

SUPPORTING INFORMATION FOR

Genetic and environmental influence on maize kernel proteome

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Supplementary table 1. Effect of genotype (Amadeo, ES Shorty, Fangio, Flavi, Gomera EU and Lukas) and environment (Frankendorf, Strassmoos, Thann, Mittich and Ansbach) on maize kernel protein contents in samples collected during the 2004 growing season.

Spot	Separation ^a	Difference between lowest and highest contents				R ² ^b
		Minimum	Maximum	Range	Relative	
404	Genotype	Flavi 97	Amadeo 819	722	8.4	0.70
1112	Genotype	Flavi 65	ES Shorty 720	656	11.1	0.95
1212	Genotype	Flavi 14	ES Shorty 362	348	25.4	0.70
1408	Genotype	Flavi 37	Lukas 347	310	9.4	0.68
	Environment	Strassmoos 47	Frankendorf 347	301	7.4	0.74
1607	Genotype	Gomera EU 192	Fangio 925	733	4.8	0.86
1809	Genotype	Lukas 243	Gomera EU 1427	1184	5.9	0.73
	Environment	Frankendorf 243	Ansbach 1485	1242	6.1	0.78
2103	Genotype	Amadeo 999	Gomera EU 6008	5009	6.0	0.77
	Environment	Thann 605	Ansbach 5105	4500	8.4	0.83
2107	Genotype	Flavi 364	Lukas 2174	1809	6.0	0.85
2113	Environment	Thann 7073	Ansbach 10374	3301	1.5	0.76
2126	Genotype	ES Shorty 22	Fangio 181	160	8.3	0.70
2202	Genotype	Gomera EU 181	Flavi 3982	3801	22.0	0.97
2202	Environment	Ansbach 1403	Strassmoos 3604	2201	2.6	0.88
2204	Genotype	Gomera EU 519	Fangio 3498	2979	6.7	0.91
2205	Genotype	Gomera EU 303	Flavi 6106	5804	20.2	0.94
2303	Genotype	Flavi 372	Fangio 2438	2066	6.6	0.85
2309	Genotype	Flavi 1776	Gomera EU 8087	6311	4.6	0.92
	Environment	Ansbach 1288	Strassmoos 5726	4438	4.4	0.71
2312	Genotype	Gomera EU 416	Fangio 2991	2575	7.2	0.88
	Environment	Thann 859	Ansbach 2609	1749	3.0	0.87
2314	Environment	Ansbach 91	Frankendorf 687	597	7.6	0.74
2317	Environment	Ansbach 52	Mittich 485	433	9.3	0.82
2406	Genotype	Fangio 322	Gomera EU 1692	1370	5.3	0.80
2420	Genotype	Amadeo 1462	Flavi 3229	1767	2.2	0.78
2503	Environment	Strassmoos 215	Mittich 1547	1331	7.2	0.71
2517	Environment	Strassmoos 84	Mittich 638	554	7.6	0.77
2613	Genotype	Gomera EU 95	Fangio 709	614	7.5	0.83
3113	Genotype	Flavi 382	ES Shorty 2159	1777	5.7	0.80
3115	Environment	Ansbach 7	Frankendorf 70	63	9.9	0.72

Supplementary table 1. Continued

Spot	Separation ^a	Difference between lowest and highest contents					R ^{2b}	
		Minimum		Maximum		Range		Relative
3119	Genotype	ES Shorty	210	Fangio	1068	858	5.1	0.68
3212	Genotype	Gomera EU	114	Lukas	801	687	7.0	0.69
3302	Genotype	Flavi	632	Gomera EU	2964	2332	4.7	0.68
3306	Genotype	Lukas	1187	Fangio	4855	3668	4.1	0.89
3405	Genotype	Lukas	1115	Fangio	3161	2045	2.8	0.71
3414	Genotype	ES Shorty	47	Lukas	981	934	21.0	0.75
3507	Genotype	ES Shorty	193	Lukas	994	800	5.1	0.76
3510	Environment	Strassmoos	28	Mittich	388	360	14.0	0.77
3725	Environment	Thann	20	Ansbach	212	192	10.8	0.71
3727	Environment	Ansbach	106	Thann	537	431	5.1	0.83
4102	Genotype	Flavi	280	Lukas	2862	2583	10.2	0.80
4104	Genotype	Flavi	327	Gomera EU	2826	2499	8.6	0.72
	Environment	Ansbach	777	Thann	3594	2816	4.6	0.84
4105	Environment	Mittich	550	Strassmoos	1426	877	2.6	0.76
4111	Environment	Ansbach	460	Strassmoos	2085	1625	4.5	0.79
4112	Genotype	Gomera EU	85	Lukas	4712	4627	55.2	0.96
4113	Environment	Ansbach	73	Thann	1654	1581	22.8	0.89
4201	Genotype	Gomera EU	1429	Lukas	5350	3922	3.7	0.84
4202	Environment	Thann	1154	Ansbach	2167	1013	1.9	0.76
4311	Environment	Ansbach	484	Mittich	1425	942	2.9	0.74
4401	Genotype	Gomera EU	242	Lukas	2495	2253	10.3	0.92
4412	Genotype	ES Shorty	1936	Fangio	3949	2013	2.0	0.76
4415	Environment	Mittich	1118	Strassmoos	2977	1859	2.7	0.86
4422	Genotype	Gomera EU	75	ES Shorty	390	315	5.2	0.70
4508	Environment	Mittich	210	Strassmoos	1293	1082	6.1	0.79
4509	Genotype	Gomera EU	251	Flavi	641	390	2.6	0.72
4514	Environment	Ansbach	62	Mittich	405	343	6.6	0.89
4601	Genotype	Lukas	256	ES Shorty	839	582	3.3	0.75
	Environment	Ansbach	221	Thann	677	456	3.1	0.76
4615	Environment	Ansbach	86	Thann	432	347	5.1	0.78
4708	Genotype	Flavi	133	ES Shorty	887	754	6.7	0.73
4708	Environment	Strassmoos	113	Thann	578	466	5.1	0.72
4719	Environment	Ansbach	33	Thann	418	385	12.7	0.94
4809	Environment	Strassmoos	29	Thann	564	535	19.4	0.72
5101	Genotype	Flavi	872	Gomera EU	6455	5583	7.4	0.81
5101	Environment	Ansbach	886	Thann	5030	4144	5.7	0.83
5106	Genotype	ES Shorty	391	Flavi	4038	3647	10.3	0.87
5207	Environment	Frankendorf	112	Strassmoos	637	525	5.7	0.86
5301	Genotype	ES Shorty	431	Lukas	1394	964	3.2	0.70
5304	Genotype	Gomera EU	317	Fangio	1985	1668	6.3	0.77

Supplementary table 1. Continued

Spot	Separation ^a	Difference between lowest and highest contents					R ^{2b}	
		Minimum		Maximum		Range		Relative
5305	Genotype	Fangio	114	Amadeo	1928	1814	16.9	0.88
5416	Environment	Mittich	48	Strassmoos	313	266	6.6	0.71
5503	Genotype	ES Shorty	746	Flavi	1711	965	2.3	0.84
5509	Genotype	Lukas	968	Fangio	2183	1215	2.3	0.69
5511	Genotype	Gomera EU	50	Fangio	389	339	7.8	0.69
5519	Environment	Mittich	7	Ansbach	380	373	53.6	0.82
5604	Genotype	ES Shorty	338	Gomera EU	1921	1582	5.7	0.68
5617	Genotype	ES Shorty	28	Flavi	410	382	14.7	0.82
5715	Genotype	Lukas	515	Amadeo	2791	2275	5.4	0.69
6101	Genotype	Flavi	5186	Gomera EU	14678	9492	2.8	0.85
6105	Genotype	Flavi	4566	ES Shorty	13972	9405	3.1	0.71
6117	Genotype	Gomera EU	465	Fangio	1912	1447	4.1	0.76
6119	Genotype	Fangio	255	Flavi	9800	9545	38.4	0.85
6207	Genotype	Flavi	104	Gomera EU	4208	4104	40.4	0.87
6611	Genotype	ES Shorty	1574	Flavi	4545	2971	2.9	0.82
6612	Environment	Frankendorf	354	Ansbach	1462	1108	4.1	0.76
6720	Environment	Thann	72	Ansbach	298	226	4.1	0.78
6803	Genotype	Lukas	798	Fangio	3544	2747	4.4	0.73
6808	Genotype	Fangio	218	Amadeo	1425	1207	6.5	0.86
7102	Genotype	Fangio	513	Gomera EU	2802	2289	5.5	0.81
7104	Genotype	Gomera EU	781	ES Shorty	5286	4506	6.8	0.69
7106	Genotype	Fangio	386	Lukas	9171	8785	23.8	0.91
7108	Genotype	Fangio	399	Lukas	2995	2596	7.5	0.71
7217	Environment	Thann	159	Strassmoos	1157	998	7.3	0.79
7305	Environment	Thann	272	Mittich	759	487	2.8	0.72
7314	Genotype	Lukas	215	Gomera EU	6532	6317	30.4	0.96
7408	Environment	Thann	97	Strassmoos	492	396	5.1	0.71
7509	Environment	Mittich	674	Ansbach	2124	1450	3.2	0.71
7513	Environment	Thann	2719	Ansbach	4744	2025	1.7	0.78
7515	Genotype	Lukas	1660	ES Shorty	8856	7196	5.3	0.90
7518	Environment	Thann	547	Ansbach	2498	1952	4.6	0.71
7520	Environment	Strassmoos	152	Ansbach	814	662	5.3	0.74
7526	Genotype	ES Shorty	186	Fangio	1149	964	6.2	0.73
7704	Genotype	Fangio	546	Lukas	2796	2250	5.1	0.68
	Environment	Ansbach	1117	Frankendorf	2796	1679	2.5	0.71
7708	Genotype	Fangio	838	ES Shorty	2782	1944	3.3	0.70
	Environment	Ansbach	1005	Thann	2577	1571	2.6	0.79
7711	Genotype	ES Shorty	150	Flavi	597	447	4.0	0.68
7803	Genotype	Fangio	279	Gomera EU	2785	2506	10.0	0.70
7806	Genotype	ES Shorty	528	Flavi	4720	4192	8.9	0.68

Supplementary table 1. Continued

Spot	Separation ^a	Difference between lowest and highest contents				R ^{2b}
		Minimum	Maximum	Range	Relative	
7811	Environment	Mittich 179	Frankendorf 676	496	3.8	0.79
8314	Genotype	Flavi 3306	Fangio 8423	5117	2.5	0.69
8320	Genotype	Fangio 260	Gomera EU 5404	5144	20.8	0.73
8811	Environment	Frankendorf 158	Ansbach 1175	1017	7.4	0.90
8817	Genotype	Flavi 759	Gomera EU 2291	1531	3.0	0.81

^a Based on ANOVA analysis (P < 0.01)

^b R² value was derived from the GLM analysis and it's used to describe how much of the variation (range 0.00 – 1.00) is assigned either to the genotype or to the environment

Supplementary table 2. Effect of genotype (Amadeo, ES Shorty, Pontos, Flavi, Gomera EU and Lukas) and environment (Frankendorf, Strassmoos and Scönbrunn) on maize kernel protein contents in samples collected during the 2005 growing season.

Spot	Identification ^a	Separation ^b	Difference between lowest and highest contents				R ^{2c}
			Minimum	Maximum	Range	Relative	
417	Unidentified	Genotype	ES Shorty 2647	Pontos 5937	3290	2.2	0.81
429	Unidentified	Genotype	Gomera EU 107	ES Shorty 427	320	4.0	0.74
504	Unidentified	Genotype	Flavi 294	ES Shorty 1358	1064	4.6	0.69
806	Unidentified	Genotype	Pontos 905	Lukas 1751	846	1.9	0.70
1103	Unidentified	Genotype	Flavi 312	ES Shorty 2030	1717	6.5	0.79
1207	Unidentified	Genotype	Lukas 3104	Flavi 8879	5776	2.9	0.74
1209	Unidentified	Genotype	Gomera EU 936	Lukas 3062	2126	3.3	0.77
1312	Unidentified	Genotype	Pontos 543	Flavi 1612	1068	3.0	0.68
1314	Unidentified	Genotype	Pontos 463	ES Shorty 2111	1648	4.6	0.91
1409	Unidentified	Genotype	Flavi 560	Gomera EU 1302	742	2.3	0.68
1412	Unidentified	Genotype	Amadeo 289	ES Shorty 954	665	3.3	0.78
1414	Unidentified	Genotype	Amadeo 161	Pontos 747	586	4.6	0.77
1416	Unidentified	Genotype	Amadeo 289	Pontos 758	469	2.6	0.71
1422	Unidentified	Genotype	Pontos 361	ES Shorty 1306	945	3.6	0.81
1518	Unidentified	Genotype	Amadeo 260	ES Shorty 925	665	3.6	0.70
2107	Unidentified	Genotype	Amadeo 2668	Flavi 14363	11696	5.4	0.92
2108	Unidentified	Genotype	Gomera EU 2584	Flavi 5700	3116	2.2	0.77
2202	Unidentified	Genotype	ES Shorty 971	Flavi 2196	1225	2.3	0.76
2203	Unidentified	Genotype	Gomera EU 988	Flavi 4238	3250	4.3	0.85
2301	Unidentified	Genotype	Flavi 1355	Pontos 9350	7995	6.9	0.88
2306	Globulin 2	Genotype	ES Shorty 3059	Amadeo 7573	4514	2.5	0.80
2404	Late embryogenesis abundant protein D-34	Genotype	Amadeo 1508	Pontos 2866	1357	1.9	0.74
2406	Unidentified	Genotype	Lukas 1610	Flavi 2985	1375	1.9	0.69
2410	Unidentified	Genotype	Pontos 1460	Flavi 2358	898	1.6	0.77

Supplementary table 2. Continued

Spot	Identification ^a	Separation ^b	Difference between lowest and highest contents						R ^{2c}
			Minimum		Maximum		Range	Relative	
2411	Unidentified	Genotype	Lukas	1301	Flavi	4227	2925	3.2	0.83
2505	Unidentified	Genotype	Amadeo	376	Lukas	888	513	2.4	0.75
2507	Unidentified	Genotype	Lukas	342	ES Shorty	938	596	2.7	0.71
2518	Unidentified	Environment	Frankendorf	635	Schönbrunn	1221	586	1.9	0.79
3105	Unidentified	Genotype	ES Shorty	1417	Flavi	6647	5230	4.7	0.74
3108	Unidentified	Genotype	Lukas	175	Gomera EU	1388	1213	7.9	0.83
	Unidentified	Environment	Schönbrunn	90	Strassmoos	840	750	9.3	0.90
3201	Unidentified	Genotype	Amadeo	660	Gomera EU	1696	1037	2.6	0.73
3206	16.9 kDa class I heat shock protein 1	Genotype	Flavi	812	Lukas	2792	1980	3.4	0.74
3217	Unidentified	Genotype	Flavi	717	Lukas	3663	2946	5.1	0.81
3305	Unidentified	Genotype	Flavi	510	Amadeo	2375	1864	4.7	0.71
3317	Unidentified	Genotype	Amadeo	167	Pontos	2376	2209	14.2	0.87
3403	Unidentified	Genotype	Flavi	338	Lukas	1277	940	3.8	0.77
3405	Unidentified	Genotype	Amadeo	356	Lukas	2541	2185	7.1	0.90
3406	Unidentified	Genotype	Flavi	346	Pontos	825	479	2.4	0.72
3407	Unidentified	Genotype	ES Shorty	526	Lukas	1240	714	2.4	0.84
	Unidentified	Environment	Strassmoos	739	Frankendorf	1240	502	1.7	0.80
3410	Unidentified	Genotype	Flavi	231	Gomera EU	2381	2150	10.3	0.94
3414	Unidentified	Genotype	Gomera EU	521	Amadeo	1280	759	2.5	0.72
3418	Glyoxalase 1	Genotype	Gomera EU	2398	Lukas	3795	1398	1.6	0.75
3421	Triosephosphate isomerase (cytosolic)	Environment	Schönbrunn	5694	Frankendorf	7417	1723	1.3	0.79
3507	Unidentified	Environment	Strassmoos	706	Frankendorf	964	258	1.4	0.83
3514	Protein b-32	Genotype	Pontos	334	Flavi	695	361	2.1	0.82
3610	Unidentified	Genotype	Pontos	294	ES Shorty	984	690	3.3	0.78
3616	Unidentified	Genotype	ES Shorty	243	Amadeo	1004	762	4.1	0.81
3617	Unidentified	Genotype	Amadeo	316	Pontos	1782	1466	5.6	0.94
3620	Unidentified	Genotype	Pontos	168	Lukas	392	225	2.3	0.73
3628	Unidentified	Environment	Strassmoos	326	Schönbrunn	632	306	1.9	0.81
3630	Unidentified	Genotype	Flavi	208	ES Shorty	437	230	2.1	0.70
	Unidentified	Environment	Schönbrunn	165	Frankendorf	295	130	1.8	0.85
3709	Brittle 2	Genotype	Pontos	329	Flavi	1163	833	3.5	0.77
3920	Unidentified	Genotype	Amadeo	48	Flavi	135	88	2.8	0.76
4103	Superoxide dismutase [Cu-Zn] 4AP	Genotype	Flavi	1822	ES Shorty	3939	2117	2.2	0.75
4104	Unidentified	Environment	Schönbrunn	1038	Strassmoos	2536	1498	2.4	0.94
4306	Unidentified	Genotype	Flavi	435	Pontos	1442	1008	3.3	0.83
4405	Unidentified	Genotype	Pontos	57	ES Shorty	602	545	10.6	0.75
4505	Unidentified	Genotype	Gomera EU	362	ES Shorty	1237	876	3.4	0.74
4508	Protein b-32	Genotype	Pontos	1702	Flavi	2506	804	1.5	0.74

Supplementary table 2. Continued

Spot	Identification ^a	Separation ^b	Difference between lowest and highest contents						R ^{2c}
			Minimum		Maximum		Range	Relative	
4519	Unidentified	Genotype	Gomera EU	122	Pontos	1219	1097	10.0	0.78
4625	Unidentified	Genotype	Flavi	56	Amadeo	388	332	6.9	0.82
4721	Unidentified	Genotype	Pontos	75	ES Shorty	259	184	3.5	0.80
4826	Unidentified	Genotype	Flavi	114	Amadeo	518	403	4.5	0.77
4910	Unidentified	Environment	Strassmoos	610	Schönbrunn	913	303	1.5	0.85
5104	Globulin 3	Genotype	Gomera EU	842	ES Shorty	2192	1350	2.6	0.82
5310	Unidentified	Genotype	ES Shorty	296	Lukas	772	476	2.6	0.83
5313	1-Cys peroxiredoxin antioxidant	Genotype	Gomera EU	2831	Lukas	4726	1895	1.7	0.70
5314	Unidentified	Genotype	Flavi	200	Amadeo	493	294	2.5	0.74
	Unidentified	Environment	Schönbrunn	235	Strassmoos	588	353	2.5	0.83
5414	Unidentified	Genotype	ES Shorty	352	Flavi	770	418	2.2	0.75
5415	Unidentified	Genotype	Flavi	336	Pontos	1323	987	3.9	0.74
5512	Glyceraldehyde-3-phosphate dehydrogenase (cytosolic)	Genotype	Gomera EU	1723	Lukas	2835	1113	1.6	0.78
	Glyceraldehyde-3-phosphate dehydrogenase (cytosolic)	Environment	Strassmoos	1648	Schönbrunn	2984	1337	1.8	0.81
5614	Unidentified	Genotype	Flavi	1014	Pontos	3015	2001	3.0	0.73
5701	Unidentified	Genotype	ES Shorty	638	Lukas	1274	636	2.0	0.80
5703	Unidentified	Genotype	ES Shorty	515	Flavi	1026	510	2.0	0.77
5708	Unidentified	Genotype	Gomera EU	136	Lukas	322	186	2.4	0.72
5720	Unidentified	Genotype	Flavi	1671	Lukas	2741	1070	1.6	0.76
5722	Unidentified	Genotype	Lukas	82	Flavi	611	529	7.4	0.84
5902	Unidentified	Environment	Strassmoos	428	Schönbrunn	726	298	1.7	0.79
6101	16.9 kDa class I heat shock protein 1	Genotype	ES Shorty	336	Flavi	8467	8131	25.2	0.86
6103	Nucleoside diphosphate kinase I	Genotype	Pontos	2365	ES Shorty	4441	2076	1.9	0.71
6104	Unidentified	Genotype	Flavi	831	ES Shorty	4295	3465	5.2	0.81
6109	Unidentified	Genotype	Gomera EU	616	Pontos	6392	5776	10.4	0.97
6202	Unidentified	Environment	Strassmoos	1673	Schönbrunn	6853	5180	4.1	0.80
6307	1-Cys peroxiredoxin antioxidant	Genotype	Gomera EU	4490	Lukas	8957	4467	2.0	0.84
6308	Unidentified	Genotype	Flavi	435	Lukas	1159	724	2.7	0.87
6315	Unidentified	Genotype	Gomera EU	429	Amadeo	2502	2073	5.8	0.90
6405	Unidentified	Environment	Strassmoos	400	Schönbrunn	1035	634	2.6	0.83
6513	Unidentified	Genotype	Amadeo	1911	Lukas	3234	1324	1.7	0.68
6516	Unidentified	Environment	Strassmoos	642	Frankendorf	1270	628	2.0	0.92
6615	Unidentified	Genotype	Amadeo	243	Lukas	558	315	2.3	0.71

Supplementary table 2. Continued

Spot	Identification ^a	Separation ^b	Difference between lowest and highest contents					R ^{2c}	
			Minimum		Maximum		Range		Relative
6705	Unidentified	Genotype	Amadeo	1342	Flavi	4116	2774	3.1	0.82
6706	unknown sequence	Genotype	Pontos	467	Amadeo	1360	893	2.9	0.69
6719	Vicilin-like embryo storage protein	Genotype	Amadeo	1603	Flavi	4663	3060	2.9	0.79
6802	Vicilin-like embryo storage protein	Genotype	Lukas	1959	ES Shorty	4344	2385	2.2	0.68
6803	Unidentified	Genotype	Pontos	163	ES Shorty	319	156	2.0	0.71
7225	Unidentified	Genotype	Amadeo	356	Flavi	3714	3357	10.4	0.87
7302	Unidentified	Genotype	Amadeo	309	Lukas	1938	1629	6.3	0.86
7305	Unidentified	Genotype	Amadeo	1333	Gomera EU	3271	1938	2.5	0.71
7404	Unidentified	Genotype	Pontos	1102	ES Shorty	2164	1062	2.0	0.73
7501	Unidentified	Genotype	Gomera EU	1700	ES Shorty	6117	4418	3.6	0.86
7504	Unidentified	Genotype	Gomera EU	759	Amadeo	5064	4304	6.7	0.78

^a See table 3

^b Based on ANOVA analysis (P < 0.01)

^c R² value was derived from the GLM analysis and it's used to describe how much of the variation (range 0.00 – 1.00) is assigned either to the genotype or to the environment

Supplementary table 3. Proteins identified from the kernels of maize grown in 2005 by MS/MS and using MASCOT search engine (www.matrixscience.com).

Spot	Identification, species, function	Accession	Score (threshold) ^b	Peptides (modifications, charge, m/z, Δ mass) ^c	Sequence coverage, %
2306	Globulin 2, <i>Z. mays</i> , nutrient reservoir activity	1802402A	120 (43)	VAELEAAPR, +2, 478.21, -0.09 GEITTASEEQIR, +2, 667.30, -0.04	4
2404 ^a	Late embryogenesis abundant protein D-34, <i>Z. mays</i> , stress response	NP_001152643	91 (44)	<u>R</u> VVTESVGGQVVGK, MTC, +2, 707.86, -0.08	5
3206 ^a	16.9 kDa class I heat shock protein 1, <i>Z. mays</i> , stress response	P12810	68 (43)	AGLENGVLTVTVPK, +2, 699.43, +0.07	9
3418 ^a	Glyoxalase 1, <i>Z. mays</i> , stress response	NP_001105217	77 (42)	SAEAVDLATK, +2, 502.69, -0.13	3
3421	Triosephosphate isomerase (cytosolic), <i>Z. mays</i> , carbohydrate metabolism	NP_001140424	160 (42)	TNASPEVAESTR, +2, 631.29, -0.01 ALLGESNEFVGDK, +2, 689.79, -0.09 ALLGESNEFVGDKVAYALSQGLK, MTC, +3, 803.75, -0.00	13
3514 ^a	Protein b-32, <i>Z. mays</i> , plant defence	CAA49722	47 (40)	GLETVTMGR, MO, +2, 490.31, +0.14	2
3709	Brittle 2, <i>Z. mays</i> , starch synthesis	AAN39297	84 (41)	ATAFGLMK, MO, +1, 854.47, +0.02 INHSAVGLR, +2, 497.86, +0.14	3
4103 ^a	Superoxide dismutase [Cu-Zn] 4AP, <i>Z. mays</i> , antioxidative enzyme	P23346	54 (42)	AVAVLGSSDGVK, +2, 551.81, +0.00	7
4508	Protein b-32, <i>Z. mays</i> , plant defence	CAA49722	91 (41)	LVALVK, +1, 642.48, +0.02 GLETVTMGR, MO, +1, 490.31, +0.14	4
5104	Globulin 3, <i>Triticum aestivum</i> , nutrient reservoir activity	ACJ65514	45 (42)	RPYVFGPR, +2, 496.20, -0.14 SISIVRASEEQLR, MTC, +2, 744.40, -0.00 GSAFVPPGHPVVEIASSR, +2, 635.97, -0.09	6
5313	1-Cys peroxiredoxin antioxidant, <i>Z. mays</i> , antioxidant enzyme	NP_001105998	59 (43)	DAAGR, +1, 489.34, +0.09 LSFLYPATTGR, +2, 613.37, +0.09	6

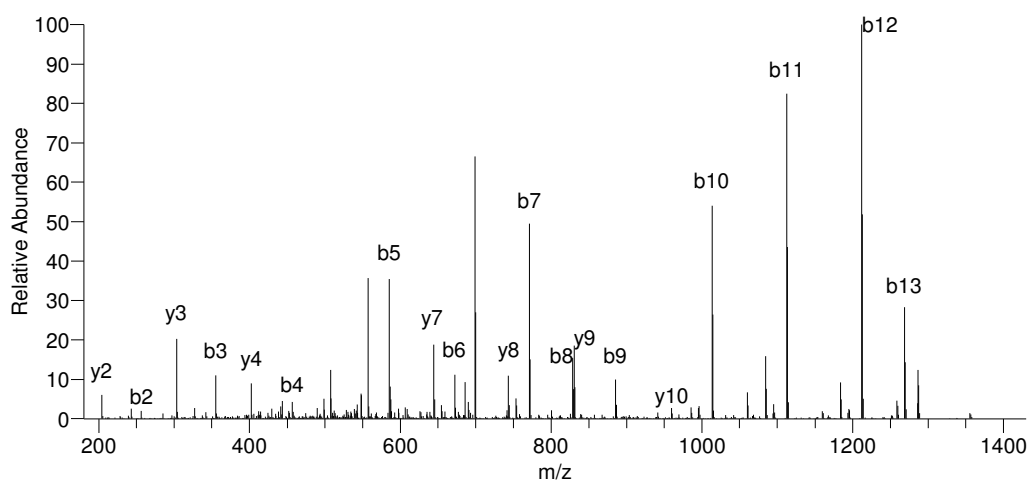
Supplementary table 3. Continued

5512	Glyceraldehyde-3-phosphate dehydrogenase (cytosolic), <i>Z. mays</i> , glycolysis	P08735	54 (41)	VVDLIR, +1, 714.59, +0.13 SSIFDAK, +1, 767.40, +0.00	3
6101	16.9 kDa class I heat shock protein 1. <i>Z. mays</i> , stress response	NP_001149666	119 (42)	SIQISG, +1, 604.24, -0.09 SIVPSSSSSGSETAAFASAR, +2, 949.92, -0.06	17
6103 ^a	Nucleoside diphosphate kinase I, <i>Z. mays</i> , NTP synthesis	ACQ73318	48 (42)	IIGATRPWEAAPGTIR, +3, 570.30, -0.05	14
6307	1-Cys peroxiredoxin antioxidant, <i>Z. mays</i> , antioxidant enzyme	NP_001105998	196 (41)	NMDEVLR + MO, +2, 446.69, -0.02 AVDSLLTAAK, +2, 494.75, -0.05 VTFPILADPAR, +2, 600.29, -0.08 QLN M VDPDEKDAAGR, MO, MTC, +3, 558.92, -0.01 KM FPQGFETADLP S KK, MO, 2MTC, +3, 613.93, -0.13 PGLTIGDTPNLELDSTHGK, +3, 688.68, -0.03	34
6706 ^a	unknown, <i>Z. mays</i> , no assigned function or homology with known proteins	ACL52677	63 (42)	ALASEQTVR, +2, 487.73, -0.06	2
6719	Vicilin-like embryo storage protein, <i>Z. mays</i> , nutrient reservoir activity	CAA41809	66 (42)	RPYVFDR, +2, 476.67, -0.14 VLRPFDEVSR, +2, 609.37, +0.08 VFLAGADNVLQK, +2, 637.92, +0.12 SFVVPSTDAH C ICYVAEGEGVTTIENGER, 2CAM, +4, 859.18, +0.12	10
6802	Vicilin-like embryo storage protein, <i>Z. mays</i> , nutrient reservoir activity	CAA41809	67 (42)	RPYVFDR, +2, 476.67, -0.14 VLRPFDEVSR, +2, 609.30, -0.06 NPESFLSSFSK, +2, 621.75, -0.09	4

^a Supplementary identification data are provided in supplementary figures 2-8.

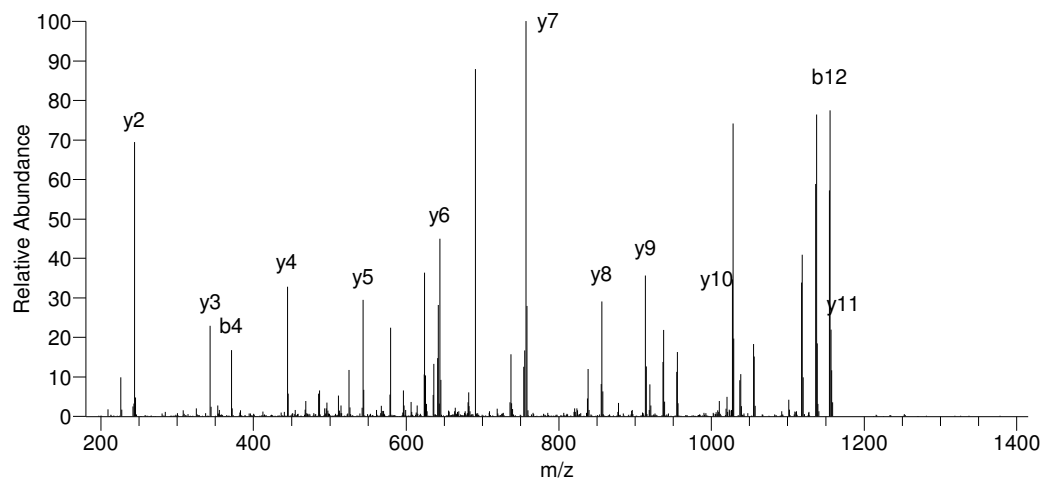
^b Probability based mowse scores were used to define the quality of identification. Threshold values were calculated based on 5% possibility for false identification.

^c The position of the amino acid modifications are indicated in bold (MO = methionine oxidation and CAM = carbamidomethylation). Missed trypsin cleavages (MTC) are indicated by underline. Δ mass indicates the difference between calculated peptide mass and the expected mass.



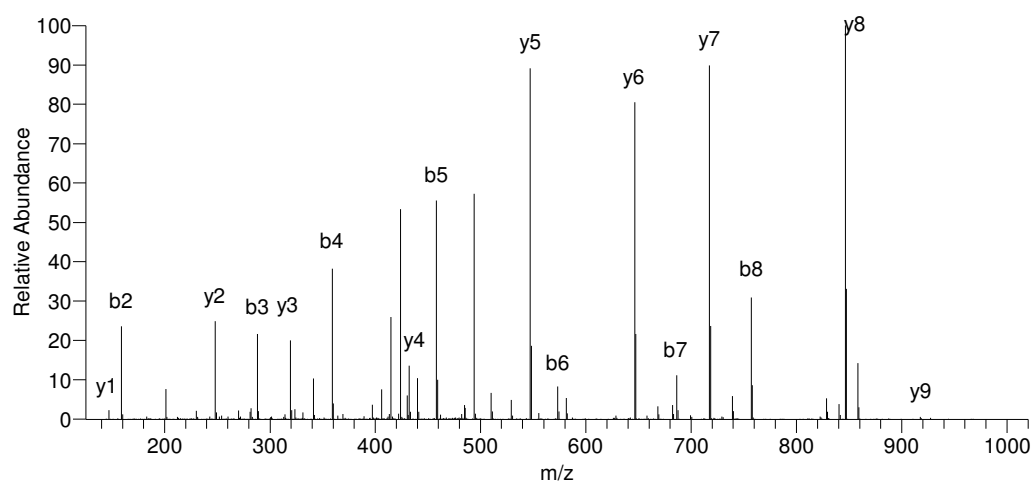
m/z				m/z				Sequence
b ions	Expected	Measured	Δ mass	y ions	Expected	Measured	Δ mass	
1	157.10	ND		14	-	-	-	R
2	256.17	256.24	-0.07	13	1258.70	ND		V
3	355.24	355.30	-0.06	12	1159.63	ND		V
4	456.29	456.47	-0.18	11	1060.56	ND		T
5	585.33	585.34	-0.01	10	959.51	959.52	-0.01	E
6	672.36	672.40	-0.04	9	830.47	830.46	0.01	S
7	771.43	771.43	0.00	8	743.44	743.45	-0.01	V
8	828.45	828.48	-0.03	7	644.37	644.39	-0.02	G
9	885.47	885.44	0.03	6	587.35	ND		G
10	1013.53	1013.51	0.02	5	530.32	ND		Q
11	1112.60	1112.53	0.07	4	402.27	402.30	-0.03	V
12	1211.67	1211.54	0.13	3	303.20	303.26	-0.06	V
13	1268.69	1268.60	0.09	2	204.13	204.08	0.05	G
14	-	-	-	1	147.11	ND		K

Supplementary figure 1. MS/MS fragmentation of the peptide RVTESVGGQVVGK with m/z 707.86 (+2) from the spot 2404 (ND = not detected).



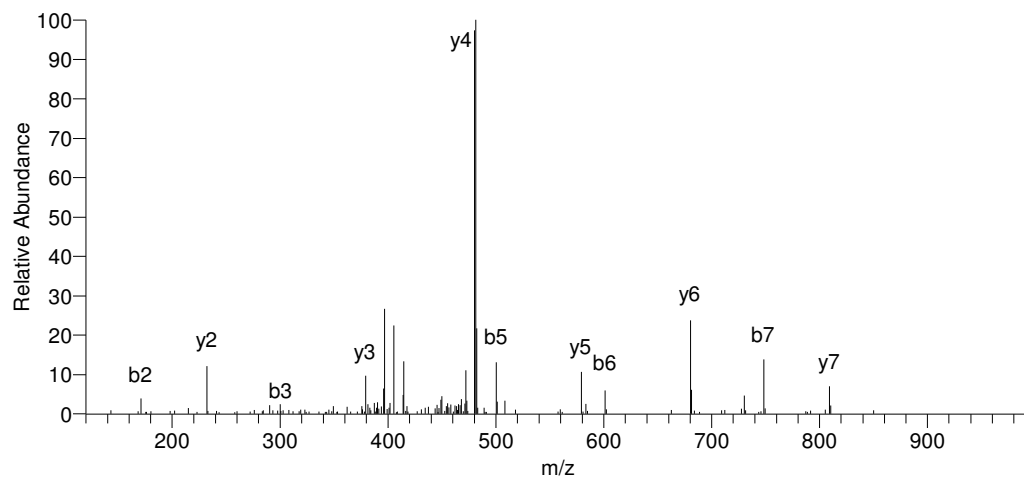
m/z				m/z				Sequence
b ions	Expected	Measured	Δ mass	y ions	Expected	Measured	Δ mass	
1	72.04	ND		14	-	-	-	A
2	129.06	ND		13	1326.76	ND		G
3	242.14	ND		12	1269.74	ND		L
4	371.19	371.18	0.01	11	1156.65	1156.46	0.19	E
5	485.23	ND		10	1027.61	1027.73	-0.12	N
6	542.25	ND		9	913.57	913.49	0.08	G
7	641.32	ND		8	856.55	856.44	0.11	V
8	754.40	ND		7	757.48	757.40	0.08	L
9	855.45	ND		6	644.39	644.39	0.00	T
10	954.52	ND		5	543.35	543.34	0.01	V
11	1055.57	ND		4	444.28	444.28	0.00	T
12	1154.64	1154.45	0.19	3	343.23	343.21	0.02	V
13	1251.69	ND		2	244.16	244.14	0.02	P
14	-	-	-	1	147.11	ND		K

Supplementary figure 2. MS/MS fragmentation of the peptide AGLENGVLTVTPK with m/z 699.43 (+2) from the spot 3206 (ND = not detected).



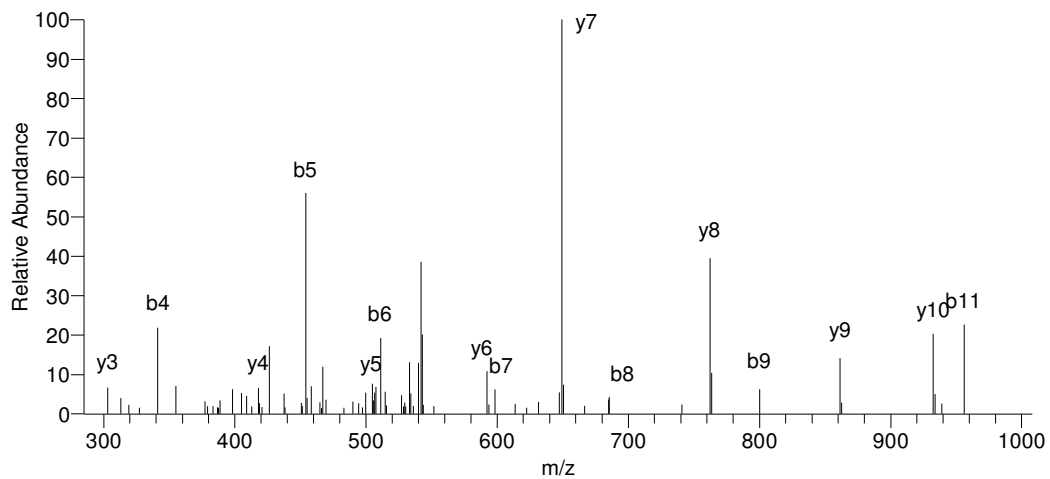
b ions	m/z			y ions	m/z			Sequence
	Expected	Measured	Δ mass		Expected	Measured	Δ mass	
1	88.03	ND		10	-	-	-	S
2	159.07	159.00	0.07	9	917.49	917.56	-0.07	A
3	288.11	288.13	-0.02	8	846.45	846.40	0.05	E
4	359.15	359.19	-0.04	7	717.41	717.38	0.03	A
5	458.22	458.18	0.04	6	646.37	646.38	-0.01	V
6	573.25	573.20	0.05	5	547.30	547.35	-0.05	D
7	686.33	686.24	0.09	4	432.28	432.34	-0.06	L
8	757.37	757.25	0.12	3	319.19	319.27	-0.08	A
9	858.42	858.29	0.13	2	248.16	248.19	-0.03	T
10	-	-	-	1	147.11	147.08	0.03	K

Supplementary figure 3. MS/MS fragmentation of the peptide SAEAVDLATK with m/z 502.69 (+2) from the spot 3418 (ND = not detected).



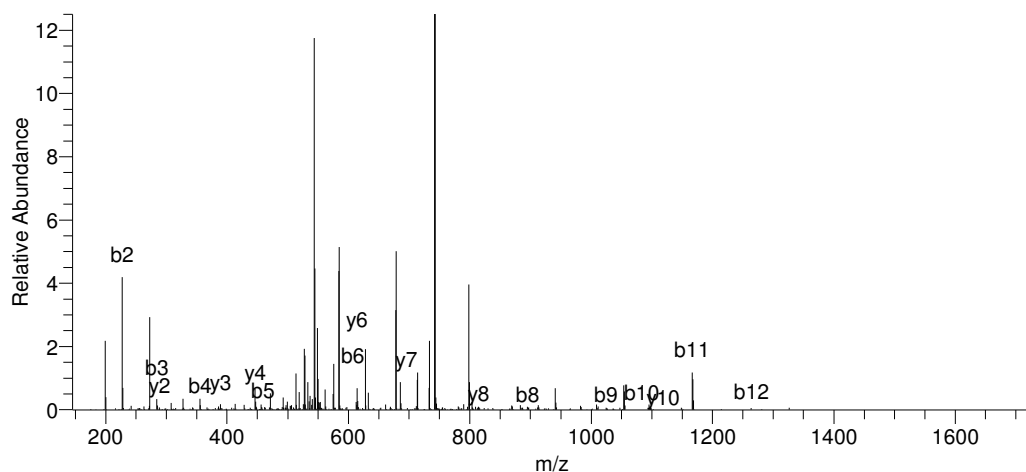
b ions	m/z			y ions	m/z			Sequence
	Expected	Measured	Δ mass		Expected	Measured	Δ mass	
1	58.02	ND		9	-	-	-	G
2	171.11	171.07	0.04	8	922.46	ND		L
3	300.15	300.04	0.11	7	809.38	809.30	0.08	E
4	401.20	ND		6	680.33	680.37	-0.04	T
5	500.27	500.28	-0.01	5	579.29	579.34	-0.05	V
6	601.31	601.18	0.13	4	480.22	480.28	-0.06	T
7	748.35	748.28	0.07	3	379.17	379.28	-0.11	M
8	805.37	ND		2	232.14	232.20	-0.06	G
9	-	-	-	1	175.11	ND		R

Supplementary figure 4. MS/MS fragmentation of the peptide GLEVTMGR containing single methionine oxidation with m/z 490.31 (+2) from the spot 3514 (ND = not detected).



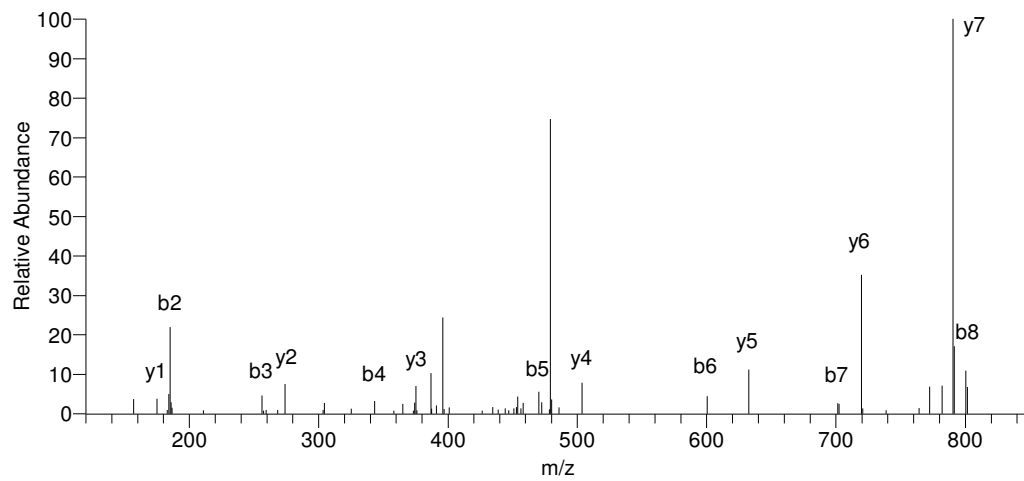
b ions	m/z			y ions	m/z			Sequence
	Expected	Measured	Δ mass		Expected	Measured	Δ mass	
1	72.04	ND		12	-	-	-	A
2	171.11	ND		11	1031.57	ND		V
3	242.14	ND		10	932.50	932.55	-0.05	A
4	341.21	341.11	0.10	9	861.46	861.48	-0.02	V
5	454.30	454.14	0.16	8	762.39	762.48	-0.09	L
6	511.32	511.31	0.01	7	649.31	649.29	0.02	G
7	598.35	598.33	0.02	6	592.29	592.28	0.01	S
8	685.38	685.57	-0.19	5	505.26	505.55	-0.29	S
9	800.41	799.99	0.42	4	418.22	418.17	0.05	D
10	857.43	ND		3	303.20	303.15	0.05	G
11	956.50	956.23	0.27	2	246.18	ND		V
12	-	-	-	1	147.11	ND		K

Supplementary figure 5. MS/MS fragmentation of the peptide AVAVLGSSDGVK with m/z 551.81 (+2) from the spot 4103 (ND = not detected).



b ions	m/z			y ions	m/z			Sequence
	Expected	Measured	Δ mass		Expected	Measured	Δ mass	
1	114.09	ND		16	-	-	-	I
2	227.17	227.12	0.05	15	1595.86	ND		I
3	284.19	284.19	0.00	14	1482.78	ND		G
4	355.23	355.31	-0.08	13	1425.75	ND		A
5	456.28	456.28	0.00	12	1354.72	ND		T
6	612.38	612.50	-0.12	11	1253.67	ND		R
7	709.43	ND		10	1097.57	1097.49	0.08	P
8	895.51	895.35	0.16	9	1000.52	ND		W
9	1024.55	1024.46	0.09	8	814.44	814.46	-0.02	E
10	1095.59	1095.32	0.27	7	685.39	685.54	-0.15	A
11	1166.63	1166.60	0.03	6	614.36	614.45	-0.09	A
12	1263.68	1263.98	-0.30	5	543.32	543.43	-0.11	P
13	1320.70	ND		4	446.27	446.42	-0.15	G
14	1421.75	ND		3	389.25	389.40	-0.15	T
15	1534.83	ND		2	288.20	288.39	-0.19	I
16	-	-	-	1	175.11	ND		R

Supplementary figure 6. MS/MS fragmentation of the peptide with m/z 570.30 (+3) from the spot 6103 (ND = not detected).



b ions	m/z			y ions	m/z			Sequence
	Expected	Measured	Δ mass		Expected	Measured	Δ mass	
1	72.04	ND		9	-	-	-	A
2	185.12	185.04	-0.08	8	903.48	ND		L
3	256.16	256.11	-0.05	7	790.40	790.45	0.05	A
4	343.19	343.27	0.08	6	719.36	719.40	0.04	S
5	472.24	472.36	0.12	5	632.33	632.45	0.12	E
6	600.29	600.44	0.15	4	503.29	503.50	0.21	Q
7	701.34	701.43	0.09	3	375.23	375.36	0.13	T
8	800.41	800.24	-0.17	2	274.18	274.01	-0.17	V
9	-	-	-	1	175.11	175.08	-0.03	R

Supplementary figure 8. MS/MS fragmentation of the peptide ALASEQTVR with m/z 487.73 (+2) from the spot 6706 (ND = not detected).