

Figure. S1: Cluster map of the protein expression patterns at 6 development stages of *G. parvifolium* seeds (yellow, higher expression; black, lower expression).

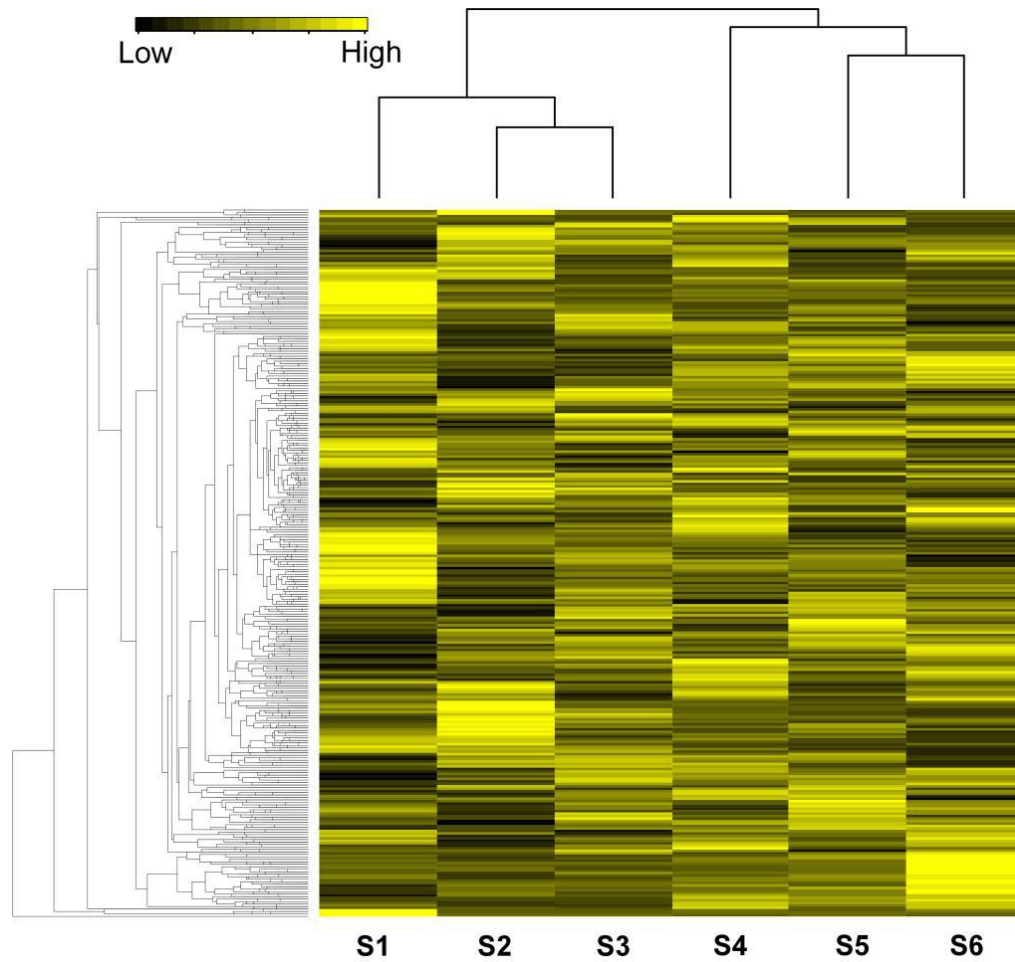
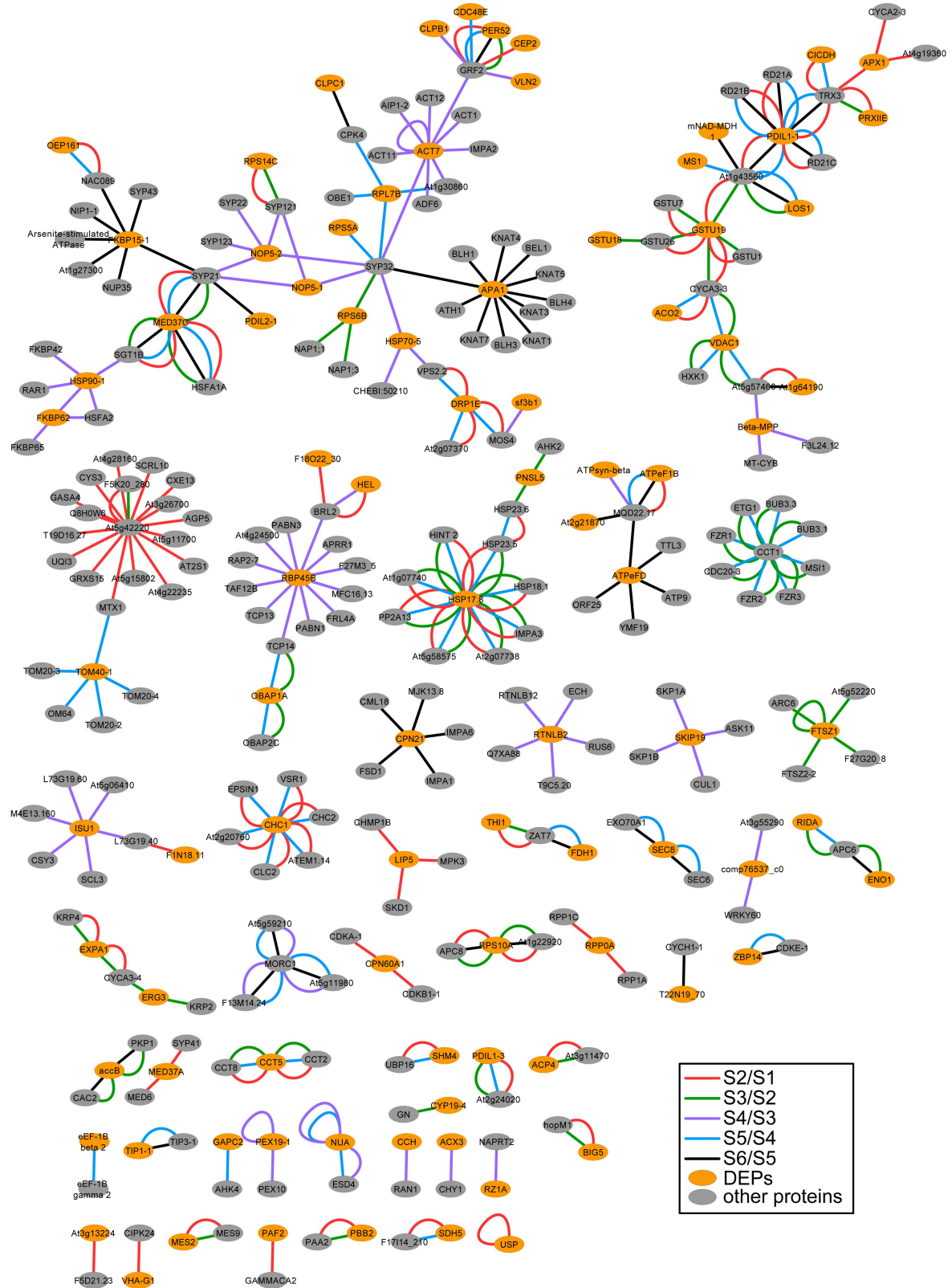


Figure. S2: GO annotation of 12 protein expression clusters (bars, numbers of proteins with one annotation; colors, different GO categories).



Figure. S3: Interaction network of DEPs identified of S2/S1, S3/S2, S4/S3, S5/S4, and S6/S5 with their predicted predicted by mapping them according to the *A. thaliana* interactions.



Supplementary Table 1 Primers of candidate genes for qRT-PCR.

Gene abbreviation	Gene name	Primer sequence (5'-3')	Size (bp)
PRXIIIE-1	Peroxisiredoxin-2E-1	AATGTCGGTGACAAGCTTCC	186
	(comp77905_c0)	GAGGTCATCAGCCTTGAAAA	
HSP21	Small heat shock protein	CCCGGATGCTTCTGTATAA	197
	(comp78352_c0)	CATGGTGTCCAGCATCTGTC	
GME-1	GDP-mannose 3,5-epimerase 1	AGGTTTGAAATGTGGGGTGA	151
	(comp72458_c0)	CAGCCATTTTCATTCATGCTG	
GALM	Aldose 1-epimerase	TTTCCCTGGAGACCTTGATG	186
	(comp95518_c0)	GAGGCCCAAATCTTGATTGA	
INV1	Beta-fructofuranosidase	CTTCCGGAACAAAGTTTGGA	153
	(comp93643_c1)	ACGAGTTATCCGGCACGTAG	
CPK	calcium-dependent protein kinase	AGTGGGGGAGCCAAGAATGT	158
	(comp75922_c0)	AGCACTCTGCCCATCTCTGC	
GARS	glycyl-tRNA synthetase	GGAGCTTAAAGGGGCTATG	174
	(comp90806_c0)	ACACCCATCGAATGACAGGT	
GST	glutathione S-transferase	AAGAGGCGAAAGTGAACGTG	185
	(comp96166_c0)	AGCAGGAGCAGTCTGTTGGT	
AP2	AP2-associated kinase	ATTTAGGCGAAATGCTGCTG	152
	(comp92905_c0)	TTGCCCAAAATGCACCTAAT	
ACTF	actin-7	GGTGATGAGGCCCAAGTCTAA	184
	(comp80220_c0)	TGTTAGCCTTTGGGTTTCAGG	
TPI	triosephosphate isomerase (TIM)	GTTTTTCGTTGGTGGCAACT	189
	(comp89124_c0)	ATCCATGAGTTTTGGGCAGA	
MDH2	malate dehydrogenase	TCTGAGAAGAGCGAGCAACA	154
	(comp82270_c0)	ATAAAGCGCGAGCTGAGAAA	

Supplementary Table 2. Expression pattern of important proteins during dormancy and germination.

Antioxidant proteins	S2 vs S1	S3 vs S2	S4 vs S3	S5 vs S4	S6 vs S5	Reference
Peroxidase	1.91	5.65	1.21	2.07	0.91	[12]
Glutathione S-transferase	1.75	1.72	0.92	1.27	0.86	[30]
Superoxide dismutase	0.45	0.57	1.33	1.42	0.38	[24]
L-ascorbate peroxidase 1	0.13	1.79	0.48	3.80	0.63	[14]
Cationic peroxidase 1	5.45	6.03	0.78	0.47	9.38	[17]
Glutathione S-transferase L3	3.31	11.80	0.16	5.65	0.36	[30]
Glutathione reductase	2.27	2.29	1.92	0.60	2.23	[12]
Peroxisomal	1.45	1.64	1.39	0.67	1.15	[30]
Peroxiredoxin-2E-1	5.45	0.39	1.39	0.59	2.78	[31]
Peroxidase 4	1.79	0.34	2.73	0.90	5.45	[12], [30]
2-Cys peroxiredoxin BAS1	0.69	1.01	1.04	1.10	0.66	[12]
Catalase isozyme 2	0.91	1.27	0.85	0.90	0.84	[12]
Peroxidase 57	0.46	1.75	0.98	0.93	1.51	[12], [30]
Carbohydrate metabolism	S2 vs S1	S3 vs S2	S4 vs S3	S5 vs S4	S6 vs S5	Reference
Isocitrate dehydrogenase	0.57	0.96	0.77	0.63	0.91	[13]
ATP synthase subunit alpha	1.87	1.80	0.64	2.73	0.70	[28], [30]
S-adenosylmethionine synthase 2	3.91	1.92	0.79	2.09	1.17	[30], [31]
phosphoglucomutase	0.17	0.10	4.37	0.89	1.89	[34], [13]
Malate dehydrogenase	0.67	1.03	0.77	1.32	1.01	[13], [17]
Aldose 1-epimerase	0.34	0.79	1.84	0.30	2.36	[13], [30]
UTP--glucose-1-phosphate uridylyltransferase	2.01	1.19	1.19	1.67	0.95	[33]
Sucrose synthase 3	1.08	1.06	0.79	1.45	1.02	[30]

Supplementary legends

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Supplementary file 1: GO biological process between S2 and S1.

Supplementary file 2: GO biological process between S3 and S2.

Supplementary file 3: GO biological process between S4 and S3.

Supplementary file 4: GO biological process between S5 and S4.

Supplementary file 5: GO biological process between S6 and S5.

Supplementary file 6: Interaction network of DEPs identified of S2/S1, S3/S2, S4/S3, S5/S4, and S6/S5 with their predicted predicted by mapping them according to the *A. thaliana* interactions

Supplementary table 1: Primers of candidate genes designed for qRT-PCR.

Supplementary table 2: Expression patterns of important proteins during dormancy and germination.