

Additional file 1

Regulation of Zn and Fe transporters by the *GPC1* gene during early wheat monocarpic senescence

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Figures S1 to S10.

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Figure S1. Relative chlorophyll content of flag leaves taken from (a) TAU-2012, (b) NY-2012 and (c) NY-2013 experiments.

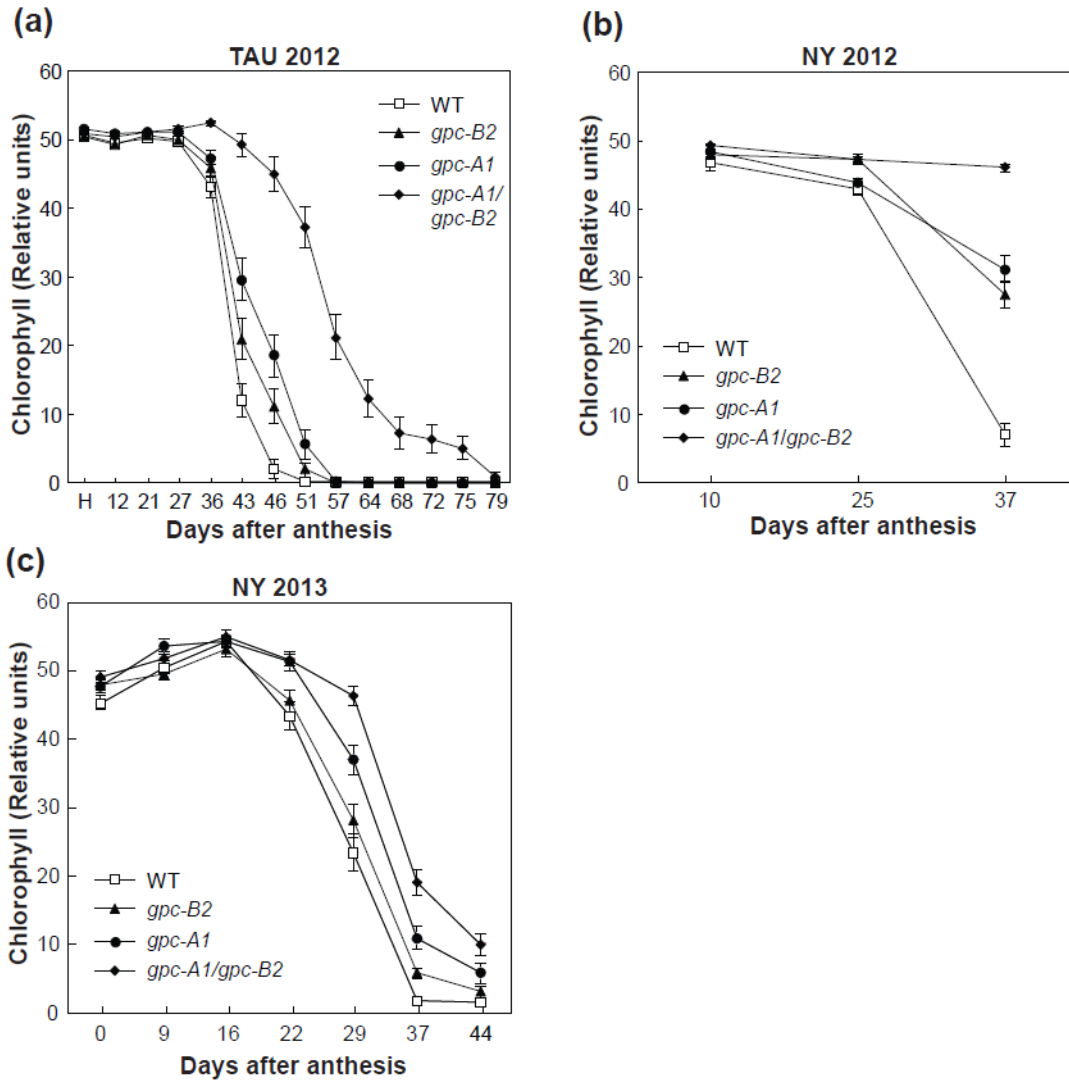


Figure S2. Spike and grain phenotypes in tetraploid *GPC* mutants. (a) Thousand kernel weight from three field experiments. Two-way factorial ANOVA was performed for TKW including location and genotype ($P=0.02$) (b) Dry spike weight at three timepoints from the UCD 2012 experiment. *** = $P<0.001$, difference when compared to WT control sample from Dunnett's test. UCD = UC Davis 2012 experiment, TAU = Tel Aviv University 2012 experiment, NY = Newe Ya'ar research center 2013 experiment. DAA = Days after anthesis.

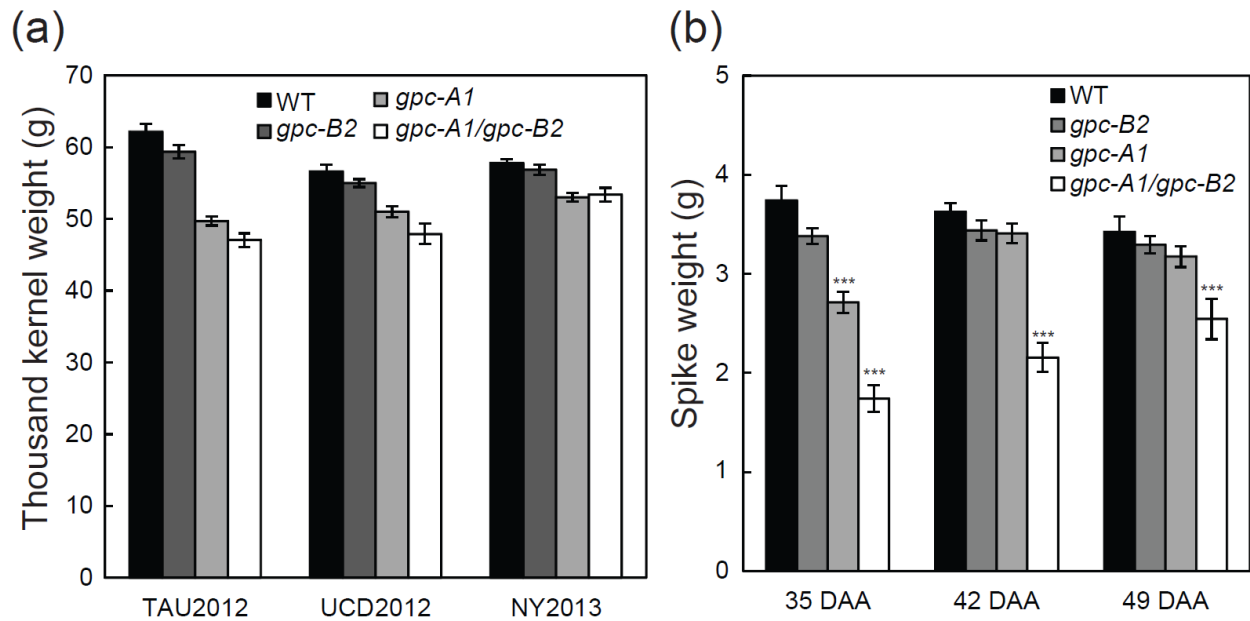


Figure S3. Phenotype of WT, *gpc-A1* and *gpc-A1/gpc-B2* TILLING mutants at 22 DAA (a-c) and at 60 DAA (d-f). In all panels, order of plants from left to right is WT, *gpc-A1*, *gpc-A1/gpc-B2*.

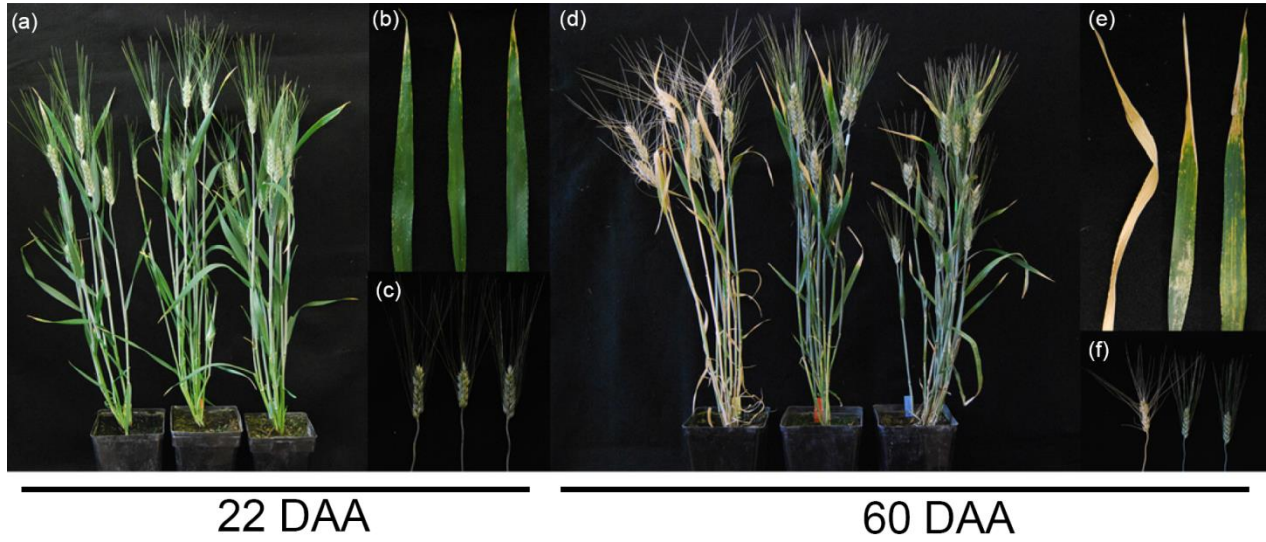


Figure S4. Principal component analyses of biological samples according to normalized expression values per locus of all genes by time point (a-c) and genotype (d-f).

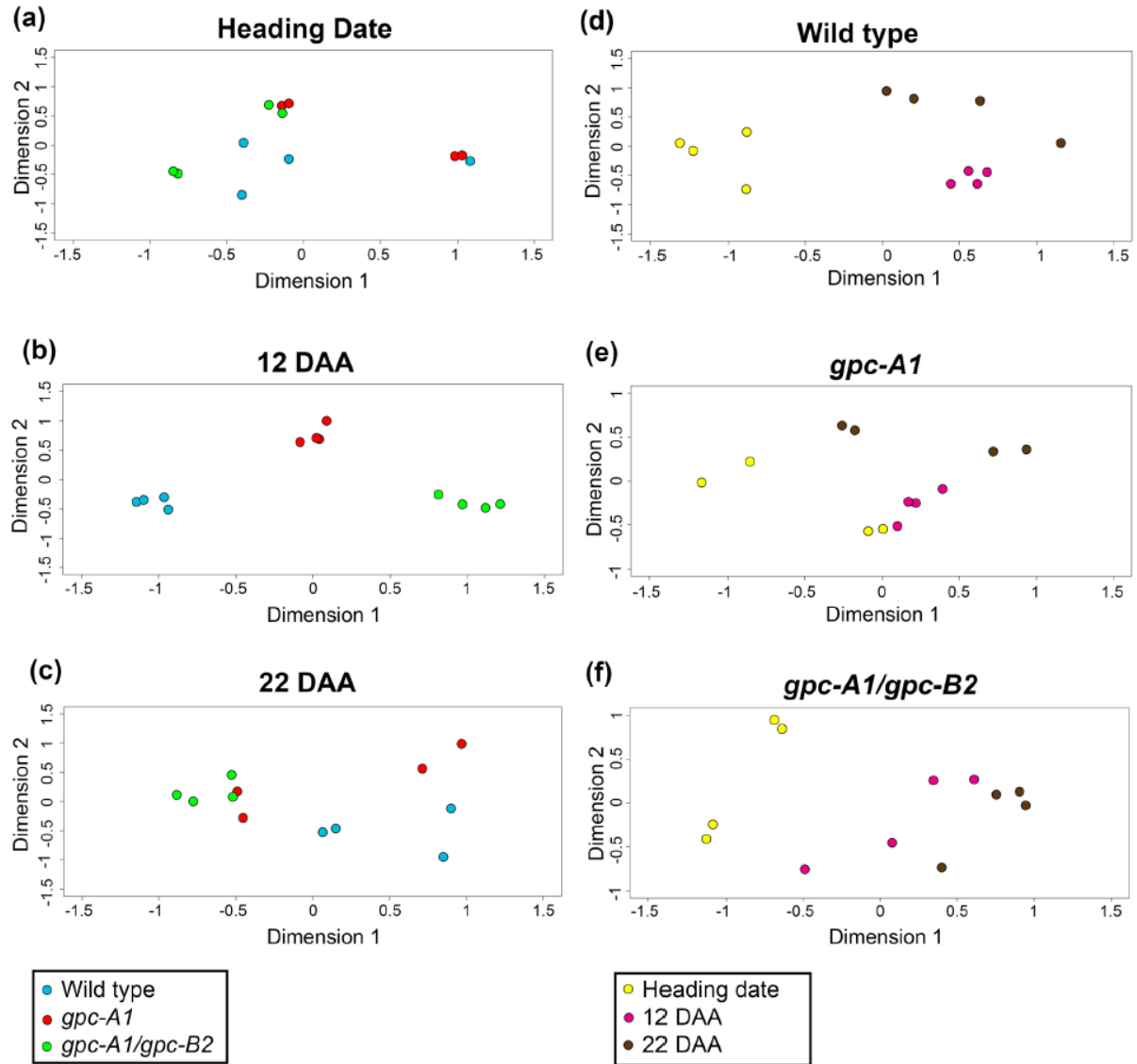


Figure S5. Relative expression of *GPC* genes in WT, *gpc-A1* and *gpc-A1/gpc-B2* lines. Expression presented as RPKM from four biological replicates \pm SE of normalized reads mapping to the loci representing each *GPC* gene.

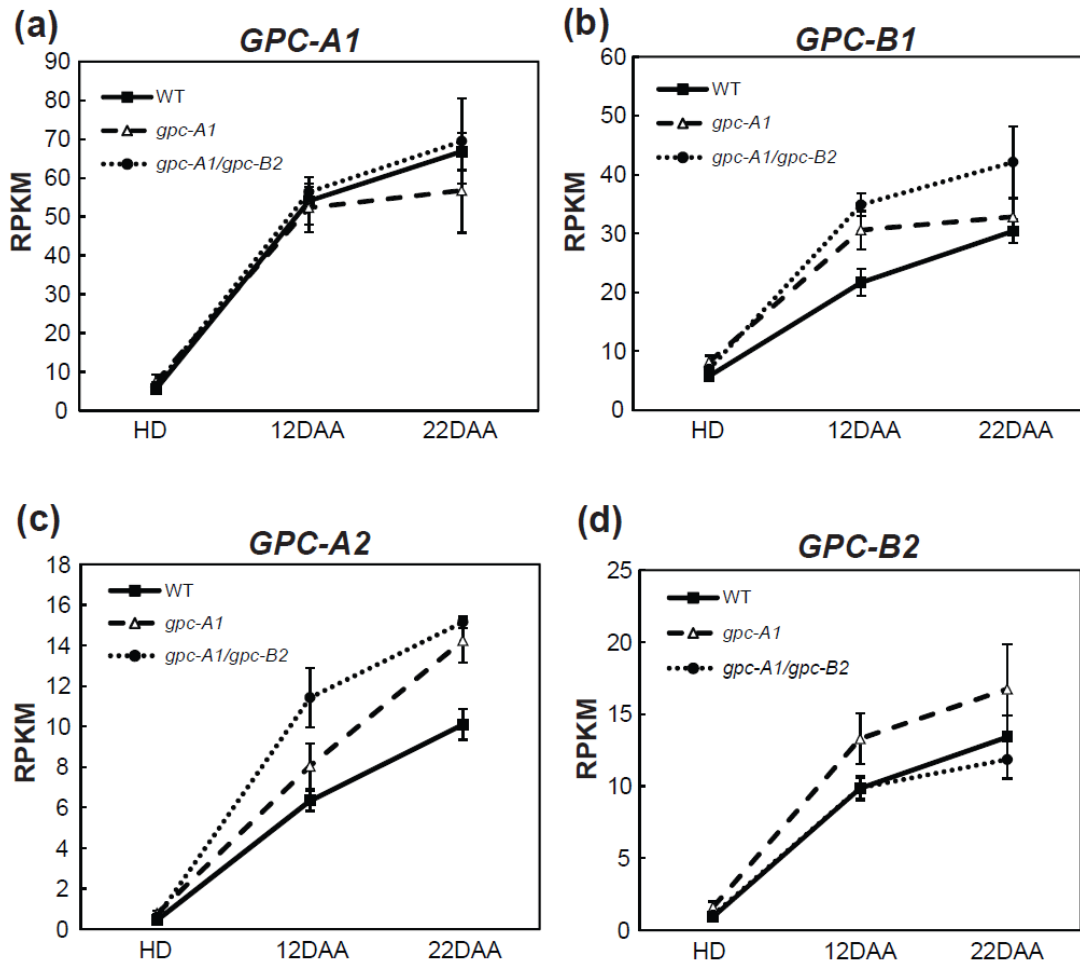


Figure S6. HMA phylogeny. Rice protein IDs (blue): OsHMA1 (NP_001058417.1), OsHMA2 (BAM36049.1), OsHMA3 (BAJ25742.1). Wheat protein IDs (red): TaHMA1 (Traes_7BL_041308E74), TaHMA1-like (Traes_5AL_C89EEBE50), TaHMA2 (Traes_7AL_8304348B7), TaHMA2-like (Traes_7AL_6AE850114), TaHMA3 (Traes_5BL_D6C3DC326). Arrows indicate up or downregulation during senescence in WT plants. * denotes differential expression in at least one *GPC* mutant genotype.

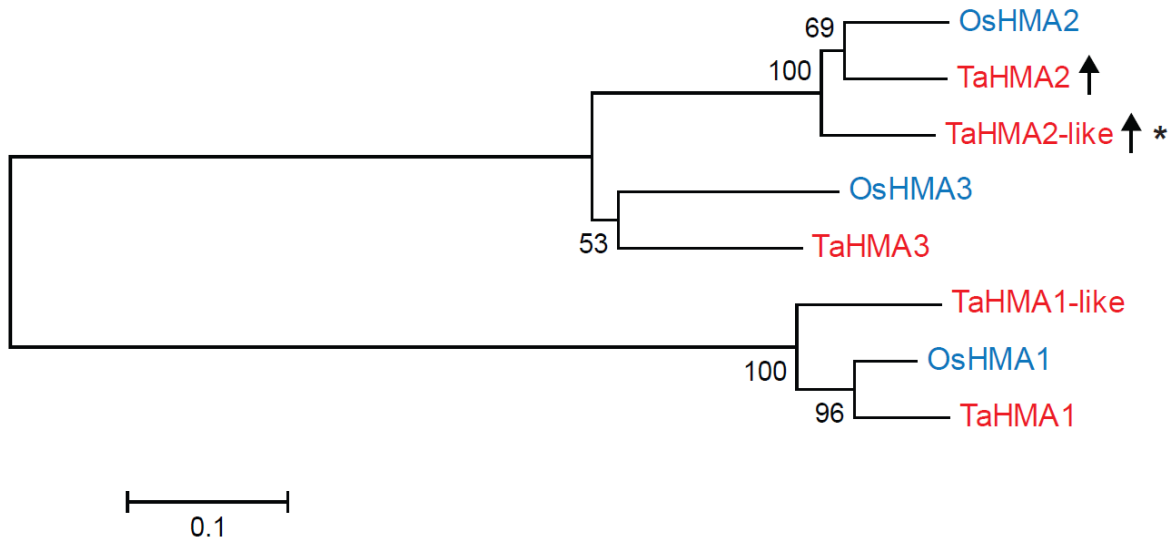


Figure S7. ZIFL phylogeny. Rice protein IDs (blue): OsZIFL1 (NP_001042690.1), OsZIFL2 (NP_001042748.1), OsZIFL3 (BAG89474), OsZIFL4 (NP_001065681.1), OsZIFL5 (NP_001065682.1), OsZIFL6 (ABA91327.1), OsZIFL7 (ABG22349.1), OsZIFL8 (ABA91341.1), OsZIFL9 (ABA95719), OsZIFL10 (NP_001066084.1), OsZIFL11 (NP_001066085.1), OsZIFL12 (ABG21873.1), OsZIFL13 (ABA95731.1). Wheat protein IDs (red): TaZIFL1 (Traes_3AS_C25151458), TaZIFL1-like (Traes_3AS_02DE247DA), TaZIFL2 (Traes_5BL_A0B9DE62E), TaZIFL3 (Traes_4BS_1DCF82CB7), TaZIFL7 (Traes_5AL_37BFFFD9E), TaZIFL8 (Traes_4AL_5C7A4DA54), TaZIFL9 (Traes_5AL_0599F7BC5). TaZIFL2-like1 was not included in the phylogeny. Arrows indicate up or downregulation during senescence in WT plants. * denotes differential expression in at least one *GPC* mutant genotype.

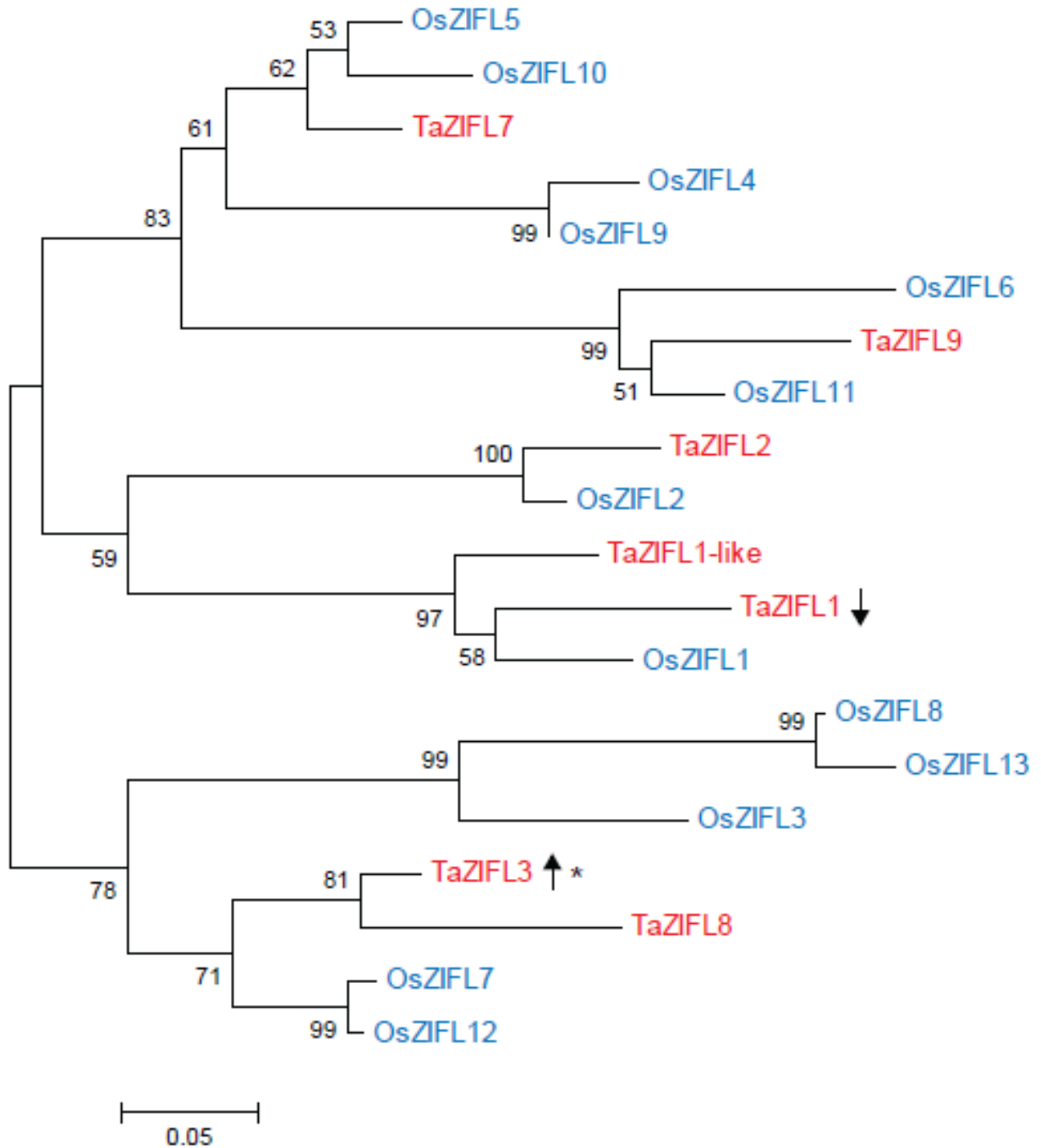


Figure S8. YSL phylogeny. Rice protein IDs (blue): OsYSL1 (NP_001042539.1), OsYSL2 (BAD90812.1), OsYSL3 (BAE91883.1), OsYSL4 (BAE91884.1), OsYSL5 (BAE91885.1), OsYSL6 (BAE91886.1), OsYSL7 (BAE91887.1), OsYSL8 (BAE91888.1), OsYSL9 (BAE91889.1), OsYSL10 (BAE91890.1), OsYSL11 (BAE91891.1), OsYSL12 (BAE91892.1), OsYSL13 (BAE44204.1), OsYSL14 (BAE44205.1), OsYSL15 (BAE91893.1), OsYSL16 (BAE91894.1), OsYSL17 (BAE91895.1), OsYSL18 (BAE91896.1). Wheat protein IDs (red): TaYSL1 (Traes_3B_17BC3E1E2), TaYSL2 (Traes_6BL_3DD0BA741), TaYSL6 (Traes_2BL_0CBCC13AD), TaYSL9 (Traes_2AL_CFCA01C76), TaYSL10 (Traes_6AL_5642D5B44), TaYSL11 (Traes_2BL_68E0CA743), TaYSL12 (Traes_2BL_2BE05F104), TaYSL13 (Traes_2AL_F707FF2C3), TaYSL13-like (Traes_2BL_A14EA5AE4), TaYSL14 (Traes_6AL_7FB45D4DE), TaYSL15 (Traes_6AL_E36CFCE64), TaYSL15-like (Traes_1BL_CA93E6359), TaYSL16 (Traes_2BL_4A1181B731), TaYSL18 (Traes_2BL_6C5206B6D). Arrows indicate up or downregulation during senescence in WT plants. * denotes differential expression in at least one *GPC* mutant genotype.

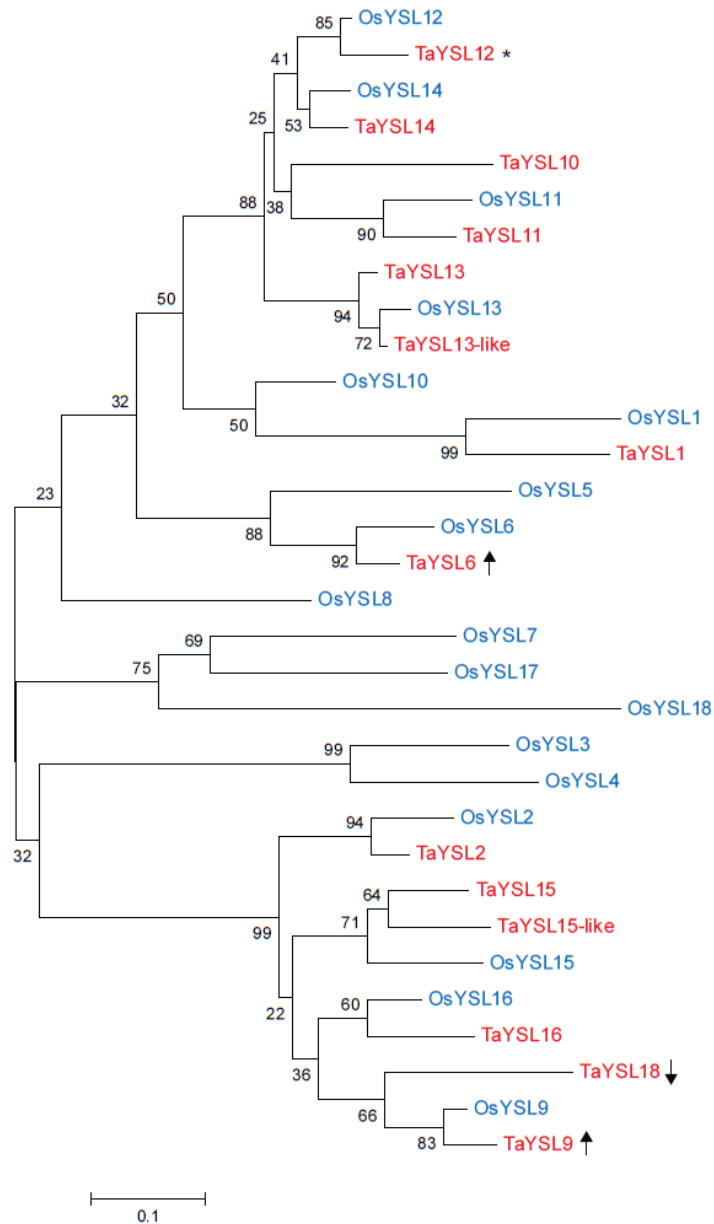


Fig. S9. ZIP phylogeny. Rice protein IDs (Blue): OsIRT1 (NP_001050853.1), OsIRT2 (ABF98082.1), OsZIP1 (NP_001045540.1), OsZIP2 (NP_001050351.1), OsZIP3 (NP_001053851.1), OsZIP4 (NP_001061245.1), OsZIP5 (NP_001055818.1), OsZIP6 (NP_001054742.1), OsZIP7 (NP_001054875.1), OsZIP8 (A3B111.1), OsZIP9 (Q0DHE3.3), OsZIP10 (EEC80824.1), OsZIP11 (NP_001055173.1), OsZIP13 (NP_001046190.1), OsZIP14 (NP_001062003.1), OsZIP16 (XP_006659010.1). Wheat protein IDs (red): TaIRT-like1 (Traes_4AL_9D79BE8FB), TaIRT-like2 (Traes_4BS_6527BBD54), TaZIP10 (Traes_7AL_A13A246B4), TaZIP10-like1 (Traes_7AL_F1D611563), TaZIP13-like1 (Traes_7BL_12C63350C), TaZIP13-like2 (Traes_2BS_9D8F265EC), TaZIP13-like3 (Traes_2AL_BE05B34FF), TaZIP1 (ABF55691.1), TaZIP2 (CAJ19368.1), TaZIP2-like (Traes_6AS_75C6428051), TaZIP3 (AAW68439.1), TaZIP5 (Traes_4AS_F5F7D2A8D), TaZIP6 (AK333945.1), TaZIP7 (ABF55692.1), TaZIP11 (Traes_1AS_7DC2CB902), TaZIP14 (AK331623.1), TaZIP15 (Traes_6AS_4E1D574BC), TaZIP16 (Traes_7AL_DFE86911E). Arrows indicate up or downregulation during senescence in WT plants. * denotes differential expression in at least one *GPC* mutant genotype.

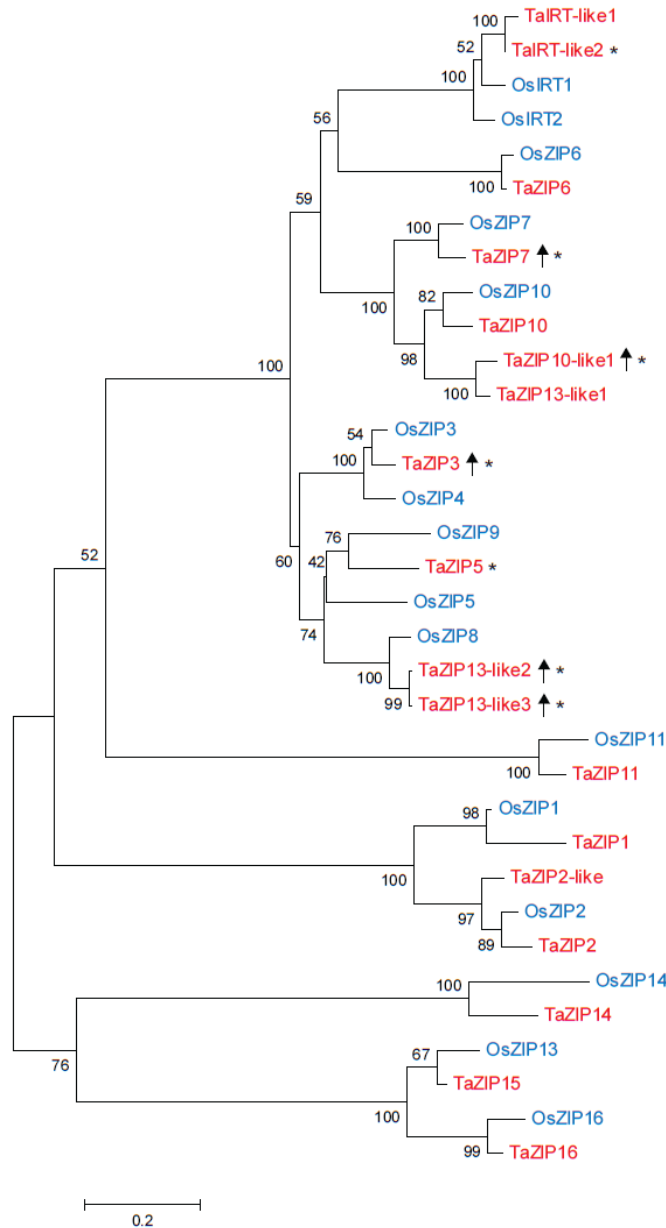


Figure S10. Validation of six transporter genes by qRT-PCR analysis. Side-by-side comparisons of the relative expression levels of each gene as assayed using RNA-seq (Normalized counts +/- SE) and qRT-PCR (fold-*ACTIN* +/- SE).

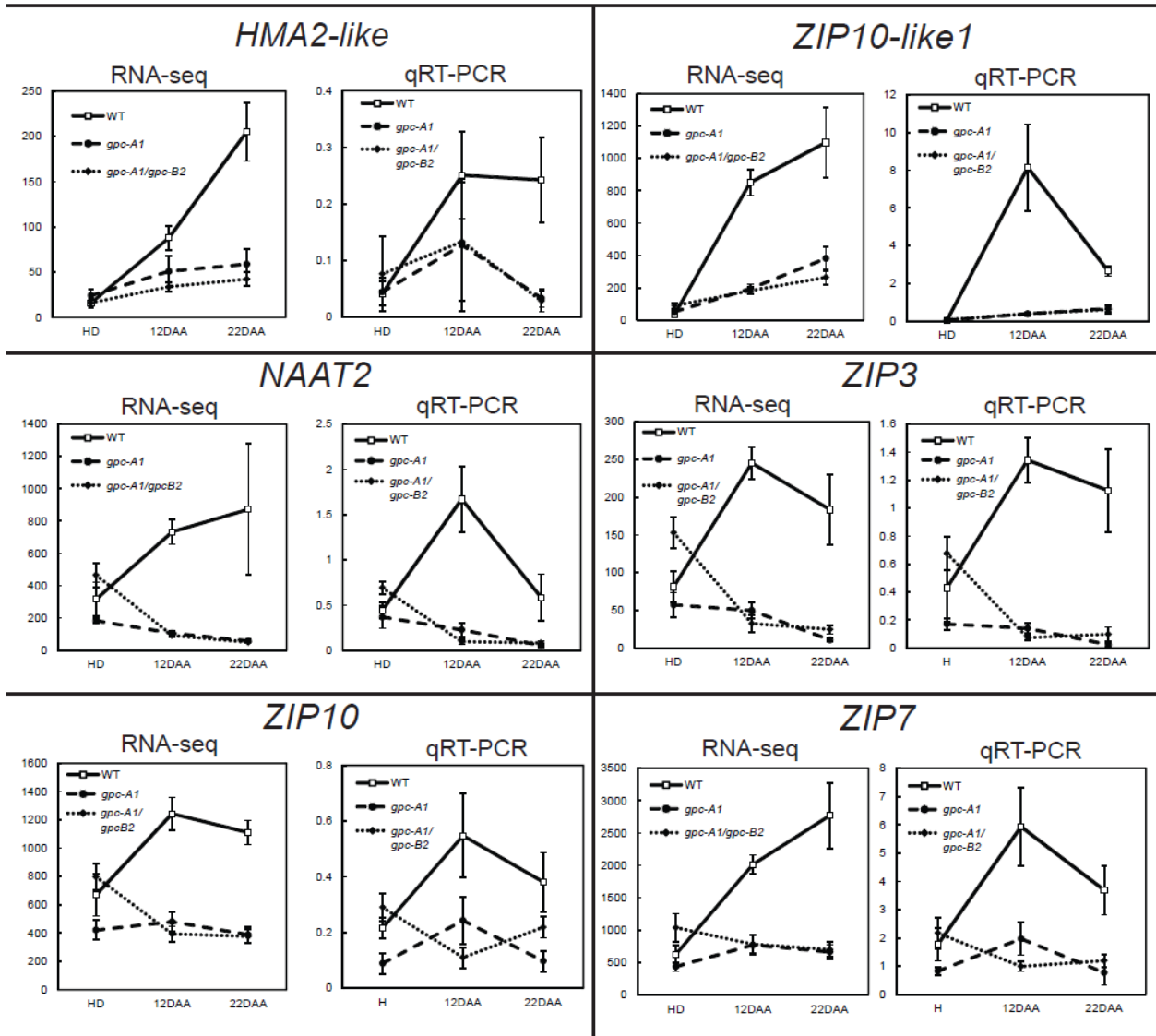


Table S1. Micronutrient concentrations in UCD-2012 and TAU-2012 experiments. GPC and micronutrient grain content for WT, single mutants and double mutant *GPC* knockout plants. Different letters denote significant differences between genotypes determined by Tukey-HSD test ($P < 0.05$).

		WT	<i>gpc-B2</i>	<i>gpc-A1</i>	<i>gpc-A1/gpc-B2</i>
N (g/kg)	UCD	29.78 ± 0.3 ^a	29.6 ± 0.3 ^a	23.16 ± 0.2 ^b	26.17 ± 0.7 ^c
	TAU	27.76 ± 0.4 ^a	29.49 ± 0.5 ^a	23.28 ± 0.6 ^b	24.4 ± 0.4 ^b
P (g/kg)	UCD	3.7 ± 0.0 ^a	3.58 ± 0.1 ^a	3.62 ± 0.0 ^a	4.15 ± 0.1 ^b
	TAU	4.13 ± 0.1 ^a	4.22 ± 0.1 ^a	4.2 ± 0.0 ^a	4.3 ± 0.1 ^a
K (g/kg)	UCD	4.88 ± 0.1 ^a	5.05 ± 0.1 ^a	5.78 ± 0.1 ^b	6.5 ± 0.9 ^c
	TAU	4.79 ± 0.1 ^a	4.53 ± 0.1 ^a	6.38 ± 0.1 ^b	6.15 ± 0.2 ^b
S (ppm)	UCD	1848.00 ± 13.2 ^a	1774.00 ± 21.6 ^b	1564.00 ± 11.7 ^c	1737.00 ± 24.1 ^b
	TAU	1783.75 ± 22.5 ^b	1866.25 ± 17.5 ^a	1690.00 ± 26.8 ^c	1777.5 ± 11.1 ^b
B (ppm)	UCD	2.42 ± 0.2 ^a	2.75 ± 0.1 ^b	2.94 ± 0.2 ^b	3.36 ± 0.1 ^c
	TAU	0.93 ± 0.0 ^a	1.3 ± 0.2 ^{ab}	1.4 ± 0.2 ^b	1.35 ± 0.1 ^{ab}
Ca (g/kg)	UCD	0.26 ± 0.1 ^{ab}	0.25 ± 0.0 ^a	0.28 ± 0.1 ^b	0.36 ± 0.1 ^c
	TAU	0.41 ± 0.0 ^a	0.42 ± 0.1 ^a	0.45 ± 0.0 ^a	0.57 ± 0.1 ^b
Mg (g/kg)	UCD	1.41 ± 0.1 ^a	1.44 ± 0.0 ^{ab}	1.51 ± 0.1 ^b	1.67 ± 0.0 ^c
	TAU	1.33 ± 0.1 ^a	1.41 ± 0.0 ^b	1.35 ± 0.0 ^{ab}	1.39 ± 0.0 ^{ab}
Zn (ppm)	UCD	50.3 ± 1.1 ^a	48.09 ± 2.1 ^a	39.42 ± 0.6 ^b	42.63 ± 1.2 ^b
	TAU	53.56 ± 4.7 ^b	61.54 ± 5.2 ^a	45.28 ± 2.8 ^c	40.93 ± 2.9 ^c
Mn (ppm)	UCD	34.68 ± 1.8 ^{bc}	32.71 ± 1.1 ^{ab}	28.52 ± 0.7 ^a	37.85 ± 2.0 ^c
	TAU	37.66 ± 1.3 ^a	52.66 ± 3.5 ^b	32.93 ± 2.3 ^a	40.48 ± 2.5 ^a
Fe (ppm)	UCD	37.66 ± 0.9 ^a	38.32 ± 1.3 ^a	28.88 ± 0.4 ^b	29.83 ± 1.7 ^b
	TAU	31.24 ± 1.6 ^b	34.24 ± 1.3 ^a	25.48 ± 1.4 ^c	24.73 ± 1.6 ^c
Cu (ppm)	UCD	5.82 ± 0.1 ^a	8.62 ± 2.5 ^a	5.72 ± 0.2 ^a	5.49 ± 0.3 ^a
	TAU	6.99 ± 0.1 ^a	6.7 ± 0.2 ^a	6.18 ± 0.1 ^b	4.83 ± 0.2 ^c

Table S2. Summary of raw and trimmed Illumina sequencing reads and mapping rates from each biological replicate.

Time point	Genotype	Replicate	Raw reads	Trimmed reads	% mapped to defined loci	% uniquely mapped to defined loci
Heading	WT	1	38,665,098	34,773,202	93.99	58.74
		2	39,475,711	39,297,400	94.15	59.59
		3	31,381,725	29,301,745	94.24	58.99
		4	33,848,760	33,264,328	93.36	58.36
	<i>gpc-A1</i>	1	32,102,685	28,868,068	94.35	58.83
		2	37,154,487	36,992,899	94.49	59.75
		3	31,889,453	29,763,897	94.52	58.80
		4	30,140,634	29,622,936	93.65	58.34
	<i>gpc-A1/gpc-B2</i>	1	41,424,154	37,211,906	94.65	52.42
		2	39,970,397	39,787,853	93.83	59.02
		3	33,530,071	31,320,928	93.64	58.27
		4	32,944,098	32,368,503	93.34	58.03
12 DAA	WT	1	39,834,397	35,863,953	93.23	58.44
		2	40,040,076	39,856,173	93.72	59.60
		3	34,534,155	32,265,656	93.00	57.59
		4	85,099,084	83,638,792	92.69	58.57
	<i>gpc-A1</i>	1	35,410,326	31,884,963	94.65	49.51
		2	39,337,625	39,151,166	93.36	59.22
		3	33,414,297	31,248,455	93.48	59.11
		4	32,263,546	31,713,135	92.51	58.12
	<i>gpc-A1/gpc-B2</i>	1	31,076,406	27,987,586	93.97	58.98
		2	35,012,331	34,832,872	91.94	58.38
		3	25,188,810	23,538,518	93.25	58.44
		4	28,255,874	27,763,518	93.85	59.00
22 DAA	WT	1	40,666,581	36,539,348	92.83	58.82
		2	37,814,738	37,635,671	92.18	59.44
		3	33,437,511	31,252,956	92.87	59.07
		4	31,528,730	30,988,194	93.16	59.17
	<i>gpc-A1</i>	1	37,399,266	33,359,639	92.56	59.56
		2	38,746,000	38,565,077	91.79	59.77
		3	28,514,156	26,523,981	93.75	59.41
		4	30,074,410	29,535,381	93.73	59.68
	<i>gpc-A1/gpc-B2</i>	1	45,208,215	40,694,293	93.20	58.49
		2	39,929,531	39,736,903	91.96	59.29
		3	36,835,190	34,436,035	93.17	59.44
		4	33,732,441	33,162,000	93.48	58.34
Average			36,552,249	34,854,109	93.40	58.46

Table S3. 26 genes commonly differentially regulated during senescence between the current study and Gregersen & Holm (2007).

Probe name (Gregersen et al. 2011)	Corresponding URGI contig	BLAST e-value	Hit description
G05_p234_plate_12	6BL-ab-k71_contig_4275858:15270-21181	0	gi 1657845 gb AAB18202.1 cold acclimation protein WCOR410c [Triticum aestivum]
H01_p436_plate_12	4BL-ab-k71_contig_6973512:3778-8889	5E-84	gi 146231063 gb ABQ12768.1 hypersensitive response protein [Triticum aestivum]
C04_p638_plate_2	2AS-ab-k71_contig_5252955:1-993	0	gi 474253786 gb EMS60319.1 Ribonuclease 1 [Triticum urartu]
B10_p234_plate_26	3AL-ab-k71_contig_4355214:1431-1859	2E-64	-
D06_p335_plate_3	1BL-ab-k71_contig_3863282:2209-5503	5E-65	gi 475538858 gb EMT09311.1 Aldehyde dehydrogenase family 2 member C4 [Aegilops tauschii]
A04_a22_plate_12	2AL-ab-k71_contig_6315374:6012-9120	1E-120	gi 475572136 gb EMT16425.1 Cysteine proteinase 1 [Aegilops tauschii]
D02_j223_plate_15	2AL-ab-k71_contig_6399751:5443-12037	1E-169	gi 475609973 gb EMT27565.1 ABC transporter C family member 9 [Aegilops tauschii]
A02_e411_plate_2	6BL-ab-k71_contig_1176509:1-8128	5E-86	gi 299482520 gb ADJ19186.1 lysine ketoglutarate reductase/saccharopine dehydrogenase [Triticum turgidum]
D10_e411_plate_13	1AL_v2-ab-k71_contig_3885764:9943-15907	1E-146	gi 460373787 ref XP_004232695.1 PREDICTED: aspartic proteinase-like [Solanum lycopersicum]
F03_N130_plate_64	6AL-ab-k71_contig_5767722:1-2056	1E-120	gi 475621610 gb EMT31542.1 3-ketoacyl-CoA thiolase 2, peroxisomal [Aegilops tauschii]
G03_p234_plate_13	3B-ab-k71_contig_10644572:1675-3600	0	gi 474436565 gb EMS68215.1 UDP-glycosyltransferase 87A1 [Triticum urartu]
C08_d26_plate_11	6BL-ab-k71_contig_4396688:584-4562	1E-68	gi 475574510 gb EMT17003.1 Acetylornithine deacetylase [Aegilops tauschii]
B03_p234_plate_11_run_2	2AS-ab-k71_contig_5303733:4078-6463	0	gi 326493682 dbj BAJ85302.1 predicted protein [Hordeum vulgare subsp. vulgare]
A11_a11_plate_3	4BS-ab-k71_contig_4861976:6480-7581	2E-36	gi 474290679 gb EMS61268.1 Metallothionein-like protein 1 [Triticum urartu]
E01_N130_plate_48	5BL-ab-k71_contig_10818068:1381-4394	0	gi 357122996 ref XP_003563199.1 PREDICTED: phospholipase C 4-like [Brachypodium distachyon]
B01_p436_plate_8_run_2	2AS-ab-k71_contig_5256148:581-5506	4E-51	gi 357116071 ref XP_003559808.1 PREDICTED: acyl-CoA dehydrogenase family member 10-like [Brachypodium distachyon]
C02_p335_plate_7	7BS-ab-k71_contig_584435:1-200	1E-99	gi 475625512 gb EMT32999.1 NAC domain-containing protein 18 [Aegilops tauschii]
B03_h116_plate_2	4BL-ab-k71_contig_7000160:3976-8945	3E-69	gi 475530866 gb EMT07974.1 Prolyl 3-hydroxylase 1 [Aegilops tauschii]
D08_n129_plate_9	1AS-ab-k71_contig_310232:674-1526	4E-99	-
H07_p436_plate_10	4AL_v2-ab-k71_contig_4AL_7112091:4128-8300	1E-170	gi 475509418 gb EMT05187.1 Glutamate decarboxylase 1 [Aegilops tauschii]
E06_p335_plate_6	5BS-ab-k71_contig_2277410:2149-11495	1E-126	gi 283970976 gb ADB54814.1 universal stress protein 9303 [Hordeum vulgare subsp. vulgare]
H08_p234_plate_14	1BL-ab-k71_contig_3868206:2733-3775	0	gi 283970978 gb ADB54815.1 universal stress protein 9303 [Hordeum vulgare subsp. vulgare]
C05_l226_plate_3	2AL-ab-k71_contig_6340847:3105-5951	4E-31	gi 473939569 gb EMS50260.1 Ferredoxin-6, chloroplastic [Triticum urartu]
E09_p335_plate_3	1AS-ab-k71_contig_2470305:166-1376	3E-72	gi 4325045 gb AAD17232.1 S-adenosylmethionine decarboxylase precursor [Triticum aestivum]
D09_p335_plate_7	3AL-ab-k71_contig_4427563:4889-5726	0	gi 473881465 gb EMS47979.1 putative glutathione S-transferase GSTF1 [Triticum urartu]
D10_p537_plate_6	3B-ab-k71_contig_10631124:2445-5741	2E-45	gi 514830677 gb AGO59325.1 MYB13 transcription factor [Triticum aestivum]
			gi 475497046 gb EMT03967.1 GDSL esterase/lipase [Aegilops tauschii]

Table S4. 196 affymetrix contigs from Jukanti et al. 2008 also differentially expressed during senescence.

Affymetrix ID (Jukanti et al. 2008)	Corresponding URGI contig	BLAST e-value	Hit description
Contig903_at	5BL-ab-k71_contig_10815975:7698-9613	1.00E-154	gi 474396172 gb EMS65694.1 Alcohol dehydrogenase 2 [Triticum urartu]
HF12K17r_at	2AS-ab-k71_contig_5273012:812-7972	8.00E-80	gi 326492077 dbj BAJ98263.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig24024_at	6AL-ab-k71_contig_5814401:2506-3427	2.00E-15	gi 326502074 dbj BAK06529.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig14921_s_at	3B-ab-k71_contig_10604827:215-5360	4.00E-78	gi 474066737 gb EMS54176.1 Purple acid phosphatase 2 [Triticum urartu]
Contig16604_at	4BS-ab-k71_contig_4901464:24-823	1E-147	#N/A
Contig15056_at	2BL-ab-k71_contig_7971302:3009-7466	9E-77	gi 326512690 dbj BAK03252.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig7857_s_at	2AS-ab-k71_contig_5225988:1-3104	1E-125	gi 326528587 dbj BAJ93475.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig1402_at	3AS-ab-k71_contig_2573541:1-247	3E-38	gi 475601114 gb EMT24719.1 GDSL esterase/lipase [Aegilops tauschii]
HW08K02u_at	4BS-ab-k71_contig_4865249:5225-6279	1E-59	gi 326514238 dbj BAJ92269.1 predicted protein [Hordeum vulgare subsp. vulgare]
HV10A20u_s_at	1AL_v2-ab-k71_contig_3912549:1123-3112	4E-16	gi 474392822 gb EMS65496.1 Cysteine proteinase RD21a [Triticum urartu]
Contig21245_at	3B-ab-k71_contig_10417977:695-3511	0	gi 326494096 dbj BAJ85510.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig26_at	5BL-ab-k71_contig_10806933:541-1198	1E-178	gi 195617694 gb ACG30677.1 histone H4 [Zea mays]
Contig7112_at	4AL_v2-ab-k71_contig_4AL_7160884:3225-4267	4E-64	gi 157312498 gb ABV32166.1 UFG2 [Triticum aestivum]
Contig7433_at	2AL-ab-k71_contig_6370536:4028-8220	1E-119	gi 474154143 gb EMS57069.1 Abscisic acid-inducible protein kinase [Triticum urartu]
Contig7433_s_at	2AL-ab-k71_contig_6370536:4028-8220	1E-119	gi 474154143 gb EMS57069.1 Abscisic acid-inducible protein kinase [Triticum urartu]
Contig19290_at	2BL-ab-k71_contig_7936650:1-1358	0	gi 474268501 gb EMS60789.1 UDP-glycosyltransferase 73C6 [Triticum urartu]
Contig22948_at	4BL-ab-k71_contig_6856755:3224-5930	2E-52	gi 326528067 dbj BAJ89085.1 predicted protein [Hordeum vulgare subsp. vulgare]
rbaal12n12_s_at	5BL-ab-k71_contig_10856642:7311-10619	1E-158	gi 475574369 gb EMT16972.1 Putative transporter [Aegilops tauschii]
Contig3935_s_at	7BL-ab-k71_contig_6509502:9-3078	4E-54	gi 473936597 gb EMS50148.1 Reticulon-like protein B2 [Triticum urartu]
HS06C20u_s_at	7BL-ab-k71_contig_6509502:9-3078	3E-88	gi 473936597 gb EMS50148.1 Reticulon-like protein B2 [Triticum urartu]
Contig7686_at	1BL-ab-k71_contig_3825950:1469-5204	0	gi 56409844 emb CAI30070.1 glycosyltransferase [Triticum aestivum]
Contig20207_s_at	3AL-ab-k71_contig_1034593:1-6300	4E-72	gi 326504974 dbj BAJ99498.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig7343_s_at	2AL-ab-k71_contig_6433511:6743-7054	1E-24	gi 326516112 dbj BAJ88079.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig14595_at	5BL-ab-k71_contig_10872426:20719-23310	0	#N/A
HS06J22u_s_at	1AL_v2-ab-k71_contig_3897631:1-3252	6E-99	gi 326488911 dbj BAJ98067.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig9006_at	1AL_v2-ab-k71_contig_3912549:1123-3112	0	gi 474392822 gb EMS65496.1 Cysteine proteinase RD21a [Triticum urartu]
Contig9352_at	3AS-ab-k71_contig_3442141:693-1706	0	gi 383100757 emb CCG47989.1 glycosyltransferase, HGA-like, expressed [Triticum aestivum]
EBpi01_SQ002_N08_at	4AL_v2-ab-k71_contig_4AL_7155714:1227-3637	9E-20	gi 326503002 dbj BAJ99126.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig9110_at	7BS-ab-k71_contig_3151221:1-523	1E-104	gi 326489587 dbj BAK01774.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 326512308 dbj BAJ99509.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 326529319 dbj BAK01053.1 predicted protein [Hordeum vulgare subsp. vulgare]
HV_CEA0011J22r2_at	3AL-ab-k71_contig_4345443:1-775	1E-41	gi 474224339 gb EMS59376.1 hypothetical protein TRIUR3_02071 [Triticum urartu]

Contig18428_at	3AL-ab-k71_contig_1034593:1-6300	0	gi 326504974 dbj BAJ99498.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig9351_s_at	3AS-ab-k71_contig_3442141:693-1706	0	gi 383100757 emb CCG47989.1 glycosyltransferase, HGA-like, expressed [Triticum aestivum]
HT12G07u_s_at	6AL-ab-k71_contig_5818539:1-7046	3E-09	gi 356463714 gb AET08895.1 vacuolar processing enzyme 2 [Aegilops tauschii]
Contig17964_at	4AS_v2-ab-k71_contig_5977931:3675-4720	0	gi 326494882 dbj BAJ94560.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig13385_s_at	2BL-ab-k71_contig_8062334:2765-3987	1E-117	gi 326530163 dbj BAK08361.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig20405_at	3B-ab-k71_contig_10615303:1399-4851	1E-103	gi 326500940 dbj BAJ95136.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig7359_at	4BL-ab-k71_contig_6887705:1-1034	1E-161	gi 475595559 gb EMT23077.1 Pheophorbide a oxygenase, chloroplastic [Aegilops tauschii]
Contig7503_at	1AL_v2-ab-k71_contig_3960754:94-4380	5E-68	gi 326523819 dbj BAJ93080.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig3892_at	2BL-ab-k71_contig_8088049:357-4123	0	gi 326531656 dbj BAJ97832.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig5654_at	2AS-ab-k71_contig_5225155:1786-5351	1E-174	gi 475588310 gb EMT20813.1 Putative quinone-oxidoreductase-like protein, chloroplastic [Aegilops tauschii]
HA18O08r_s_at	5AL-ab-k95_contig_1128960:517-4580	2E-64	gi 345447290 gb AEN92260.1 arginase [Triticum aestivum]
Contig11129_at	2BS-ab-k71_contig_5194333:8297-9616	1E-107	gi 474114511 gb EMS55823.1 putative ornithine aminotransferase [Triticum urartu]
Contig2736_s_at	5AL-ab-k95_contig_2809387:2645-5504	1E-127	gi 475510892 gb EMT05328.1 Adipocyte plasma membrane-associated protein [Aegilops tauschii]
Contig3691_at	2AS-ab-k71_contig_5252955:1-993	0	gi 473891753 gb EMS48763.1 Beta-glucosidase 31 [Triticum urartu]
Contig7997_at	6BL-ab-k71_contig_3771316:67-1562	3E-62	gi 474253786 gb EMS60319.1 Ribonuclease 1 [Triticum urartu]
Contig6152_at	7BS-ab-k71_contig_3097754:654-17033	1E-155	gi 326513484 dbj BAJ92093.1 predicted protein [Hordeum vulgare subsp. vulgare]
HV_CEb0005N09r2_at	6AS-ab-k71_contig_4359475:3564-5827	3E-85	gi 326514820 dbj BAJ99771.1 predicted protein [Hordeum vulgare subsp. vulgare]
HVSMEm0007B06r2_s_at	5AL-ab-k95_contig_22698:1-1478	1E-132	gi 326516984 dbj BAJ96484.1 predicted protein [Hordeum vulgare subsp. vulgare]
HV_C Ea0006M06r2_s_at	4AL_v2-ab-k71_contig_4AL_7075859:3208-6993	1E-59	gi 326525907 dbj BAJ93130.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig10193_at	3AL-ab-k71_contig_4336869:1-1893	1E-69	gi 475589772 gb EMT21266.1 ABC transporter C family member 10 [Aegilops tauschii]
Contig23092_at	7BS-ab-k71_contig_3088434:3365-7082	0	gi 474237122 gb EMS59633.1 Epoxide hydrolase 2 [Triticum urartu]
Contig10270_at	5AL-ab-k95_contig_2783071:1-1528	0	gi 474167057 gb EMS57469.1 KDEL-tailed cysteine endopeptidase CEP1 [Triticum urartu]
Contig24230_at	2AS-ab-k71_contig_5199858:1-856	1E-134	gi 326524432 dbj BAK00599.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig17818_at	1AS-ab-k71_contig_3288158:270-2003	0	gi 474213532 gb EMS58952.1 Elicitor-responsive protein 1 [Triticum urartu]
HV_C Ea0006E02r2_s_at	6AL-ab-k71_contig_5830900:430-3997	2E-77	gi 326522618 dbj BAK07771.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig7293_at	2BL-ab-k71_contig_8052619:2011-6240	0	gi 326505554 dbj BAJ95448.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig17276_at	5BL-ab-k71_contig_348262:1118-7118	0	gi 326515132 dbj BAK03479.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig20144_s_at	4AL_v2-ab-k71_contig_4AL_7155714:1227-3637	2E-23	gi 348549744 emb CBZ41151.1 NAC transcription factor [Hordeum vulgare subsp. vulgare]
Contig8056_at	6AL-ab-k71_contig_5760608:1-612	7E-78	gi 326518772 dbj BAJ92547.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 473922892 gb EMS49728.1 Quinone oxidoreductase PIG3 [Triticum urartu]
			gi 326519885 dbj BAK03867.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 357153424 ref XP_003576447.1 PREDICTED: ABC transporter A family member 7-like [Brachypodium distachyon]
			gi 326503002 dbj BAJ99126.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 474065824 gb EMS54111.1 Peroxisomal multifunctional enzyme type 2 [Triticum urartu]

Contig13658_at	2BS-ab-k71_contig_5208331:5065-7158	0	gi 475624481 gb EMT32631.1 Peroxisomal multifunctional enzyme type 2 [Aegilops tauschii]
Contig13046_at	1BL-ab-k71_contig_3904034:661-2554	2E-62	gi 371924997 tpe CBZ41159.1 TPA: NAC transcription factor [Hordeum vulgare subsp. vulgare]
Contig10594_at	7BS-ab-k71_contig_909259:1-1586	0	gi 326520874 dbj BAJ92800.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig5299_at	1BL-ab-k71_contig_3868206:2733-3775	0	gi 326531956 dbj BAK01354.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig10981_at	5BS-ab-k71_contig_2274553:453-5698	1E-112	gi 475558485 gb EMT13108.1 hypothetical protein F775_27330 [Aegilops tauschii]
Contig24105_at	4AS_v2-ab-k71_contig_5952279:5675-11064	1E-173	gi 473939569 gb EMS50260.1 Ferredoxin-6, chloroplastic [Triticum urartu]
Contig1403_at	3AS-ab-k71_contig_2573541:1-247	2E-67	gi 357157153 ref XP_003577703.1 PREDICTED: uncharacterized hydrolase HI_0588-like [Brachypodium distachyon]
Contig11890_at	6AL-ab-k71_contig_5830900:430-3997	3E-96	gi 326506432 dbj BAJ86534.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig20575_at	1BL-ab-k71_contig_3894079:1-345	3E-83	gi 475601114 gb EMT24719.1 GDSL esterase/lipase [Aegilops tauschii]
Contig9954_at	6BL-ab-k71_contig_4309090:343-4524	1E-132	gi 473922892 gb EMS49728.1 Quinone oxidoreductase PIG3 [Triticum urartu]
Contig6343_at	3B-ab-k71_contig_10520391:1337-6837	0	gi 326512068 dbj BAJ96015.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig1404_at	3AS-ab-k71_contig_2573541:1-247	5E-80	gi 326496777 dbj BAJ98415.1 predicted protein [Hordeum vulgare subsp. vulgare]
EBma03_SQ002_F16_s_at	4AS_v2-ab-k71_contig_5955108:4662-6252	6E-26	gi 326505418 dbj BAJ95380.1 predicted protein [Hordeum vulgare subsp. vulgare]
rbaal10h14_at	2BL-ab-k71_contig_8072661:19233-21176	3E-73	gi 475601114 gb EMT24719.1 GDSL esterase/lipase [Aegilops tauschii]
Contig1404_x_at	3AS-ab-k71_contig_2573541:1-247	5E-80	gi 326487554 dbj BAK05449.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig15869_at	4AS_v2-ab-k71_contig_352920:1089-3423	0	gi 326490093 dbj BAJ94120.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig10700_at	3B-ab-k71_contig_10699811:1993-2563	1E-91	gi 326516896 dbj BAJ96440.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig4096_at	1BS-ab-k71_contig_3454525:1-7236	1E-135	gi 475601114 gb EMT24719.1 GDSL esterase/lipase [Aegilops tauschii]
Contig5177_s_at	1BL-ab-k71_contig_3830761:5135-10857	1E-162	gi 189172063 gb ACD80387.1 WRKY40 transcription factor, partial [Triticum aestivum]
Contig4639_s_at	2AL-ab-k71_contig_6356061:2883-4074	6E-91	gi 326490638 dbj BAJ89986.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig6008_s_at	1AL_v2-ab-k71_contig_3904007:1-2701	1E-171	gi 326498703 dbj BAK02337.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig9392_at	1BS-ab-k71_contig_3431786:6994-7732	2E-37	gi 474317121 gb EMS62134.1 Actin-7 [Triticum urartu]
Contig26053_at	3AL-ab-k71_contig_4407808:2194-3672	7E-74	gi 475561024 gb EMT13696.1 Actin-7 [Aegilops tauschii]
HV_CEA0008J10r2_s_at	3AS-ab-k71_contig_3379776:1910-2481	4E-20	gi 474390725 gb EMS65281.1 hypothetical protein TRIUR3_32617 [Triticum urartu]
Contig2750_s_at	6AL-ab-k71_contig_5767722:1-2056	2E-55	gi 475600098 gb EMT24434.1 hypothetical protein F775_32163 [Aegilops tauschii]
Contig16179_s_at	1BS-ab-k71_contig_3423601:17002-26931	2E-13	gi 475514050 gb EMT05681.1 Low temperature-induced protein [Aegilops tauschii]
HVSMEI0013E16r2_s_at	6AL-ab-k71_contig_5791715:1-1294	4E-57	gi 475625209 gb EMT32886.1 Jasmonate O-methyltransferase [Aegilops tauschii]
Contig6381_at	3AL-ab-k71_contig_96597:80-1495	1E-137	#N/A
Contig16535_at	5BS-ab-k71_contig_2266199:109-6401	1E-115	gi 475621610 gb EMT31542.1 3-ketoacyl-CoA thiolase 2, peroxisomal [Aegilops tauschii]
HW02O09u_s_at	5AL-ab-k95_contig_565469:1301-3254	6E-60	gi 357130187 ref XP_003566732.1 PREDICTED: phosphatidylinositol 3-kinase, root isoform-like [Brachypodium distachyon]
			gi 326528223 dbj BAJ93293.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 326528473 dbj BAJ93418.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 473874636 gb EMS47816.1 Aldehyde dehydrogenase family 2 member C4 [Triticum urartu]
			gi 357161700 ref XP_003579177.1 PREDICTED: methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial-like [Brachypodium distachyon]
			gi 474265415 gb EMS60690.1 Auxin-induced protein

rbaal23d16_s_at	3AL-ab-k71_contig_4332102:492-3349	5E-28	5NG4 [Triticum urartu] gi 475567132 gb EMT15199.1 putative Isocitrate dehydrogenase (NADP), chloroplastic [Aegilops tauschii]
HVSMEI0010P10f_x_at	2BS-ab-k71_contig_5201747:10374-13960	8E-35	gi 345447290 gb AEN92260.1 arginase [Triticum aestivum]
Contig6659_s_at	3B-ab-k71_contig_10639283:103-4231	1E-102	gi 474156727 gb EMS57131.1 Sphingosine-1-phosphate lyase [Triticum urartu]
Contig2253_s_at	2AL-ab-k71_contig_6439401:36-885	0	gi 475515312 gb EMT05831.1 Histone H1 [Aegilops tauschii]
Contig10984_at	3AL-ab-k71_contig_4450714:278-8391	0	gi 161702907 gb ABX76295.1 neutral ceramidase [Triticum aestivum]
Contig25897_at	7BS-ab-k71_contig_3065267:1-5116	0	gi 474036949 gb EMS53193.1 FACT complex subunit SPT16 [Triticum urartu]
rbaal21e22_x_at	6AL-ab-k71_contig_5767722:1-2056	3E-18	gi 475621610 gb EMT31542.1 3-ketoacyl-CoA thiolase 2, peroxisomal [Aegilops tauschii]
HV_CEA0008J10r2_at	3AS-ab-k71_contig_3379776:1910-2481	4E-20	#N/A
Contig17260_at	6AS-ab-k71_contig_4351215:1-1669	9E-99	gi 326497895 dbj BAJ94810.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig17135_s_at	2BL-ab-k71_contig_8062334:2765-3987	3E-44	gi 326531478 dbj BAJ97743.1 predicted protein [Hordeum vulgare subsp. vulgare]
EBpi03_SQ001_I14_at	4AL_v2-ab-k71_contig_4AL_7099893:6436-10911	8E-20	gi 326530163 dbj BAK08361.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig617_x_at	6AS-ab-k71_contig_4349651:4661-5719	0	gi 326511956 dbj BAJ95959.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig433_x_at	6BS-ab-k71_contig_2935443:1-457	0	gi 475604137 gb EMT25652.1 hypothetical protein F775_43704 [Aegilops tauschii]
Contig346_at	5AL-ab-k95_contig_2799832:1371-2762	7E-91	gi 31753114 gb AAH53854.1 Unknown (protein for IMAGE:5194336), partial [Homo sapiens]
Contig6411_at	4AS_v2-ab-k71_contig_5994312:6000-8002	0	gi 11494016 gb AAI11385.1 Unknown (protein for IMAGE:5198300), partial [Homo sapiens]
Contig17360_at	6AL-ab-k71_contig_5757005:1129-7237	7E-62	gi 4090293 emb CAA10497.1 hypothetical protein [Secale cereale]
Contig13068_at	3B-ab-k71_contig_10402369:1602-2690	3E-43	gi 475605702 gb EMT26171.1 3-ketoacyl-CoA synthase 1 [Aegilops tauschii]
Contig16209_at	3B-ab-k71_contig_10690339:4659-6750	1E-58	gi 357145196 ref XP_003573558.1 PREDICTED: methionine aminopeptidase 1B, chloroplastic-like [Brachypodium distachyon]
Contig11332_at	3B-ab-k71_contig_10730106:2887-7639	9E-96	#N/A
Contig14144_at	6AL-ab-k71_contig_5764148:7642-9513	0	gi 475580681 gb EMT18662.1 Glucoamylase [Aegilops tauschii]
HVSMEh0102G02f_x_at	4AS_v2-ab-k71_contig_5945881:18664-19150	2E-29	gi 475615860 gb EMT29587.1 Putative membrane protein [Aegilops tauschii]
Contig21024_at	4AS_v2-ab-k71_contig_5970292:5240-10627	1E-108	gi 473777884 gb EMS46019.1 hypothetical protein TRIUR3_07308 [Triticum urartu]
Contig16113_at	2AL-ab-k71_contig_6364940:5698-6948	0	gi 326506444 dbj BAJ86540.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig2985_s_at	2BS-ab-k71_contig_5231013:12845-20601	0	gi 254885381 emb CBA11528.1 sulphate transporter [Triticum aestivum]
Contig12563_s_at	6AS-ab-k71_contig_4385322:6110-7798	1E-126	gi 326520605 dbj BAK07561.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig16015_at	5BS-ab-k71_contig_2287895:5743-10850	1E-146	gi 14861035 gb AAK72401.1 Mg-chelatase subunit XANTHA-F [Hordeum vulgare subsp. vulgare]
Contig2433_s_at	4AL_v2-ab-k71_contig_4AL_7151445:3859-11701	1E-161	gi 326528365 dbj BAJ93364.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig2111_s_at	2AL-ab-k71_contig_6359939:14373-15478	6E-77	gi 475534641 gb EMT08606.1 Coleoptile phototropism protein 1 [Aegilops tauschii]
Contig19029_at	7AL-ab-k71_contig_4470746:4134-4406	3E-67	gi 474074549 gb EMS4507.1 Acid phosphatase 1 [Triticum urartu]
HA14G19r_at	5AL-ab-k95_contig_13914:1-3260	2E-72	gi 326521510 dbj BAK00331.1 predicted protein [Hordeum vulgare subsp. vulgare]
X12735_at	1AL_v2-ab-k71_contig_3715806:2709-4239	1E-131	gi 475577656 gb EMT17876.1 Beta-galactosidase [Aegilops tauschii]
Contig13735_at	6BL-ab-k71_contig_127065:3397-4210	1E-125	gi 474343675 gb EMS62751.1 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Triticum urartu]
Contig21274_at	4AL_v2-ab-k71_contig_4AL_7125345:8254-15574	1E-138	gi 474060351 gb EMS53958.1 Chlorophyll a-b binding protein 3C, chloroplastic [Triticum urartu]
			gi 326488427 dbj BAJ93882.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 326492676 dbj BAJ90194.1 predicted protein [Hordeum vulgare subsp. vulgare]

Contig820_at	4AL_v2-ab-k71_contig_4AL_5754445:1016-3177	0	gi 473913339 gb EMS49688.1 Chlorophyll a-b binding protein CP26, chloroplastic [Triticum urartu]
HV_CEA0016F11f_at	4BL-ab-k71_contig_6992715:1-4024	6E-14	gi 357113513 ref XP_003558547.1 PREDICTED: uncharacterized protein LOC100823410 [Brachypodium distachyon]
Contig16020_at	4BS-ab-k71_contig_4937574:115-7508	1E-124	gi 357156916 ref XP_003577619.1 PREDICTED: uncharacterized protein LOC100836694 [Brachypodium distachyon]
Contig2412_at	2AS-ab-k71_contig_5190107:3940-11214	1E-161	gi 357122526 ref XP_003562966.1 PREDICTED: uncharacterized protein LOC100831317 [Brachypodium distachyon]
Contig3396_s_at	3B-ab-k71_contig_10628326:166-917	1E-179	gi 475559550 gb EMT13370.1 hypothetical protein F775_28691 [Aegilops tauschii]
EBro07_SQ002_K15_x_at	4BL-ab-k71_contig_7034718:16725-18998	4E-26	#N/A
Contig194_s_at	5AL-ab-k95_contig_2774278:3264-4547	0	gi 475614191 gb EMT29003.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
HVSMEi0020J05f_x_at	5BL-ab-k71_contig_10916028:1304-6876	1E-108	gi 326513480 dbj BAK06980.1 predicted protein [Hordeum vulgare subsp. vulgare]
HVSMEh0080N02r2_at	2AS-ab-k71_contig_5263481:3990-5197	3E-25	gi 400879 sp P31093.1 PSAN_HORVU RecName: Full=Photosystem I reaction center subunit N, chloroplastic; Short=PSI-N; Flags: Precursor gi 19095 emb CAA47056.1 photosystem I subunit N [Hordeum vulgare subsp. vulgare]
baak46p14_s_at	3AS-ab-k71_contig_3334610:1-2284	2E-53	gi 326517280 dbj BAK00007.1 predicted protein [Hordeum vulgare subsp. vulgare]
HVSMEi0005B04r2_x_at	2BS-ab-k71_contig_3595733:4298-5840	2E-16	gi 58339283 gb AAW66004.1 leucine zipper protein zip1 [Triticum aestivum]
Contig497_s_at	5AL-ab-k95_contig_2799832:1371-2762	3E-64	gi 326528195 dbj BAJ89149.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig3183_at	6BL-ab-k71_contig_2539176:1-221	8E-55	gi 4090293 emb CAA10497.1 hypothetical protein [Secale cereale]
Contig14542_at	3B-ab-k71_contig_10550500:5495-21268	1E-131	gi 475559300 gb EMT13311.1 Geranylgeranyl diphosphate reductase, chloroplastic [Aegilops tauschii]
Contig4700_at	3B-ab-k71_contig_10631745:24-4235	0	gi 475570720 gb EMT16094.1 Alpha-amylase [Aegilops tauschii]
Contig3146_at	1AS-ab-k71_contig_2183291:104-3156	0	gi 357141239 ref XP_003572147.1 PREDICTED: uncharacterized protein At4g01050, chloroplastic-like [Brachypodium distachyon]
HV_CEA0015D14r2_at	5BL-ab-k71_contig_10902908:2670-5635	1E-176	gi 354681874 dbj BAL04917.1 glutamyl tRNA reductase [Triticum aestivum]
Contig5026_at	6AS-ab-k71_contig_3291344:4049-4863	9E-83	gi 326531042 dbj BAK04872.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig23482_at	6AL-ab-k71_contig_5826035:1-3331	1E-55	gi 475596216 gb EMT23305.1 hypothetical protein F775_30333 [Aegilops tauschii]
HV_CEB0017F03r2_s_at	7AS-ab-k71_contig_4215480:1887-3348	1E-144	gi 326502018 dbj BAK06501.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig14841_at	5BS-ab-k71_contig_2261475:1-2128	2E-74	gi 225690802 gb ACO06087.1 chlorophyll a-b binding protein [Triticum aestivum]
Contig8679_at	5AL-ab-k95_contig_2748254:476-3293	1E-171	gi 357114424 ref XP_003559000.1 PREDICTED: uncharacterized protein LOC100832376 [Brachypodium distachyon]
S78730_at	5BL-ab-k71_contig_10916028:1304-6876	1E-149	gi 326520313 dbj BAK07415.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig7304_s_at	6BS-ab-k71_contig_3024079:10228-11218	0	gi 326513480 dbj BAK06980.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig5659_at	7BS-ab-k71_contig_3068208:1-163	7E-77	gi 475458442 gb EMT01926.1 O-methyltransferase ZRP4 [Aegilops tauschii]
Contig20267_at	5BL-ab-k71_contig_10790778:15407-18782	1E-124	gi 475558039 gb EMT12976.1 50S ribosomal protein 6, chloroplastic [Aegilops tauschii]
Contig9660_at	6AL-ab-k71_contig_5808587:152-3532	2E-63	gi 326489459 dbj BAK01710.1 predicted protein [Hordeum vulgare subsp. vulgare]
HVSMEh0080L10r2_x_at	7BS-ab-k71_contig_3164750:1-1240	1E-80	gi 326494976 dbj BAJ85583.1 predicted protein [Hordeum vulgare subsp. vulgare]
rbah53j14_at	2BL-ab-k71_contig_7993541:454-2439	5E-80	gi 326506224 dbj BAJ86430.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 225690802 gb ACO06087.1 chlorophyll a-b binding protein [Triticum aestivum]
			gi 326500100 dbj BAJ90885.1 predicted protein [Hordeum vulgare subsp. vulgare]
			gi 326527749 dbj BAK08149.1 predicted protein

Contig1208_s_at	7BS-ab-k71_contig_3164750:1-1240	0	[Hordeum vulgare subsp. vulgare] gi 225690802 gb ACO06087.1 chlorophyll a-b binding protein [Triticum aestivum]
Contig7305_at	6BS-ab-k71_contig_3024079:10228-11218	0	gi 475458442 gb EMT01926.1 O-methyltransferase ZRP4 [Aegilops tauschii]
Contig2766_s_at	1AL_v2-ab-k71_contig_3874670:3902-5985	1E-152	gi 10720236 sp Q42850.1 PORB_HORVU RecName: Full=Protochlorophyllide reductase B, chloroplastic; Short=PCR B; AltName: Full=NADPH-protochlorophyllide oxidoreductase B; Short=POR B; Flags: Precursor gi 683476 emb CAA59228.1 NADPH dehydrogenase [Hordeum vulgare] gi 326488707 dbj BAJ97965.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 326493324 dbj BAJ85123.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 326494290 dbj BAJ90414.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 474399175 gb EMS65931.1 Lipoxigenase 1 [Triticum urartu]
Contig12574_at	2AL-ab-k71_contig_6437732:12404-19901	0	gi 218191232 gb EEC73659.1 hypothetical protein OsI_08191 [Oryza sativa Indica Group]
EBed02_SQ002_E18_s_at	6AL-ab-k71_contig_5789067:4555-10598	3E-52	gi 154551059 gb ABS83562.1 boron transporter [Hordeum vulgare] gi 154551061 gb ABS83563.1 boron transporter [Hordeum vulgare]
Contig21126_at	4BL-ab-k71_contig_4768862:125-3354	2E-72	gi 160346960 gb ABX26122.1 putative boron transporter 2 [Hordeum vulgare]
Contig8854_at	6AL-ab-k71_contig_5789067:4555-10598	1E-142	gi 218191232 gb EEC73659.1 hypothetical protein OsI_08191 [Oryza sativa Indica Group]
HVSMEa0012N07r2_at	3B-ab-k71_contig_10594544:114-2512	4E-35	gi 326523645 dbj BAJ92993.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 326524189 dbj BAJ97105.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig2762_at	1AL_v2-ab-k71_contig_3874670:3902-5985	0	gi 10720236 sp Q42850.1 PORB_HORVU RecName: Full=Protochlorophyllide reductase B, chloroplastic; Short=PCR B; AltName: Full=NADPH-protochlorophyllide oxidoreductase B; Short=POR B; Flags: Precursor gi 683476 emb CAA59228.1 NADPH dehydrogenase [Hordeum vulgare] gi 326488707 dbj BAJ97965.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 326493324 dbj BAJ85123.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 326494290 dbj BAJ90414.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 354681872 dbj BAL04916.1 glutamyl tRNA reductase [Triticum aestivum]
Contig3148_at	1BS-ab-k71_contig_3481555:1190-3041	0	gi 326489448 dbj BAK01705.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig19438_at	2BL-ab-k71_contig_8039865:2256-6860	1E-175	gi 473789781 gb EMS46316.1 Photosystem I reaction center subunit XI, chloroplastic [Triticum urartu]
Contig2177_at	3B-ab-k71_contig_10484319:1384-2702	0	gi 326528371 dbj BAJ93367.1 predicted protein [Hordeum vulgare subsp. vulgare]
rbah35f01_s_at	2AS-ab-k71_contig_5307368:5342-15094	6E-96	gi 475621673 gb EMT31573.1 Ribonuclease 1 [Aegilops tauschii]
Contig5059_s_at	1BL-ab-k71_contig_3797658:2212-4443	0	#N/A
HVSMEf0013I09r2_at	2BS-ab-k71_contig_5166420:1548-4919	2E-46	gi 21668465 dbj BAA07785.3 plastid omega-3 fatty acid desaturase [Triticum aestivum]
Contig9169_at	2BS-ab-k71_contig_5200682:6276-9820	0	gi 475614190 gb EMT29002.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig628_x_at	5BL-ab-k71_contig_10831572:1917-3005	0	gi 475614190 gb EMT29002.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig418_at	1BL-ab-k71_contig_1678368:429-2096	0	gi 475614191 gb EMT29003.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig422_at	5AL-ab-k95_contig_2774278:3264-4547	0	gi 475614190 gb EMT29002.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig841_x_at	1BL-ab-k71_contig_1678368:429-2096	0	gi 475614190 gb EMT29002.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig828_s_at	1AL_v2-ab-k71_contig_3941328:9659-11114	0	gi 475614190 gb EMT29002.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig14143_s_at	6AL-ab-k71_contig_5764148:7642-9513	1E-152	gi 473777884 gb EMS46019.1 hypothetical protein TRIUR3_07308 [Triticum urartu]
Contig6_x_at	6AS-ab-k71_contig_4354575:1792-2909	0	gi 473952980 gb EMS50796.1 Chlorophyll a-b binding

Contig11957_at	2BS-ab-k71_contig_5229550:15258-16617	0	protein, chloroplastic [Triticum urartu] gi 475518448 gb EMT06200.1 Cytochrome P450 71C1 [Aegilops tauschii]
Contig347_s_at	6BS-ab-k71_contig_2981828:642-1842	0	gi 473952980 gb EMS50796.1 Chlorophyll a-b binding protein, chloroplastic [Triticum urartu]
Contig6484_at	7AL-ab-k71_contig_4554300:1636-4345	0	gi 296044566 gb ADG85703.1 putative NAC transcription factor [Triticum aestivum]
Contig2764_s_at	2BL-ab-k71_contig_7951021:10929-19547	0	gi 326507788 dbj BAJ86637.1 predicted protein [Hordeum vulgare subsp. vulgare]
HV03G23u_s_at	1BL-ab-k71_contig_3792355:1-3151	2E-63	gi 354681870 dbj BAL04915.1 glutamyl tRNA reductase [Triticum aestivum]
Contig636_at	1BL-ab-k71_contig_3813291:2683-4178	0	gi 475623771 gb EMT32357.1 Chlorophyll a-b binding protein of LHCII type III, chloroplastic [Aegilops tauschii]
Contig12240_at	6BL-ab-k71_contig_4303428:96-1083	0	gi 473822355 gb EMS47061.1 hypothetical protein TRIUR3_14995 [Triticum urartu]
baak1b18_at	7BS-ab-k71_contig_3100652:1-380	2E-92	#N/A
Contig15259_at	7BS-ab-k71_contig_3156232:805-2519	3E-37	gi 60100238 gb AAX13288.1 senescence-associated protein [Triticum aestivum]
HVSMEn0021L12r2_at	2BS-ab-k71_contig_5166420:1548-4919	2E-08	#N/A
baak1b18_x_at	7BS-ab-k71_contig_3100652:1-380	2E-92	#N/A
HVSMeg0006C07r2_at	2AL-ab-k71_contig_6363708:6428-7130	2E-58	gi 82780760 gb ABB90549.1 putative membrane protein [Triticum aestivum]
Contig18687_at	5BL-ab-k71_contig_10866110:23976-25433	3E-61	gi 475581852 gb EMT18963.1 hypothetical protein F775_26051 [Aegilops tauschii]
Contig1012_s_at	5BL-ab-k71_contig_10834918:4913-6105	0	gi 475614191 gb EMT29003.1 Chlorophyll a-b binding protein, chloroplastic [Aegilops tauschii]
Contig950_at	5AL-ab-k95_contig_1127310:1-799	1E-111	gi 131176 sp P13194.2 PSAE_HORVU RecName: Full=Photosystem I reaction center subunit IV, chloroplastic; Short=PSI-E; AltName: Full=Photosystem I 10.8 kDa polypeptide; Flags: Precursor gi 19087 emb CAA68782.1 unnamed protein product [Hordeum vulgare] gi 326503110 dbj BAJ99180.1 predicted protein [Hordeum vulgare subsp. vulgare] gi 226163 prf 1413233A 10.8kD photosystem I protein gi 82780760 gb ABB90549.1 putative membrane protein [Triticum aestivum]
Contig2859_s_at	2AL-ab-k71_contig_6363708:6428-7130	3E-98	gi 473952980 gb EMS50796.1 Chlorophyll a-b binding protein, chloroplastic [Triticum urartu]
Contig926_x_at	6BS-ab-k71_contig_2981828:642-1842	0	gi 473952980 gb EMS50796.1 Chlorophyll a-b binding protein, chloroplastic [Triticum urartu]
Contig26393_at	2BL-ab-k71_contig_7955957:1964-3724	1E-169	gi 326527993 dbj BAJ89048.1 predicted protein [Hordeum vulgare subsp. vulgare]
Contig2411_at	2AS-ab-k71_contig_5190107:3940-11214	1E-134	gi 357122526 ref XP_003562966.1 PREDICTED: uncharacterized protein LOC100831317 [Brachypodium distachyon]
Contig168_at	4AL_v2-ab-k71_contig_4AL_5754445:1016-3177	0	gi 473913339 gb EMS49688.1 Chlorophyll a-b binding protein CP26, chloroplastic [Triticum urartu]
Contig960_s_at	6AS-ab-k71_contig_4354575:1792-2909	1E-116	gi 473952980 gb EMS50796.1 Chlorophyll a-b binding protein, chloroplastic [Triticum urartu]
HO08B11S_at	4AL_v2-ab-k71_contig_4AL_7099598:762-2473	1E-44	gi 475559215 gb EMT13284.1 3-ketoacyl-CoA synthase 6 [Aegilops tauschii]

Table S5. List of 33 loci significantly upregulated between HD and 12 DAA in WT plants but not in *gpc-A1* plants.

Locus	IWGSC ID	Sequence description	Gene name
IWGSC_CSS_7AL_scaff_4381790:1-1789	Traes_7AL_6AE850114	Cadmium zinc-transporting ATPase 3	<i>TaHMA2-likeA</i>
IWGSC_CSS_7BL_scaff_6741649:1-1191	Traes_7BL_0CF58CF4E	Cadmium zinc-transporting ATPase 3	<i>TaHMA2-likeB</i>
IWGSC_CSS_3AS_scaff_3289235:1-527	Traes_3AS_E59FB52EC	Probable peptide nitrate transporter at3g43790-like	<i>TaZIFL2-like1A</i>
IWGSC_CSS_4BS_scaff_4884666:3611-13951	Traes_4BS_1DCF82CB7	Protein zinc induced facilitator-like 1-like	<i>TaZIFL3B</i>
IWGSC_CSS_7AL_scaff_4404279:2840-3532	Traes_7AL_F1D611563	Zinc transporter 10	<i>TaZIP10-like1A</i>
IWGSC_CSS_2BS_scaff_5173470:2532-5129	Traes_2BS_9D8F265EC	Zinc transporter 1	<i>TaZIP13-like2B</i>
IWGSC_CSS_2BL_scaff_8072119:162-3787	Traes_2BL_A1BCBD2BE	Zinc transporter 1	<i>TaZIP13-likeB</i>
IWGSC_CSS_2AL_scaff_1213723:1-2131	Traes_2AL_3983FD077	Zinc transporter zip1	<i>TaZIP3A</i>
IWGSC_CSS_1AS_scaff_3313103:14-652	Traes_1AS_EC8891094	Zinc transporter protein zip7	<i>TaZIP7A</i>
IWGSC_CSS_1AS_scaff_3258126:5939-9519	Traes_1AS_50323685E	Zinc transporter 7-like	<i>TaZIP7A</i>
IWGSC_CSS_1BS_scaff_3424485:2111-5600	Traes_1BS_D68F0BED6	Zinc transporter 7-like	<i>TaZIP7B</i>
IWGSC_CSS_7BS_scaff_3097754:654-17033	Traes_7BS_BB0FECDBE	ABC transporter C family member 10	
IWGSC_CSS_3AS_scaff_3280126:1-370	N/A	Aquaporin TIP4-3-like	
IWGSC_CSS_3B_scaff_7192099:7-5760	N/A	Coatomer subunit beta -1	
IWGSC_CSS_2BL_scaff_8006213:433-3492	Traes_2BL_ACB3018DD	Ferredoxin--NADP embryo chloroplastic	
IWGSC_CSS_2AL_scaff_6420325:2830-4395	Traes_2AL_D24C65691	Ferredoxin--NADP embryo chloroplastic	
IWGSC_CSS_4BS_scaff_4865990:1587-2676	Traes_4BS_FFF12BA9E	Ferritin 2a	
IWGSC_CSS_2BL_scaff_8011889:2013-8385	Traes_2BL_F2772688F	GDSL esterase lipase EXL3	
IWGSC_CSS_1BL_scaff_814680:1-755	Traes_1BL_8DAC11230	Inwardly rectifying potassium channel AKT2	
IWGSC_CSS_5AL_scaff_2808642:7307-9079	Traes_5AL_6C8BD96CB	Nucleolar protein 58-like isoform x1	
IWGSC_CSS_6AL_scaff_5832728:1-551	N/A	Peroxisomal multifunctional enzyme type 2	
IWGSC_CSS_6BL_scaff_3861072:390-904	N/A	Peroxisomal multifunctional enzyme type 2-like	
IWGSC_CSS_7AL_scaff_4506504:232-7123	Traes_7AL_7BD10B6C7	Pleiotropic drug resistance protein 12-like	
IWGSC_CSS_2BS_scaff_5172493:6780-8736	Traes_2BS_D5A97B888	Polyol transporter 5-like	
IWGSC_CSS_5AL_scaff_2750252:1939-3125	Traes_5AL_8F16AB90F	Probable auxin efflux carrier component 4-like	
IWGSC_CSS_2BL_scaff_8087489:9565-11148	Traes_2BL_0E87D8729	Probable peptide nitrate transporter at1g22540-like	
IWGSC_CSS_3B_scaff_10437122:613-1435	Traes_3B_F81203C21	Protein HASTY1-like	
IWGSC_CSS_1AL_scaff_2791900:7869-11173	Traes_1AL_039C1D96D	Protein RUPTURED POLLEN GRAIN 1	
IWGSC_CSS_1AL_scaff_3915680:8466-19572	Traes_1AL_C921492AA	Squamosa promoter-binding-like protein 9	
IWGSC_CSS_3B_scaff_10770864:1-1807	Traes_3B_F6D9A9AEE	S-type anion channel SLAH3	
IWGSC_CSS_4AL_scaff_495051:405-909	Traes_4AL_0FEA52671	Sulfate transporter	
IWGSC_CSS_2AL_scaff_6345426:2122-3685	N/A	Sulfate transporter	
IWGSC_CSS_1BL_scaff_3829677:1628-1984	Traes_1BL_CF65BE819	Zinc transporter 9-like	

Table S6. Details of field experiments.

Experiment	UCD-2012	TAU-2012	NY-2012	NY-2013
Location	Davis, CA, 38° 32' N, 121° 46' W	Tel-Aviv University 32° 6' N 34° 48' E	Newe Ya'ar Regional Research Center 32° 42' N 35° 10' E	Newe Ya'ar Regional Research Center 32° 42' N 35° 10' E
Planting date	11/23/2011	12/12/2011	12/7/2011	12/2/2012
Sowing	50 seeds per row	8 pre-germinated seedlings per row	8 pre-germinated seedlings per row	8 pre-germinated seedlings per row
Soil	Yolo loam soil (fine silty, mixed, superactive, nonacid, thermic Mollic Xerofluvent)	Hamra soil (90% sand, 10% clay, soil N 8.2 mg kg ⁻¹)	Heavy soil (18.7% inorganic matter, 22.6% sand, 57.0% silt, 1.7% clay and organic matter)	Heavy soil (18.7% inorganic matter, 22.6% sand, 57.0% silt, 1.7% clay and organic matter)
Precipitation during growing season (mm)	232	522	566	682
Irrigation	1 acre foot (326,000 gallons) added 05/17/2012	-	-	-
Fertilizer	11 g/row ammonium sulfate added 2/13/2012	100 kg ha ⁻¹ basal N fertilization	100 kg ha ⁻¹ basal N fertilization	100 kg ha ⁻¹ basal N fertilization
Randomized complete blocks	10	4	5	4

Table S7. qRT-PCR primers used in this study and their efficiency.

Target	F primer	R primer	Efficiency (%)
<i>HMA2-like</i>	GAGATCCATGGGCATCAAGT	CTCCGGCAAAAGTTCAGAG	97.4%
<i>NAAT2</i>	ACCCAGCAACCTTCATTCAG	CAGACCGATAATCCCCTTGA	95.5%
<i>ZIP10-like1</i>	GCCTTCTTCTTTGCCATCAC	GGGCTGTATGGGTCGTAGAA	95.0%
<i>ZIP10</i>	GTGGATCTCATTGCTGCTGA	AGCCCAAATAGCCAGTGATG	95.8%
<i>ZIP3</i>	CTTTGAAGGCATAGGCTTGG	GATGGTTGCCCTTACCTTGA	95.3%
<i>ZIP7</i>	CAGGGCTCTAGTGGTCGAAG	AGAAATCGGCTGCGATTAGA	97.3%