Table S2. Additional protein identifications of preferentially accumulated in *hsp101* mutant (mut) or wild-type (WT) quiescent (0 h) and 24 h-imbibed (24 h) maize embryos.

***Protein (species)/ AC*[a]	***Spot No.***	***Spot presence*[b]	***MASCOT Score*[c]	***Sequence coverage (%)*[d]	***Mr predicted/ Mr gel***	***pI predicted/ pI gel***	***No. unique peptides***	***emPAI*[e]
0 h								
ubiquitin-conjugating enzyme spm2 (*Zea mays*)/ ACG25186	29	2	129	35	16.7/16.7	6.42/6.7	3	0.74
abscisic acid-responsive gene rab28 (*Zea mays*)/ CAA41854	28	1	276	52	27.6/17.0	4.9/5.55	1	1.22
HSP17.2 class I (*Zea mays*)/NP_001105442	28	1	226	35	17.2/17.0	5.54/5.55	3	0.43
embryonic abundant protein 1 (*Zea mays*)/ACG33377	28	1	189	59	12.07/17.0	5.42/5.55	4	1.72
late embryogenesis abundant protein Lea14-A (*Zea mays*)/ NP_001152646	28	1	133	51	16.0/17.0	5.64/5.55	5	0.77
hypothetical protein LOC100279096 (*Zea mays*)/ NP_001145613	30	2	159	57	13.4/16.0	5.62/6.07	6	0.57
late embryogenesis abundant protein Lea14-A (*Zea mays*)/ NP_001152646	30	2	125	47	16.0/16.0	5.64/6.07	6	0.77
HSP17.4 class I heat shock protein 3 (*Zea mays*) ACG35098	31	2	156	43	17.7/17.0	5.55/5.92	3	1.01
superoxide dismutase (Cu-Zn) 4AP (*Zea mays*)/NP_001105704	31	2	239	44	15.1/17.0	5.65/5.92	1	0.84
abscisic acid-responsive gene rab28 (*Zea mays*)/CAA41854	32	2	344	64	27.69/15.9	4.9/5.95	5	1.49
HSP17.2 class I heat shock protein (*Zea mays*)/NP_001105442	32	2	155	44	17.15	5.54/5.95	2	1.05
hypothetical protein (*Zea mays*)	13	1	112	57	13.4	5.62/5.8	5	2.11

/NP_001145613								
HSP17.5 class II heat shock protein (*Zea mays*)/ NP_001105705	13	1	169	49	17.5/17.2	5.56/5.8	8	1.02
24 h								
Unknown protein 18/ P85925	29	2	98	100	1.39	5.8/6.8	3	15.56
40S ribosomal protein S18 (*Zea mays*)/NP_001151612	29	2	35	88	17.69	10.74/6.8	1	0.69
HSP16.9A class I heat shock protein 1 (*Zea mays*))/ACG36285	27	1	236	49	16.9/38.7	6.77/4.6	3	1.04
HSP17.5 class II heat shock protein (*Zea mays*)/ NP_001105705	13	1	261	49	17.5/16.1	5.56/6.08	3	1.41

[a] Accession number from the maizesequences.org database.

[b] Indicates whether the protein identification was from a given spot in wild type (1) or *hsp101* mutant (2), respectively.

[c] Probability based MASCOT score is defined as -10∗Log(p), where p is the probability that the observed match is a random event. Scores > 43 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

[d] Percentage of protein coverage by peptide sequencing.

[e] Exponentially Modified Protein Abundance Index (emPAI) for Estimation of Absolute Protein Amount is Equal to $10^{PAI} - 1$, which is proportional to protein content in a protein mixture.