

Supplementary Material

Transcriptomic profiling revealed genes involved in response to cold stress in maize

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Additional files

Fig. S1 Venn diagram showing number of transcripts detected in M54 and 753F after cold stress for 4 and 24 h.

Fig. S2 COG function classification of consensus sequence. A, M54 after cold treatment for 4 h; B, M54 for 24 h; C, 753F for 4 h; D, 753F for 24 h.

Fig. S3 KEGG map of the photosynthesis-antenna proteins pathway. Results are an analysis of DEGs as determined by RNA-seq, comparing cold-treated samples to untreated controls. Boxes with a red frame indicate the corresponding DEGs were upregulated in the cold-treated samples, boxes with a green frame indicate the corresponding DEGs were downregulated in the cold-treated samples, boxes with a blue frame indicate some of the corresponding DEGs were downregulated and others were upregulated, and those without any colored frame indicate the expression levels of the corresponding genes were not changed.

Fig. S4 KEGG map of the photosynthesis pathway. Results are an analysis of DEGs as determined by RNA-seq, comparing cold-treated samples with untreated controls. Boxes with a red frame indicate the corresponding DEGs were upregulated in the cold-treated samples, boxes with a green frame indicate the corresponding DEGs were downregulated in the cold-treated samples, boxes with a blue frame indicate some of the corresponding DEGs were downregulated and others were upregulated, and those without any colored frame indicate the expression levels of the corresponding genes were not changed.

Fig. S5 KEGG map of the carbon fixation in photosynthetic organisms pathway. Results are an analysis of DEGs as determined by RNA-seq, comparing cold-treated samples to untreated controls. Boxes with a red frame indicate the corresponding DEGs were upregulated in the cold-treated samples, boxes with a green frame indicate the corresponding DEGs were downregulated in the cold-treated samples, boxes with a blue frame indicate some of the corresponding DEGs were downregulated and others were upregulated, and

those without any colored frame indicate the expression levels of the corresponding genes were not changed.

Fig. S6 DEGs mapped to KEGG pathways related to secondary metabolism

Table S1 Primer pairs for real-time quantitative PCR

Table S2 Clean reads used for further analysis

Table S3 DEGs mapped to KEGG pathways related to lipid metabolism

Table S4 DEGs mapped to KEGG pathways related to secondary metabolism

Table S5 Upregulated genes related to transcription factors

Fig. S1

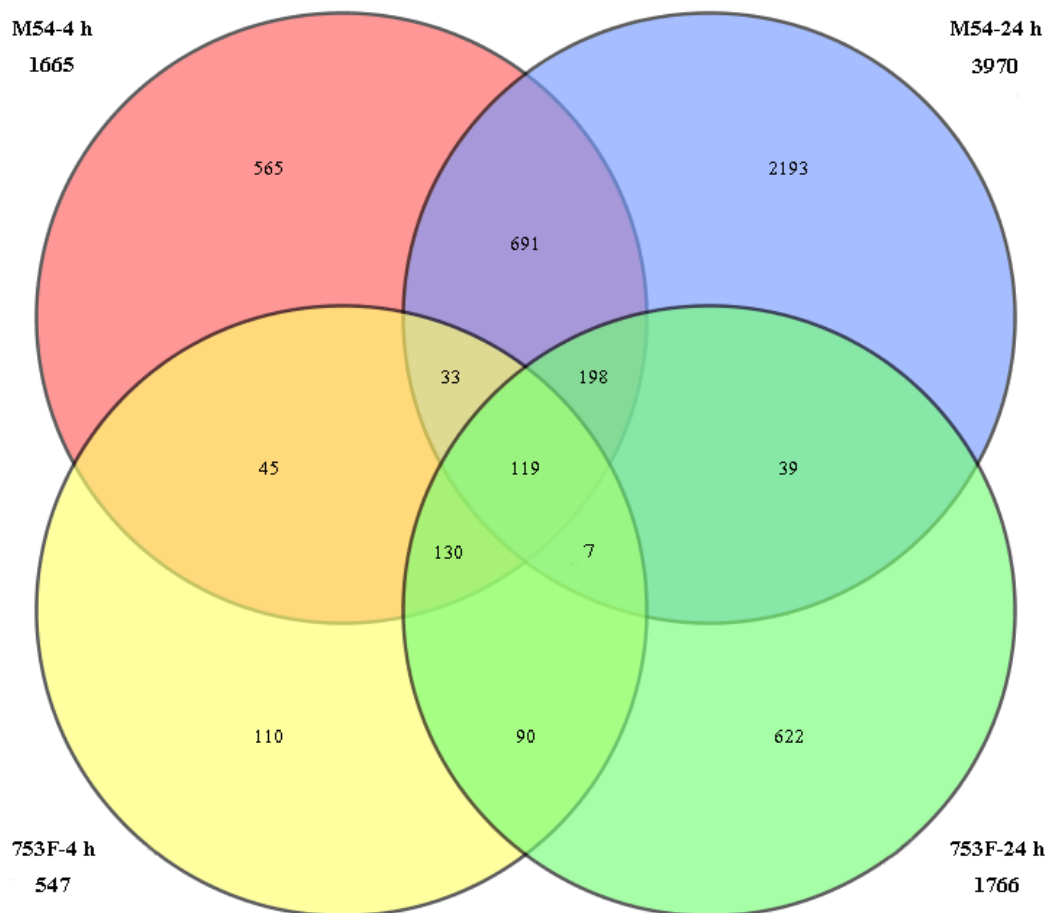


Fig. S2

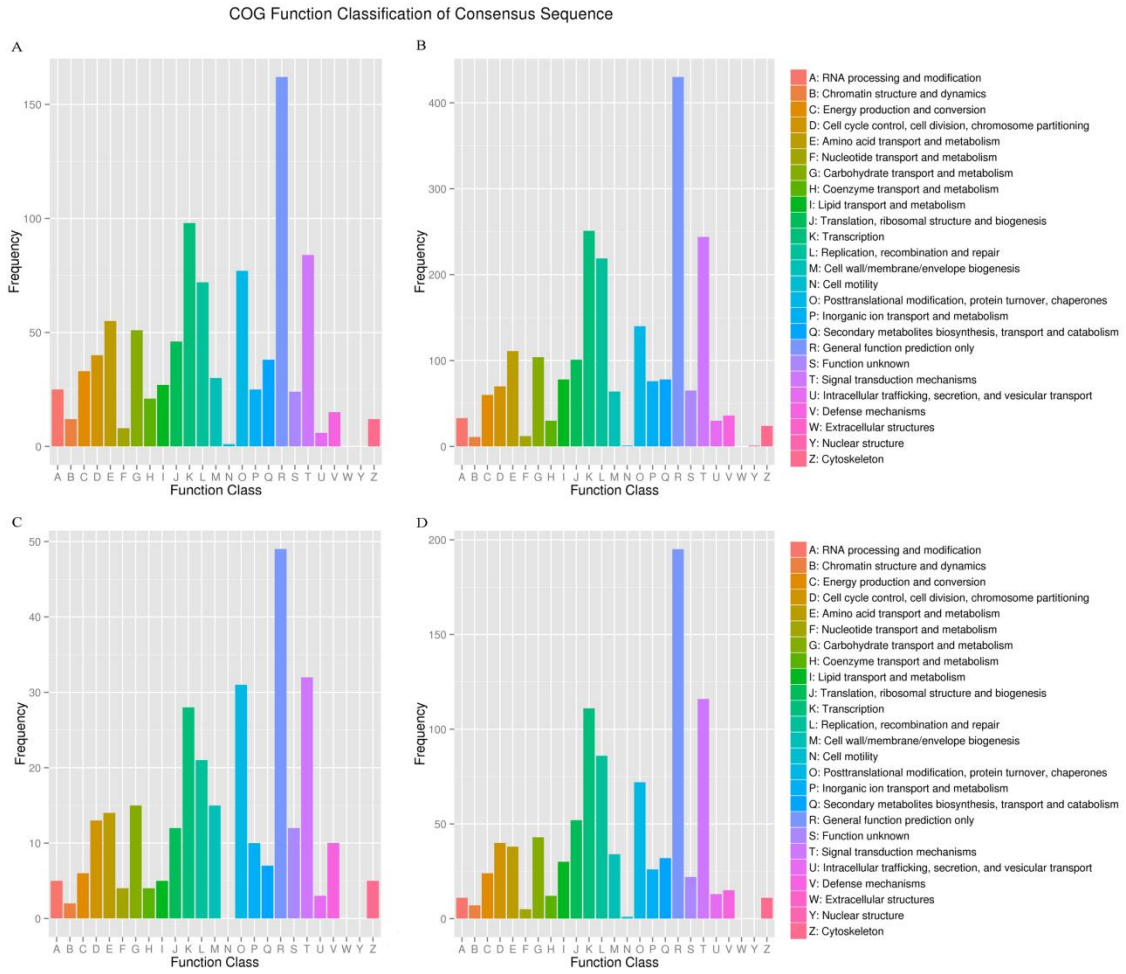


Fig. S3

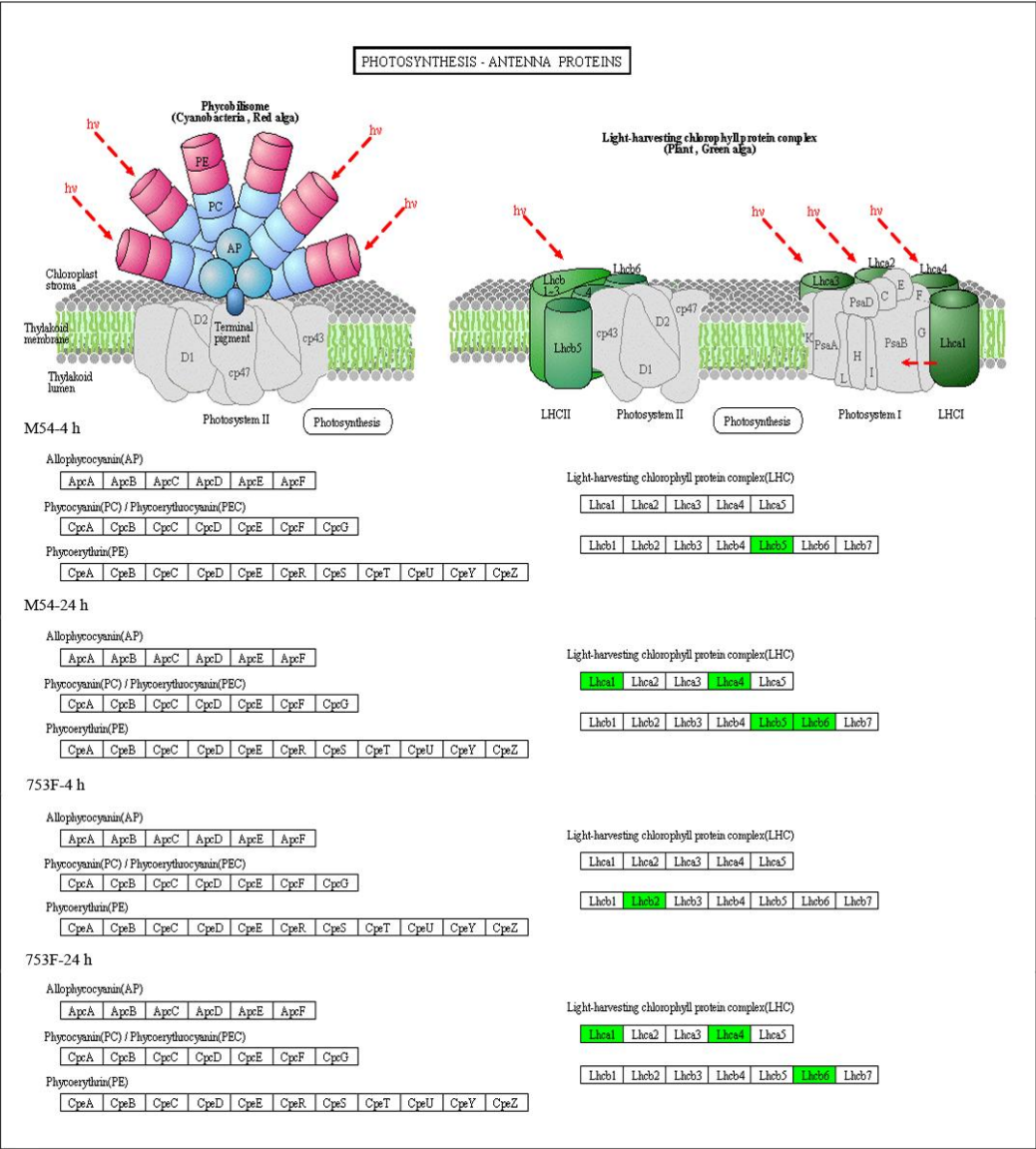


Fig. S4

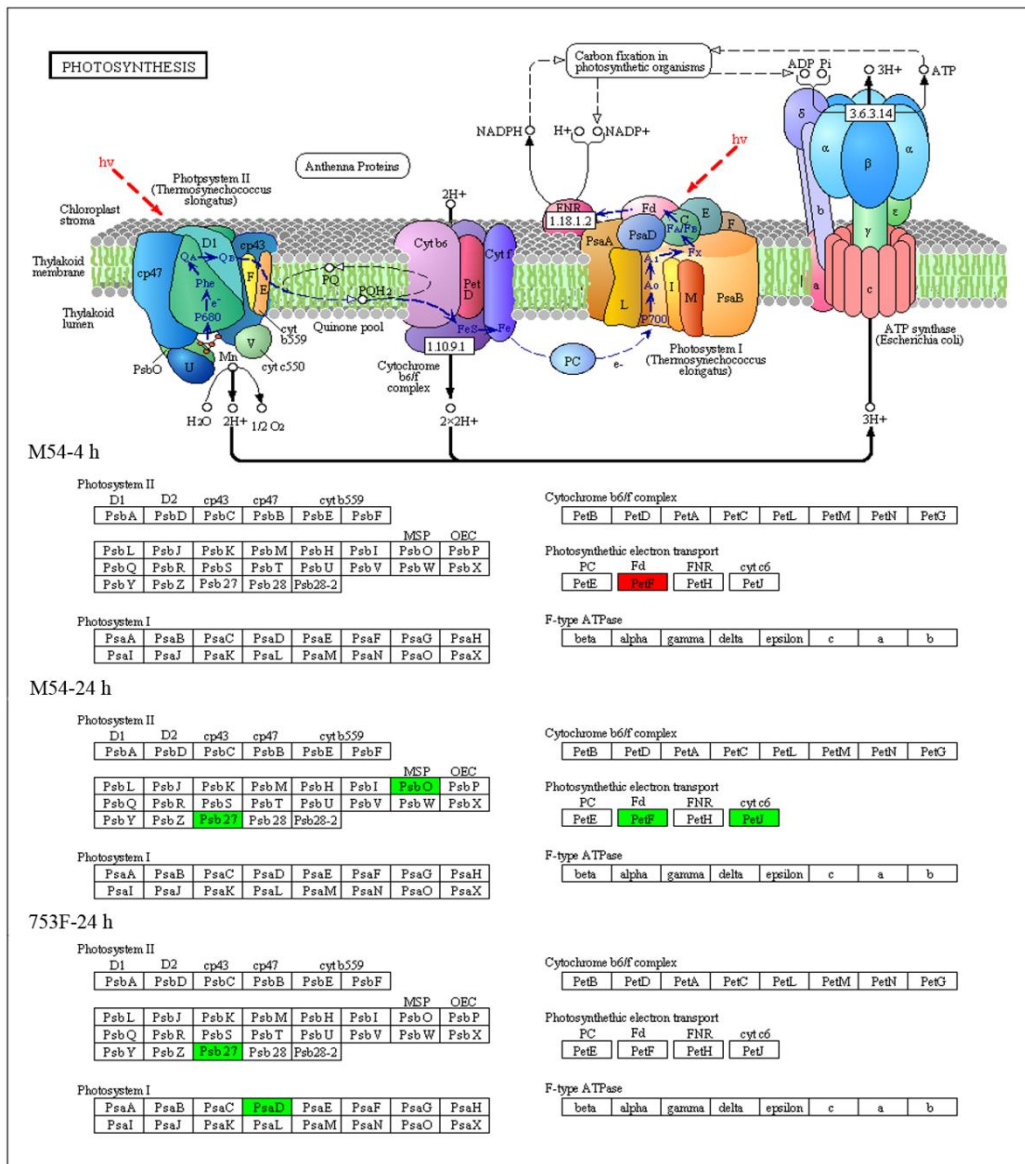


Fig. S5

Fig. S6

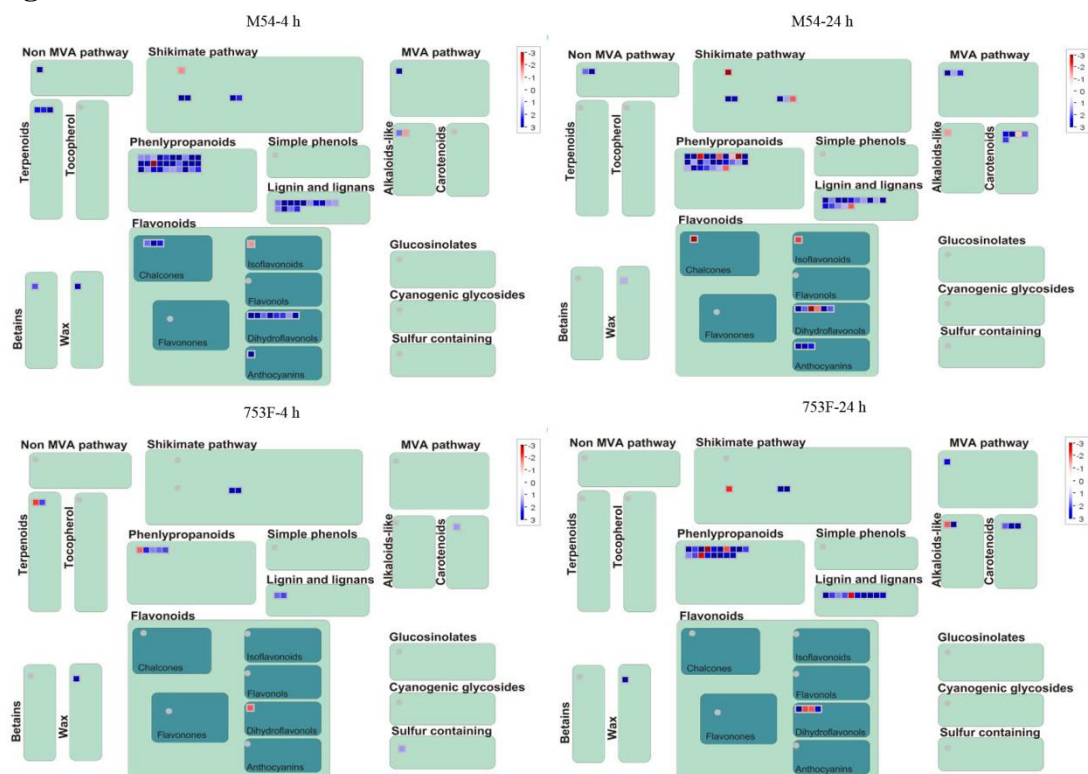


Table S1 Primer pairs for real-time quantitative PCR

Genes	Sequence
GRMZM2G069542	Sense: CCTACAATGCTCCTCTC Antisense: CCTCTGGTGTACTCTTG
GRMZM2G007489	Sense: CCTATGCCTGTCTTCTAAT Antisense: GTGTGACTGTGATGGTTA
GRMZM2G179792	Sense: GTACGTGTTCTCTTCTCC Antisense: CGAGGATCTGTCTGTCTT
GRMZM2G109056	Sense: CCTTCAAATATCATCAGATCAG Antisense: AACTCTTCGTCGGTCCTC
GRMZM6G617209	Sense: ATTCCAGACCCCAGCAAG Antisense: GAGTCCTATGGTGTGAACTT
GRMZM2G051262	Sense: TTGGTGAGCATAAGGTTT Antisense: GCTTCCCATATCTTCTTG
GRMZM2G427815	Sense: GCTCCACAGTGAACCTAAG Antisense: TCGTTGAATATACCACTAGC
GRMZM2G127948	Sense: TCAACAAGCTCAACAACCT Antisense: GTGGCGAGGAGGGAGTAG
GRMZM2G139874	Sense: CTAGAAATCAATGCGTGTT Antisense: GAAATACATCTCTCTTAGTAAA
GRMZM2G106263	Sense: ATCTTGCGAGTGAATATC Antisense: TTGTTGTATGGAGAATGG

GRMZM2G089698	Sense: CCTAGTATTCTCATGTGGTT
	Antisense: GATAGTACGGTGGATAGC
GRMZM2G029048	Sense: AAGGCAGCTCGTACATGA
	Antisense: GTATCTGTCCTGCTTCGG
GRMZM2G132898	Sense: CTATCTTCTCGTCGGATG
	Antisense: ATTCGTATCGCTCTTCCT
GRMZM2G036340	Sense: GGAGACTGATGCTGATGA
	Antisense: GGATCGATATGCCAGGTT
GRMZM2G144730	Sense: GAGCACTGAAGACACTGT
	Antisense: CATTCCCCATCCACTAAC
GRMZM2G156517	Sense: TTTGGTCACTATTCATTTTC
	Antisense: CCGTTGCTGTTGATATTC
GRMZM2G365160	Sense: CAAAGGAGGGTAGGAATA
	Antisense: CACTAAGCATCAACAA
GRMZM2G003331	Sense: AAATCCGAGGCAATACTG
	Antisense: TCCATCAAGAACTGTAACC
GRMZM5G867185	Sense: TTCACTGCTAACTGTATCT
	Antisense: CCAACATCTCATCATTCC
GRMZM2G032602	sense: ATCAATATGTTTCAGCAAT
	antisense: CCAGCCAATAATCAACTA
GRMZM2G141931	Sense: CATCATCAACTCACTCTACAG
	Antisense: CTAATCTTATCCAACGCATCA
GRMZM2G456471	sense: TCTGAATGTCCACGAACCT
	antisense: TACGAGCCAATCCACCAA
GRMZM2G352855	sense: CAGAAGATTCCATCCTAA
	antisense: ATGTCTAAACCATCACTT
GRMZM2G022679	sense: GACAACAATAACAACCACCAT
	antisense: TCTTCACCTTCTTCTTCTTCTT
GRMZM2G139874	Sense: CTAGAAATCAATGCGTGTT
	antisense: GAAATACATCTCCTCTTAGT
GRMZM2G046382	Sense: CTAAGACGGAGCAGATCA
	Antisense: AATGGACTTCACTTCAGG
GRMZM2G083810	Sense: GAGGAATAATCGTAGTCT
	Antisense: TCAGATAGGAATTGGTAG
GRMZM2G112609	Sense: GGTATGATTGCTGGACAT
	Antisense: CTTAATGAAGGACGGTGT
GRMZM5G883417	Sense:GGCTCCGTCATGCTCATG
	Antisense:GGCTCCGTCATGCTCATG
GRMZM2G354558	Sense:AATCAAACCAATTCCATC
	Antisense:AATCAAACCAATTCCATC
GRMZM2G064701	Sense:TCTTTCTTCACACTTTATCTACA
	Antisense:GCGAGTTTGGTTCAACTT
AC205703.4_FG006	Sense:CGTATGTTGACCAATTCT

	Antisense:TTGAGACAAGATACATTTCG
AC205703.4_FG006	Sense:CGTATGTTGACCAATTCT
	Antisense:TTGAGACAAGATACATTTCG
GRMZM2G128971	Sense:TTCCCGTTATACTTGTTT
	Antisense:GATGTTATGATGTCATTCTT
GRMZM2G110201	Sense:GCTGTTGAGTCACATAGA
	Antisense:GTATGAACTGGCACAATT
GRMZM2G085381	Sense:AAGCCAAGAACAACAACCT
	Antisense:TGATCTCCTTCATCCTGTCT
GRMZM2G085661	Sense:GACGACGATAAGGACTTCA
	Antisense:CTTGATATGGTCTCTGGTGA
GRMZM2G167549	Sense:ACTACGGACAATCTCAAG
	Antisense:TACTCTAGCGTCAGGTAA
GRMZM6G617209	Sense:ATTCCAGACCCCAGCAAG
	Antisense:GAGTCCTATGGTGTGAACTT
GRMZM2G427618	Sense:TACATTGCTCTGCTTCTTCT
	Antisense:AGGGAGATTTGGTCGAGA
GRMZM2G025832	Sense:ACACTAGGTTCAACGAGACTG
	Antisense:CGTGCTGGATGTCGTGTC
GRMZM2G035584	Sense:CRACTTCACGGACGACATCTC
	Antisense:ATGCCAACGCCGATAGCC
GRMZM2G062396	Sense:TCAAGAAGCAGGTCAAGG
	Antisense:CAAGAATGGCGTCGAGAG
GRMZM2G029048	Sense:TGAACGACTACTACAACAAC
	Antisense:TTGAAGCCGTAGTCCAAG
GRMZM2G042347	Sense:GAAGCCTAACAACAACCTC
	Antisense:CAAGCATATCGTGTTTAC

Table S2 Clean reads used for further analysis

Samples	Total reads	Total bases	GC%	Q30%
M54-C1	10,733,328	536,564,772	56.62%	93.58%
M54-C2	12,352,925	620,628,673	57.91%	93.39%
M54-C3	24,943,475	1,247,173,750	59.71%	96.69%
M54-4 h1	10,722,526	536,028,985	59.58%	93.12%
M54-4 h2	10,368,333	518,323,431	58.72%	93.17%
M54-4 h3	30,721,534	1,536,076,700	59.35%	96.71%
M54-24 h1	10,301,485	514,982,900	58.73%	93.36%
M54-24 h2	10,406,570	520,234,609	58.91%	93.12%
M54-24 h3	23,928,096	1,196,404,800	59.36%	96.67%
753F-C1	11,529,603	577,980,277	57.58%	93.23%
753F-C2	11,132,314	557,943,074	58.36%	93.16%
753F-C3	25,995,744	1,299,787,200	59.50%	96.64%
753F-4 h1	12,330,091	620,214,088	58.36%	93.18%
753F-4 h2	10,013,764	500,601,354	60.09%	93.05%
753F-4 h3	25,405,926	1,270,296,300	59.73%	96.64%
753F-24 h1	10,668,802	533,346,649	59.48%	92.73%
753F-24 h2	11,629,193	581,354,633	59.25%	92.87%
753F-24 h3	29,169,685	1,458,484,250	59.44%	96.60%

M54-C, M54-4 h and M54-24 h were used for leaves of M54 treated by chilling stress for 0, 4 and 24 h, respectively. 753F-C, 753F-4 h and 753F-24 h were used for leaves of 753F treated by chilling stress for 0, 4 and 24 h, respectively.

Table S3 DEGs mapped to KEGG pathways related to lipid metabolism

Gene ID	Annotation	M54-4 h		M54-24 h		753F-4 h		753F-24 h	
		FDR	Log ₂ F C	FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC
A: Biosynthesis of unsaturated fatty acids									
AC205703.4_FG006	glossy8	5.43E-04	1.96	-	-	-	-	-	-
GRMZM2G064701	omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2	2.79E-03	1.83	-	-	-	-	-	-
GRMZM2G354558	TPA: omega-3 fatty acid desaturase	4.01E-09	5.11	-	-	-	-	-	-
GRMZM5G883417	TPA: acyl-desaturase	2.26E-03	Inf	-	-	-	-	-	-
GRMZM2G099666	Acyl-coenzyme A oxidase 2, peroxisomal (Precursor)	-	-	2.51E-03	-1.77	-	-	-	-
GRMZM2G110201	3-ketoacyl-CoA thiolase 2, peroxisomal (Precursor)	-	-	5.78E-03	1.25	-	-	-	-
GRMZM2G128971	omega-3 fatty acid desaturase	-	-	4.41E-09	2.83	9.22E-05	2.07	-	-
GRMZM2G151087	PAS2	-	-	5.95E-03	-1.38	-	-	-	-
GRMZM2G181266	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase	-	-	3.67E-03	-2.77	-	-	-	-
GRMZM2G099666	Acyl-coenzyme A oxidase 2, peroxisomal (Precursor)	-	-	-	-	-	-	2.63E-06	3.22
B: Fatty acid biosynthesis									
GRMZM2G007489	Palmitoyl-acyl carrier protein thioesterase, chloroplastic (Precursor)	6.97E-07	2.30	3.03E-19	4.01	3.39E-06	2.41	2.68E-06	2.84
GRMZM2G101875	Long chain acyl-CoA synthetase 1	1.85E-05	2.02	-	-	-	-	-	-
GRMZM5G883417	TPA: acyl-desaturase	2.26E-03	Inf	-	-	-	-	-	-
GRMZM2G135498	3-oxoacyl-synthase I	-	-	5.38E-03	1.26	-	-	-	-
GRMZM2G406603	Palmitoyl-acyl carrier protein thioesterase, chloroplastic (Precursor)	-	-	1.73E-03	1.85	-	-	-	-
GRMZM2G464176	putative acyl-ACP thioesterase family protein	-	-	1.47E-05	4.81	-	-	-	-

C: Fatty acid degradation

GRMZM2G101875	Long chain acyl-CoA synthetase 1	1.85E-05	2.02	-	-	-	-	-	-
GRMZM2G152975	Alcohol dehydrogenase-like 4	2.18E-03	1.48	-	-	-	-	-	-
GRMZM2G099666	Acyl-coenzyme A oxidase 2, peroxisomal (Precursor)	-	-	2.51E-03	-1.77	-	-	2.63E-06	3.22
GRMZM2G110201	3-ketoacyl-CoA thiolase 2, peroxisomal (Precursor)	-	-	5.78E-03	1.25	-	-	-	-

D: Fatty acid metabolism

AC205703.4_FG006	glossy8	5.43E-04	1.96	3.03E-19	4.01	-	-	-	-
GRMZM2G007489	Palmitoyl-acyl carrier protein thioesterase, chloroplast (Precursor)	6.97E-07	2.30	3.03E-19	4.01	3.39E-06	2.41	2.68E-06	2.84
GRMZM2G064701	omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2	2.79E-03	1.83	-	-	-	-	-	-
GRMZM2G101875	Long chain acyl-CoA synthetase 1	1.85E-05	2.02	-	-	-	-	-	-
GRMZM2G354558	TPA: omega-3 fatty acid desaturase	4.01E-09	5.11	-	-	-	-	-	-
GRMZM5G883417	TPA: acyl-desaturase	2.26E-03	Inf	-	-	-	-	-	-
GRMZM2G099666	Acyl-coenzyme A oxidase 2, peroxisomal (Precursor)	-	-	2.51E-03	-1.77	-	-	2.63E-06	3.22
GRMZM2G110201	3-ketoacyl-CoA thiolase 2, peroxisomal (Precursor)	-	-	5.78E-03	1.25	-	-	-	-
GRMZM2G128971	omega-3 fatty acid desaturase	-	-	4.41E-09	2.83	9.22E-05	2.07	-	-
GRMZM2G135498	3-oxoacyl-synthase I	-	-	5.38E-03	1.26	-	-	-	-
GRMZM2G151087	PAS2	-	-	5.95E-03	-1.38	-	-	-	-
GRMZM2G181266	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase	-	-	3.67E-03	-2.77	-	-	-	-
GRMZM2G406603	Palmitoyl-acyl carrier protein thioesterase,	-	-	1.73E-03	1.85	-	-	-	-

GRMZM2G464176	chloroplastic (Precursor) putative acyl-ACP thioesterase family protein	-	-	1.47E-05	4.81	-	-	-	-	
E: Glycerolipid metabolism										
AC233887.1_FG006	Digalactosyldiacylglycerol synthase 1, chloroplastic	7.01E-05	-1.89	1.64E-05	-1.96	6.18E-03	-1.64	-	-	
GRMZM2G020320	glycerol-3-phosphate acyltransferase 8	5.85E-03	1.36	-	-	-	-	-	-	
GRMZM2G072298	TPA: glycerol-3-phosphate acyltransferase 1	2.24E-11	4.49	-	-	-	-	-	-	
GRMZM2G447433	Lipid phosphate phosphatase 2	1.86E-05	-2.23	2.41E-10	-2.75	-	-	1.12E-04	-2.38	
GRMZM2G037104	1-acyl-sn-glycerol-3-phosp hate acyltransferase PLS1	-	-	1.64E-03	-1.49	-	-	-	-	
GRMZM2G099481	uncharacterized protein LOC100279857	-	-	4.65E-05	1.74	-	-	1.94E-03	2.01	
GRMZM2G146463	Alpha-galactosidase (Precursor) Probable	-	-	1.97E-28	7.44	-	-	1.31E-03	3.63	
GRMZM2G178892	monogalactosyldiacylglyce rol synthase 3, chloroplastic (Precursor)	-	-	7.87E-04	3.40	-	-	-	-	
GRMZM2G059637	Glycerol-3-phosphate acyltransferase 5	-	-	-	-	-	-	3.40E-03	1.81	
GRMZM2G062429	Diacylglycerol kinase 5 Probable	-	-	-	-	-	-	3.55E-04	2.26	
GRMZM2G070304	glycerol-3-phosphate acyltransferase 3	-	-	-	-	-	-	6.85E-09	3.64	
GRMZM2G128214	diacylglycerol kinase isoform 1	-	-	-	-	-	-	8.66E-03	1.75	
GRMZM2G177150	Glycerol-3-phosphate acyltransferase 1	-	-	-	-	-	-	3.93E-03	4.39	
F: Glycerophospholipid metabolism										
GRMZM2G015908	Inorganic pyrophosphatase 1	5.97E-05	2.13	-	-	-	-	1.59E-03	3.98	
GRMZM2G020320	glycerol-3-phosphate	5.85E-03	1.36	-	-	-	-	-	-	

	acyltransferase 8								
GRMZM2G072298	TPA: glycerol-3-phosphate acyltransferase 1	2.24E-11	4.49	-	-	-	-	-	-
GRMZM2G122296	Phosphoethanolamine N-methyltransferase 1	6.67E-06	2.21	2.18E-03	1.55	-	-	-	-
GRMZM2G132898	choline-phosphate cytidyltransferase B	5.19E-04	1.70	2.76E-11	2.90	-	-	-	-
GRMZM2G170400	Phosphoethanolamine N-methyltransferase 1	3.52E-08	2.56	-	-	-	-	-	-
GRMZM2G179792	Phospholipase D alpha 1	1.13E-04	2.03	8.06E-05	2.01	-	-	-	-
GRMZM2G447433	Lipid phosphate phosphatase2	1.86E-05	-2.23	2.41E-10	-2.75	-	-	1.12E-04	-2.38
GRMZM5G836174	Inorganic pyrophosphatase 1	3.01E-05	3.68	-	-	-	-	-	-
GRMZM2G015692	hypothetical protein ZEAMMB73_017576	-	-	1.51E-03	-1.50	-	-	-	-
GRMZM2G034697	uncharacterized protein LOC100276493	-	-	9.94E-03	-1.20	-	-	-	-
GRMZM2G037104	1-acyl-sn-glycerol-3-phosph ate acyltransferase PLS1	-	-	1.64E-03	-1.49	-	-	-	-
GRMZM2G081719	Vegetative cell wall protein gp1 (Precursor)	-	-	3.23E-05	-3.56	-	-	-	-
GRMZM2G085926	uncharacterized protein LOC100191152	-	-	4.51E-03	-1.25	-	-	-	-
GRMZM2G099481	uncharacterized protein LOC100279857	-	-	4.65E-05	1.74	-	-	1.94E-03	2.01
GRMZM2G100333	uncharacterized protein LOC100280298	-	-	4.24E-08	2.39	-	-	1.04E-07	3.25
GRMZM2G155357	hypothetical protein ZEAMMB73_658422	-	-	8.96E-05	1.86	-	-	-	-
GRMZM2G337128	Manganese-dependent ADP-ribose/CDP-alcohol diphosphatase	-	-	7.35E-04	-3.26	-	-	-	-
GRMZM2G352855	Lecithin-cholesterol acyltransferase-like 1	-	-	5.74E-03	-2.70	7.64E-04	-2.33	1.16E-05	-3.22
GRMZM2G469409	TPA: hypothetical protein ZEAMMB73_138989	-	-	3.44E-06	2.07	-	-	1.83E-05	2.57

GRMZM2G477340	phosphatidylserine synthase2	-	-	2.08E-07	2.55	-	-	5.86E-04	2.29
GRMZM2G017550	Probable glycerophosphoryl diester phosphodiesterase 1 (Precursor)	-	-	-	-	-	-	1.51E-03	Inf
GRMZM2G059637	Glycerol-3-phosphate acyltransferase 5	-	-	-	-	-	-	3.40E-03	1.81
GRMZM2G062429	Diacylglycerol kinase 5 Probable	-	-	-	-	-	-	3.55E-04	2.26
GRMZM2G070304	glycerol-3-phosphate acyltransferase 3	-	-	-	-	-	-	6.85E-09	3.64
GRMZM2G128214	diacylglycerol kinase isoform 1	-	-	-	-	-	-	8.66E-03	1.75
GRMZM2G177150	Glycerol-3-phosphate acyltransferase 1	-	-	-	-	-	-	3.93E-03	4.39
G: Linoleic acid metabolism									
GRMZM2G015419	Lipoxygenase 2.3, chloroplastic (Precursor)	6.88E-07	2.32	-	-	-	-	-	-
GRMZM2G102760	lipoxygenase	5.87E-04	2.52	-	-	-	-	-	-
GRMZM2G106748	lipoxygenase	2.70E-13	3.48	-	-	-	-	-	-
GRMZM2G109056	Probable linoleate 9S-lipoxygenase 4	2.99E-07	2.40	4.82E-18	3.88	-	-	3.73E-05	2.67
GRMZM2G156861	lipoxygenase	9.59E-03	4.33	-	-	-	-	-	-
GRMZM2G147752	Secologanin synthase	-	-	2.75E-08	3.17	-	-	-	-
GRMZM5G822593	Probable lipoxygenase 8, chloroplastic (Precursor)	-	-	-	-	-	-	6.68E-05	3.39
H: Sphingolipid metabolism									
GRMZM2G134248	Long chain base biosynthesis protein 1a	7.27E-04	-4.26	-	-	-	-	-	-
GRMZM2G165613	Long chain base biosynthesis protein 1a	3.15E-03	-1.55	-	-	-	-	-	-
GRMZM2G444378	Long chain base biosynthesis protein 1a	4.88E-03	-1.50	-	-	-	-	-	-
GRMZM2G044175	Sphinganine C(4)-monooxygenase 1	-	-	2.82E-03	-1.87	-	-	-	-
GRMZM2G146463	Alpha-galactosidase (Precursor)	-	-	1.97E-28	7.44	-	-	1.31E-03	3.63

GRMZM2G300944	hypothetical protein	-	-	3.36E-03	-1.43	-	-	-	-
GRMZM2G374827	Vegetative cell wall protein gp1 (Precursor)	-	-	4.57E-03	1.29	-	-	-	-
GRMZM5G836378	Sphinganine C(4)-monooxygenase 1	-	-	6.59E-06	1.91	-	-	6.51E-04	2.14
GRMZM2G003526	Sphinganine C(4)-monooxygenase 1	-	-	-	-	-	-	2.36E-03	3.69

Legend: DEGs mapped to the metabolism pathway of photosynthesis, photosynthesis-antenna proteins and carbon fixation in photosynthetic organisms. "FDR" means false discovery rate, "FC" means fold change, "Inf" means Infinite, "-" means the expression of the gene was not changed under salt stress. Some of the DEGs appeared several times in the table as they are involved in multiple pathways.

Table S4 DEGs mapped to KEGG pathways related to secondary metabolism

Gene ID	Annotation	M54-4 h		M54-24 h		753F-4 h		753F-24 h	
		FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC
A: Benzoxazinoid biosynthesis									
GRMZM2G063756	Cytochrome P450 monooxygenase CYP71C3v2	2.28E-03	1.75	5.93E-03	-1.91	-	-	-	-
GRMZM2G085381	Indole-3-glycerol phosphate lyase, chloroplastic (Precursor)	1.64E-22	9.04	-	-	-	-	-	-
GRMZM2G085661	Indole-2-monooxygenase	5.48E-07	Inf	-	-	-	-	-	-
GRMZM2G167549	Cytochrome P450 CYP71C2v2	5.89E-04	2.22	-	-	-	-	-	-
GRMZM6G617209	DIBOA-glucoside dioxygenase BX6	3.87E-09	4.15	5.36E-17	3.81	-	-	-	-
GRMZM2G046163	Indole-3-glycerol phosphate lyase, chloroplastic (Precursor)	-	-	2.15E-03	1.70	-	-	-	-
GRMZM2G085054	Benzoxazinone synthesis8	-	-	4.71E-04	1.58	-	-	-	-
B: Diterpenoid biosynthesis									
GRMZM2G022679	Gibberellin 2-beta-dioxygenase	2.72E-23	5.56	3.13E-17	8.60	7.19E-06	2.32	2.44E-03	4.50
GRMZM2G036340	GA 3-oxidase 1	1.30E-11	4.51	2.76E-11	4.65	-	-	5.46E-03	2.91
GRMZM2G427618	Gibberellin 2-beta-dioxygenase	1.89E-03	Inf	-	-	-	-	-	-

GRMZM2G051619	Gibberellin 2-beta-dioxygenase	-	-	3.16E-06	4.78	-	-	9.36E-16	6.49
GRMZM2G155686	Gibberellin 2-beta-dioxygenase	-	-	-	-	-	-	4.48E-03	Inf
GRMZM2G022679	Gibberellin 2-beta-dioxygenase	2.72E-23	5.56	3.13E-17	8.60	7.19E-06	2.32	2.44E-03	4.50

C: Flavonoid biosynthesis

GRMZM2G025832	Red aleurone1 Shikimate	9.60E-04	4.22	-	-	-	-	-	-
GRMZM2G035584	O-hydroxycinnamoyltransferase	6.10E-03	1.38	-	-	-	-	-	-
GRMZM2G062396	Naringenin,2-oxoglutarate 3-dioxygenase	1.80E-06	2.22	-	-	-	-	-	-
GRMZM2G089698	Anthranilate N-benzoyltransferase protein 1	3.49E-03	1.69	4.14E-08	4.95	-	-	1.24E-05	3.45
GRMZM2G099363	Caffeoyl-CoA O-methyltransferase 2	4.85E-04	1.77	1.49E-11	2.99	-	-	7.44E-07	3.38
GRMZM2G127948	Caffeoyl-CoA 3-O-methyltransferase 1	9.05E-04	2.25	5.44E-06	2.12	-	-	8.16E-06	2.87
GRMZM2G139874	Trans-cinnamate 4-monooxygenase	2.22E-07	2.79	2.13E-19	4.73	5.26E-04	1.87	1.13E-03	3.24
GRMZM2G155329	Chalcone--flavonone isomerase	2.64E-04	1.84	-	-	-	-	-	-
GRMZM2G004138	TPA: caffeoyl-CoA O-methyltransferase 1	-	-	4.20E-04	2.40	-	-	-	-
GRMZM2G097841	Leucoanthocyanidin reductase	-	-	1.15E-04	-1.82	-	-	-	-
GRMZM2G138074	Cytochrome P450 98A1	-	-	7.21E-04	1.61	-	-	-	-
GRMZM2G010468	Putative cytochrome P450 superfamily protein	-	-	-	-	-	-	3.05E-03	-2.25

D: Isoquinoline alkaloid biosynthesis

GRMZM2G146677	Aspartate aminotransferase	-	-	3.08E-03	1.38	-	-	-	-
GRMZM2G002652	Probable aminotransferase TAT2	-	-	-	-	-	-	5.55E-03	-1.75
GRMZM2G006480	Nicotianamine aminotransferase A	-	-	-	-	-	-	8.89E-04	2.18
GRMZM2G056469	Tyrosine decarboxylase	-	-	-	-	-	-	1.50E-03	5.39

E: Monoterpenoid biosynthesis

AC210013.4_FG006	Salutaridine reductase	6.27E-04	1.63	-	-	-	-	-	-
GRMZM2G170017	Salutaridine reductase	9.67E-03	Inf	1.02E-03	Inf	-	-	-	-

F: N-Glycan biosynthesis

GRMZM2G051262	Dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase	2.68E-04	-2.13	3.07E-06	-2.77	2.74E-04	-2.44	1.19E-05	-3.13
GRMZM2G062488	Acetylglucosaminyltransferase/transferase	1.54E-06	-2.31	1.28E-10	-2.74	-	-	-	-
GRMZM2G079682	DNA-directed RNA polymerase II subunit RPB1	6.45E-03	2.13	-	-	-	-	5.07E-03	1.81
GRMZM2G045435	Uncharacterized protein LOC100501240	-	-	1.53E-04	2.49	-	-	-	-
GRMZM2G056036	TPA: hypothetical protein ZEAMMB73_746806	-	-	4.16E-03	-1.65	-	-	-	-
GRMZM2G059393	TPA: hypothetical protein ZEAMMB73_651652	-	-	6.65E-03	-2.40	-	-	-	-
GRMZM2G084515	Vegetative cell wall protein gp1 (Precursor)	-	-	1.44E-05	-2.72	-	-	-	-
GRMZM2G128914	Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1 Probable	-	-	1.56E-03	2.09	-	-	5.18E-03	1.78
GRMZM2G149946	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 3 (Precursor)	-	-	1.13E-03	-1.87	-	-	-	-
GRMZM2G104118	N-acetylglucosaminyltransferase III	-	-	-	-	-	-	4.22E-04	2.31
GRMZM2G124671	UDP-N-acetylglucosamine transferase subunit alg13	-	-	-	-	-	-	7.61E-03	-4.22
GRMZM2G133048	Hypothetical protein ZEAMMB73_937323	-	-	-	-	-	-	9.48E-03	1.64

G: Phenylpropanoid biosynthesis

GRMZM2G008247	Beta-glucosidase2	1.32E-05	3.70	-	-	-	-	-	-
GRMZM2G017186	TPA: exhydrolase II	2.08E-04	2.43	-	-	-	-	-	-
GRMZM2G029048	Phenylalanine ammonia-lyase	1.83E-06	2.59	9.38E-04	1.73	-	-	-	-
GRMZM2G035584	Shikimate O-hydroxycinnamoyltransferase	6.10E-03	1.38	-	-	-	-	-	-
GRMZM2G042347	Cationic peroxidase 1 (Precursor)	2.93E-04	Inf	1.72E-08	Inf	-	-	-	-
GRMZM2G047456	Peroxidase 35 (Precursor)	8.72E-04	3.14	-	-	-	-	-	-

GRMZM2G054013	Probable 4-coumarate--CoA ligase 2	5.35E-03	1.48	5.05E-08	2.38	-	-	-	-
GRMZM2G063917	Phenylalanine ammonia-lyase	9.24E-03	4.94	-	-	-	-	-	-
GRMZM2G069024	Beta-glucosidase 5 (Precursor)	5.10E-03	-1.46	1.72E-03	-1.37	-	-	8.22E-04	-2.04
GRMZM2G071021	Cytosolic aldehyde dehydrogenase RF2C	5.47E-11	3.07	2.72E-03	3.06	-	-	-	-
GRMZM2G074604	Phenylalanine/tyrosine ammonia-lyase	2.31E-03	1.59	-	-	-	-	-	-
GRMZM2G076946	Beta-glucosidase, chloroplastic (Precursor)	2.63E-04	2.39	-	-	-	-	-	-
GRMZM2G077015	Beta-glucosidase, chloroplastic (Precursor)	1.61E-06	2.60	-	-	-	-	-	-
GRMZM2G080183	Peroxidase 16 (Precursor)	4.06E-03	1.47	3.40E-06	2.09	-	-	-	-
GRMZM2G081582	Phenylalanine ammonia-lyase	1.67E-04	1.84	-	-	-	-	-	-
GRMZM2G085967	Peroxidase 3 (Precursor)	1.51E-06	4.62	1.23E-12	4.76	-	-	-	-
GRMZM2G089698	Shikimate O-hydroxycinnamoyltransferase	3.49E-03	1.69	4.14E-08	4.95	-	-	1.24E-05	3.45
GRMZM2G099363	Caffeoyl-CoA O-methyltransferase 2	4.85E-04	1.77	1.49E-11	2.99	-	-	7.44E-07	3.38
GRMZM2G108153	Cationic peroxidase SPC4 (Precursor)	1.49E-04	3.04	-	-	-	-	-	-
GRMZM2G117706	Peroxidase 70 (Precursor)	9.37E-08	4.01	2.50E-29	7.26	-	-	1.83E-05	4.33
GRMZM2G118003	Beta-glucosidase 7 (Precursor)	2.69E-03	1.57	-	-	-	-	-	-
GRMZM2G126261	Peroxidase 42 (Precursor)	6.17E-03	1.58	-	-	-	-	-	-
GRMZM2G127948	Caffeoyl-CoA 3-O-methyltransferase 1	9.05E-04	2.25	5.44E-06	2.12	-	-	8.16E-06	2.87
GRMZM2G139874	Trans-cinnamate 4-monooxygenase	2.22E-07	2.79	2.13E-19	4.73	5.26E-04	1.87	1.13E-03	3.24
GRMZM2G147687	TPA: exoglucanase Precursor	7.66E-04	1.61	-	-	-	-	-	-
GRMZM2G150893	Peroxidase 54 precursor	1.43E-09	3.17	-	-	-	-	-	-
GRMZM2G170692	Phenylalanine ammonia-lyase	2.43E-04	6.06	-	-	-	-	-	-
GRMZM2G334660	Phenylalanine ammonia-lyase	7.22E-10	Inf	4.41E-13	Inf	-	-	-	-
GRMZM2G394500	Peroxidase 2 (Precursor)	1.14E-08	2.66	-	-	-	-	-	-
GRMZM2G405581	Peroxidase 70 (Precursor)	1.17E-03	2.27	5.08E-08	3.24	-	-	1.60E-04	3.56
GRMZM2G427815	TPA: peroxidase J	1.23E-12	4.62	2.37E-05	4.49	-	-	-	-
GRMZM2G441347	TPA: phenylalanine ammonia-lyase	7.15E-04	3.15	-	-	-	-	-	-
GRMZM2G471357	Peroxidase 52 isoform 1	1.94E-07	-2.44	8.50E-25	-5.11	-	-	4.30E-06	-3.43
AC196475.3_FG004	Catechol O-methyltransferase	-	-	4.55E-03	1.29	-	-	-	-

AC210173.4_FG005	Cytochrome P450 84A1	-	-	4.03E-04	1.65	-	-	-	-
GRMZM2G004138	TPA: caffeoyl-CoA O-methyltransferase 1	-	-	4.20E-04	2.40	-	-	-	-
GRMZM2G023840	Peroxidase 72 (Precursor)	-	-	2.92E-04	3.99	-	-	-	-
GRMZM2G075333	Probable 4-coumarate--CoA ligase 3	-	-	1.49E-05	1.89	-	-	2.05E-03	2.05
GRMZM2G108207	Cationic peroxidase SPC4 (Precursor)	-	-	5.81E-04	2.18	-	-	4.03E-04	3.22
GRMZM2G118610	Putative cinnamyl-alcohol dehydrogenase family protein	-	-	6.05E-06	-1.96	-	-	-	-
GRMZM2G130904	TPA: peroxidase R11	-	-	9.04E-05	3.04	-	-	-	-
GRMZM2G135108	Peroxidase	-	-	1.91E-05	-2.25	-	-	-	-
GRMZM2G136534	Peroxidase 55 (Precursor)	-	-	4.61E-06	1.96	-	-	-	-
GRMZM2G138074	Cytochrome P450 98A1	-	-	7.21E-04	1.61	-	-	-	-
GRMZM2G163544	Beta-glucosidase 25 (Precursor)	-	-	7.25E-03	-3.15	-	-	-	-
GRMZM2G320269	Peroxidase 1 (Precursor)	-	-	2.44E-03	-Inf	-	-	-	-
GRMZM2G365774	Peroxidase 2 (Precursor)	-	-	3.23E-04	-2.42	-	-	-	-
GRMZM2G408963	Peroxidase 65 precursor	-	-	1.09E-04	-2.60	-	-	-	-
GRMZM5G810727	Beta-glucosidase	-	-	4.14E-05	-2.26	-	-	-	-
GRMZM2G167613	Probable cinnamyl alcohol dehydrogenase 6	-	-	-	-	7.60E-05	2.08	1.89E-05	2.76
GRMZM2G010468	Trans-cinnamate 4-monooxygenase	-	-	-	-	-	-	3.05E-03	-2.25
GRMZM2G048522	Probable 4-coumarate--CoA ligase 5	-	-	-	-	-	-	1.26E-04	-2.63
GRMZM2G055320	Probable 4-coumarate--CoA ligase 4	-	-	-	-	-	-	8.18E-03	1.67
GRMZM2G070603	Peroxidase 1	-	-	-	-	-	-	4.90E-09	-3.53
GRMZM2G104109	Peroxidase 1 precursor	-	-	-	-	-	-	1.07E-04	Inf
GRMZM2G116823	Peroxidase 54 (Precursor)	-	-	-	-	-	-	2.08E-05	-Inf
GRMZM2G129493	Polygalacturonase inhibitor (Precursor)	-	-	-	-	-	-	1.69E-05	-4.52
GRMZM2G174732	Probable 4-coumarate--CoA ligase 1	-	-	-	-	-	-	2.60E-05	2.53
GRMZM2G321839	Peroxidase 1 (Precursor)	-	-	-	-	-	-	3.17E-03	1.87

H: Sesquiterpenoid and triterpenoid biosynthesis

GRMZM2G105787	Squalene monooxygenase	4.88E-08	2.53	-	-	-	-	-	-
GRMZM2G091456	Squalene monooxygenase	-	-	1.11E-11	-2.91	-	-	-	-

I: Steroid biosynthesis

AC233853.1_FG003	Cytochrome P450 710A1	6.46E-03	1.35	-	-	-	-	-	-	-
GRMZM2G006937	Achilleol B synthase	5.01E-05	2.30	-	-	-	-	-	-	-
GRMZM2G100060	Achilleol B synthase	6.34E-08	2.51	-	-	-	-	-	-	-
GRMZM2G105787	Squalene monooxygenase	4.88E-08	2.53	-	-	-	-	-	-	-
GRMZM2G091456	Squalene monooxygenase	-	-	1.11E-11	-2.91	-	-	-	-	-
GRMZM2G126682	24-methylenesterol C-methyltransferase 2	-	-	2.96E-17	4.05	3.03E-04	1.92	1.08E-04	2.47	-
GRMZM5G850019	Delta(7)-sterol-C5(6)-desaturase	-	-	8.46E-03	-1.29	-	-	-	-	-
GRMZM5G899349	Obtusifoliol 14-alpha demethylase	-	-	2.57E-04	-1.72	-	-	8.28E-06	-2.77	-

J: Stilbenoid, diarylheptanoid and gingerol biosynthesis

GRMZM2G035584	Shikimate O-hydroxycinnamoyltransferase	6.10E-03	1.38	-	-	-	-	-	-	-
GRMZM2G089698	Anthranilate N-benzoyltransferase protein 1	3.49E-03	1.69	4.14E-08	4.95	-	-	1.24E-05	3.45	-
GRMZM2G099363	Caffeoyl-CoA O-methyltransferase 2	4.85E-04	1.77	1.49E-11	2.99	-	-	7.44E-07	3.38	-
GRMZM2G127948	Caffeoyl-CoA 3-O-methyltransferase 1	9.05E-04	2.25	5.44E-06	2.12	-	-	8.16E-06	2.87	-
GRMZM2G139874	Putative cytochrome P450 superfamily protein	2.22E-07	2.79	2.13E-19	4.73	5.26E-04	1.87	1.13E-03	3.24	-
GRMZM2G004138	TPA: caffeoyl-CoA O-methyltransferase1	-	-	4.20E-04	2.40	-	-	-	-	-
GRMZM2G138074	Cytochrome P450 98A1	-	-	7.21E-04	1.61	-	-	-	-	-
GRMZM2G010468	Putative cytochrome P450 superfamily protein	-	-	-	-	-	-	3.05E-03	-2.25	-

K: Synthesis and degradation of ketone bodies

GRMZM2G106263	Hydroxymethylglutaryl-CoA synthase	7.00E-03	3.62	1.63E-06	3.33	-	-	-	-	-
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L: Terpenoid backbone biosynthesis

GRMZM2G106263	Hydroxymethylglutaryl-CoA synthase	7.00E-03	3.62	1.63E-06	3.33	-	-	-	-	-
GRMZM2G493395	TPA: 1-deoxy-D-xylulose 5-phosphate synthase	3.58E-03	7.00	-	-	-	-	-	-	-
AC234201.1_FG003	Farnesylcysteine lyase (Precursor)	-	-	3.25E-04	-2.29	-	-	-	-	-
GRMZM2G001645	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3	-	-	1.33E-03	1.43	-	-	-	-	-
GRMZM2G007957	Dehydrodolichyl diphosphate synthase 6	-	-	1.88E-03	-1.47	-	-	-	-	-

GRMZM2G036290	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic (Precursor)	-	-	3.20E-05	1.88	-	-	-	-
GRMZM2G058095	3-hydroxy-3-methylglutaryl-coenzyme A reductase	-	-	3.70E-03	2.32	-	-	-	-
GRMZM2G123503	CAAX prenyl protease 2	-	-	7.98E-03	-2.45	-	-	-	-
GRMZM2G146437	Dehydrololichyl diphosphate synthase 2	-	-	1.85E-03	-1.88	-	-	-	-
GRMZM2G439203	Carboxylesterase-like protein	-	-	5.58E-04	1.49	-	-	-	-
GRMZM2G473976	Probable isoprenylcysteine alpha-carbonyl methylesterase ICME	-	-	3.87E-08	2.67	-	-	4.98E-03	2.15
GRMZM5G856881	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase, chloroplastic (Precursor)	-	-	4.24E-10	2.93	-	-	-	-
GRMZM2G054803	Dehydrololichyl diphosphate synthase 2	-	-	-	-	2.52E-04	-2.14	-	-
GRMZM2G058095	3-hydroxy-3-methylglutaryl-coenzyme A reductase	-	-	-	-	-	-	6.69E-05	2.48

M: Tropane, piperidine and pyridine alkaloid biosynthesis

GRMZM2G097981	Tropinone reductase 2	-	-	2.82E-05	2.25	-	-	-	-
GRMZM2G146677	Aspartate aminotransferase	-	-	3.08E-03	1.38	-	-	-	-
GRMZM2G002652	Probable aminotransferase TAT2	-	-	-	-	-	-	5.55E-03	-1.75
GRMZM2G006480	Nicotianamine aminotransferase A	-	-	-	-	-	-	8.89E-04	2.18

N: Ubiquinone and other terpenoid-quinone biosynthesis

GRMZM2G054013	Putative AMP-dependent synthetase and ligase superfamily protein	5.35E-03	1.48	5.05E-08	2.38	-	-	-	-
GRMZM2G139874	Putative cytochrome P450 superfamily protein	2.22E-07	2.79	2.13E-19	4.73	5.26E-04	1.87	1.13E-03	3.24
GRMZM2G075333	Probable 4-coumarate--CoA ligase 3	-	-	1.49E-05	1.89	-	-	2.05E-03	2.05
GRMZM2G002652	Probable aminotransferase TAT2	-	-	-	-	-	-	5.55E-03	-1.75
GRMZM2G006480	Nicotianamine aminotransferase A	-	-	-	-	-	-	8.89E-04	2.18
GRMZM2G010468	Trans-cinnamate 4-monooxygenase	-	-	-	-	-	-	3.05E-03	-2.25
GRMZM2G048522	Probable 4-coumarate--CoA ligase 5	-	-	-	-	-	-	1.26E-04	-2.63
GRMZM2G055320	Putative AMP-dependent synthetase and ligase superfamily protein	-	-	-	-	-	-	8.18E-03	1.67

GRMZM2G174732	Putative AMP-dependent synthetase and ligase superfamily protein	-	-	-	-	-	-	2.60E-05	2.53
O: Vitamin B6 metabolism									
GRMZM2G120652	TPA: Pyridoxin biosynthesis protein ER1	-	-	2.83E-05	-2.01	-	-	-	-
GRMZM5G850015	Pyridoxin biosynthesis protein ER1	-	-	1.73E-03	-1.51	-	-	-	-

Legend: DEGs mapped to the metabolism pathway of photosynthesis, photosynthesis-antenna proteins and carbon fixation in photosynthetic organisms. "FDR" means false discovery rate, "FC" means fold change, "Inf" means Infinite, "-" means the expression of the gene was not changed under salt stress. Some of the DEGs appeared several times in the table as they are involved in multiple pathways.

Table S5 Up-regulated genes related to transcription factor

Gene ID	Annotation	Log ₂ FC			
		M54-4 h	M54-24 h	753F-4 h	753F-24 h
GRMZM2G068715_T01	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	--	--	2.202	3.527
GRMZM2G158835_T01	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	--	--	1.726	2.372
GRMZM5G841101_T01	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	--	--	--	-1.742
GRMZM2G037444_T02	agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	--	-1.17	--	--
AC217050.4_FGT004	agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	--	-1.58	--	--
GRMZM2G441583_T01	AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding	--	1.557	--	--
GRMZM2G105250_T01	AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding	--	--	--	2.587
GRMZM2G007791_T01	AGO2 (argonaute 2); nucleic acid binding	--	1.902	--	--
GRMZM2G158918_T01	AL6 (ALFIN-LIKE 6); DNA binding / methylated histone residue binding	--	-1.935	--	--
GRMZM2G153087_T01	AL7 (ALFIN-LIKE 7); DNA binding / methylated histone residue binding	--	-1.344	--	--
GRMZM2G107807_T02	AL7 (ALFIN-LIKE 7); DNA binding / methylated histone residue binding	--	-2.047	--	-1.898
GRMZM2G004531_T01	anac017 (Arabidopsis NAC domain containing protein 17); transcription factor	--	1.643	--	--

GRMZM2G068973_T01	anac032 (Arabidopsis NAC domain containing protein 32); transcription factor	--	3.947	--		2.419
GRMZM2G030325_T01	ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor	--	2.06	--	--	
GRMZM2G126817_T01	anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	--	4.581	--	--	
GRMZM2G386163_T01	ANAC038 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 38); transcription factor	--	--	--	--	5.501
GRMZM2G011598_T01	anac047 (Arabidopsis NAC domain containing protein 47); transcription factor	--	-2.091	--	--	
GRMZM2G079632_T01	ANAC055 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 55); transcription factor	--	2.053	--	--	
GRMZM2G082709_T01	anac071 (Arabidopsis NAC domain containing protein 71); transcription factor	--	8.21	--	--	
GRMZM2G159500_T02	ANAC087; transcription factor	--	--	--	--	2.326
GRMZM2G031001_T01	ANAC087; transcription factor	--	--	--	--	2.345
GRMZM2G116658_T01	ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	--	2.592	--	--	
GRMZM2G367834_T01	APRR5 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator	3.721	5.918		5.414	5.891
GRMZM2G179024_T01	APRR5 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator	3.838	5.451		3.854	4.521
GRMZM2G017187_T02	ARF1 (AUXIN RESPONSE FACTOR 1); DNA binding / transcription factor	--	2.978	--	--	2.376
GRMZM2G081406_T01	ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	--	1.568	--	--	

GRMZM2G160005_T01	ARF19 (AUXIN RESPONSE FACTOR 19); DNA binding / transcription factor	1.515	--	--	--	
GRMZM2G116557_T03	ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	--		1.84	--	--
GRMZM2G338259_T01	ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	--		2.34	--	2.133
GRMZM2G317900_T01	ARF6 (AUXIN RESPONSE FACTOR 6); transcription factor	1.376		1.726	--	--
GRMZM2G110109_T01	ARID/BRIGHT DNA-binding domain-containing protein	--		1.835	--	--
GRMZM2G409974_T01	ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	--		2.948	--	--
GRMZM2G136884_T01	aspartyl protease family protein	2.156		2.501		2.14
GRMZM2G381739_T01	aspartyl protease family protein	--		4.136	--	--
GRMZM2G376825_T01	aspartyl protease family protein	--		3.181	--	--
GRMZM2G128333_T01	aspartyl protease family protein	--		4.825	--	--
GRMZM2G036134_T01	aspartyl protease family protein	--		2.312	--	--
GRMZM2G153523_T01	aspartyl protease family protein	--	--			1.611
GRMZM2G475265_T01	aspartyl protease family protein	--	--			-2.672
GRMZM2G014653_T03	ATAF1; transcription activator/ transcription factor	--		2.046	--	2.212
GRMZM2G180328_T01	ATAF1; transcription activator/ transcription factor	--	--		--	2.88
GRMZM2G347043_T01	ATAF2; transcription activator	--		1.716	--	--
GRMZM2G143211_T01	AtATG18d	-1.88		-1.701	--	--
GRMZM2G118690_T02	ATBPC6; DNA binding / transcription factor	--		-1.93	--	--
GRMZM2G065566_T01	ATEXO70B1 (exocyst subunit EXO70 family protein B1); protein binding	--		1.254	--	--
GRMZM5G869403_T02	ATEXO70B1 (exocyst subunit EXO70 family protein B1); protein binding	--	--		--	1.87
GRMZM2G162065_T01	ATEXO70G1 (exocyst subunit EXO70 family protein G1); protein binding	--		2.878	--	1.792
GRMZM2G129261_T02	AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc	--		1.978	--	--

	ion binding				
GRMZM2G004957_T02	ATML1 (MERISTEM LAYER 1); DNA binding / sequence-specific DNA binding / transcription factor	--	-2.019	--	--
GRMZM2G158700_T02	AtMYB78 (myb domain protein 78); DNA binding / transcription factor	2.84	--	--	--
GRMZM2G143046_T02	AtMYB78 (myb domain protein 78); DNA binding / transcription factor	2.359	--	--	--
GRMZM2G134279_T01	AtMYB78 (myb domain protein 78); DNA binding / transcription factor	--	3.362	--	--
GRMZM2G160840_T01	AtMYB78 (myb domain protein 78); DNA binding / transcription factor	--	--	--	6.403
GRMZM2G430849_T01	ATNAC2 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 2); transcription factor	--	1.252	--	--
GRMZM2G087787_T01	ATNFXL1 (ARABIDOPSIS THALIANA NF-X-LIKE 1); protein binding / transcription factor/ zinc ion binding	-2.533	--	--	--
GRMZM2G012453_T01	ATP-dependent RNA helicase, putative ATRBL14 (ARABIDOPSIS	--	--	1.528	2.588
GRMZM2G053066_T01	RHOMBOID-LIKE PROTEIN 14); zinc ion binding	-5.141	-4.526	--	-2.483
GRMZM2G467907_T02	ATRBP47B (RNA-binding protein 47B); RNA binding	2.733	4.23	--	1.934
GRMZM2G069678_T01	ATRBP47C' (RNA-binding protein 47C'); RNA binding	--	1.606	--	--
GRMZM2G076636_T01	basic helix-loop-helix (bHLH) family protein	-2.523	-2.442	--	-2.11
GRMZM2G064466_T01	BEL1 (BELL 1); DNA binding / protein binding / transcription factor	--	2.07	--	--
GRMZM2G458728_T05	BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	--	1.452	1.764	1.912
GRMZM2G396114_T02	BLH4 (BEL1-LIKE HOMEODOMAIN 4); DNA binding / transcription factor	--	2.003	1.734	1.964
GRMZM2G024851_T01	bZIP family transcription factor	1.737	2.757	--	--

GRMZM2G094352_T01	bZIP family transcription factor	--	--	--		2.273
GRMZM2G055413_T07	bZIP transcription factor family protein	--		-1.395	--	--
GRMZM2G162749_T01	CDF3 (CYCLING DOF FACTOR 3); DNA binding / protein binding / transcription factor	--	--			1.828
GRMZM2G052416_T01	CHC1	--		-1.822	--	--
GRMZM2G089506_T01	chloroplast nucleoid DNA-binding protein, putative	--	--			-3.375
GRMZM2G025592_T01	CMT3 (chromomethylase 3); DNA (cytosine-5-)-methyltransferase		1.546	--	--	--
GRMZM2G075562_T01	COL9 (CONSTANS-LIKE 9); transcription factor/ zinc ion binding	--		1.683	--	--
GRMZM2G011173_T01	DCP1 (decapping 1); m7G(5')pppNdiphosphatase/ protein homodimerization	--	--			-2.522
GRMZM2G403636_T01	DEAD box RNA helicase, putative (RH11)	--	--		2.056	3.334
GRMZM2G448104_T03	DNA binding	--		1.334	--	--
GRMZM2G436226_T01	DNA binding / nucleic acid binding / protein binding / zinc ion binding	--		1.745	--	--
GRMZM2G393471_T01	DNA binding / nucleic acid binding / protein binding / zinc ion binding	--		2.182	--	1.924
GRMZM2G468479_T01	DNA binding / nucleic acid binding / transcription factor	--		3.336	--	--
GRMZM2G097726_T02	DNA binding / protein binding / zinc ion binding		-2.096	-3.044	--	-2.342
GRMZM5G871463_T02	DNA binding / protein binding / zinc ion binding	--		-1.499	--	--
GRMZM2G091265_T02	DNA binding / protein binding / zinc ion binding	--		-1.404	--	--
GRMZM2G447745_T01	DNA binding / transcription factor	--	--			1.869
GRMZM2G047370_T02	DNA binding protein GT-1	--		-2.433	-2.603	-3.708
GRMZM2G353779_T01	DNA-binding bromodomain-containing protein	--		-1.564	--	--
GRMZM2G072117_T02	DNA-binding family protein / AT-hook protein 1 (AHP1)		2.493	4.056	--	--
GRMZM2G089163_T02	DRB3 (dsRNA-binding protein 3); RNA binding / double-stranded RNA binding	--	--			-2.508

GRMZM2G393742_T01	DRD1 (DEFECTIVE IN RNA-DIRECTED DNA METHYLATION 1); ATP binding / DNA binding / helicase/ nucleic acid binding	--	--	--	-3.565
AC233850.1_FGT005	E2F3 (E2F TRANSCRIPTION FACTOR 3); DNA binding / transcription factor	--	4.172	--	--
GRMZM2G041701_T02	E2F3 (E2F TRANSCRIPTION FACTOR 3); DNA binding / transcription factor	--	2.163	--	3.067
GRMZM2G431243_T02	EICBP.B (ETHYLENE INDUCED CALMODULIN BINDING PROTEIN); calmodulin binding / transcription activator/ transcription regulator	--	2.431	--	--
AC234203.1_FGT011	EIL3 (ETHYLENE-INSENSITIVE3-LIKE3); DNA binding / transcription factor	--	-2.039	--	--
GRMZM2G426154_T01	EMB2219 (embryo defective 2219)	--	-2.34	--	-3.092
GRMZM2G171395_T01	EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	3.861	--	5.138	4.866
GRMZM2G312712_T01	EMB2454 (embryo defective 2454); protein binding / zinc ion binding	--	-2.364	--	--
GRMZM2G044322_T01	ethylene insensitive 3 family protein	0	--	--	--
GRMZM2G030710_T01	ETT (ETTIN); DNA binding / transcription factor	1.861	2.191	--	--
GRMZM2G056120_T01	ETT (ETTIN); DNA binding / transcription factor	--	1.254	--	--
GRMZM2G362557_T01	FUNCTIONS IN: molecular_functionunknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF659 (InterPro:IPR007021); BEST Arabidopsis thaliana protein match is: protein dimerization (TAIR:AT5G31412.1); Has	--	1.345	--	--

GRMZM2G024550_T01	<p>380 Blast hits to 376 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 2; Plants - 368; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).</p> <p>FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial transcription termination factor-related (InterPro:IPR003690); BEST Arabidopsis thaliana protein match is: EMB2219 (embryo defective 2219) (TAIR:AT2G21710.1); Has 760 Blast hits to 374 proteins in 45 species: Archae - 0; Bacteria - 0; Metazoa - 99; Fungi - 0; Plants - 624; Viruses - 0; Other Eukaryotes - 37 (source: NCBI BLink).</p>	-2.079	--	--	-2.98
GRMZM2G101518_T01	<p>FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDC (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink).</p>	--	1.524	1.617	--
GRMZM2G123159_T01	<p>GCN5-related N-acetyltransferase (GNAT) family protein</p>	-1.383	-1.826	--	--

GRMZM2G010075_T02	GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUPE 4); DNA binding	1.619	2.111	1.479	2.021
GRMZM2G167718_T02	GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUPE 4); DNA binding	--	-2.447	--	--
GRMZM2G148074_T01	HAT3 (HOMEODOMAIN ZIPPER PROTEIN 3); transcription factor	--	3.023	--	2.487
GRMZM2G126646_T01	HDG11 (HOMEODOMAIN GLABROUS 11); DNA binding / transcription factor	2.493	--	--	--
GRMZM2G145690_T01	HDG11 (HOMEODOMAIN GLABROUS 11); DNA binding / transcription factor	--	--	--	inf
AC198361.3_FGT004	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative	--	--	1.752	2.299
GRMZM2G158162_T01	HSI2 (HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE 2); transcription factor/ transcription repressor	--	1.287	--	--
GRMZM2G173534_T02	ICE1 (INDUCER OF CBF EXPRESSION 1); DNA binding / transcription activator/ transcription factor	--	2.731	--	2.535
GRMZM2G117441_T01	Kin17 DNA-binding protein-related	-2.064	-2.339	--	--
GRMZM2G060507_T01	KNAT7 (KNOTTED-LIKE HOMEODOMAIN OF ARABIDOPSIS THALIANA 7); DNA binding / transcription activator/ transcription factor	--	--	--	3.171
GRMZM2G072518_T01	leucine-rich repeat family protein	1.468	--	--	--
GRMZM2G144097_T01	LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	2.226	--	--	--
GRMZM2G070446_T01	LZF1 (LIGHT-REGULATED ZINC FINGER PROTEIN 1); transcription factor/ zinc ion binding	--	1.65	--	--
GRMZM2G106233_T01	MFP1 (MAR BINDING FILAMENT-LIKE PROTEIN 1); DNA binding	--	--	--	-2.377

GRMZM2G022213_T01	MGP (Magpie); nucleic acid binding / protein binding / transcription factor/ zinc ion binding	--	1.203	--	--	
GRMZM2G061542_T01	mitochondrial transcription termination factor-related / mTERF-related	--	2.07	--	--	
GRMZM5G862467_T01	mob1/phocein family protein	--	3.235	--	--	
GRMZM2G010920_T01	myb family transcription factor	-1.669	-2.437	--	--	-2.229
GRMZM2G400489_T01	myb family transcription factor	2.733	4.47	--	--	
GRMZM2G348238_T01	myb family transcription factor	--	2.131	--	--	1.885
GRMZM2G173943_T02	myb family transcription factor	--	2.253	--	--	2.147
GRMZM2G057408_T01	myb family transcription factor	--	2.002	--	--	
GRMZM2G034110_T01	myb family transcription factor	--	--	--	--	2.047
GRMZM2G047600_T01	MYB112 (myb domain protein 112); DNA binding / transcription factor	6.22	--	--	--	-3.782
GRMZM2G055158_T01	MYB20 (myb domain protein 20); DNA binding / transcription factor	--	2.842	--	--	
GRMZM2G117244_T01	MYB36 (myb domain protein 36); DNA binding / transcription factor	--	3.484	--	--	
GRMZM2G405094_T01	MYB4; DNA binding / transcription factor	1.315	--	--	--	
GRMZM2G084583_T01	MYB4; DNA binding / transcription factor	-4.883	-4.066	--	--	-2.044
GRMZM2G050305_T01	MYB4; DNA binding / transcription factor	2.96	3.877	--	--	
GRMZM2G160838_T01	MYB4; DNA binding / transcription factor	1.471	--	--	--	
GRMZM2G089244_T01	MYB4; DNA binding / transcription factor	--	4.2	--	--	2.657
GRMZM2G041415_T01	MYB4; DNA binding / transcription factor	--	-2.218	--	--	
GRMZM2G431156_T02	MYB4; DNA binding / transcription factor	--	--	--	1.763	--
GRMZM2G048136_T02	MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor	-3.266	-3.43	--	--	
GRMZM2G108959_T01	MYB60 (myb domain protein 60); DNA binding / transcription factor	-1.884	--	--	--	
GRMZM2G017520_T01	MYB61 (MYB DOMAIN PROTEIN	2.495	--	--	--	

GRMZM2G171781_T01	61); DNA binding / transcription factor MYB61 (MYB DOMAIN PROTEIN 61); DNA binding / transcription factor	3.202	--	--	--	
GRMZM2G127490_T01	61); DNA binding / transcription factor MYB61 (MYB DOMAIN PROTEIN 61); DNA binding / transcription factor	7.616		7.818	--	5.253
GRMZM2G139688_T01	65); DNA binding / transcription factor MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	--	--	--	--	-2.548
GRMZM2G006352_T01	84); DNA binding / transcription factor MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	--	--	2.214	--	2.822
GRMZM2G037650_T01	MYB85 (myb domain protein 85); DNA binding / transcription activator/transcription factor	-3.522		-3.572	--	--
GRMZM2G048910_T01	MYB85 (myb domain protein 85); DNA binding / transcription activator/transcription factor	--	--	2.259	4.477	4.556
GRMZM2G050550_T01	MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor	--	--	2.107	--	--
GRMZM2G701218_T01	MYR1 (MYb-related protein 1); transcription factor	--	--	-2.038	--	--
GRMZM2G035465_T04	PAP2 (PHYTOCHROME-ASSOCIATED PROTEIN 2); transcription factor	--	--	1.266	--	1.675
GRMZM2G067702_T02	PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor	1.696		3.753	2.204	3.333
GRMZM2G339736_T01	PCS1 (PROMOTION OF CELL SURVIVAL 1); aspartic-type endopeptidase/ peptidase	--	--	3.016	--	1.697
GRMZM2G426888_T01	pentatricopeptide repeat-containing protein (PPR)	-2.248		-4.376	--	-1.844
GRMZM2G399750_T02	pentatricopeptide repeat-containing protein (PPR)	--	--	-3.234	--	--
GRMZM2G073460_T01	pentatricopeptide repeat-containing protein (PPR)	--	--	-5.238	--	-3.167
GRMZM2G440349_T01	pentatricopeptide repeat-containing protein (PPR)	--	--	-2.117	--	--
GRMZM2G033884_T01	pentatricopeptide repeat-containing protein (PPR)	--	--	4.046	--	--
GRMZM2G053396_T01	pentatricopeptide (PPR)	--	--	0	--	--

	repeat-containing protein						
GRMZM2G017197_T02	pentatricopeptide	(PPR)	--	4.527	--		3.441
	repeat-containing protein						
GRMZM2G703373_T01	pentatricopeptide	(PPR)	--	5.094	--	--	
	repeat-containing protein						
GRMZM2G171994_T01	pentatricopeptide	(PPR)	--	-2.156	--		-2.13
	repeat-containing protein						
GRMZM2G481373_T01	pentatricopeptide	(PPR)	--		--		-3.226
	repeat-containing protein						
GRMZM2G076950_T01	pentatricopeptide	(PPR)	--		--		-2.086
	repeat-containing protein						
GRMZM2G068331_T02	PHD finger family protein		--		--		5.435
	PMH2 (putative mitochondrial RNA						
GRMZM2G565140_T01	helicase 2); ATP binding / ATP-dependent		--		--	1.687	2.22
	helicase/ helicase/ nucleic acid binding						
	PMH2 (putative mitochondrial RNA						
GRMZM2G107984_T02	helicase 2); ATP binding / ATP-dependent		--		--		2.422
	helicase/ helicase/ nucleic acid binding						
	PUX2 (PLANT UBX						
GRMZM2G327459_T01	DOMAIN-CONTAINING PROTEIN 2);		--	2.814	--		1.816
	nucleic acid binding / zinc ion binding						
GRMZM2G021483_T01	PWWP domain-containing protein		--	1.541	--	--	
GRMZM2G163717_T04	receptor/ zinc ion binding		--	-1.297	--	--	
GRMZM2G100641_T01	receptor/ zinc ion binding		--	4.737	--		2.711
	REF6 (RELATIVE OF EARLY						
GRMZM2G431157_T01	FLOWERING 6); nucleic acid binding /		--	-2.005	--		-3.112
	transcription factor/ zinc ion binding						
GRMZM2G119426_T02	remorin family protein			4.379	4.929	--	--
GRMZM2G162598_T01	remorin family protein		--	4.323	2.447	--	
	RHL1 (ROOT HAIRLESS 1); DNA						
GRMZM2G406101_T03	binding / protein binding		--	3.273	--		2.293
	RNA recognition motif						
GRMZM2G125529_T01	(RRM)-containing protein		--		--	-2.823	-4.149
	RNA recognition motif						
GRMZM2G127559_T01	(RRM)-containing protein		--		--		2.338
	RNA-binding protein 45 (RBP45),						
GRMZM2G426591_T01	putative		--	2.788	--		2.158

GRMZM2G005459_T01	RNA-binding protein, putative	--	--		2.889	--	
GRMZM5G814159_T01	RNA-binding protein, putative	--	--	--			-2.164
GRMZM2G074645_T01	RPL (REPLUMLESS); DNA binding / sequence-specific DNA binding / transcription factor		1.574	2.603	1.629		2.475
GRMZM2G154641_T01	RPL (REPLUMLESS); DNA binding / sequence-specific DNA binding / transcription factor		2.354	2.871	--		1.681
GRMZM2G105004_T02	RWP-RK domain-containing protein		-1.72	--	--	--	
GRMZM2G031398_T01	RWP-RK domain-containing protein		-2.164	-2.934	--		-1.769
GRMZM2G042278_T01	RWP-RK domain-containing protein	--		2.756	--		4.737
GRMZM2G124576_T02	SAR DNA-binding protein, putative		1.605	2.388	--	--	
GRMZM2G313078_T01	scarecrow transcription factor family protein	--		-4.379	--	--	
GRMZM2G028608_T01	scarecrow transcription factor family protein	--		1.989	--	--	
GRMZM2G051785_T01	scarecrow-like transcription factor 6 (SCL6)	--		-1.537	--	--	
GRMZM2G346706_T01	scarecrow-like transcription factor 9 (SCL9)		-2.564	-3.195	--		-4.366
GRMZM2G049159_T01	scarecrow-like transcription factor 9 (SCL9)		-1.438	-2.141	--	--	
GRMZM2G163427_T01	scarecrow-like transcription factor 9 (SCL9)	--		1.792	--	--	
GRMZM2G073779_T01	scarecrow-like transcription factor 9 (SCL9)	--		3.184	--	--	
GRMZM2G073805_T01	scarecrow-like transcription factor 9 (SCL9)	--		2.552	--		2.618
GRMZM2G179325_T01	scarecrow-like transcription factor 9 (SCL9)	--		1.865	--	--	
GRMZM2G157679_T01	SCL14 (SCARECROW-LIKE 14); transcription factor	--		1.569	--	--	
GRMZM5G868355_T01	SCL14 (SCARECROW-LIKE 14); transcription factor	--		3.637	--	--	
GRMZM2G156099_T02	SE (SERRATE); DNA binding / transcription factor	--		-1.634	--	--	
GRMZM2G454176_T01	sequence-specific DNA binding / transcription factor	--		2.463	--		2.419

GRMZM2G143392_T01	SIG2 (RNA POLYMERASE SIGMA SUBUNIT 2); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	--	--	--	--	-1.713
GRMZM2G133646_T01	SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor	--	1.467	1.642	--	
GRMZM2G102711_T01	splicing factor Prp18 family protein	--	--	--	-4.016	-5.152
GRMZM5G806358_T02	SPT16 (global transcription factor C)	--	-1.382	--	--	
GRMZM2G023988_T04	STOP1 (sensitive to proton rhizotoxicity 1); nucleic acid binding / transcription factor/ zinc ion binding	--	--	--	--	1.936
GRMZM2G139710_T02	SUVH1 (SU(VAR)3-9 HOMOLOG 1); histone methyltransferase	--	-1.496	--	--	
AC233961.1_FGT001	SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase	--	-2.58	--	--	-2.161
GRMZM2G165011_T01	SUVH9; histone-lysine N-methyltransferase/ zinc ion binding	--	-3.999	--	--	
GRMZM2G318803_T01	SUVR1 (ARABIDOPSIS HOMOLOG OF SU(VAR)3-9 1); histone-lysine N-methyltransferase/ zinc ion binding	--	--	--	--	-3.177
GRMZM2G149238_T02	TBP2 (TATA BINDING PROTEIN 2); DNA binding / RNA polymerase II transcription factor/ TATA-binding protein binding	--	--	--	--	2.275
GRMZM2G161418_T02	TBP2 (TATA BINDING PROTEIN 2); DNA binding / RNA polymerase II transcription factor/ TATA-binding protein binding	--	--	--	--	1.709
AC205574.3_FGT006	TCP4 (TCP family transcription factor 4); transcription factor	2.186	--	--	--	
GRMZM2G108716_T01	TFIIS (TRANSCRIPT ELONGATION FACTOR IIS); DNA binding / RNA polymerase II transcription elongation factor/ transcription factor	-2.339	-3.035	--	--	
GRMZM2G020081_T01	TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator/ two-component response regulator	3.541	5.171	4.449	4.858	

GRMZM2G060919_T01	transcription factor jumonji (jnj) family protein	2.012	1.97	--		3.288
GRMZM2G057466_T01	transcription factor jumonji (jnj) family protein	2.588	4.288	--	--	
GRMZM2G180086_T01	transcription factor jumonji (jnj) family protein	--	3.425	--		2.181
AC197122.3_FGT003	transcription regulator NOT2/NOT3/NOT5 family protein	--	1.643	--	--	
GRMZM2G132644_T01	transducin family protein / WD-40 repeat family protein	--	-1.497	--	--	
AC207890.3_FGT002	tudor domain-containing protein / nuclease family protein	--	5.233	--		2.659
GRMZM2G136296_T02	tudor domain-containing protein / nuclease family protein	--	2.568	--	--	
GRMZM2G177229_T08	U2AF35B; RNA binding / nucleic acid binding / nucleotide binding / zinc ion binding	--	--		-3.423	-3.489
GRMZM2G029101_T01	unknown protein	2.316	2.705	--		1.916
GRMZM2G140179_T01	unknown protein	--	-2.685	--	--	
GRMZM2G173763_T01	unknown protein	--	--	--		1.65
GRMZM2G113078_T01	WRI1 (WRINKLED 1); DNA binding / transcription factor	--	4.269	--	--	
GRMZM2G052671_T01	WRKY2; transcription factor	--	--	--		1.762
GRMZM2G076657_T02	WRKY3; transcription factor	--	-2.008	--	--	
GRMZM2G148087_T01	WRKY33; transcription factor	--	2.366	--	--	
GRMZM5G871347_T01	WRKY6; transcription factor	--	3.731	--		2.568
GRMZM2G083350_T01	WRKY72; transcription factor	--	--	--		4.3
GRMZM2G064868_T01	XRN3; 5'-3' exoribonuclease	--	--		2.428	2.899
GRMZM2G114137_T01	zinc finger (B-box type) family protein	-1.941	-3.764	--	--	
GRMZM2G107886_T01	zinc finger (B-box type) family protein	3.922	3.697		1.542	--
GRMZM2G086277_T02	zinc finger (C2H2 type) family protein	--	-2.872		-2.466	-2.703
GRMZM5G885700_T02	zinc finger (C2H2 type) family protein	--	-1.285	--	--	
GRMZM2G140016_T01	zinc finger (C2H2 type) family protein	--	-2.132	--	--	
GRMZM2G000836_T01	zinc finger (C2H2 type) protein (WIP4)	--	2.534	--	--	
GRMZM2G081782_T01	zinc finger (C2H2 type, AN1-like) family protein	--	--	--		1.852

