

Supplementary Material

Figure S1. PCR analysis of the presence of transgenes and mRNA expression in T₀ and T₁ generations of wheat plants transformed with *TaBWPR-1.2* constructs. T₀: (**top**) analysis of leaf genomic DNA of 20 (for *Ubi:TaBWPR-1.2#2*) and 12 (for *Ubi:TaBWPR-1.2#13*) putative T₀ lines; (**bottom**) analysis of leaf mRNA from the same plants. T₁: to confirm the 3:1 segregation ratio, 16 plants were examined from each of the *Ubi:TaBWPR-1.2#2* and *Ubi:TaBWPR-1.2#13* lines. Seven DNA-positive plants and one DNA-negative plant were tested by RT-PCR. For each construct, four representative independent transgenic lines that were isolated as homozygous T₂ are shown. P, positive plasmid controls; N, non-transgenic control.

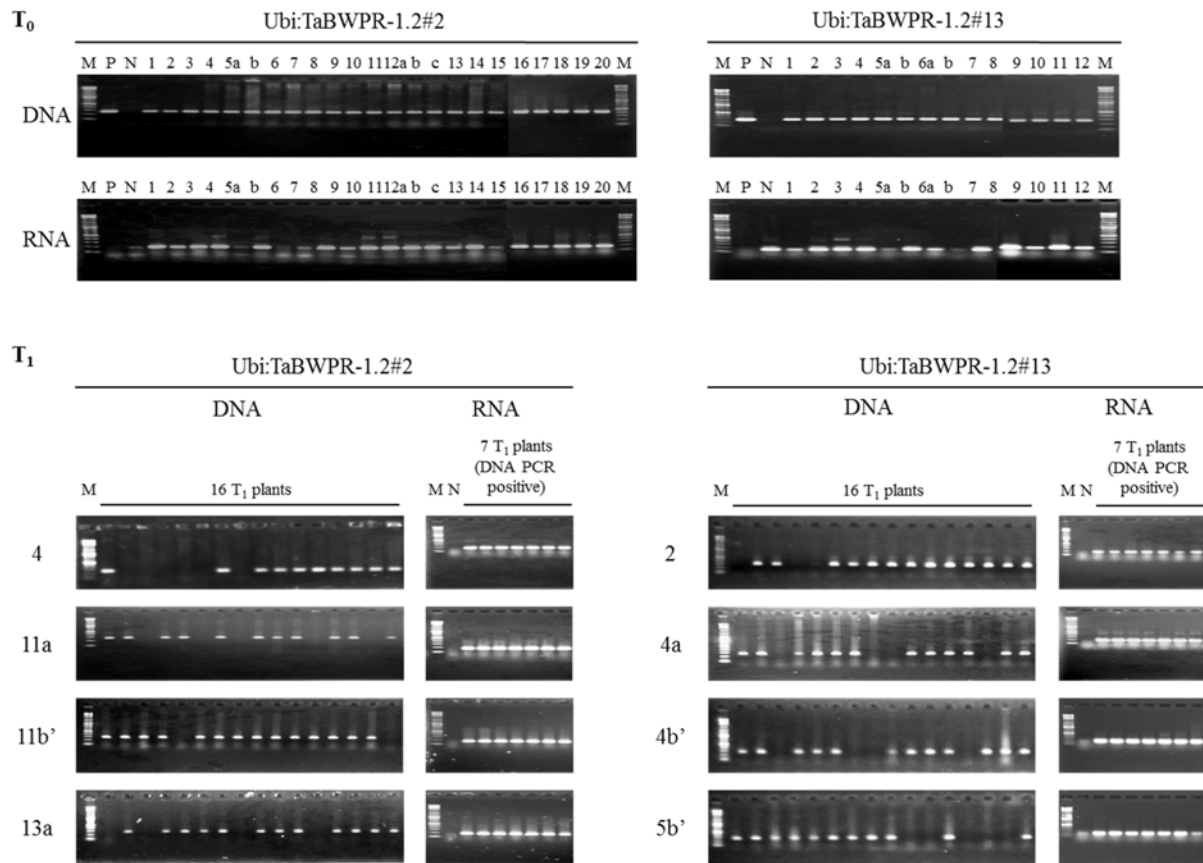


Figure S2. Organ-specific expression of *Ubi:TaBWPR-1.2#13* (as a representative of both transgenes) detected by RT-PCR. **(Top)** A four-day-old germinating embryo. **(Middle)** Leaf, root base (1 cm), middle of root (3–5 cm) and root tip (1 cm) of an eight-day-old seedling. **(Bottom, left)** Whole leaf and root of a 15-day-old seedling grown in a pot. **(Bottom, right)** Spikes (before anthesis) of 90-day-old plants grown in pots. N, respective null-segregant; P, positive plasmid controls.

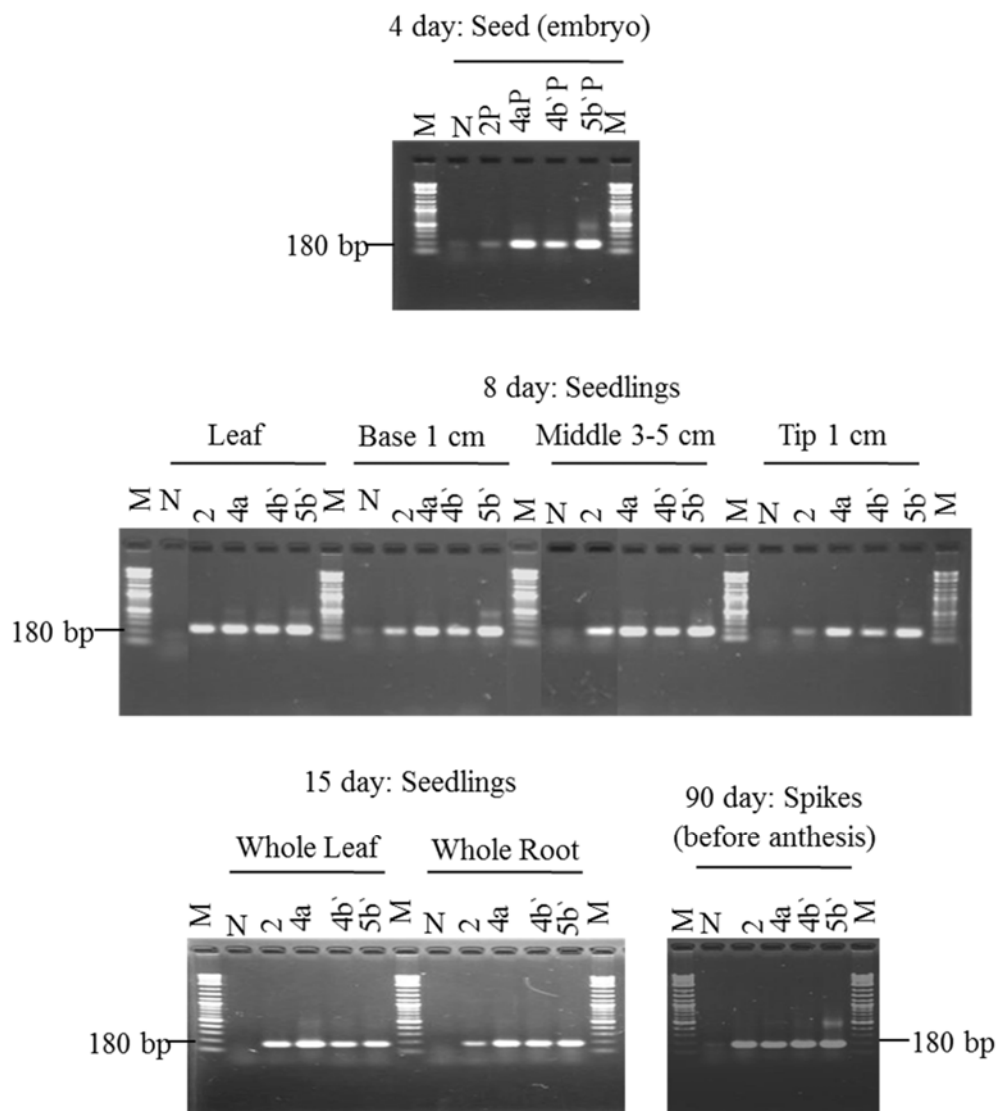


Figure S3. The levels of TaBWPR-1.2 proteins in the roots of homozygous transformants under control conditions and five days of WL. Immunoblotting was performed with anti-rice PR-1 antibody. The molecular weight of TaBWPR-1.2 is shown.

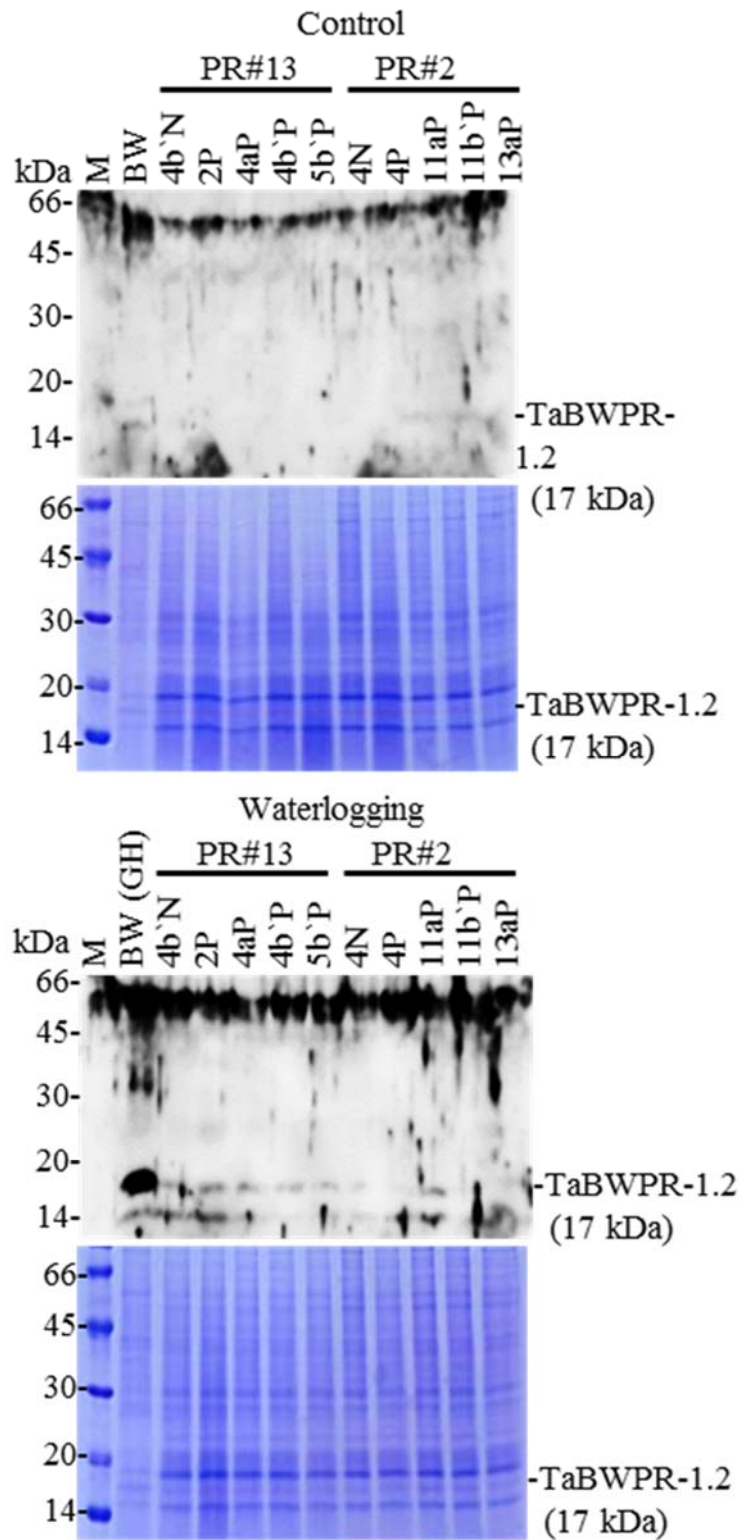


Table S1. Composition of media.

Medium Name	Composition
Callus induction: 0.2 M mannitol (CI-0.2Man)	MS salts and vitamins [1], 0.2 M mannitol, 1 mg·L ⁻¹ thiamin-HCl, 1.95 g·L ⁻¹ MES, 3.5 mM Gln, 1 mM Pro, 1 mM Asn, 100 mg·L ⁻¹ casein hydrolysate, pH 5.8, 2 g·L ⁻¹ Phytigel (Sigma), autoclaved. Picloram (2 mg·L ⁻¹), 2 mg·L ⁻¹ 2,4-dichlorophenoxyacetic acid (2,4-D), 100 mg·L ⁻¹ ascorbic acid, and 150 g·L ⁻¹ maltose added after autoclaving
Callus maintenance: 3 mg·L ⁻¹ phosphinothricin (CM-3P)	Same as CI-0.2Man, but no mannitol, and 0.5 mg·L ⁻¹ 2,4-D. Add 3 mg·L ⁻¹ phosphinothricin (PPT) after autoclaving.
Shoot growth: 1 mg·L ⁻¹ PPT (SG-1P)	Macrosalts (1.4 g·L ⁻¹ KNO ₃ , 300 mg·L ⁻¹ NH ₄ NO ₃ , 200 mg·L ⁻¹ KH ₂ PO ₄ , 450 mg·L ⁻¹ CaCl ₂ ·2H ₂ O, 350 mg·L ⁻¹ MgSO ₄ ·7H ₂ O); microsals (40 mg·L ⁻¹ Fe·Na·EDTA, 11.2 mg·L ⁻¹ MnSO ₄ ·5H ₂ O, 5 mg·L ⁻¹ H ₃ BO ₃ , 7.5 mg·L ⁻¹ ZnSO ₄ ·7H ₂ O, 0.75 mg·L ⁻¹ KI, 0.25 mg·L ⁻¹ Na ₂ MoO ₄ ·7H ₂ O, 0.025 mg·L ⁻¹ CuSO ₄ ·5H ₂ O, 0.025 mg·L ⁻¹ CoCl ₂ ·6H ₂ O); 30 g·L ⁻¹ maltose, 200 mg·L ⁻¹ myo-inositol, pH 5.7, 5 g·L ⁻¹ agar, autoclaved. Zeatin (5 mg·L ⁻¹), 0.1 mg·L ⁻¹ 2,4-D, vitamins (10 mg·L ⁻¹ thiamin-HCl, 1 mg·L ⁻¹ pyridoxine-HCl, 1 mg·L ⁻¹ nicotinic acid, 1 mg·L ⁻¹ Ca-pantothenate, 1 mg·L ⁻¹ ascorbic acid) and 1 mg·L ⁻¹ PPT added after autoclaving.
Root growth: 3 mg·L ⁻¹ PPT (RG-3P)	Same as SG-1P, but no zeatin or 2,4-D and 3 mg·L ⁻¹ PPT

Table S2. The list of proteins identified in seminal roots of the wheat transgenic line and the wild-type under control condition.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
Increase							
UniRef100_F8S6U7	Pathogenesis_related protein 1_17 n = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6U7_WHEAT	4	7	62	2.88	0.46	0.00
UniRef100_F8S6U4	Pathogenesis_related protein 1_14 n = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6U4_WHEAT	2	3	15	1.60	0.57	0.00
RFL_Contig3922	_pep_1:127_2472	4	4	6	1.33	0.22	0.03
gi_257637546_emb_CBD24658.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	3	7	1.30	0.21	0.01
RFL_Contig60	_pep_1:127_2376	2	2	3	1.28	0.15	0.01
UniRef100_Q9ZR95	Gamma_type tonoplast intrinsic protein n = 1 Tax = <i>Triticum aestivum</i> RepID = Q9ZR95_WHEAT	2	3	25	1.26	0.26	0.00
UniRef100_Q45NB5	Glutamine synthetase n = 1 Tax = <i>Triticum aestivum</i> RepID = Q45NB5_WHEAT	2	3	17	1.26	0.28	0.03
UniRef100_D2KZ10	Alanine_glyoxylate aminotransferase n = 1 Tax = <i>Triticum aestivum</i> RepID = D2KZ10_WHEAT	3	3	10	1.25	0.12	0.02
RFL_Contig5231	_pep_1:85_540	3	3	17	1.22	0.21	0.00
RFL_Contig267	_pep_1:103_981	3	3	7	1.22	0.11	0.00
RFL_Contig168	_pep_3:78_440	2	2	15	1.21	0.17	0.00
UniRef100_Q9FXQ8	TaWIN2 n = 1 Tax = <i>Triticum aestivum</i> RepID = Q9FXQ8_WHEAT	6	7	17	1.20	0.11	0.00
RFL_Contig1992	_pep_2:74_1693	5	5	19	1.19	0.19	0.04
RFL_Contig5189	_pep_3:90_845	2	2	14	1.19	0.17	0.00
UniRef100_Q401N6	Aspartic proteinase n = 1 Tax = <i>Triticum aestivum</i> RepID = Q401N6_WHEAT	4	4	32	1.19	0.11	0.00
UniRef100_H9CWE9	12_oxo_phytodienoic acid reductase n = 1 Tax = <i>Triticum aestivum</i> RepID = H9CWE9_WHEAT	2	2	15	1.19	0.09	0.00
UniRef100_A9P8I4	Predicted protein n = 6 Tax = Magnoliophyta RepID = A9P8I4_POPTR	2	2	23	1.18	0.07	0.00
gi_227473231_emb_CAY33013.1_	unnamed protein product (<i>Triticum aestivum</i>)	7	8	39	1.17	0.10	0.00
UniRef100_B4F6E5	Root peroxidase n = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E5_WHEAT	6	6	14	1.17	0.14	0.00
UniRef100_B4F6F2	Root peroxidase n = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6F2_WHEAT	7	7	15	1.16	0.13	0.00
UniRef100_Q84MJ5	Methylmalonate semialdehyde dehydrogenase (Fragment) n = 1 Tax = <i>Triticum aestivum</i> RepID = Q84MJ5_WHEAT	5	7	42	1.16	0.10	0.05
RFL_Contig4308	_pep_3:60_830	3	3	11	1.15	0.10	0.03
UniRef100_O81331	Vacuolar invertase (Fragment) n = 1 Tax = <i>Triticum aestivum</i> RepID = O81331_WHEAT	5	6	33	1.14	0.25	0.01
RFL_Contig5913	_pep_1:166_957	4	6	36	1.14	0.13	0.00
UniRef100_Q7X729	Acidic ribosomal protein P2 (Fragment) n = 1 Tax = <i>Triticum aestivum</i> RepID = Q7X729_WHEAT	2	4	30	1.14	0.09	0.00
UniRef100_Q75QN9	Cold shock domain protein 2 n = 1 Tax = <i>Triticum aestivum</i> RepID = Q75QN9_WHEAT	4	4	32	1.13	0.07	0.00
UniRef100_A3FKE5	Superoxide dismutase (Fragment) n = 1 Tax = <i>Triticum aestivum</i> RepID = A3FKE5_WHEAT	2	2	8	1.12	0.19	0.01

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig3422	_pep_2:98_514	2	2	22	1.12	0.13	0.00
RFL_Contig2381	_pep_2:65_808	2	4	20	1.12	0.11	0.00
RFL_Contig1475	_pep_1:52_537	2	2	3	1.11	0.13	0.04
gi_218381856_emb_CAV24596.1	unnamed protein product (<i>Triticum aestivum</i>)	2	3	30	1.11	0.09	0.00
UniRef100_Q24396	Adenylosuccinate synthetase_chloroplastic (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = PURA_WHEAT	3	3	18	1.11	0.08	0.02
UniRef100_A5JPR2	Peroxisomal ascorbate peroxidase <i>n</i> = 2 Tax = Triticeae RepID = A5JPR2_WHEAT	4	4	26	1.11	0.06	0.00
UniRef100_Q5G1T9	Gamma glutamylcysteine synthetase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q5G1T9_WHEAT	4	5	29	1.11	0.11	0.01
UniRef100_B4F6E6	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E6_WHEAT	9	9	65	1.10	0.11	0.00
UniRef100_B4F6E7	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E7_WHEAT	9	10	91	1.10	0.10	0.00
RFL_Contig3447	_pep_3:195_1160	2	2	6	1.10	0.07	0.01
UniRef100_I0AW27	Mitochondrial manganese superoxide dismutase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = I0AW27_WHEAT	3	3	5	1.09	0.17	0.02
UniRef100_Q7X9L9	QM (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7X9L9_WHEAT	2	2	17	1.09	0.33	0.01
RFL_Contig2937	_pep_3:102_1607	5	6	27	1.09	0.09	0.03
UniRef100_G1FUU8	Superoxide dismutase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = G1FUU8_WHEAT	3	3	19	1.08	0.11	0.02
gi_257667483_emb_CBD31968.1	unnamed protein product (<i>Triticum aestivum</i>)	4	5	36	1.08	0.08	0.00
RFL_Contig3430	_pep_3:291_1733	5	5	22	1.08	0.06	0.04
UniRef100_Q7XYD5	Acidic ribosomal protein (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7XYD5_WHEAT	4	6	68	1.08	0.08	0.00
UniRef100_Q2QKB2	MRNA transport factor <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q2QKB2_WHEAT	2	2	13	1.08	0.13	0.00
UniRef100_D8L9A5	Putative PDI_like protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9A5_WHEAT	5	5	20	1.08	0.05	0.00
RFL_Contig3855	_pep_3:126_1601	5	6	44	1.07	0.06	0.00
RFL_Contig3939	_pep_2:125_1702	8	10	53	1.07	0.08	0.01
gi_296524610_emb_CBM36960.1	unnamed protein product (<i>Triticum aestivum</i>)	7	8	59	1.06	0.05	0.00
gi_296525620_emb_CBM37262.1	unnamed protein product (<i>Triticum aestivum</i>)	6	6	43	1.06	0.10	0.01
UniRef100_C6K7G3	Lipoxygenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C6K7G3_WHEAT	7	8	22	1.06	0.05	0.00
RFL_Contig2671	_pep_1:118_1575	8	8	66	1.06	0.07	0.01
RFL_Contig825	_pep_1:61_3579	9	9	40	1.06	0.05	0.00
gi_219890652_emb_CAW94684.1	unnamed protein product (<i>Triticum aestivum</i>)	10	13	72	1.05	0.04	0.00
gi_227289532_emb_CAY02762.1	unnamed protein product (<i>Triticum aestivum</i>)	2	2	10	1.05	0.06	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
gi_219890650_emb_CAW94682.1_	unnamed protein product (<i>Triticum aestivum</i>)	6	7	28	1.05	0.05	0.00
RFL_Contig2744	_pep_1:109_1791	4	4	13	1.05	0.14	0.00
gi_219914284_emb_CAW74911.1_	unnamed protein product (<i>Triticum aestivum</i>)	7	8	48	1.05	0.11	0.01
UniRef100_Q8VYX1	Phosphoethanolamine methyltransferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8VYX1_WHEAT	9	10	62	1.04	0.04	0.05
UniRef100_G3E8E1	Aquaporin 7 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = G3E8E1_WHEAT	5	7	70	1.04	0.07	0.00
RFL_Contig2753	_pep_3:177_1784	6	7	30	1.03	0.04	0.05
UniRef100_Q9M7C4	Plasma membrane intrinsic protein 1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9M7C4_WHEAT	2	3	31	1.03	0.14	0.00
RFL_Contig2735	_pep_1:76_2670	11	14	93	1.03	0.04	0.00
UniRef100_P55313	Catalase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CATA2_WHEAT	8	10	58	1.03	0.04	0.04
RFL_Contig3291	_pep_3:81_1841	10	13	96	1.03	0.05	0.00
UniRef100_C7C4X1	Glyceraldehyde_3_phosphate dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C7C4X1_WHEAT	10	21	184	1.03	0.04	0.00
RFL_Contig1280	_pep_3:195_1787	3	4	36	1.03	0.02	0.01
RFL_Contig3876	_pep_2:95_1588	5	6	15	1.03	0.10	0.00
RFL_Contig3093	_pep_1:85_957	3	4	7	1.03	0.13	0.00
RFL_Contig3171	_pep_2:98_1981	6	6	20	1.02	0.07	0.00
gi_315113253_pdb_3IZR_H	Chain H_ Localization Of The Large Subunit Ribosomal Proteins Into A 5.5 A Cryo_Em Map of <i>Triticum aestivum</i> Translating 80s Ribosome	5	5	13	1.02	0.04	0.00
RFL_Contig2987	_pep_2:68_565	5	5	31	1.02	0.14	0.02
gi_227483057_emb_CAY37266.1_	unnamed protein product (<i>Triticum aestivum</i>)	11	14	89	1.02	0.03	0.00
RFL_Contig6066	_pep_3:69_2492	13	13	95	1.02	0.04	0.00
UniRef100_P46524	Dehydrin COR410 <i>n</i> = 2 Tax = <i>Triticum aestivum</i> RepID = CO410_WHEAT	3	4	26	1.01	0.11	0.00
RFL_Contig2913	_pep_2:56_544	4	5	31	1.01	0.03	0.00
RFL_Contig3927	_pep_3:123_1715	5	5	30	1.01	0.05	0.00
RFL_Contig5059	_pep_1:97_1608	7	8	47	1.01	0.05	0.00
UniRef100_C5H4Q0	Class III peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C5H4Q0_WHEAT	5	6	38	1.01	0.09	0.01
RFL_Contig308	_pep_1:73_1512	10	15	113	1.01	0.06	0.01
UniRef100_D8L9J3	Dolichyl_diphosphooligosaccharide__protein glycosyltransferase_putative_expressed <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9J3_WHEAT	11	12	64	1.01	0.04	0.01

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
Decrease							
UniRef100_H2KXF7	Pathogenesis_related protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H2KXF7_WHEAT	4	5	16	0.44	0.08	0.00
UniRef100_B5B3P8	Pathogenesis related protein 10 <i>n</i> = 2 Tax = commelinids RepID = B5B3P8_WHEAT	4	4	16	0.47	0.08	0.00
RFL_Contig2907	_pep_2:905_1681	5	5	11	0.58	0.05	0.00
RFL_Contig2814	_pep_2:74_1759	6	6	19	0.59	0.03	0.00
UniRef100_Q41629	ADP_ATP carrier protein 1_mitochondrial <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = ADT1_WHEAT	7	10	68	0.60	0.03	0.00
UniRef100_Q43223	Sucrose synthase type 2 <i>n</i> = 2 Tax = <i>Triticum aestivum</i> RepID = Q43223_WHEAT	6	8	40	0.69	0.07	0.00
RFL_Contig4468	_pep_3:39_2093	2	2	15	0.70	0.23	0.01
RFL_Contig154	_pep_3:54_440	2	3	18	0.73	0.18	0.00
UniRef100_Q515K7	Small GTP_binding protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q515K7_WHEAT	8	9	40	0.74	0.07	0.00
UniRef100_I1HEK5	Uncharacterized protein <i>n</i> = 2 Tax = Pooidae RepID = I1HEK5_BRADI	2	2	17	0.76	0.07	0.00
UniRef100_A4K4Z0	Alpha tubulin_5B <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Z0_WHEAT	4	7	68	0.77	0.05	0.00
UniRef100_Q8LGQ9	Betaine_aldehyde dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8LGQ9_WHEAT	6	6	38	0.77	0.06	0.00
UniRef100_A2WN93	Calmodulin_1 <i>n</i> = 18 Tax = Magnoliophyta RepID = CALM1_ORYSI	3	3	6	0.78	0.06	0.00
UniRef100_P04464	Calmodulin <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CALM_WHEAT	3	3	34	0.78	0.06	0.00
UniRef100_Q8RW03	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW03_WHEAT	4	4	8	0.79	0.04	0.00
RFL_Contig2611	_pep_1:163_2028	4	4	19	0.79	0.05	0.00
UniRef100_Q8RW02	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW02_WHEAT	5	6	37	0.79	0.04	0.00
UniRef100_Q8L808	Putative cytochrome c oxidase subunit <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8L808_WHEAT	2	2	10	0.79	0.12	0.00
RFL_Contig3301	_pep_1:73_1101	3	3	12	0.80	0.11	0.01
RFL_Contig3551	_pep_3:141_1922	4	4	17	0.81	0.10	0.00
RFL_Contig3524	_pep_2:224_3232	4	4	13	0.81	0.09	0.00
UniRef100_Q8RW01	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW01_WHEAT	2	2	10	0.81	0.13	0.00
gi_315113258_pdb_3IZR_Q	Chain Q_ Localization Of The Large Subunit Ribosomal Proteins Into A 5.5 A Cryo_Em Map of <i>Triticum aestivum</i> Translating 80s Ribosome	3	3	10	0.82	0.06	0.00
UniRef100_Q9ZR33	Glycosyltransferase 75 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9ZR33_WHEAT	11	13	118	0.82	0.05	0.00
RFL_Contig3262	_pep_3:150_1172	3	4	14	0.82	0.09	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
gi_257669840_emb_CBD25095.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	4	41	0.83	0.07	0.00
RFL_Contig3224	_pep_2:101_2215	20	22	228	0.83	0.04	0.00
RFL_Contig608	_pep_1:118_1374	2	2	7	0.83	0.19	0.02
UniRef100_F6H5Z7	Putative uncharacterized protein <i>n</i> = 11 Tax = Viridiplantae RepID = F6H5Z7_VITVI	3	9	82	0.84	0.08	0.00
RFL_Contig3004	_pep_1:253_1263	2	2	11	0.84	0.14	0.00
RFL_Contig4661	_pep_3:114_1046	5	5	23	0.84	0.07	0.00
UniRef100_Q6IY71	Mitochondrial ATP synthase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q6IY71_WHEAT	5	6	32	0.84	0.11	0.01
UniRef100_Q43199	Adenine phosphoribosyltransferase 1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = APT1_WHEAT	5	6	32	0.85	0.07	0.01
UniRef100_G9HXG9	60S ribosomal protein L5 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = G9HXG9_WHEAT	3	5	50	0.85	0.07	0.00
UniRef100_Q08G39	Ribosomal protein L3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q08G39_WHEAT	6	10	56	0.86	0.05	0.00
RFL_Contig3052	_pep_3:75_488	2	2	12	0.86	0.17	0.02
UniRef100_Q517K2	Ribosomal protein S7 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q517K2_WHEAT	6	8	33	0.86	0.12	0.00
UniRef100_Q1W692	Calcium dependent protein kinase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1W692_WHEAT	3	3	15	0.86	0.12	0.01
UniRef100_G5DFC5	14_3_3 protein <i>n</i> = 2 Tax = <i>Triticum aestivum</i> RepID = G5DFC5_WHEAT	7	11	107	0.86	0.06	0.00
UniRef100_P93616	Poly(A) binding protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = P93616_WHEAT	4	4	19	0.87	0.10	0.00
UniRef100_Q08G36	14_3_3 protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q08G36_WHEAT	8	12	94	0.87	0.04	0.00
RFL_Contig3269	_pep_2:77_985	6	10	70	0.87	0.05	0.00
UniRef100_B2B9T8	V_type proton ATPase subunit F <i>n</i> = 2 Tax = Triticeae RepID = B2B9T8_WHEAT	4	5	22	0.87	0.12	0.01
RFL_Contig1864	_pep_3:60_566	2	3	14	0.87	0.10	0.00
gi_257719940_emb_CBD33082.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	4	15	0.87	0.09	0.02
UniRef100_Q9FXQ9	TaWIN1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9FXQ9_WHEAT	7	9	62	0.87	0.04	0.00
UniRef100_F2VQK3	Atp4_1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F2VQK3_WHEAT	3	4	22	0.87	0.11	0.01
RFL_Contig1443	_pep_3:513_887	2	2	8	0.87	0.15	0.01
UniRef100_A1YE31	Ribosomal protein L3_A3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A1YE31_WHEAT	8	13	67	0.87	0.04	0.02
RFL_Contig876	_pep_3:159_1526	2	2	5	0.87	0.11	0.02
RFL_Contig3677	_pep_3:54_725	2	3	6	0.87	0.10	0.00
UniRef100_B2ZGK6	Plastid acetyl-CoA carboxylase <i>n</i> = 50 Tax = Pooideae RepID = B2ZGK6_TRIUA	9	9	20	0.87	0.06	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig3128	_pep_3:87_524	2	2	16	0.87	0.08	0.00
UniRef100_A4K4Y7	Alpha tubulin_4D n = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Y7_WHEAT	10	15	145	0.88	0.03	0.00
gi_219736721_emb_CAW66961.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	3	11	0.88	0.08	0.01
RFL_Contig773	_pep_2:83_862	3	4	17	0.88	0.08	0.00
UniRef100_A7J2I0	Plasma membrane intrinsic protein n = 1 Tax = <i>Triticum aestivum</i> RepID = A7J2I0_WHEAT	3	3	23	0.88	0.04	0.00
RFL_Contig3347	_pep_1:43_1236	2	2	14	0.88	0.12	0.01
RFL_Contig5794	_pep_2:89_2389	17	31	234	0.88	0.03	0.00
RFL_Contig5814	_pep_3:78_2375	19	35	299	0.88	0.03	0.00
RFL_Contig3640	_pep_1:91_3054	4	5	19	0.89	0.06	0.01
gi_295422633_emb_CBL75153.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	3	19	0.89	0.08	0.00
gi_257672159_emb_CBD32171.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	8	60	0.89	0.07	0.03
gi_257672167_emb_CBD32175.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	8	66	0.89	0.07	0.03
UniRef100_O82073	Sucrose synthase type I n = 2 Tax = <i>Triticum aestivum</i> RepID = O82073_WHEAT	19	26	192	0.90	0.05	0.01
gi_227473233_emb_CAY33014.1_	unnamed protein product (<i>Triticum aestivum</i>)	7	7	14	0.90	0.05	0.00
gi_227295766_emb_CAY03053.1_	unnamed protein product (<i>Triticum aestivum</i>)	4	4	25	0.90	0.10	0.00
gi_296514140_emb_CBM39929.1_	unnamed protein product (<i>Triticum aestivum</i>)	6	6	59	0.90	0.11	0.00
gi_257672153_emb_CBD32168.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	10	129	0.90	0.05	0.00
gi_257672155_emb_CBD32169.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	10	129	0.90	0.05	0.00
RFL_Contig4300	_pep_2:125_586	2	2	13	0.90	0.10	0.00
RFL_Contig3604	_pep_2:149_973	4	4	24	0.90	0.05	0.00
RFL_Contig3076	_pep_1:130_1965	4	4	15	0.90	0.06	0.04
RFL_Contig6144	_pep_1:88_1224	3	5	18	0.90	0.03	0.00
RFL_Contig3937	_pep_3:258_1649	3	3	10	0.90	0.07	0.01
UniRef100_Q1XH04	Beta_glucosidase n = 1 Tax = <i>Triticum aestivum</i> RepID = Q1XH04_WHEAT	8	11	22	0.90	0.05	0.00
gi_219772365_emb_CAW48568.1_	unnamed protein product (<i>Triticum aestivum</i>)	13	18	129	0.90	0.05	0.00
UniRef100_P02276	Histone H2A.2.1 n = 1 Tax = <i>Triticum aestivum</i> RepID = H2A2_WHEAT	2	10	132	0.90	0.07	0.00
UniRef100_D5MTF8	Beta_glucosidase n = 1 Tax = <i>Triticum aestivum</i> RepID = D5MTF8_WHEAT	12	17	128	0.91	0.05	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
gi_257672171_emb_CBD32177.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	4	12	0.91	0.07	0.00
UniRef100_Q1XIR9	Beta_glucosidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1XIR9_WHEAT	10	14	105	0.91	0.05	0.00
UniRef100_Q1XH05	Beta_glucosidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1XH05_WHEAT	9	14	89	0.91	0.05	0.00
UniRef100_P38076	Cysteine synthase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CYSK_WHEAT	7	10	77	0.91	0.08	0.00
RFL_Contig1936	_pep_ 1:130_579	2	2	18	0.91	0.07	0.00
RFL_Contig3987	_pep_ 2:107_1024	4	6	23	0.91	0.07	0.00
gi_295422149_emb_CBL74911.1_	unnamed protein product (<i>Triticum aestivum</i>)	5	5	41	0.91	0.08	0.00
UniRef100_P02275	Histone H2A.1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H2A1_WHEAT	2	10	135	0.91	0.07	0.00
UniRef100_F2E390	Ribosomal protein <i>n</i> = 2 Tax = Triticeae RepID = F2E390_HORVD	5	8	16	0.91	0.07	0.05
RFL_Contig3661	_pep_ 1:106_3954	2	2	15	0.91	0.15	0.01
UniRef100_F2VQM4	Nad9 <i>n</i> = 1 Tax= <i>Triticum aestivum</i> RepID=F2VQM4_WHEAT	3	3	17	0.91	0.06	0.01
UniRef100_Q53UC8	Delta1_pyrraline_5_carboxylate synthetase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q53UC8_WHEAT	7	7	18	0.91	0.03	0.00
UniRef100_Q9FVJ9	COP alpha homolog (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9FVJ9_WHEAT	6	6	16	0.91	0.05	0.00
RFL_Contig2923	_pep_ 1:160_1344	6	7	26	0.91	0.05	0.00
UniRef100_P02277	Histone H2A.2.2 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H2A3_WHEAT	2	11	146	0.91	0.07	0.00
gi_257672157_emb_CBD32170.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	11	146	0.91	0.07	0.00
UniRef100_Q9ZRB0	Tubulin beta_3 chain <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = TBB3_WHEAT	13	19	178	0.91	0.03	0.00
RFL_Contig2971	_pep_ 1:64_600	5	5	30	0.92	0.04	0.00
UniRef100_Q0PMD7	J_domain protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q0PMD7_WHEAT	2	2	7	0.92	0.08	0.03
UniRef100_Q9SP56	Glutathione S_transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9SP56_WHEAT	5	7	55	0.92	0.05	0.00
gi_257659932_emb_CBD33996.1_	unnamed protein product (<i>Triticum aestivum</i>)	5	7	55	0.92	0.05	0.00
UniRef100_Q8GTB7	Glutathione transferase F1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8GTB7_WHEAT	2	4	10	0.92	0.06	0.00
gi_257711213_emb_CBD35086.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	2	8	0.92	0.09	0.01
UniRef100_Q58QF6	Delta 1_pyrraline_5_carboxylate synthetase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q58QF6_WHEAT	8	8	16	0.92	0.03	0.00
UniRef100_A4K4Z3	Alpha tubulin_1A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Z3_WHEAT	9	15	136	0.92	0.04	0.00
RFL_Contig5566	_pep_ 3:78_905	6	8	29	0.92	0.05	0.01
RFL_Contig3435	_pep_ 2:95_865	8	12	106	0.92	0.07	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_O82072	Phosphoenolpyruvate carboxylase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = O82072_WHEAT	25	33	268	0.92	0.02	0.00
RFL_Contig3489	_pep_3:129_1109	5	6	49	0.92	0.08	0.00
gi_295415556_emb_CBL76033.1_	unnamed protein product (<i>Triticum aestivum</i>)	8	10	49	0.93	0.08	0.00
UniRef100_Q9ZRA8	Tubulin beta_5 chain <i>n</i> = 4 Tax = Pooideae RepID = TBB5_WHEAT	11	14	171	0.93	0.03	0.00
UniRef100_A4K4Y1	Alpha tubulin_2A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Y1_WHEAT	11	19	173	0.93	0.03	0.00
UniRef100_P83970	Plasma membrane ATPase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = PMA1_WHEAT	20	28	190	0.93	0.05	0.00
gi_218409192_emb_CAV27654.1_	unnamed protein product (<i>Triticum aestivum</i>)	20	24	197	0.93	0.03	0.01
RFL_Contig3549	_pep_1:88_426	4	4	52	0.93	0.13	0.00
RFL_Contig3111	_pep_2:80_682	2	3	36	0.93	0.07	0.00
UniRef100_Q9ZRR5	Tubulin alpha_3 chain <i>n</i> = 3 Tax = Triticeae RepID = TBA3_HORVU	11	18	174	0.93	0.03	0.00
RFL_Contig618	_pep_2:116_700	2	2	3	0.93	0.09	0.00
RFL_Contig63	_pep_2:113_733	5	5	40	0.93	0.07	0.00
RFL_Contig1587	_pep_2:131_1375	11	11	62	0.93	0.04	0.00
gi_295415558_emb_CBL76034.1_	unnamed protein product (<i>Triticum aestivum</i>)	7	11	85	0.93	0.08	0.00
RFL_Contig4735	_pep_3:96_3362	3	3	14	0.93	0.07	0.00
UniRef100_Q9ZRB1	Tubulin beta_2 chain <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = TBB2_WHEAT	11	17	190	0.93	0.03	0.00
RFL_Contig2042	_pep_3:180_1829	9	9	46	0.94	0.04	0.00
gi_257726669_emb_CBD21804.1_	unnamed protein product (<i>Triticum aestivum</i>)	10	12	41	0.94	0.04	0.00
RFL_Contig4145	_pep_2:26_508	3	3	17	0.94	0.09	0.05
UniRef100_Q41583	Initiation factor (Iso)4f p82 subunit <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q41583_WHEAT	11	14	39	0.94	0.03	0.00
RFL_Contig3507	_pep_2:59_1102	6	9	69	0.94	0.04	0.00
UniRef100_Q8VX48	Phosphoglucosmutase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8VX48_WHEAT	12	12	87	0.94	0.06	0.00
UniRef100_Q93YY0	68 kDa protein HP68 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q93YY0_WHEAT	4	4	10	0.94	0.09	0.00
UniRef100_A5YVV3	Glyceraldehyde_3_phosphate dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A5YVV3_WHEAT	11	22	184	0.94	0.05	0.00
UniRef100_Q9FS79	Triosephosphate isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9FS79_WHEAT	9	12	74	0.94	0.06	0.00
UniRef100_A7J2I1	Plasma membrane intrinsic protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7J2I1_WHEAT	4	5	33	0.94	0.04	0.00
UniRef100_Q03387	Eukaryotic initiation factor iso_4F subunit p82_34 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = IF41_WHEAT	13	16	66	0.94	0.03	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_B0LXM0	S_adenosylmethionine synthase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = METK_WHEAT	5	9	67	0.94	0.05	0.03
UniRef100_Q7X9L6	40S ribosomal protein (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7X9L6_WHEAT	4	4	7	0.94	0.02	0.00
UniRef100_Q8L804	Putative 40S ribosomal protein S3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8L804_WHEAT	6	7	53	0.94	0.02	0.00
UniRef100_F6IB54	Putative feruloyl transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F6IB54_WHEAT	2	2	16	0.94	0.03	0.00
RFL_Contig4437	_pep_2:137_2578	6	6	24	0.95	0.10	0.02
UniRef100_A7J2I2	Plasma membrane intrinsic protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7J2I2_WHEAT	5	7	64	0.95	0.03	0.00
UniRef100_Q41534	ATP synthase subunit beta <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q41534_WHEAT	19	35	272	0.95	0.04	0.00
UniRef100_C9EF64	Dehydroascorbate reductase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C9EF64_WHEAT	7	9	63	0.95	0.04	0.00
gi_296511813_emb_CBM39048.1	unnamed protein product (<i>Triticum aestivum</i>)	2	2	2	0.95	0.06	0.00
UniRef100_Q84UH6	Dehydroascorbate reductase <i>n</i> = 2 Tax = <i>Triticum</i> RepID = Q84UH6_WHEAT	7	10	63	0.95	0.03	0.00
RFL_Contig3778	_pep_3:354_3464	4	4	18	0.95	0.05	0.01
RFL_Contig2570	_pep_1:94_1038	6	7	27	0.96	0.08	0.00
UniRef100_Q9ZRA9	Tubulin beta_4 chain <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = TBB4_WHEAT	13	18	183	0.96	0.03	0.00
RFL_Contig3647	_pep_3:66_1604	5	6	29	0.96	0.10	0.01
UniRef100_O82571	Superoxide dismutase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = O82571_WHEAT	3	3	9	0.96	0.08	0.00
RFL_Contig31	_pep_3:72_440	3	3	15	0.96	0.04	0.05
RFL_Contig1940	_pep_1:7_954	6	8	40	0.96	0.05	0.03
RFL_Contig3378	_pep_2:140_1723	12	14	102	0.96	0.06	0.00
RFL_Contig2911	_pep_2:110_1441	8	9	66	0.96	0.05	0.00
UniRef100_G4XH71	Peptidyl_prolyl cis_trans isomerase <i>n</i> = 2 Tax = Triticeae RepID = G4XH71_9POAL	3	5	48	0.96	0.06	0.00
gi_257672699_emb_CBD34755.1	unnamed protein product (<i>Triticum aestivum</i>)	16	21	157	0.97	0.05	0.00
UniRef100_A7LM55	Peptidyl_prolyl cis_trans isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7LM55_WHEAT	3	7	63	0.97	0.06	0.00
UniRef100_Q332R4	ATP synthase subunit alpha <i>n</i> = 3 Tax = Triticeae RepID = Q332R4_WHEAT	13	14	113	0.97	0.03	0.05
UniRef100_P43650	Putative ATP synthase protein YMF19 <i>n</i> = 2 Tax = Triticeae RepID = YMF19_WHEAT	3	3	23	0.97	0.03	0.00
UniRef100_C3VQ52	Ascorbate peroxidase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C3VQ52_WHEAT	9	11	76	0.97	0.07	0.01
UniRef100_B9A8E2	Protein disulfide isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B9A8E2_WHEAT	11	13	91	0.97	0.04	0.00
UniRef100_B9A8E3	Protein disulfide isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B9A8E3_WHEAT	13	15	65	0.97	0.04	0.00

Table S2. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_B2BA44	Vacuolar proton ATPase subunit H <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B2BA44_WHEAT	9	11	73	0.97	0.05	0.04
UniRef100_P52589	Protein disulfide isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = PDI_WHEAT	11	12	53	0.97	0.04	0.00
UniRef100_Q8L806	Putative ribosomal protein S18 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8L806_WHEAT	3	3	19	0.97	0.05	0.01
RFL_Contig3770	_pep_3:33_1130	11	18	152	0.97	0.05	0.00
UniRef100_Q9ZRA7	Beta_tubulin 6 (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9ZRA7_WHEAT	6	10	47	0.97	0.04	0.00
RFL_Contig3321	_pep_3:156_1730	10	14	106	0.97	0.04	0.00
RFL_Contig4151	_pep_3:126_5297	29	34	190	0.97	0.03	0.00
gi_257711217_emb_CBD35088.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	2	26	0.97	0.07	0.05
RFL_Contig3538	_pep_1:112_1083	6	7	60	0.98	0.05	0.01
RFL_Contig5895	_pep_2:608_3703	3	3	33	0.98	0.06	0.00
RFL_Contig4724	_pep_3:228_3104	8	10	46	0.98	0.07	0.01
RFL_Contig3118	_pep_2:137_1474	3	3	36	0.98	0.08	0.02
UniRef100_D8L9U6	Eukaryotic translation initiation factor_putative_expressed <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9U6_WHEAT	6	6	24	0.98	0.08	0.03
RFL_Contig5602	_pep_2:71_748	6	9	79	0.98	0.04	0.00
UniRef100_F4Y592	Heat shock protein 90 <i>n</i> = 2 Tax = <i>Triticum</i> RepID = F4Y592_WHEAT	8	8	16	0.98	0.05	0.00
UniRef100_A3KLL4	Malate dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A3KLL4_WHEAT	6	10	99	0.98	0.08	0.04
RFL_Contig4129	_pep_1:262_1017	3	4	18	0.98	0.04	0.01
RFL_Contig259	_pep_3:63_1403	13	17	162	0.98	0.05	0.00
UniRef100_F4Y594	Heat shock protein 90 <i>n</i> = 2 Tax = <i>Triticeae</i> RepID = F4Y594_WHEAT	8	10	14	0.98	0.05	0.00
RFL_Contig3043	_pep_1:235_2394	7	7	42	0.98	0.06	0.00
UniRef100_Q03033	Elongation factor 1_alpha <i>n</i> = 3 Tax = <i>Triticeae</i> RepID = EF1A_WHEAT	10	22	176	0.99	0.05	0.00
UniRef100_F4Y589	Heat shock protein 90 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F4Y589_WHEAT	6	7	24	0.99	0.04	0.00
RFL_Contig3625	_pep_3:405_2606	4	4	9	0.99	0.15	0.03
RFL_Contig3308	_pep_1:88_2154	10	11	82	0.99	0.04	0.04
UniRef100_Q9SAU8	HSP70 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9SAU8_WHEAT	15	19	162	0.99	0.03	0.00
gi_296511811_emb_CBM39047.1_	unnamed protein product (<i>Triticum aestivum</i>)	10	10	68	0.99	0.04	0.00

Table S3. The list of proteins identified in seminal roots of the wheat transgenic line and wild type under waterlogging.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
Increase							
UniRef100_Q8S3J5	Ferredoxin <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8S3J5_WHEAT	2	2	6	2.02	2.29	0.01
UniRef100_F8S6T6	Pathogenesis_related protein 1_6 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6T6_WHEAT	2	3	15	1.97	0.66	0.00
UniRef100_Q9M7S5	Elongation factor_2 (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9M7S5_WHEAT	2	2	9	1.87	1.15	0.03
UniRef100_F8S6U7	Pathogenesis_related protein 1_17 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6U7_WHEAT	5	8	82	1.53	0.10	0.00
RFL_Contig2626	_pep_2:92_1075	2	2	2	1.35	0.11	0.02
RFL_Contig2940	_pep_2:62_583	2	3	22	1.33	0.40	0.00
UniRef100_Q7XYB6	Elongation factor (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7XYB6_WHEAT	2	3	35	1.30	0.30	0.01
RFL_Contig246	_pep_3:57_590	2	2	3	1.24	0.16	0.01
RFL_Contig2363	_pep_2:65_1267	4	5	20	1.22	0.12	0.00
RFL_Contig5163	_pep_2:125_1489	3	3	14	1.22	0.09	0.00
RFL_Contig2035	_pep_1:49_1818	2	2	3	1.22	0.34	0.02
UniRef100_A2WN93	Calmodulin_1 <i>n</i> = 18 Tax = Magnoliophyta RepID = CALM1_ORYSI	3	3	22	1.21	0.18	0.00
UniRef100_Q84MJ5	Methylmalonate semialdehyde dehydrogenase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q84MJ5_WHEAT	3	5	56	1.19	0.16	0.00
RFL_Contig3223	_pep_2:116_607	5	6	28	1.19	0.13	0.00
UniRef100_A9U8G4	Alcohol dehydrogenase ADH1A <i>n</i> = 2 Tax = <i>Triticum</i> RepID = A9U8G4_WHEAT	9	14	89	1.18	0.07	0.00
RFL_Contig3037	_pep_1:118_786	3	3	26	1.18	0.11	0.00
RFL_Contig4868	_pep_3:54_1019	3	3	6	1.17	0.12	0.00
UniRef100_I1HEK5	Uncharacterized protein <i>n</i> = 2 Tax = Pooideae RepID = I1HEK5_BRADI	3	3	13	1.16	0.17	0.00
RFL_Contig2784	_pep_2:128_631	3	4	40	1.16	0.13	0.00
UniRef100_Q8GTC0	Glutathione transferase F3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8GTC0_WHEAT	2	3	35	1.16	0.19	0.00
UniRef100_A4GSN7	Ferritin <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4GSN7_WHEAT	3	3	4	1.14	0.15	0.00
UniRef100_D1MBU0	Type II metacaspase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D1MBU0_WHEAT	5	5	39	1.14	0.11	0.00
RFL_Contig3391	_pep_3:87_767	2	2	16	1.13	0.06	0.00
UniRef100_A7XDG5	Peptidyl_prolyl cis_trans isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7XDG5_WHEAT	2	2	15	1.13	0.08	0.00
RFL_Contig2286	_pep_2:107_1555	8	12	74	1.13	0.07	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig2640	_pep_2:101_1549	10	13	40	1.13	0.07	0.00
UniRef100_A9U8G5	Alcohol dehydrogenase ADH1D <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A9U8G5_WHEAT	9	15	80	1.12	0.08	0.00
RFL_Contig1157	_pep_1:55_1080	6	7	57	1.11	0.13	0.00
gi_219914282_emb_CAW74910.1_	unnamed protein product (<i>Triticum aestivum</i>)	4	5	65	1.10	0.04	0.00
UniRef100_B8YEL1	Ferredoxin_nitrite reductase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B8YEL1_WHEAT	5	7	34	1.10	0.08	0.04
UniRef100_O04437	Glutathione S_transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = GSTZ_WHEAT	2	2	10	1.10	0.16	0.04
UniRef100_H8ZI06	HSP70 (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H8ZI06_WHEAT	4	5	22	1.10	0.07	0.00
UniRef100_A9U8G1	Alcohol dehydrogenase ADH2D <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A9U8G1_WHEAT	6	9	43	1.09	0.10	0.00
RFL_Contig3621	_pep_3:84_2090	6	6	20	1.09	0.06	0.00
gi_359828768_gb_AEV76986.1_	beta_glucosidase 4_partial (<i>Triticum aestivum</i>)	2	2	7	1.08	0.18	0.00
RFL_Contig3509	_pep_2:197_1150	2	2	15	1.08	0.17	0.04
RFL_Contig2792	_pep_2:62_1270	2	2	14	1.07	0.14	0.00
UniRef100_D8L9G6	Phosphorylase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9G6_WHEAT	5	6	9	1.06	0.14	0.04
UniRef100_Q6RUJ1	Glutamine synthetase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q6RUJ1_WHEAT	5	6	20	1.05	0.16	0.01
UniRef100_D8L9B3	Putative PDI_like protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9B3_WHEAT	6	9	84	1.05	0.10	0.00
RFL_Contig4839	_pep_3:18_1208	4	5	22	1.05	0.13	0.01
RFL_Contig37	_pep_3:117_1193	7	9	49	1.05	0.05	0.01
gi_296523708_emb_CBM36708.1_	unnamed protein product (<i>Triticum aestivum</i>)	6	6	11	1.05	0.10	0.00
gi_291047854_emb_CBK51440.1_	unnamed protein product (<i>Triticum aestivum</i>)	3	3	4	1.04	0.09	0.05
UniRef100_O82073	Sucrose synthase type I <i>n</i> = 2 Tax = <i>Triticum aestivum</i> RepID = O82073_WHEAT	24	50	419	1.04	0.03	0.00
gi_257667483_emb_CBD31968.1_	unnamed protein product (<i>Triticum aestivum</i>)	2	3	26	1.04	0.18	0.00
RFL_Contig3777	_pep_2:104_1627	2	3	11	1.04	0.16	0.00
UniRef100_P20973	Ubiquitin_activating enzyme E1 1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = UBE11_WHEAT	10	12	71	1.04	0.07	0.00
RFL_Contig2547	_pep_2:83_1108	6	8	80	1.03	0.07	0.00
UniRef100_Q8VWM9	Fructose_bisphosphate aldolase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8VWM9_WHEAT	9	15	110	1.03	0.06	0.05
RFL_Contig3134	_pep_3:120_1937	5	5	19	1.03	0.11	0.00
UniRef100_F2CQ27	Predicted protein <i>n</i> = 2 Tax = <i>Triticeae</i> RepID = F2CQ27_HORVD	4	4	32	1.03	0.03	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_C1J959	Fructose_bisphosphate aldolase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C1J959_WHEAT	13	21	132	1.03	0.05	0.04
RFL_Contig5913	_pep_1:166_957	5	6	47	1.02	0.16	0.03
RFL_Contig1280	_pep_3:195_1787	3	5	33	1.02	0.14	0.00
UniRef100_P41378	Eukaryotic initiation factor 4A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = IF4A_WHEAT	7	8	15	1.01	0.05	0.00
UniRef100_Q401N7	Aspartic proteinase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q401N7_WHEAT	6	7	27	1.01	0.08	0.03
Decrease							
RFL_Contig2907	_pep_2:905_1681	4	4	14	0.56	0.06	0.00
UniRef100_H2KXF7	Pathogenesis_related protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H2KXF7_WHEAT	4	5	17	0.61	0.10	0.00
UniRef100_H9CWE9	12_oxo_phytodienoic acid reductase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H9CWE9_WHEAT	2	2	9	0.73	0.17	0.03
UniRef100_Q8GTB9	Glutathione transferase F4 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8GTB9_WHEAT	2	3	16	0.76	0.07	0.00
UniRef100_D8LAL9	Hydroquinone glucosyltransferase_putative_expressed <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8LAL9_WHEAT	2	2	15	0.77	0.17	0.02
UniRef100_Q43199	Adenine phosphoribosyltransferase 1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = APT1_WHEAT	4	5	36	0.78	0.06	0.00
RFL_Contig2919	_pep_2:80_598	3	3	7	0.79	0.04	0.00
UniRef100_P38076	Cysteine synthase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CYSK_WHEAT	8	9	90	0.79	0.06	0.00
UniRef100_P59232	Ubiquitin_40S ribosomal protein S27a_2 <i>n</i> = 18 Tax = Eukaryota RepID = R27AB_ARATH	4	8	63	0.79	0.08	0.00
UniRef100_A1YE34	Ribosomal protein L3_B2 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A1YE34_WHEAT	6	9	23	0.79	0.05	0.00
RFL_Contig2772	_pep_3:60_4160	6	6	18	0.80	0.10	0.01
UniRef100_A1YE31	Ribosomal protein L3_A3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A1YE31_WHEAT	8	12	72	0.80	0.05	0.00
RFL_Contig3907	_pep_3:174_1214	2	2	11	0.80	0.11	0.00
UniRef100_B5B3P8	Pathogenesis related protein 10 <i>n</i> = 2 Tax = commelinids RepID = B5B3P8_WHEAT	3	3	13	0.80	0.12	0.00
UniRef100_P04464	Calmodulin <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CALM_WHEAT	4	4	17	0.80	0.06	0.00
UniRef100_P43650	Putative ATP synthase protein YMF19 <i>n</i> = 2 Tax = Triticeae RepID = YMF19_WHEAT	3	3	19	0.80	0.06	0.00
UniRef100_Q8RW03	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW03_WHEAT	5	5	17	0.81	0.07	0.00
UniRef100_Q08G39	Ribosomal protein L3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q08G39_WHEAT	8	11	53	0.81	0.05	0.00
UniRef100_Q8LL15	Glutathione_S_transferase 28e45 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8LL15_WHEAT	3	3	31	0.81	0.13	0.00
gi_295422149_emb_CBL74911.1_	unnamed protein product (<i>Triticum aestivum</i>)	6	7	39	0.81	0.06	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig1200	_pep_1:70_1410	2	2	3	0.81	0.10	0.00
UniRef100_Q517L5	60S ribosomal protein L36 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q517L5_WHEAT	2	2	17	0.82	0.14	0.00
UniRef100_A4K4Y7	Alpha tubulin_4D <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Y7_WHEAT	12	17	162	0.82	0.06	0.00
UniRef100_Q7XYE4	40S ribosomal protein S9 (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7XYE4_WHEAT	2	3	26	0.82	0.02	0.00
UniRef100_Q9ZRA8	Tubulin beta_5 chain <i>n</i> = 4 Tax = Pooideae RepID = TBB5_WHEAT	13	18	183	0.82	0.05	0.00
RFL_Contig2002	_pep_2:95_1294	2	2	3	0.83	0.18	0.05
gi_295415558_emb_CBL76034.1	unnamed protein product (<i>Triticum aestivum</i>)	8	10	97	0.83	0.06	0.00
UniRef100_Q8RW02	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW02_WHEAT	4	5	38	0.83	0.07	0.00
gi_218389472_emb_CAV25023.1	unnamed protein product (<i>Triticum aestivum</i>)	2	2	9	0.83	0.08	0.00
gi_295422633_emb_CBL75153.1	unnamed protein product (<i>Triticum aestivum</i>)	5	5	8	0.83	0.06	0.00
gi_295415556_emb_CBL76033.1	unnamed protein product (<i>Triticum aestivum</i>)	8	10	74	0.83	0.07	0.00
UniRef100_Q515K7	Small GTP_binding protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q515K7_WHEAT	7	8	38	0.83	0.07	0.00
RFL_Contig3884	_pep_1:124_2052	3	3	9	0.84	0.09	0.01
UniRef100_I0JTW5	Eukaryotic translation initiation factor 3 subunit A_putative_expressed <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = I0JTW5_WHEAT	2	2	3	0.84	0.14	0.00
RFL_Contig2682	_pep_2:98_1111	13	17	138	0.84	0.04	0.00
UniRef100_A4K4Y1	Alpha tubulin_2A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Y1_WHEAT	12	19	192	0.84	0.06	0.00
UniRef100_Q9ZRR5	Tubulin alpha_3 chain <i>n</i> = 3 Tax = Triticeae RepID = TBA3_HORVU	12	18	191	0.84	0.06	0.00
gi_227295766_emb_CAY03053.1	unnamed protein product (<i>Triticum aestivum</i>)	3	4	15	0.84	0.07	0.00
UniRef100_Q332R4	ATP synthase subunit alpha <i>n</i> = 3 Tax = Triticeae RepID = Q332R4_WHEAT	13	16	127	0.85	0.04	0.00
RFL_Contig501	_pep_1:91_1434	12	18	111	0.85	0.05	0.01
UniRef100_A4K4Z0	Alpha tubulin_5B <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Z0_WHEAT	4	7	72	0.85	0.07	0.00
RFL_Contig2895	_pep_1:73_1257	6	6	40	0.85	0.05	0.00
UniRef100_A0MA43	Ran_binding protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A0MA43_WHEAT	2	2	12	0.85	0.17	0.05
RFL_Contig3526	_pep_1:115_1941	9	11	92	0.85	0.06	0.00
UniRef100_A4K4Z3	Alpha tubulin_1A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A4K4Z3_WHEAT	10	16	161	0.86	0.07	0.00
UniRef100_B4F6F0	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6F0_WHEAT	9	12	75	0.86	0.08	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_Q8RW00	Glutathione transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8RW00_WHEAT	4	5	32	0.86	0.09	0.00
RFL_Contig2924	_pep_1:124_831	3	3	21	0.86	0.09	0.00
UniRef100_Q9ZRA7	Beta_tubulin 6 (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9ZRA7_WHEAT	8	13	79	0.86	0.06	0.00
UniRef100_B4F6E7	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E7_WHEAT	12	17	156	0.86	0.06	0.00
gi_226885722_emb_CAX86813.1	unnamed protein product (<i>Triticum aestivum</i>)	2	2	16	0.86	0.07	0.00
UniRef100_Q9ZRA9	Tubulin beta_4 chain <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = TBB4_WHEAT	13	20	202	0.86	0.05	0.00
UniRef100_B4F6E6	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E6_WHEAT	12	17	158	0.86	0.07	0.00
UniRef100_Q9ZRB0	Tubulin beta_3 chain <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = TBB3_WHEAT	13	21	190	0.86	0.05	0.00
gi_259662493_emb_CBG02800.1	unnamed protein product (<i>Triticum aestivum</i>)	4	4	21	0.86	0.06	0.00
gi_259662491_emb_CBG02799.1	unnamed protein product (<i>Triticum aestivum</i>)	4	4	11	0.86	0.06	0.00
RFL_Contig478	_pep_1:70_783	4	4	26	0.87	0.06	0.00
RFL_Contig1627	_pep_1:127_1104	3	3	12	0.87	0.10	0.00
RFL_Contig3205	_pep_1:145_2199	3	4	7	0.87	0.04	0.00
RFL_Contig259	_pep_3:63_1403	17	24	207	0.87	0.03	0.00
UniRef100_B4F6E5	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6E5_WHEAT	10	14	107	0.87	0.07	0.00
UniRef100_C6ETB5	Class III peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C6ETB5_WHEAT	2	4	16	0.87	0.05	0.01
RFL_Contig2129	_pep_1:19_1374	2	3	21	0.87	0.10	0.00
RFL_Contig2512	_pep_3:63_794	3	3	14	0.88	0.07	0.04
UniRef100_Q0PMD7	J_domain protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q0PMD7_WHEAT	3	3	7	0.88	0.05	0.00
RFL_Contig2839	_pep_3:132_584	2	3	8	0.88	0.14	0.00
RFL_Contig5814	_pep_3:78_2375	20	33	311	0.88	0.05	0.00
UniRef100_B4F6F2	Root peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B4F6F2_WHEAT	10	13	135	0.88	0.07	0.00
RFL_Contig2680	_pep_1:142_753	3	3	4	0.88	0.06	0.00
UniRef100_A7J2I2	Plasma membrane intrinsic protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7J2I2_WHEAT	6	8	55	0.88	0.05	0.00
UniRef100_F4Y589	Heat shock protein 90 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F4Y589_WHEAT	4	5	12	0.89	0.07	0.00
UniRef100_P51823	ADP_ribosylation factor 2 <i>n</i> = 6 Tax = Poaceae RepID = ARF2_ORYSJ	4	6	66	0.89	0.07	0.00
RFL_Contig4822	_pep_3:99_1934	2	2	2	0.89	0.21	0.05

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig1072	_pep_1:223_2271	6	6	24	0.89	0.08	0.01
UniRef100_A7J211	Plasma membrane intrinsic protein <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A7J211_WHEAT	5	7	32	0.89	0.05	0.00
UniRef100_D8L9U6	Eukaryotic translation initiation factor_putative_ expressed <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D8L9U6_WHEAT	5	6	22	0.89	0.09	0.00
UniRef100_C6ETB6	Class III peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C6ETB6_WHEAT	3	6	23	0.89	0.05	0.01
RFL_Contig3253	_pep_1:121_996	6	7	50	0.89	0.04	0.00
gi_330728034_emb_CCA64660.1	unnamed protein product (<i>Triticum aestivum</i>)	4	5	41	0.89	0.10	0.02
UniRef100_Q6IY71	Mitochondrial ATP synthase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q6IY71_WHEAT	5	5	28	0.89	0.09	0.01
RFL_Contig2992	_pep_3:111_908	2	2	3	0.89	0.06	0.02
RFL_Contig4724	_pep_3:228_3104	9	11	39	0.90	0.05	0.01
RFL_Contig3855	_pep_3:126_1601	9	9	42	0.90	0.04	0.00
RFL_Contig1865	_pep_2:104_901	8	10	59	0.90	0.05	0.01
UniRef100_F4Y592	Heat shock protein 90 <i>n</i> = 2 Tax = <i>Triticum</i> RepID = F4Y592_WHEAT	9	13	39	0.90	0.04	0.00
gi_227248192_emb_CAY07658.1	unnamed protein product (<i>Triticum aestivum</i>)	6	8	61	0.90	0.06	0.00
RFL_Contig5048	_pep_2:134_1606	2	2	2	0.90	0.03	0.01
RFL_Contig3532	_pep_3:99_1424	8	8	9	0.90	0.03	0.03
UniRef100_Q9LRJ0	Glucose_6_phosphate 1_dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9LRJ0_WHEAT	10	11	51	0.90	0.07	0.00
RFL_Contig3581	_pep_2:92_883	3	3	16	0.90	0.09	0.01
RFL_Contig1629	_pep_2:140_1102	7	11	66	0.90	0.04	0.00
gi_313103631_pdb_3IZ6_D	Chain D_ Localization Of The Small Subunit Ribosomal Proteins Into A 5.5 A Cryo_Em Map of <i>Triticum aestivum</i> Translating 80s Ribosome	4	4	27	0.90	0.07	0.01
gi_313103629_pdb_3IZ6_A	Chain A_ Localization Of The Small Subunit Ribosomal Proteins Into A 5.5 A Cryo_Em Map of <i>Triticum aestivum</i> Translating 80s Ribosome	6	6	31	0.91	0.04	0.00
RFL_Contig5445	_pep_1:130_1044	3	3	22	0.91	0.06	0.00
UniRef100_F4Y5B2	Heat shock protein 90 <i>n</i> = 5 Tax = Triticeae RepID = F4Y5B2_AEGTA	13	19	119	0.91	0.04	0.00
UniRef100_Q03387	Eukaryotic initiation factor iso_4F subunit p82_34 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = IF41_WHEAT	13	15	71	0.91	0.05	0.00
gi_257672781_emb_CBD34794.1	unnamed protein product (<i>Triticum aestivum</i>)	3	3	25	0.91	0.09	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig3279	_pep_2:122_1471	5	6	32	0.91	0.06	0.00
UniRef100_Q41591	Voltage dependent anion channel (VDAC) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q41591_WHEAT	5	5	21	0.91	0.05	0.02
RFL_Contig5794	_pep_2:89_2389	16	26	238	0.91	0.05	0.00
UniRef100_Q9M7C2	Plasma membrane intrinsic protein 3 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9M7C2_WHEAT	3	4	6	0.91	0.16	0.04
UniRef100_C3UZE7	Germin_like protein 2 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C3UZE7_WHEAT	2	2	4	0.91	0.24	0.04
UniRef100_F8S6U4	Pathogenesis_related protein 1_14 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6U4_WHEAT	3	4	24	0.91	0.12	0.00
RFL_Contig6069	_pep_2:41_1012	4	5	31	0.91	0.07	0.00
RFL_Contig2656	_pep_2:95_1369	5	5	15	0.91	0.10	0.02
UniRef100_Q7XY23	Cyc07 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7XY23_WHEAT	5	7	35	0.91	0.05	0.00
UniRef100_F4Y593	Heat shock protein 90 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F4Y593_WHEAT	10	12	71	0.92	0.04	0.00
UniRef100_Q9ZR33	Glycosyltransferase 75 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9ZR33_WHEAT	10	16	138	0.92	0.05	0.02
RFL_Contig1308	_pep_3:153_1403	4	5	53	0.92	0.08	0.00
UniRef100_F4Y595	Heat shock protein 90 <i>n</i> = 3 Tax = <i>Triticum</i> RepID = F4Y595_WHEAT	13	21	63	0.92	0.04	0.00
RFL_Contig5919	_pep_2:74_865	6	9	93	0.92	0.03	0.00
UniRef100_P83970	Plasma membrane ATPase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = PMA1_WHEAT	21	27	185	0.92	0.03	0.00
RFL_Contig4608	_pep_2:86_1918	10	14	101	0.92	0.03	0.00
RFL_Contig3501	_pep_2:206_1009	3	3	26	0.92	0.06	0.01
UniRef100_Q1XIR9	Beta_glucosidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1XIR9_WHEAT	8	9	73	0.92	0.09	0.00
UniRef100_Q8GTB7	Glutathione transferase F1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8GTB7_WHEAT	3	4	10	0.92	0.10	0.02
UniRef100_Q8S4X5	Aquaporin PIP1 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q8S4X5_WHEAT	2	3	21	0.92	0.18	0.01
UniRef100_Q5I7L0	60S ribosomal protein L18 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q5I7L0_WHEAT	4	5	23	0.92	0.07	0.01
RFL_Contig3135	_pep_3:48_797	5	6	25	0.93	0.04	0.00
UniRef100_Q41583	Initiation factor (Iso)4f p82 subunit <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q41583_WHEAT	12	14	60	0.93	0.05	0.00
UniRef100_Q1W681	Vacuolar proton_ATPase subunit A <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1W681_WHEAT	17	21	126	0.93	0.04	0.00
RFL_Contig2911	_pep_2:110_1441	8	8	48	0.93	0.04	0.00
UniRef100_C9EF64	Dehydroascorbate reductase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C9EF64_WHEAT	8	9	61	0.93	0.03	0.00
RFL_Contig3954	_pep_3:162_1994	11	14	111	0.93	0.03	0.00

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
UniRef100_Q41629	ADP_ATP carrier protein 1_mitochondrial <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = ADT1_WHEAT	8	12	105	0.93	0.06	0.02
UniRef100_Q9SP56	Glutathione S_transferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9SP56_WHEAT	4	6	63	0.93	0.08	0.04
gi_257659932_emb_CBD33996.1_	unnamed protein product (<i>Triticum aestivum</i>)	4	6	63	0.93	0.08	0.04
RFL_Contig3640	_pep_1:91_3054	7	8	40	0.93	0.08	0.00
RFL_Contig5920	_pep_1:85_912	8	11	52	0.93	0.05	0.04
gi_219914284_emb_CAW74911.1_	unnamed protein product (<i>Triticum aestivum</i>)	8	11	65	0.93	0.05	0.00
UniRef100_G1FFN0	Glutamine synthetase <i>n</i> = 2 Tax = Triticeae RepID = G1FFN0_9POAL	6	9	40	0.93	0.11	0.01
UniRef100_A9LIN4	Malic enzyme <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = A9LIN4_WHEAT	9	10	68	0.93	0.06	0.01
UniRef100_C6ETA8	Class III peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C6ETA8_WHEAT	3	4	10	0.93	0.05	0.00
RFL_Contig4067	_pep_2:110_1627	8	9	81	0.93	0.06	0.00
RFL_Contig3580	_pep_3:9_563	2	3	34	0.94	0.08	0.00
UniRef100_C6ES53	Class III peroxidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = C6ES53_WHEAT	4	6	18	0.94	0.05	0.00
UniRef100_Q7XYD5	Acidic ribosomal protein (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q7XYD5_WHEAT	4	6	71	0.94	0.08	0.00
RFL_Contig4097	_pep_3:123_1553	6	9	22	0.94	0.07	0.05
RFL_Contig3158	_pep_2:62_631	7	8	79	0.94	0.05	0.00
RFL_Contig3111	_pep_2:80_682	4	5	51	0.94	0.11	0.00
gi_315113252_pdb_3IZR_F	Chain F_ Localization Of The Large Subunit Ribosomal Proteins Into A 5.5 A Cryo_Em Map of <i>Triticum aestivum</i> Translating 80s Ribosome	3	3	8	0.94	0.05	0.00
RFL_Contig4002	_pep_3:30_1007	2	3	13	0.94	0.12	0.01
UniRef100_B9A8E3	Protein disulfide isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B9A8E3_WHEAT	13	17	135	0.95	0.04	0.01
RFL_Contig3538	_pep_1:112_1083	10	10	76	0.95	0.03	0.00
RFL_Contig3549	_pep_1:88_426	4	4	56	0.95	0.09	0.00
UniRef100_E3KLJ3	Calmodulin <i>n</i> = 2 Tax = Eukaryota RepID = E3KLJ3_PUCGT	2	2	3	0.95	0.22	0.00
gi_296525616_emb_CBM37260.1_	unnamed protein product (<i>Triticum aestivum</i>)	6	7	35	0.95	0.07	0.00
UniRef100_Q41534	ATP synthase subunit beta <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q41534_WHEAT	19	42	284	0.95	0.03	0.01
UniRef100_H9ZWY2	Plastid 3_phosphoglycerate kinase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H9ZWY2_WHEAT	5	5	41	0.95	0.07	0.00
RFL_Contig3766	_pep_1:112_2550	12	15	86	0.95	0.04	0.03

Table S3. Cont.

PROTEIN ID	DESCRIPTION	Matched Peptides	FRAMES	HITS	Ratio	SD	p-Value
RFL_Contig3291	_pep_3:81_1841	14	16	91	0.95	0.05	0.02
RFL_Contig3722	_pep_3:144_1124	2	2	21	0.95	0.06	0.00
UniRef100_Q1XH05	Beta_glucosidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1XH05_WHEAT	9	9	66	0.95	0.08	0.00
RFL_Contig3927	_pep_3:123_1715	7	7	38	0.95	0.05	0.01
RFL_Contig2067	_pep_1:118_1539	5	5	25	0.95	0.14	0.02
RFL_Contig4151	_pep_3:126_5297	32	34	203	0.96	0.03	0.00
RFL_Contig3262	_pep_3:150_1172	2	4	22	0.96	0.18	0.03
RFL_Contig308	_pep_1:73_1512	14	23	146	0.96	0.05	0.00
UniRef100_B2BA41	Vacuolar proton_ATPase C subunit <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = B2BA41_WHEAT	5	8	65	0.96	0.07	0.00
UniRef100_F8S6V1	Pathogenesis_related protein 1_21 <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = F8S6V1_WHEAT	3	4	26	0.96	0.16	0.00
gi_257672153_emb_CBD32168.1	unnamed protein product (<i>Triticum aestivum</i>)	3	11	95	0.96	0.06	0.04
gi_257672155_emb_CBD32169.1	unnamed protein product (<i>Triticum aestivum</i>)	3	11	117	0.96	0.06	0.04
UniRef100_Q36813	NADH dehydrogenase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q36813_WHEAT	4	4	25	0.96	0.07	0.04
UniRef100_Q1PBI3	Glucose_6_phosphate isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q1PBI3_WHEAT	4	4	34	0.96	0.02	0.00
UniRef100_Q9FS79	Triosephosphate isomerase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q9FS79_WHEAT	9	14	100	0.96	0.07	0.02
UniRef100_Q53UC8	Delta1_pyrroline_5_carboxylate synthetase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = Q53UC8_WHEAT	5	5	29	0.97	0.08	0.05
UniRef100_D5MTD9	Benzoxazinone:UDP_Glc glucosyltransferase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D5MTD9_WHEAT	5	5	14	0.97	0.11	0.02
RFL_Contig3604	_pep_2:149_973	3	3	28	0.97	0.09	0.00
UniRef100_P55313	Catalase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = CATA2_WHEAT	9	9	47	0.97	0.06	0.04
RFL_Contig6066	_pep_3:69_2492	15	15	111	0.98	0.04	0.00
UniRef100_D5MTF8	Beta_glucosidase <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = D5MTF8_WHEAT	11	12	89	0.98	0.08	0.00
RFL_Contig3091	_pep_3:108_1586	11	11	57	0.98	0.06	0.05
RFL_Contig1587	_pep_2:131_1375	13	15	83	0.99	0.04	0.00
UniRef100_H9ZWY1	Plastid_3_phosphoglycerate kinase (Fragment) <i>n</i> = 1 Tax = <i>Triticum aestivum</i> RepID = H9ZWY1_WHEAT	4	4	10	0.99	0.09	0.00
RFL_Contig4165	_pep_1:100_963	4	4	22	0.99	0.12	0.05

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