

Table S1 Primers used in this paper

Name	ID_maize	Forward primer SEQ	Reverse primer SEQ
Primers used for real-time RT-PCR			
ABA1	GRMZM2G127139	TCCCTCCGATGTCATTGAGT	TGTGGCTGATGATAGTGGTG
NPQ1	GRMZM2G027219	TGGGATGGTTATGGTGGTTC	CCACAGGTGTTGTCGGTCAT
AAO3	GRMZM2G141473	CCTTGGCATTCCATTCACA	GCAACATTGGGCTCACATCC
AAO3	GRMZM2G141535	CGCACTAGACACTAACACCG	TTGGTCGAAGATTAACCTCATA
AAO3	GRMZM2G406830	GTTGCACCGTCCTGTCCGTAT	CCGCATCGCAGACTTTGTAG
AAO3	GRMZM2G019799	TGAAGCACCCACATACACGC	GCCCGAAGACTCACCTCATA
AAO3	GRMZM5G899851	CTTTGAGACTTTCCGAGCAG	AGGGAGGATAGGAAGGTAAACA
ABA2	GRMZM2G332976	GCTCTGGGATTGGGAGGGAGTA	GCAACGCTGTAGGACGAAATTGTA
ABA2	GRMZM2G069523	GCGTTGGAGCAGGCAATGGA	TACAAAGCCGGTGCCGGTGA
NCED	GRMZM2G150363	AGGACGACGGCTACTTGGTG	GTATCCAGCGCGTGTCTTCT
NCED	GRMZM2G417954	TGTCGTGTCCAAGCCGTTCTT	CGGGATGATGGCGTGGTTCT
NCED	GRMZM2G014392	CGGAGGAGGAACAGAGGAGCCA	GCAACCAAGATCCCAGACACCC
NCED	GRMZM5G838285	CCCACCATGATCCACGACTTCGC	CGTCTTCTCCCTGTCCAGCACCC
ZmPTF1	GRMZM2G024530	TCAACTTCTGTGCTGCTCAA	GCAGCAGCATGTCTTTATTT
ZmPTF1-like	GRMZM2G116785	ATCCTTCTGATGTACAAACT	AGGCAGAGGTTGGCCGTGGTA
ZmAct1	GRMZM2G126010	ATCACCATTGGGTCAGAAAGG	GTGCTGAGAGAAGCCAAAATAGAG
Primers used for Yeast-one-hybridization			
Pro_AZF2	GRMZM2G113860	acggtaccGCGTAGTTGGAGGCTGGTTT	TGGCTAGCTGATCTGATGACGcagctgtg
Pro_NAC30	AC212859.3_FG008	acggtaccTTCTACACAAGCCGGTCGTC	GATCAGGGTCAGGGATCGGAcagctgtg
Pro_ATAF2	GRMZM2G347043	acggtaccAAAGATGTCAGTACCCGCCG	TTAGCTCGGATCTGCGTGTGcagctgtg
Pro_NCED9_1	GRMZM2G014392	acggtaccCACGCGATAAATCCTGTGCC	CATCGCGGTGACTGGAATTGcagctgtg
Pro_NCED9_2	GRMZM2G417954	acggtaccCCACCACTTTCCAAAGTTCAGA	GTCAGAGAGCTGGGGTTGTcagctgtg
Pro_CBF4_1	GRMZM2G069082	acggtaccCACAGGCACTGTCTGTCTT	GGGTTCTTTGTCTCGGGATcagctgtg
Pro_CBF4_2	GRMZM2G124037	acggtaccAGCAAGACCCTCTCGCTACC	GTGTGGTTTTGTGGGAGGTGcagctgtg
Primers used for mutant genotyping			
mu1046031	ptf1	GCACTAGCCAGAAGAAGGCATAA	AGGCCCTCAGCAAACATCAA
	TIRmix+3'-n(ptf1)		AAGCGTAATCGAAGTTCCAACAAT
mu1030095&mu1040158	ptf2/3	AGGCTCGTTCTCAAACCCAT	CATCAATCAATCCCACCCAC
	TIRmix+3'-n(ptf2/3)		GAGGAAACAGACTTGACGCT
	TIR8a	CGCTCCATTTGTCGAATCCCCTS	
	TIR8b	CGCTCCATTTGTCGAATCCSCTT	
TIR Forward primer	TIR8c	SGCTCCATTTGTCGAATCCCKT	
	TIR8d	CGCTCCATTTGTCGAATCACCTC	

Table S1

Table S2 Sequences of probes and mutated probes used in electrophoretic mobility shift assay

Gene ID	Nam	Sequence of the probe (5' to 3')
GRMZM2G11386	F	GAAGTCTAAATCCAGTGCACGCAGTAGCCCGTGCACCTTTGCCTCTA
GRMZM2G11386	R	GCTTAGAGGCAAAGGTGCACGGGCTACTGCGTGCCTGGATTTAGAC
GRMZM2G11386	MF	GAAGTCTAAATCCAACAACAGCAGTAGCCACACAACACTTTGCCTCTA
GRMZM2G11386	MR	GCTTAGAGGCAAAGTGTGTGGGCTACTGCTGTTGTTGGATTTAGAC
AC212859.3_FG0	F	AGAAGTAGATGGCTGCGAATCCTCAAGTGCCTCAAAGAAACATGC
AC212859.3_FG0	R	GCATGCATGTTTCTTTGAGTGCCTTGAGGATTCGCAGCCATCTACTT
AC212859.3_FG0	MF	AGAAGTAGATGGCTGCGAATCCTCAAACAACATCAAAGAAACATGC
AC212859.3_FG0	MR	GCATGCATGTTTCTTTGATGTTGTTGAGGATTCGCAGCCATCTACTT
GRMZM2G34704	F	TCATCCAGCTGCCCCGCCCAACCACACGTGCCAATTCGGCTTTTCGGC
GRMZM2G34704	R	TGCGCGAAAGCGGAATTGGCAGGTGTGGTTGGGCGGGGGCAGCTGG
GRMZM2G34704	MF	TCATCCAGCTGCCCCGCCCAACCAACAACCAATTCGGCTTTTCGGC
GRMZM2G34704	MR	TGCGCGAAAGCGGAATTGGTGTGTTGGTTGGGCGGGGGCAGCTGGA
GRMZM2G01439	F	GCCCCCGCAGCGCACACAGTGGGCGCCCCGTGTCGGCGTCGCGAATT
GRMZM2G01439	R	ATGAATTCGCGACGCCGACAGGGGCGCCACGTGGTGCCTGCGGG
GRMZM2G01439	MF	GCCCCCGCAGCGCACACAACAGGCGCCCCGTGTCGGCGTCGCGAATT
GRMZM2G01439	MR	ATGAATTCGCGACGCCGACAGGGGCGCCTGTTGTGTGCGCTGCGGGG
GRMZM2G41795	F	GAAGAGGACAGCCACAGACACGGCTGCAGTGCACGCGCGCGTCCC
GRMZM2G41795	R	ACGGGGACGCGCCGCGTGCCTGCAGCCGTGTCTGTGGCTGTCTCT
GRMZM2G41795	MF	GAAGAGGACAGCCACAGACACGGCTGCAACAACAGCGCGCGTCCC
GRMZM2G41795	MR	ACGGGGACGCGCCGCGTGTGTTGCAGCCGTGTCTGTGGCTGTCTCTT
GRMZM2G06908	F	GCCCATGTCCTCCACTGCAGTGCCTACAAAAACCACTGTCAATGTC
GRMZM2G06908	R	CTTGACATTGACAGTGGTTTTTGTAGTGCCTGCAGTGGAGGACATG
GRMZM2G06908	MF	GCCCATGTCCTCCACTGCAACAACATAAAAAACCACTGTCAATGTC
GRMZM2G06908	MR	CTTGACATTGACAGTGGTTTTTGTATGTTGTTGCAGTGGAGGACATGG
GRMZM2G12403	F	CCTCCACTTCACTGCAGCTGCAGTGCACACCACTCTGTCTGTTTGTGA
GRMZM2G12403	R	CTTCACAAACAGACAGAGTGGTGTGCTGCAGTGCAGTGAAGTGG
GRMZM2G12403	MF	CCTCCACTTCACTGCAGCTGCAACAACAACCACTCTGTCTGTTTGTGA
GRMZM2G12403	MR	CTTCACAAACAGACAGAGTGGTGTGTTGCTGCAGTGCAGTGAAGTGG

Table S2

Table S3 GO enrichment analysis between the ZmPTF1 overexpression line (L+4) and WT

GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
GO:0042221	P	response to chemical stimulus	212	3978	1.50E-38	7.60E-35
GO:0050896	P	response to stimulus	276	6292	1.00E-37	2.60E-34
GO:0010033	P	response to organic substance	163	2754	1.80E-33	3.00E-30
GO:0010200	P	response to chitin	59	421	1.90E-28	2.40E-25
GO:0006950	P	response to stress	192	4089	2.10E-27	2.10E-24
GO:0009743	P	response to carbohydrate stimulus	73	812	4.50E-24	3.80E-21
GO:0009719	P	response to endogenous stimulus	105	1615	6.60E-24	4.70E-21
GO:0009628	P	response to abiotic stimulus	134	2635	2.90E-21	1.80E-18
GO:0070887	P	cellular response to chemical stimulus	91	1417	2.30E-20	1.30E-17
GO:0045087	P	innate immune response	70	930	3.90E-19	1.90E-16
GO:0044283	P	small molecule biosynthetic process	104	1865	5.00E-19	2.30E-16
GO:0051716	P	cellular response to stimulus	119	2355	1.40E-18	5.00E-16
GO:0009607	P	response to biotic stimulus	97	1687	1.40E-18	5.00E-16
GO:0009725	P	response to hormone stimulus	86	1375	1.40E-18	5.00E-16
GO:0002376	P	immune system process	71	984	1.80E-18	5.60E-16
GO:0006955	P	immune response	71	984	1.80E-18	5.60E-16
GO:0071310	P	cellular response to organic substance	80	1234	3.70E-18	1.10E-15
GO:0009737	P	response to abscisic acid stimulus	55	621	4.70E-18	1.30E-15
GO:0046394	P	carboxylic acid biosynthetic process	73	1116	8.10E-17	2.00E-14
GO:0016053	P	organic acid biosynthetic process	73	1116	8.10E-17	2.00E-14
GO:0071495	P	cellular response to endogenous stimulus	61	815	1.10E-16	2.70E-14
GO:0051707	P	response to other organism	83	1421	2.60E-16	5.90E-14
GO:0006811	P	ion transport	68	1019	4.10E-16	8.80E-14
GO:0006952	P	defense response	90	1653	7.00E-16	1.50E-13
GO:0007242	P	intracellular signaling cascade	76	1252	8.00E-16	1.60E-13
GO:0009611	P	response to wounding	38	340	9.60E-16	1.90E-13
GO:0009620	P	response to fungus	45	499	3.10E-15	5.80E-13
GO:0051704	P	multi-organism process	93	1820	8.50E-15	1.50E-12
GO:0009753	P	response to jasmonic acid stimulus	43	471	8.90E-15	1.50E-12
GO:0006091	P	generation of precursor metabolites and energy	54	730	1.10E-14	1.90E-12
GO:0034641	P	cellular nitrogen compound metabolic process	77	1373	2.70E-14	4.40E-12
GO:0009751	P	response to salicylic acid stimulus	42	470	3.60E-14	5.70E-12
GO:0006812	P	cation transport	56	813	5.80E-14	8.70E-12
GO:0015979	P	photosynthesis	40	435	6.40E-14	9.40E-12
GO:0009266	P	response to temperature stimulus	61	962	1.20E-13	1.70E-11
GO:0043436	P	oxoacid metabolic process	99	2103	1.30E-13	1.70E-11
GO:0019752	P	carboxylic acid metabolic process	99	2103	1.30E-13	1.70E-11
GO:0006082	P	organic acid metabolic process	99	2105	1.40E-13	1.80E-11
GO:0050832	P	defense response to fungus	35	342	1.40E-13	1.90E-11
GO:0065007	P	biological regulation	210	6222	1.70E-13	2.20E-11
GO:0002679	P	respiratory burst during defense response	22	121	2.30E-13	2.60E-11
GO:0009605	P	response to external stimulus	65	1087	2.30E-13	2.60E-11
GO:0042180	P	cellular ketone metabolic process	99	2123	2.20E-13	2.60E-11
GO:0045730	P	respiratory burst	22	121	2.30E-13	2.60E-11
GO:0019684	P	photosynthesis, light reaction	34	333	3.40E-13	3.80E-11
GO:0023052	P	signaling	106	2376	3.90E-13	4.20E-11
GO:0006810	P	transport	140	3577	4.80E-13	4.90E-11
GO:0044237	P	cellular metabolic process	330	11509	4.70E-13	4.90E-11
GO:0009987	P	cellular process	391	14419	4.60E-13	4.90E-11
GO:0044281	P	small molecule metabolic process	153	4065	5.60E-13	5.60E-11
GO:0033554	P	cellular response to stress	77	1473	8.10E-13	7.80E-11
GO:0008152	P	metabolic process	374	13633	7.90E-13	7.80E-11

GO:0009863	P	salicylic acid mediated signaling pathway	34	349	1.20E-12	1.10E-10
GO:0071446	P	cellular response to salicylic acid stimulus	34	351	1.30E-12	1.20E-10
GO:0051179	P	localization	145	3819	1.50E-12	1.40E-10
GO:0000096	P	sulfur amino acid metabolic process	39	465	1.90E-12	1.70E-10
GO:0051234	P	establishment of localization	140	3652	2.10E-12	1.90E-10
GO:0010941	P	regulation of cell death	36	405	2.90E-12	2.50E-10
GO:0023034	P	intracellular signaling pathway	37	433	4.30E-12	3.60E-10
GO:0030001	P	metal ion transport	43	576	4.90E-12	4.10E-10
GO:0006519	P	cellular amino acid and derivative metabolic pr	70	1324	6.10E-12	5.00E-10
GO:0006790	P	sulfur metabolic process	47	683	6.90E-12	5.60E-10
GO:0043067	P	regulation of programmed cell death	35	397	7.30E-12	5.80E-10
GO:0042743	P	hydrogen peroxide metabolic process	32	335	8.70E-12	6.80E-10
GO:0032870	P	cellular response to hormone stimulus	45	641	1.10E-11	8.20E-10
GO:0009867	P	jasmonic acid mediated signaling pathway	29	282	1.60E-11	1.20E-09
GO:0071395	P	cellular response to jasmonic acid stimulus	29	282	1.60E-11	1.20E-09
GO:0009755	P	hormone-mediated signaling pathway	43	600	1.70E-11	1.20E-09
GO:0044106	P	cellular amine metabolic process	56	947	1.80E-11	1.30E-09
GO:0006800	P	oxygen and reactive oxygen species metabolic	32	347	2.00E-11	1.40E-09
GO:0010363	P	regulation of plant-type hypersensitive respons	33	371	2.40E-11	1.70E-09
GO:0009414	P	response to water deprivation	35	416	2.40E-11	1.70E-09
GO:0009814	P	defense response, incompatible interaction	40	536	2.80E-11	1.90E-09
GO:0050794	P	regulation of cellular process	161	4595	3.00E-11	2.10E-09
GO:0009862	P	systemic acquired resistance, salicylic acid med	27	251	3.20E-11	2.20E-09
GO:0009738	P	abscisic acid mediated signaling pathway	27	252	3.50E-11	2.30E-09
GO:0050789	P	regulation of biological process	177	5235	3.60E-11	2.40E-09
GO:0009415	P	response to water	35	424	4.00E-11	2.50E-09
GO:0080135	P	regulation of cellular response to stress	33	379	4.00E-11	2.50E-09
GO:0009626	P	plant-type hypersensitive response	34	401	3.90E-11	2.50E-09
GO:0023033	P	signaling pathway	39	519	4.10E-11	2.50E-09
GO:0034050	P	host programmed cell death induced by symbic	34	402	4.10E-11	2.50E-09
GO:0012501	P	programmed cell death	36	451	5.00E-11	3.00E-09
GO:0009308	P	amine metabolic process	58	1034	5.40E-11	3.20E-09
GO:0008219	P	cell death	38	500	5.40E-11	3.20E-09
GO:0016265	P	death	38	500	5.40E-11	3.20E-09
GO:0009696	P	salicylic acid metabolic process	25	222	7.20E-11	4.20E-09
GO:0045088	P	regulation of innate immune response	34	415	9.10E-11	5.20E-09
GO:0007165	P	signal transduction	78	1670	1.10E-10	6.00E-09
GO:0050776	P	regulation of immune response	34	419	1.20E-10	6.30E-09
GO:0002682	P	regulation of immune system process	34	419	1.20E-10	6.30E-09
GO:0071215	P	cellular response to abscisic acid stimulus	27	267	1.20E-10	6.30E-09
GO:0009697	P	salicylic acid biosynthetic process	24	209	1.20E-10	6.50E-09
GO:0009723	P	response to ethylene stimulus	31	353	1.30E-10	6.90E-09
GO:0019438	P	aromatic compound biosynthetic process	44	680	2.10E-10	1.10E-08
GO:0006520	P	cellular amino acid metabolic process	51	882	3.10E-10	1.60E-08
GO:0006612	P	protein targeting to membrane	32	392	3.60E-10	1.80E-08
GO:0042742	P	defense response to bacterium	32	394	4.00E-10	2.10E-08
GO:0010310	P	regulation of hydrogen peroxide metabolic proc	22	187	4.70E-10	2.40E-08
GO:0009627	P	systemic acquired resistance	34	445	5.00E-10	2.50E-08
GO:0080010	P	regulation of oxygen and reactive oxygen speci	22	188	5.20E-10	2.60E-08
GO:0023060	P	signal transmission	79	1767	5.60E-10	2.70E-08
GO:0023046	P	signaling process	79	1768	5.70E-10	2.80E-08
GO:0019344	P	cysteine biosynthetic process	23	210	6.80E-10	3.30E-08
GO:0002252	P	immune effector process	26	273	8.40E-10	4.00E-08
GO:0006534	P	cysteine metabolic process	23	213	8.80E-10	4.10E-08
GO:0031323	P	regulation of cellular metabolic process	111	2928	1.40E-09	6.60E-08
GO:0009642	P	response to light intensity	26	282	1.60E-09	7.30E-08
GO:0009070	P	serine family amino acid biosynthetic process	23	222	1.80E-09	8.40E-08
GO:0030968	P	endoplasmic reticulum unfolded protein respon:	21	185	2.10E-09	9.60E-08

Table S3

GO:0034620	P	cellular response to unfolded protein	21	187	2.50E-09	1.10E-07
GO:0006986	P	response to unfolded protein	21	187	2.50E-09	1.10E-07
GO:0019222	P	regulation of metabolic process	117	3186	2.80E-09	1.20E-07
GO:0031347	P	regulation of defense response	36	529	2.80E-09	1.20E-07
GO:0000165	P	MAPKKK cascade	22	209	3.10E-09	1.40E-07
GO:0009069	P	serine family amino acid metabolic process	25	271	3.20E-09	1.40E-07
GO:0044271	P	cellular nitrogen compound biosynthetic proces	46	804	3.30E-09	1.40E-07
GO:0044272	P	sulfur compound biosynthetic process	34	486	4.10E-09	1.70E-07
GO:0006984	P	ER-nuclear signaling pathway	21	193	4.20E-09	1.80E-07
GO:0071445	P	cellular response to protein stimulus	21	194	4.50E-09	1.90E-07
GO:0009612	P	response to mechanical stimulus	13	63	4.90E-09	2.00E-07
GO:0070838	P	divalent metal ion transport	21	195	4.90E-09	2.00E-07
GO:0006725	P	cellular aromatic compound metabolic process	53	1022	5.10E-09	2.10E-07
GO:0009651	P	response to salt stress	45	788	5.20E-09	2.10E-07
GO:0010035	P	response to inorganic substance	55	1086	5.60E-09	2.20E-07
GO:0080134	P	regulation of response to stress	36	544	5.60E-09	2.20E-07
GO:0071216	P	cellular response to biotic stimulus	21	197	5.80E-09	2.30E-07
GO:0031408	P	oxylipin biosynthetic process	18	142	6.30E-09	2.40E-07
GO:0009409	P	response to cold	39	629	7.00E-09	2.70E-07
GO:0009617	P	response to bacterium	37	577	7.50E-09	2.90E-07
GO:0009309	P	amine biosynthetic process	35	527	8.40E-09	3.20E-07
GO:0008652	P	cellular amino acid biosynthetic process	34	503	9.20E-09	3.50E-07
GO:0007243	P	protein kinase cascade	22	223	9.30E-09	3.50E-07
GO:0048583	P	regulation of response to stimulus	40	667	1.10E-08	4.00E-07
GO:0051606	P	detection of stimulus	18	148	1.10E-08	4.20E-07
GO:0006970	P	response to osmotic stress	46	842	1.30E-08	4.60E-07
GO:0043069	P	negative regulation of programmed cell death	19	170	1.50E-08	5.60E-07
GO:0031348	P	negative regulation of defense response	24	273	1.60E-08	5.70E-07
GO:0019748	P	secondary metabolic process	59	1247	1.60E-08	5.70E-07
GO:0006807	P	nitrogen compound metabolic process	177	5675	1.80E-08	6.40E-07
GO:0060548	P	negative regulation of cell death	19	174	2.20E-08	7.70E-07
GO:0009595	P	detection of biotic stimulus	15	104	2.50E-08	8.60E-07
GO:0048585	P	negative regulation of response to stimulus	27	349	2.40E-08	8.60E-07
GO:0009058	P	biosynthetic process	230	7962	2.80E-08	9.90E-07
GO:0034976	P	response to endoplasmic reticulum stress	27	352	2.90E-08	9.90E-07
GO:0000097	P	sulfur amino acid biosynthetic process	25	309	3.60E-08	1.20E-06
GO:0009873	P	ethylene mediated signaling pathway	16	125	3.80E-08	1.30E-06
GO:0044249	P	cellular biosynthetic process	224	7737	4.20E-08	1.40E-06
GO:0080090	P	regulation of primary metabolic process	101	2761	5.20E-08	1.70E-06
GO:0031407	P	oxylipin metabolic process	18	168	6.60E-08	2.20E-06
GO:0015674	P	di-, tri-valent inorganic cation transport	25	321	7.10E-08	2.40E-06
GO:0048519	P	negative regulation of biological process	57	1243	7.80E-08	2.60E-06
GO:0030003	P	cellular cation homeostasis	18	172	9.20E-08	3.00E-06
GO:0010286	P	heat acclimation	13	84	1.00E-07	3.30E-06
GO:0009695	P	jasmonic acid biosynthetic process	16	136	1.10E-07	3.50E-06
GO:0042398	P	cellular amino acid derivative biosynthetic proci	33	534	1.10E-07	3.50E-06
GO:0043900	P	regulation of multi-organism process	15	118	1.10E-07	3.50E-06
GO:0055080	P	cation homeostasis	20	217	1.20E-07	3.90E-06
GO:0071369	P	cellular response to ethylene stimulus	16	144	2.30E-07	7.10E-06
GO:0009416	P	response to light stimulus	54	1188	2.30E-07	7.10E-06
GO:0006873	P	cellular ion homeostasis	18	185	2.50E-07	7.70E-06
GO:0055082	P	cellular chemical homeostasis	18	186	2.70E-07	8.30E-06
GO:0044238	P	primary metabolic process	308	11717	3.00E-07	9.30E-06
GO:0006633	P	fatty acid biosynthetic process	23	303	3.60E-07	1.10E-05
GO:0009408	P	response to heat	23	303	3.60E-07	1.10E-05
GO:0019725	P	cellular homeostasis	24	328	3.80E-07	1.10E-05
GO:0032787	P	monocarboxylic acid metabolic process	62	1481	4.30E-07	1.30E-05
GO:0009773	P	photosynthetic electron transport in photosyste	10	51	4.50E-07	1.30E-05

Table S3

GO:0050801	P	ion homeostasis	20	240	5.40E-07	1.60E-05
GO:0046686	P	response to cadmium ion	29	470	6.70E-07	2.00E-05
GO:0010038	P	response to metal ion	34	610	6.80E-07	2.00E-05
GO:0016311	P	dephosphorylation	20	245	7.30E-07	2.10E-05
GO:0009694	P	jasmonic acid metabolic process	16	160	8.20E-07	2.40E-05
GO:0006778	P	porphyrin metabolic process	19	226	9.20E-07	2.60E-05
GO:0033013	P	tetrapyrrole metabolic process	19	227	9.70E-07	2.80E-05
GO:0006575	P	cellular amino acid derivative metabolic proces	37	714	1.10E-06	3.30E-05
GO:0000160	P	two-component signal transduction system (ph	16	165	1.20E-06	3.40E-05
GO:0009314	P	response to radiation	54	1263	1.40E-06	3.90E-05
GO:0048878	P	chemical homeostasis	21	281	1.50E-06	4.10E-05
GO:0006470	P	protein amino acid dephosphorylation	18	214	1.80E-06	4.90E-05
GO:0031399	P	regulation of protein modification process	15	150	1.80E-06	5.00E-05
GO:0035304	P	regulation of protein amino acid dephosphoryla	14	135	2.70E-06	7.40E-05
GO:0009767	P	photosynthetic electron transport chain	11	80	2.70E-06	7.50E-05
GO:0010207	P	photosystem II assembly	16	177	2.80E-06	7.60E-05
GO:0035303	P	regulation of dephosphorylation	14	137	3.20E-06	8.50E-05
GO:0009644	P	response to high light intensity	18	224	3.20E-06	8.60E-05
GO:0051789	P	response to protein stimulus	24	376	3.60E-06	9.60E-05
GO:0044275	P	cellular carbohydrate catabolic process	30	545	3.90E-06	0.0001
GO:0006979	P	response to oxidative stress	31	582	5.10E-06	0.00013
GO:0006631	P	fatty acid metabolic process	31	587	6.00E-06	0.00016
GO:0015994	P	chlorophyll metabolic process	16	189	6.10E-06	0.00016
GO:0009765	P	photosynthesis, light harvesting	8	41	6.60E-06	0.00017
GO:0006007	P	glucose catabolic process	27	474	6.60E-06	0.00017
GO:0019320	P	hexose catabolic process	27	476	7.10E-06	0.00018
GO:0032268	P	regulation of cellular protein metabolic process	17	215	7.30E-06	0.00019
GO:0015849	P	organic acid transport	20	289	7.60E-06	0.00019
GO:0046365	P	monosaccharide catabolic process	27	480	8.20E-06	0.00021
GO:0060255	P	regulation of macromolecule metabolic process	94	2829	8.80E-06	0.00022
GO:0009056	P	catabolic process	77	2182	8.90E-06	0.00022
GO:0016052	P	carbohydrate catabolic process	30	573	9.80E-06	0.00025
GO:0048523	P	negative regulation of cellular process	37	789	1.00E-05	0.00025
GO:0015672	P	monovalent inorganic cation transport	18	245	1.00E-05	0.00025
GO:0042592	P	homeostatic process	27	488	1.10E-05	0.00027
GO:0046164	P	alcohol catabolic process	27	491	1.20E-05	0.00029
GO:0006972	P	hyperosmotic response	18	251	1.40E-05	0.00034
GO:0042538	P	hyperosmotic salinity response	14	162	1.80E-05	0.00045
GO:0046942	P	carboxylic acid transport	19	283	1.90E-05	0.00046
GO:0051246	P	regulation of protein metabolic process	17	237	2.40E-05	0.00057
GO:0019318	P	hexose metabolic process	30	602	2.40E-05	0.00057
GO:0006865	P	amino acid transport	18	266	2.80E-05	0.00068
GO:0043269	P	regulation of ion transport	13	147	2.90E-05	0.00069
GO:0006006	P	glucose metabolic process	28	554	3.50E-05	0.00083
GO:0015837	P	amine transport	18	272	3.70E-05	0.00088
GO:0006813	P	potassium ion transport	8	54	3.90E-05	0.00092
GO:0044248	P	cellular catabolic process	72	2095	4.10E-05	0.00095
GO:0009692	P	ethylene metabolic process	12	131	4.30E-05	0.00099
GO:0009693	P	ethylene biosynthetic process	12	131	4.30E-05	0.00099
GO:0006740	P	NADPH regeneration	15	201	4.60E-05	0.0011
GO:0051186	P	cofactor metabolic process	34	753	4.70E-05	0.0011
GO:0043449	P	cellular alkene metabolic process	12	133	4.90E-05	0.0011
GO:0043450	P	alkene biosynthetic process	12	133	4.90E-05	0.0011
GO:0046483	P	heterocycle metabolic process	42	1023	5.10E-05	0.0012
GO:0006739	P	NADP metabolic process	15	204	5.40E-05	0.0012
GO:0009733	P	response to auxin stimulus	23	431	8.00E-05	0.0018
GO:0046496	P	nicotinamide nucleotide metabolic process	15	212	8.10E-05	0.0018
GO:0006769	P	nicotinamide metabolic process	15	212	8.10E-05	0.0018

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GO:0019362	P	pyridine nucleotide metabolic process	15	214	8.90E-05	0.002
GO:0070482	P	response to oxygen levels	10	104	0.00013	0.0028
GO:0051049	P	regulation of transport	13	172	0.00013	0.0028
GO:0043603	P	cellular amide metabolic process	15	222	0.00013	0.0029
GO:0044282	P	small molecule catabolic process	38	932	0.00013	0.0029
GO:0042440	P	pigment metabolic process	20	361	0.00014	0.0031
GO:0009820	P	alkaloid metabolic process	15	225	0.00015	0.0032
GO:0009066	P	aspartate family amino acid metabolic process	17	278	0.00015	0.0032
GO:0006098	P	pentose-phosphate shunt	14	200	0.00015	0.0033
GO:0005996	P	monosaccharide metabolic process	34	804	0.00016	0.0033
GO:0006605	P	protein targeting	37	906	0.00016	0.0034
GO:0051252	P	regulation of RNA metabolic process	77	2388	0.00016	0.0034
GO:0005975	P	carbohydrate metabolic process	73	2249	0.0002	0.0042
GO:0022900	P	electron transport chain	11	133	0.0002	0.0043
GO:0032879	P	regulation of localization	14	207	0.00022	0.0045
GO:0009646	P	response to absence of light	6	37	0.00024	0.0049
GO:0006820	P	anion transport	19	350	0.00027	0.0055
GO:0031326	P	regulation of cellular biosynthetic process	82	2631	0.00028	0.0057
GO:0009889	P	regulation of biosynthetic process	82	2634	0.00029	0.0059
GO:0006733	P	oxidoreduction coenzyme metabolic process	16	267	0.00029	0.0059
GO:0006355	P	regulation of transcription, DNA-dependent	75	2372	0.00035	0.007
GO:0070647	P	protein modification by small protein conjugatic	21	418	0.00035	0.0071
GO:0045449	P	regulation of transcription	75	2376	0.00036	0.0073
GO:0006096	P	glycolysis	14	219	0.00037	0.0074
GO:0046907	P	intracellular transport	50	1423	0.0004	0.008
GO:0001666	P	response to hypoxia	9	100	0.00043	0.0085
GO:0043170	P	macromolecule metabolic process	234	9246	0.00043	0.0085
GO:0044255	P	cellular lipid metabolic process	49	1395	0.00046	0.0091
GO:0006066	P	alcohol metabolic process	42	1143	0.0005	0.0098
GO:0051649	P	establishment of localization in cell	53	1554	0.00053	0.01
GO:0052542	P	callose deposition during defense response	7	62	0.00054	0.011
GO:0010556	P	regulation of macromolecule biosynthetic proce	77	2491	0.00055	0.011
GO:0006464	P	protein modification process	84	2773	0.00055	0.011
GO:0010468	P	regulation of gene expression	82	2695	0.00057	0.011
GO:0019219	P	regulation of nucleobase, nucleoside, nucleotide	77	2496	0.00058	0.011
GO:0009698	P	phenylpropanoid metabolic process	20	405	0.00059	0.011
GO:0019220	P	regulation of phosphate metabolic process	14	231	0.00061	0.012
GO:0051174	P	regulation of phosphorus metabolic process	14	231	0.00061	0.012
GO:0008610	P	lipid biosynthetic process	42	1159	0.00065	0.012
GO:0043623	P	cellular protein complex assembly	23	504	0.00067	0.013
GO:0051641	P	cellular localization	54	1613	0.00071	0.013
GO:0042542	P	response to hydrogen peroxide	15	263	0.00071	0.013
GO:0051171	P	regulation of nitrogen compound metabolic pro	77	2517	0.00073	0.014
GO:0006555	P	methionine metabolic process	14	236	0.00074	0.014
GO:0006779	P	porphyrin biosynthetic process	11	157	0.00076	0.014
GO:0009744	P	response to sucrose stimulus	13	210	0.00078	0.014
GO:0006461	P	protein complex assembly	25	577	0.00081	0.015
GO:0070271	P	protein complex biogenesis	25	577	0.00081	0.015
GO:0044262	P	cellular carbohydrate metabolic process	58	1778	0.00082	0.015
GO:0009699	P	phenylpropanoid biosynthetic process	17	327	0.00087	0.016
GO:0033014	P	tetrapyrrole biosynthetic process	11	160	0.00088	0.016
GO:0034285	P	response to disaccharide stimulus	13	213	0.00088	0.016
GO:0007154	P	cell communication	30	758	0.001	0.019
GO:0006636	P	unsaturated fatty acid biosynthetic process	7	70	0.001	0.019
GO:0043687	P	post-translational protein modification	65	2075	0.0011	0.02
GO:0033559	P	unsaturated fatty acid metabolic process	7	71	0.0011	0.02
GO:0034622	P	cellular macromolecular complex assembly	25	592	0.0011	0.02
GO:0052545	P	callose localization	8	93	0.0012	0.021

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GO:0065008	P	regulation of biological quality	54	1654	0.0012	0.021
GO:0033037	P	polysaccharide localization	8	94	0.0012	0.022
GO:0006629	P	lipid metabolic process	57	1772	0.0012	0.022
GO:0065003	P	macromolecular complex assembly	27	665	0.0013	0.022
GO:0034613	P	cellular protein localization	38	1059	0.0014	0.024
GO:0015824	P	proline transport	7	74	0.0014	0.024
GO:0043090	P	amino acid import	7	75	0.0015	0.026
GO:0010167	P	response to nitrate	12	199	0.0015	0.026
GO:0019722	P	calcium-mediated signaling	6	55	0.0016	0.027
GO:0015992	P	proton transport	10	147	0.0016	0.027
GO:0006818	P	hydrogen transport	10	147	0.0016	0.027
GO:0018130	P	heterocycle biosynthetic process	14	258	0.0017	0.028
GO:0010218	P	response to far red light	8	99	0.0017	0.029
GO:0010155	P	regulation of proton transport	7	77	0.0017	0.029
GO:0015804	P	neutral amino acid transport	7	77	0.0017	0.029
GO:0006598	P	polyamine catabolic process	5	38	0.0018	0.031
GO:0015995	P	chlorophyll biosynthetic process	9	125	0.0019	0.031
GO:0044260	P	cellular macromolecule metabolic process	215	8616	0.0019	0.031
GO:0009117	P	nucleotide metabolic process	27	685	0.0019	0.032
GO:0006886	P	intracellular protein transport	37	1044	0.0019	0.032
GO:0034621	P	cellular macromolecular complex subunit organ	25	617	0.002	0.032
GO:0009637	P	response to blue light	9	126	0.002	0.032
GO:0006753	P	nucleoside phosphate metabolic process	27	687	0.002	0.033
GO:0006364	P	rRNA processing	16	324	0.002	0.033
GO:0015996	P	chlorophyll catabolic process	6	58	0.002	0.033
GO:0046149	P	pigment catabolic process	6	58	0.002	0.033
GO:0016072	P	rRNA metabolic process	16	325	0.0021	0.033
GO:0015706	P	nitrate transport	12	207	0.0021	0.033
GO:0031668	P	cellular response to extracellular stimulus	18	388	0.0021	0.033
GO:0071496	P	cellular response to external stimulus	18	389	0.0021	0.034
GO:0016567	P	protein ubiquitination	14	266	0.0022	0.034
GO:0043933	P	macromolecular complex subunit organization	27	691	0.0022	0.034
GO:0010114	P	response to red light	8	104	0.0023	0.036
GO:0070727	P	cellular macromolecule localization	38	1093	0.0023	0.037
GO:0006595	P	polyamine metabolic process	6	60	0.0024	0.037
GO:0009581	P	detection of external stimulus	6	60	0.0024	0.037
GO:0009657	P	plastid organization	18	398	0.0027	0.042
GO:0006787	P	porphyrin catabolic process	6	62	0.0028	0.043
GO:0033015	P	tetrapyrrole catabolic process	6	62	0.0028	0.043
GO:0000302	P	response to reactive oxygen species	16	338	0.003	0.046
GO:0043412	P	macromolecule modification	90	3199	0.0031	0.047
GO:0006351	P	transcription, DNA-dependent	76	2618	0.0031	0.047
GO:0006350	P	transcription	76	2620	0.0031	0.048
GO:0032774	P	RNA biosynthetic process	76	2621	0.0032	0.048
GO:0005488	F	binding	303	11247	3.20E-08	1.50E-05
GO:0005515	F	protein binding	99	2709	7.60E-08	1.50E-05
GO:0046872	F	metal ion binding	103	2853	7.00E-08	1.50E-05
GO:0043167	F	ion binding	106	3030	2.00E-07	2.40E-05
GO:0043169	F	cation binding	106	3029	1.90E-07	2.40E-05
GO:0003700	F	transcription factor activity	67	1682	7.80E-07	7.90E-05
GO:0030528	F	transcription regulator activity	67	1740	2.40E-06	0.00021
GO:0016168	F	chlorophyll binding	7	32	1.30E-05	0.0009
GO:0046873	F	metal ion transmembrane transporter activity	14	157	1.30E-05	0.0009
GO:0046914	F	transition metal ion binding	77	2313	6.00E-05	0.0036
GO:0043565	F	sequence-specific DNA binding	22	402	8.10E-05	0.0045
GO:0005509	F	calcium ion binding	16	258	0.0002	0.0089
GO:0046915	F	transition metal ion transmembrane transporte	7	52	0.0002	0.0089
GO:0003677	F	DNA binding	77	2399	0.00018	0.0089

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GO:0022890	F	inorganic cation transmembrane transporter ac	15	241	0.0003	0.012
GO:0008270	F	zinc ion binding	52	1521	0.00056	0.021
GO:0005516	F	calmodulin binding	12	190	0.001	0.037
GO:0031976	C	plastid thylakoid	40	425	3.20E-14	3.00E-12
GO:0055035	C	plastid thylakoid membrane	35	324	3.40E-14	3.00E-12
GO:0009579	C	thylakoid	45	518	1.10E-14	3.00E-12
GO:0009535	C	chloroplast thylakoid membrane	35	322	2.90E-14	3.00E-12
GO:0009534	C	chloroplast thylakoid	40	425	3.20E-14	3.00E-12
GO:0031984	C	organelle subcompartment	40	428	3.90E-14	3.00E-12
GO:0034357	C	photosynthetic membrane	36	355	8.30E-14	5.40E-12
GO:0042651	C	thylakoid membrane	35	341	1.30E-13	7.60E-12
GO:0044436	C	thylakoid part	37	388	2.10E-13	1.10E-11
GO:0044434	C	chloroplast part	68	1211	9.70E-13	4.40E-11
GO:0016020	C	membrane	203	6122	3.10E-12	1.30E-10
GO:0044435	C	plastid part	68	1252	4.10E-12	1.50E-10
GO:0009521	C	photosystem	16	68	1.50E-11	5.30E-10
GO:0009522	C	photosystem I	10	22	5.50E-10	1.80E-08
GO:0009941	C	chloroplast envelope	37	573	6.30E-09	1.90E-07
GO:0031090	C	organelle membrane	62	1327	1.00E-08	3.00E-07
GO:0009526	C	plastid envelope	37	598	1.80E-08	4.90E-07
GO:0031975	C	envelope	48	929	3.10E-08	7.50E-07
GO:0031967	C	organelle envelope	48	929	3.10E-08	7.50E-07
GO:0005886	C	plasma membrane	127	3740	4.50E-08	1.00E-06
GO:0010287	C	plastoglobule	12	68	8.80E-08	1.90E-06
GO:0044446	C	intracellular organelle part	115	3379	2.10E-07	4.40E-06
GO:0044422	C	organelle part	115	3385	2.30E-07	4.60E-06
GO:0044464	C	cell part	518	22455	9.60E-07	1.80E-05
GO:0005623	C	cell	518	22455	9.60E-07	1.80E-05
GO:0044424	C	intracellular part	465	19957	2.10E-05	0.00038
GO:0005622	C	intracellular	466	20042	2.80E-05	0.00047
GO:0009536	C	plastid	121	4037	4.20E-05	0.00068
GO:0030076	C	light-harvesting complex	6	28	6.10E-05	0.00097
GO:0009507	C	chloroplast	118	3959	6.70E-05	0.001
GO:0048046	C	apoplast	22	406	9.30E-05	0.0014
GO:0005737	C	cytoplasm	302	12233	0.00015	0.0022
GO:0044425	C	membrane part	77	2448	0.00033	0.0046
GO:0009523	C	photosystem II	6	46	0.00068	0.0089
GO:0009570	C	chloroplast stroma	26	603	0.00069	0.0089
GO:0009532	C	plastid stroma	27	637	0.0007	0.0089

The criterion “ $FDR \leq 0.001$ and the absolute value of $\log_2\text{Ratio}(L+4/WT) \geq 1$ ” was used as the threshold to judge the significance of gene expression differences. GO enrichment analysis were done using AgriGO (<http://bioinfo.cau.edu.cn/agriGO/>).

Table S4 Differentially expressed key genes involved in plant growth and development between *ZmPTF1* overexpression line (L+4) and WT

Gene	log2 (L+4/WT)	Best-hit- Arabi-name	Arabi-symbol	Function
Transcription factor				
GRMZM2G063522	1.26	AT1G56010.2	anac021,ANAC022,NAC1	shoot apical meristem formation,auxin-mediated lateral root formation, stress responses
AC212859.3_FG008	8.01	AT1G71930.1	ANAC030,VND7	xylem formation
GRMZM2G011598	1.33	AT3G04070.1	anac047,NAC047	Regulates Flooding-Induced Leaf Movement
GRMZM2G127379	1.99	AT3G04070.2	anac047,NAC047	
GRMZM2G068973	2.28	AT5G08790.1	anac081,ATAF2	
GRMZM2G123667	-1.35	AT5G08790.1	anac081,ATAF2	integrates brassinosteroid inactivation and seedling photomorphogenesis
GRMZM2G162739	1.96	AT5G08790.1	anac081,ATAF2	
GRMZM2G347043	2.07	AT5G08790.1	anac081,ATAF2	
GRMZM2G106548	-1.96	AT5G41920.1	SCL23	bundle sheath cell fate specification
GRMZM2G069126	4.52	AT4G25470.1	ATCBF2,CBF2,DREB1C,F	Stunted growth, darker, less elongated and prostate leaves, delayed flowering.
GRMZM2G069146	3.08	AT4G25470.1	ATCBF2,CBF2,DREB1C,F	
GRMZM2G130149	-1.58	AT5G59780.3	ATMYB59,MYB59	root growth and cell cycle progression
GRMZM2G001930	1.30	AT1G32640.1	ATMYC2,JAI1,JIN1,RD22I	Positive regulator of lateral root formation.
GRMZM2G059562	3.17	AT2G46400.1	ATWRKY46,WRKY46	stress-dependent LR inhibition via regulation of ABA signaling and auxin homeostasis.
GRMZM2G093404	-2.54	AT1G03790.1	SOM	SOM negatively regulates light-dependent seed germination downstream of PIL5 (AT2G20180)
GRMZM2G163813	9.63	AT5G43270.3	SPL2	development of lateral organs in association with shoot maturation in the reproductive phase.
GRMZM2G465553	-1.18	AT2G38560.1	TFIIS	Mutant flower slightly earlier than the wild type and show clearly reduced seed dormancy.
GRMZM2G181551	1.48	AT2G41430.1	CID1,ERD15,LSR1	It acts together with additional CIB1-related proteins to promote CRY2-dependent floral initiation.
GRMZM2G037189	1.20	AT2G41430.4	CID1,ERD15,LSR1	
GRMZM2G025685	-1.21	AT1G46264.1	AT-HSFB4,HSFB4,SCZ	Functions as a nuclear factor regulating asymmetry of stem cell divisions.
Plant hormone				
GRMZM2G115357	2.42	AT1G04240.1	IAA3,SHY2	SHY2/IAA3 regulates multiple auxin responses in roots.
GRMZM2G081158	-1.18	AT1G30330.2	ARF6	Acts redundantly with ARF8 to control stamen elongation and flower maturation.
GRMZM2G414727	1.97	AT2G46690.1	SAUR32	
GRMZM2G442000	-1.44	AT1G19840.1	SAUR53	SAUR-like auxin-responsive protein family
GRMZM2G430052	1.17	AT5G50760.1	SAUR55	
GRMZM2G146108	8.51	AT1G56150.1	SAUR71	
GRMZM2G446858	-1.63	AT4G32810.1	ATCCD8,CCD8,MAX4	shoot branching, and light-dependent defects in hook opening and hypocotyl/root elongation.
GRMZM2G044537	3.26	AT3G61460.1	BRH1	
GRMZM2G071277	3.04	AT3G61460.1	BRH1	Expression is down regulated by brassinolide.
GRMZM2G318408	1.80	AT3G61460.1	BRH1	
GRMZM2G173630	1.32	AT5G27320.1	ATGID1C,GID1C	Rosette radius and root length
GRMZM2G440543	2.24	AT5G48170.1	SLY2	Promoting growth
GRMZM2G045820	-1.11	AT1G47056.1	VFB1	Growth and reduced expression of auxin response genes.
GRMZM2G005840	3.30	AT2G04240.2	XERICO	Transcripts levels are induced by DELLA proteins and repressed by gibberellic acid. Involved in ABA metabolism.
GRMZM2G022972	1.78	AT1G73805.1	SARD1	Key regulator for ICS1 (Isochorismate Synthase 1) induction and salicylic acid (SA) synthesis.
GRMZM2G126749	2.26	AT1G73805.1	SARD1	
GRMZM2G061043	-1.01	AT2G45000.1	EMB2766	A major negative regulator of auxin signalling. Loss of function mutants are embryo lethal.
GRMZM2G141031	-1.68	AT1G25250.1	AtIDD16,IDD16	Regulates auxin biosynthesis and transport and thus aerial organ morphogenesis and gravitropic responses.

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GRMZM2G153683	1.20	AT5G61210.1	ATSNAP33,SNAP33,SNP3	Involved in cytokinesis and cell plate formation
GRMZM2G410766	1.65	AT2G39050.1	EULS3	Involved in ABA mediated stomatal movement.
GRMZM2G162200	-2.69	AT2G39730.2	RCA	Required for the light activation of rubisco. Involved in jasmonate-induced leaf senescence.
GRMZM2G325650	-1.58	AT1G80440.1	KFB20	Targets type-B ARR proteins for degradation and is involved in the negative regulation of the cytokinin response.
GRMZM2G445634	5.54	AT1G19180.1	JAZ1,TIFY10A	Involved in jasmonate signaling. JAZ1 can interact with the COI1 F-box subunit of an SCF E3 ubiquitin ligase only in the presence of jasmonate-isoleucine (JA-ILE) or coronatine.
Others				
GRMZM2G474755	5.42	AT1G24620.1	CML25	Root hairs under phosphate-deficient conditions.
GRMZM2G097900	3.28	AT5G37770.1	CML24,TCH2	Resistant to ABA inhibition of germination and seedling growth, are defective in long-day induction of flowering.
GRMZM2G309327	1.47	AT4G20780.1	CML42	trichome branching.
GRMZM2G312661	1.22	AT4G20780.1	CML42	trichome branching.
GRMZM2G173965	4.61	AT5G55090.1	MAPKKK15	MAPKKK15, MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 15
GRMZM2G174896	1.64	AT2G26980.4	CIPK3,SnRK3.17	Germination efficiency
GRMZM2G138770	2.09	AT5G40010.1	AATP1	Seed and silique development.
GRMZM2G178645	1.89	AT5G40010.1	AATP1	Seed and silique development.
GRMZM2G010251	2.54	AT1G08090.1	ACH1,ATNRT2.1,ATNRT	Lateral root initiation independently of nitrate uptake.
GRMZM2G437912	2.13	AT1G08090.1	2:1,LIN1,NRT2,NRT2.1	Lateral root initiation independently of nitrate uptake.
GRMZM2G108976	1.49	AT4G01710.1	ARPC5,CRK	Cell expansion of trichome.
GRMZM2G352431	1.07	AT1G77300.1	ASHH2,CCR1,EFS,SDG8	Ovule, embryo sac, anther and pollen development.
GRMZM2G064159	1.07	AT5G08170.1	ATAIH,EMB1873	EMBRYO DEFECTIVE 1873
GRMZM2G028677	-2.15	AT2G30490.1	ATC4H,C4H,CYP73A5,RE	Phenylpropanoid metabolism, growth and development.
GRMZM2G436583	-3.11	AT2G24610.1	ATCNGC14,CNGC14	Tip-Growth in Root Hairs, Root Gravitropism in Arabidopsis thaliana
GRMZM2G436299	1.15	AT3G03050.1	ATCSLD3,CSLD3,KJK	mutations initiate root hairs that rupture at their tip soon after initiation.
GRMZM2G048313	-3.09	AT1G60950.1	ATFD2,FED A	Retarded growth, with thin leaves of a lighter yellowish-green color, and more roundly shape
GRMZM2G122327	-1.66	AT1G60950.1	ATFD2,FED A	Retarded growth, with thin leaves of a lighter yellowish-green color, and more roundly shape
GRMZM2G122337	-1.67	AT1G60950.1	ATFD2,FED A	Retarded growth, with thin leaves of a lighter yellowish-green color, and more roundly shape
GRMZM2G059637	1.52	AT3G11430.1	ATGPAT5,GPAT5	The mutant seeds have a reduced germination rate under high salt and lower tolerance to salt stress.
GRMZM5G873519	-8.58	AT1G32080.1	ATLRGB	Involved in chloroplast development, carbon partitioning and leaf senescence.
GRMZM2G128171	-1.19	AT2G47470.1	ATPD111,ATPDIL2-1,MEE	Reduced seed set due to delayed development of embryo sacs and resulting defect in pollen tube guidance
GRMZM2G058039	1.05	AT5G53180.1	ATPTB2,PTB2	Pollen germination.
GRMZM2G038598	1.01	AT4G23920.1	ATUGE2,UGE2	Involved in growth and cell wall carbohydrate biosynthesis.
GRMZM2G117935	2.08	AT1G17730.1	CHMP1B,VPS46.1	CHMP1A and B mediate multivesicular body sorting of auxin carriers and are required for plant development.
GRMZM5G875502	1.23	AT2G23380.1	CLF,ICU1,SDG1,SET1	Involved in the control of leaf morphogenesis.
GRMZM2G107199	-1.11	AT3G50660.1	CLM,CYP90B1,DWF4,PSI	CLM is an epi-allele with small, compressed rosette, reduced internode length, and reduced fertility.
GRMZM2G056975	-1.04	AT5G62790.1	DXR,PDE129	DXR knockout or strongly silenced lines have a seedling lethal, albino phenotype.
GRMZM2G382341	1.05	AT5G35700.1	FIM2	Encodes FIMBRIN5, an actin bundling factor required for pollen germination and pollen tube growth.
GRMZM2G010555	2.81	AT4G22260.1	IM,IM1	im mutants have a variegated phenotype and fail to differentiate chloroplasts.
GRMZM2G461447	-1.11	AT1G57820.1	ORTH2,VIM1	Root growth and flowering.
GRMZM2G098637	1.97	AT5G22000.3	RHF2A	RHF2a may be involved in targetting ICK4KRP6 for degradation following meiosis in order to allow the mitoses associated with megagametogenesis and microgametogenesis to occur.
GRMZM2G001205	-1.51	AT5G59820.1	RHL41,ZAT12	lines overexpressing this gene exhibits a small but reproducible increase in freeze tolerance.
GRMZM2G318860	1.07	AT1G31480.1	SGR2	Abnormal gravitropism in inflorescence stems and hypocotyls.
GRMZM2G311898	1.49	AT1G28480.1	GRX480,roxy19	GRX480 transcription is SA-inducible and requires NPR1. Maybe involved in SA/JA cross-talk.

The criterion "FDR \leq 0.001 and the absolute value of $\log_2\text{Ratio}(L+4/WT) \geq 1$ " was used as the threshold to judge the significance of gene expression differences.

Table S4

Table S5 Differentially expressed key genes involved in ABA metabolic and signaling pathway between *ZmPTF1* overexpression line (L+4) and WT

Gene	log2 (L+4/WT)	Best-hit- arabi-name	Arabi-symbol	Annotation
abscisic acid metabolic process				
GRMZM2G446858	-1.63	AT4G32810.1	ATCCD8,CCD8,MAX4	carotenoid cleavage dioxygenase 8
GRMZM2G417954	8.59	AT1G78390.1	ATNCED9,NCED9	nine-cis-epoxycarotenoid dioxygenase 9
GRMZM2G014392	2.63	AT1G78390.1	ATNCED9,NCED9	nine-cis-epoxycarotenoid dioxygenase 9
GRMZM2G149317	-1.81	AT5G17230.1	PSY	PHYTOENE SYNTHASE
abscisic acid core signaling pathway				
GRMZM2G119370	8.23	AT2G26040.1	PYL2,RCAR14	PYR1-like 2
GRMZM2G112524	1.17	AT2G26040.1	PYL2, RCAR14	PYR1-like 2
GRMZM2G057959	-1.90	AT5G05440.1	PYL5,RCAR8	Polyketide cyclase/dehydrase and lipid transport superfamily protein
GRMZM2G158328	9.37	AT1G66600.1	ABO3,WRKY63	ABA overly sensitive mutant 3
GRMZM2G174896	1.64	AT2G26980.4	CIPK3,SnRK3.17	CBL-interacting protein kinase 3
GRMZM2G465287	2.91	AT2G30020.1	AP2C1	Protein phosphatase 2C family protein
GRMZM2G033413	1.13	AT3G19290.1	ABF4, AREB2	ABRE binding factor 4
GRMZM2G117164	1.66	AT5G65310.1	ATHB-5, ATHB5, HB5	homeobox protein 5
GRMZM2G117851	1.74	AT2G46270.2	GBF3	G-box binding factor 3
abscisic acid-activated signaling pathway				
GRMZM2G061568	1.23	AT1G15080.1	ATLPP2,ATPAP2,LPP2	lipid phosphate phosphatase 2
GRMZM2G001930	1.30	AT1G32640.1	ATMYC2,JAI1,RD22BP1	Basic helix-loop-helix (bHLH) DNA-binding family protein
GRMZM2G394450	2.13	AT1G62660.1		Glycosyl hydrolases family 32 protein
GRMZM2G005840	3.30	AT2G04240.2	XERICO	RING/U-box superfamily protein
GRMZM2G113860	8.33	AT3G19580.1	AZF2,ZF2	zinc-finger protein 2
GRMZM2G567897	1.98	AT3G46620.1	ATRDUF1	zinc finger (C3HC4-type RING finger) family protein
GRMZM2G077809	1.49	AT5G14420.1	RGLG2	RING domain ligase2
GRMZM2G069082	11.05	AT5G51990.1	CBF4,DREB1D	C-repeat-binding factor 4
GRMZM2G124037	10.09	AT5G51990.1	CBF4,DREB1D	C-repeat-binding factor 4
GRMZM2G364612	2.31	AT5G59550.1	ATRDUF2	zinc finger (C3HC4-type RING finger) family protein
GRMZM2G145444	1.10	AT5G67300.1	ATMYB44,MYB44	myb domain protein r1
AC226248.1_FG002	1.02	AT1G11050.1		Protein kinase superfamily protein
GRMZM2G445634	5.54	AT1G19180.1	JAZ1,TIFY10A	jasmonate-zim-domain protein 1
GRMZM2G013236	1.49	AT1G30270.1	ATCIPK23,SnRK3.23	CBL-interacting protein kinase 23
GRMZM2G066120	1.31	AT4G08500.1	ATMEKK1,MAPKKK8	MAPK/ERK kinase kinase 1
GRMZM2G080516	2.04	AT4G17500.1	ATERF-1,ERF-1	ethylene responsive element binding factor 1
GRMZM2G466044	1.56	AT4G17500.1	ATERF-1,ERF-1	ethylene responsive element binding factor 1

The criterion “FDR ≤ 0.001 and the absolute value of log2Ratio(L+4/WT) ≥ 1” was used as the threshold to judge the significance of gene expression differences.

Table S6 Differentially expressed key genes between *ZmPTF1* overexpression line (L+4) and WT

Gene	log2 (L+4/WT)	Best-hit- Arabidopsis	Name in Arabidopsis	Function
AP2/DREBP family transcription factors				
GRMZM2G069082	11.05	AT5G51990.1	CBF4,DREB1D (A-1 subfamily)	There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to drought stress and abscisic acid treatment, but not to low temperature.
GRMZM2G124037	10.09	AT5G51990.1		
GRMZM2G069126	4.52	AT4G25470.1	ATCBF2,DREB1C,FTQ4 (A-1 subfamily)	This gene is involved in response to low temperature, abscisic acid, etc. Overexpressing CBF2 leads to increased freeze tolerance. May be involved in a negative regulatory/feedback circuit of the CBF pathway.
GRMZM2G069146	3.08	AT4G25470.1		
GRMZM2G061487	2.22	AT1G78080.1	RAP2.4 (A-6 subfamily)	Role in mediating light and ethylene signaling.
GRMZM2G113060	1.21	AT1G78080.1		
GRMZM2G438202	3.16	AT3G15210.1	ATERF-4,ATERF4,RAP2.5(B-1 subfamily)	Acts as a negative regulator of JA-responsive defense gene expression and resistance to the necrotrophic fungal pathogen <i>Fusarium oxysporum</i> and antagonizes JA inhibition of root elongation.
GRMZM2G020150	2.67	AT3G15210.1		
GRMZM2G020054	5.78	AT3G20310.1	ATERF-7,ATERF7,ERF7(B-1 subfamily)	Phosphorylated by PKS3 in vitro. Involved in ABA-mediated responses. Acts as a repressor of GCC box-mediated transcription together with AtSin3 and HDA19.
GRMZM2G068967	3.88	AT3G20310.1		
GRMZM2G089995	3.62	AT3G20310.1		
GRMZM2G174347	3.09	AT5G44210.1	ATERF-9,ATERF9,ERF9(B-1 subfamily)	here are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.
GRMZM2G310368	2.50	AT5G44210.1		
GRMZM2G132185	1.32	AT5G44210.1		
GRMZM2G369472	10.30	AT3G16770.1	ATEBP,EBP,ERF72,RAP2.3 (B-2 subfamily)	Acts as a transcriptional activator through the GCC-box. It was a suppressor of Bax-induced cell death. Confers resistance to H ₂ O ₂ and heat stresses. It is part of the ethylene signaling pathway and is predicted to act downstream of EIN2 and CTR1, but not under EIN3.
GRMZM2G173771	8.23	AT3G16770.1		
GRMZM2G080516	2.04	AT4G17500.1	ATERF-1,ERF-1(B-3 subfamily)	There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.
GRMZM2G466044	1.56	AT4G17500.1		
WRKY family transcription factors				
GRMZM2G012724	3.15	AT2G38470.1	ATWRKY33,WRKY33 (group I)	Regulates the antagonistic relationship between defense pathways mediating responses to <i>P. syringae</i> and necrotrophic fungal pathogens. Located in nucleus. Involved in response to various abiotic stresses.
GRMZM2G148087	1.74	AT2G38470.1		
GRMZM2G120320	3.17	AT1G80840.1	ATWRKY40,WRKY40 (Group IIc)	Forms complexes with itself, WRKY40 and 60. Coexpression made plants more susceptible to biotic stress.
GRMZM2G176489	1.93	AT5G15130.1	ATWRKY72,WRKY72(Group IIb)	WRKY72-type transcription factors contribute to basal immunity in tomato and Arabidopsis.
GRMZM2G083350	1.25	AT5G15130.1		
GRMZM5G863420	1.02	AT5G64810.1	ATWRKY51,WRKY51 (Group IIc)	Involved in jasmonic acid inducible defense responses.
GRMZM2G401521	2.12	AT1G64000.1	ATWRKY56,WRKY56(Group IIc Group II-c WRKY TF.	
GRMZM2G143204	1.36	AT1G69310.2	ATWRKY57,WRKY57(Group IIc)	Activation of WRKY57 confers drought tolerance.
GRMZM2G148561	1.12	AT4G31550.2	ATWRKY11,WRKY11 (Group IIc)	Negative regulator of basal resistance to <i>Pseudomonas syringae</i> .
GRMZM2G324999	2.00	AT4G11070.1	AtWRKY41,WRKY41(Group III)	WRKY41 controls Arabidopsis seed dormancy via direct regulation of ABI3 transcript levels.
GRMZM2G059562	3.17	AT2G46400.1	ATWRKY46,WRKY46(Group III)	Feedforward inhibition of osmotic/salt stress-dependent LR inhibition via regulation of ABA and auxin signalling.
GRMZM2G158328	9.37	AT1G66600.1	ABO3,WRKY63(Group III)	Involved in the regulation of plant responses to ABA and drought stress
NAC family transcription factors				
GRMZM2G014653	1.12	AT1G01720.1	ANAC002,ATAF1	Transcript level increases in response to wounding and ABA. ATAF1 attenuates ABA signaling and synthesis.
AC196475.3_FG005	1.67	AT1G33060.2	ANAC014,NAC014	NAC domains transcription factor NAC014
GRMZM2G063522	1.26	AT1G56010.2	anac021,ANAC022,NAC1	Involved in shoot apical meristem formation and auxin-mediated lateral root formation and stress responses.
GRMZM2G146380	2.25	AT3G04060.1	anac046,NAC046	Mutants in NAC046 have delayed senescence and increased CHL content.

Table S6

GRMZM2G127379	1.99	AT3G04070.2	anac047,NAC047	NAC Transcription Factor SPEEDY HYPONASTIC GROWTH Regulates Flooding-Induced Leaf Movement in Arabidopsis
GRMZM2G011598	1.33	AT3G04070.1		
AC212859.3_FG006	8.01	AT1G71930.1	ANAC030,VND7	Involved in xylem formation. Induces transdifferentiation of various cells into protoxylem vessel elements.
GRMZM2G068973	2.28	AT5G08790.1		
GRMZM2G347043	2.07	AT5G08790.1	anac081,ATAF2	Induced by wounding, belongs to a large family of putative transcriptional activators with NAC domain.ATAF2 integrates Arabidopsis brassinosteroid inactivation and seedling photomorphogenesis
GRMZM2G162739	1.96	AT5G08790.1		
GRMZM2G123667	-1.35	AT5G08790.1		
MYB family transcription factors				
GRMZM2G145444	1.10	AT5G67300.1	ATMYB44,MYBR1	Involved in mediating plant responses to a variety of abiotic stimuli.
GRMZM2G127857	5.75	AT3G23250.1	ATMYB15,ATY19,MYB15	SG2-type R2R3-MYB transcription factor MYB15 controls defense-induced lignification and basal immunity in Arabidopsis
GRMZM2G095904	4.55	AT3G23250.1		
GRMZM2G084583	-1.76	AT4G38620.1	ATMYB4,MYB4	A R2R3 MYB protein which is involved in the response to UV-B and a repressor of target gene expression.
GRMZM2G130149	-1.58	AT5G59780.3	ATMYB59,MYB59	AtMYB59 regulates root growth and cell cycle progression in Arabidopsis
GRMZM2G078820	1.85	AT2G23290.1	AtMYB70,MYB70	Member of the R2R3 factor gene family.
bHLH family transcription factors				
GRMZM2G301089	5.11	AT5G43650.1	BHLH92	bHLH92 functions in plant responses to osmotic stresses
GRMZM2G001930	1.30	AT1G32640.1	ATMYC2,RD22BP1,ZBF1	MYC-related transcriptional activator. Binds to an extended G-Box promoter motif and interacts with Jasmonate ZIM-domain proteins. Interacts with EIN3 and EIL1 to repress hook curvature and resistance to Botrytis cinera.
GRMZM2G133675	1.23	AT3G47640.2	PYE	Encodes POPEYE, a bHLH transcription factor regulating response to iron deficiency in Arabidopsis roots.
GRMZM2G082343	2.07	AT4G37850.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
GRMZM2G006631	-1.09	AT1G72210.1	BHLH96	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
GRMZM2G101350	1.70	AT4G34530.1	CIB1	CIB1 interacts with CRY2 (cryptochrome 2) in a blue light-specific manner, CIB1 positively regulates FT expression.
other transcription factor				
GRMZM2G060216	1.83	AT1G08320.3	bZIP21,TGA9	Involved in ROS-mediated responses to bacterial PAMP flg22
GRMZM2G131961	1.51	AT5G65210.2	TGA1	A redox-controlled regulator of systemic acquired resistance. TGA1 targets the as-1 element of defense proteins genes
GRMZM2G033413	1.13	AT3G19290.1	ABF4,AREB2	Mediates ABA-dependent stress responses.ABF4 acts through SnRK2 pathway and binds to ABA response elements.
GRMZM2G139872	1.59	AT5G27920.1		F-box family protein
GRMZM2G440543	2.24	AT5G48170.1	SLY2	Overexpression of SLY2 can partially compensate sly1-10 mutant phenotype of dwarfism.
GRMZM2G138967	-1.33	AT4G16141.1	ATGATA17L	GATA type zinc finger transcription factor family protein;(source:Araport11)
GRMZM2G163427	1.56	AT2G37650.1		GRAS family transcription factor
GRMZM2G001205	-1.51	AT5G59820.1	RHL41,ZAT12	Overexpression of this putative transcription factor exhibits a small but reproducible increase in freeze tolerance.
GRMZM2G002805	9.55	AT2G28200.1		C2H2-type zinc finger family protein
GRMZM2G361210	4.24	AT3G46080.1		C2H2-type zinc finger family protein
GRMZM2G117851	1.74	AT2G46270.2	GBF3	Induced by ABA. It has been shown to bind to ABA that contains the G-box and is induced by cold and water deprivation
GRMZM2G366532	8.01	AT5G02500.1	AT-HSC70-1,HSP70-1	Important for stomatal closure and modulate abscisic acid-dependent physiological responses in Arabidopsis
mitogen-activated protein kinase				
GRMZM2G131334	-1.10	AT2G42880.1	ATMPK20,MPK20	MAP kinase 20
GRMZM2G173965	4.61	AT5G55090.1	MAPKKK15	mitogen-activated protein kinase kinase kinase 15
GRMZM2G041774	4.01	AT4G26890.1	MAPKKK16	mitogen-activated protein kinase kinase kinase 16
GRMZM2G476477	1.68	AT2G32510.1	MAPKKK17	mitogen-activated protein kinase kinase kinase 17
GRMZM2G156800	1.05	AT5G66850.1	MAPKKK5	mitogen-activated protein kinase kinase kinase 5

Table S6

VQ motif-containing protein				
GRMZM2G174558	1.26	AT1G28280.1	MPK3/6-TARGETED VQP 1	MPK3/6-TARGETED VQP 1
GRMZM2G118172	3.45	AT4G37710.1	VQ12	Arabidopsis VQ-motif-containing Protein 29 Represses Seedling De-etiolation by Interacting with PIF1
GRMZM2G333049	3.01	AT4G39720.1	VQ motif-containing protein	VQ motif-containing protein
GRMZM2G420715	2.06	AT4G39720.1	VQ motif-containing protein	VQ motif-containing protein
jasmonate-zim-domain protein				
GRMZM2G445634	5.54	AT1G19180.1	JAZ1,TIFY10A	JAZ 1 is a nuclear-localized protein involved in jasmonate signaling. JAZ 1 can interact with the CO11 F-box subunit of an SCF E3 ubiquitin ligase in a yeast-two-hybrid assay only in the presence of jasmonate-isoleucine (JA-ILE) or coronatine
GRMZM2G036351	6.00	AT1G74950.1	JAZ2,TIFY10B	TIFY domain/Divergent CCT motif family protein
GRMZM2G343157	8.74	AT3G43440.1	JAZ11,TIFY3A	
GRMZM2G145458	5.76	AT3G43440.1	JAZ11,TIFY3A	Jasmonate-zim-domain protein 11
GRMZM2G145412	5.01	AT3G43440.1	JAZ11,TIFY3A	
Auxin signaling pathway				
GRMZM2G115357	2.42	AT1G04240.1	IAA3,SHY2	SHY2/IAA3 regulates auxin responses. It is induced rapidly by IAA, and phosphorylated by oat phytochrome A in vitro.
GRMZM2G081158	-1.18	AT1G30330.2	ARF6	Mediates auxin response. Acts redundantly with ARF8 to control stamen elongation and flower maturation.
GRMZM2G442000	-1.44	AT1G19840.1	SAUR53	SAUR-like auxin-responsive protein family
GRMZM2G414727	1.97	AT2G46690.1	SAUR32	SAUR-like auxin-responsive protein family
GRMZM2G430052	1.17	AT5G50760.1	SAUR55	SAUR-like auxin-responsive protein family
GRMZM2G146108	8.51	AT1G56150.1	SAUR71	SAUR-like auxin-responsive protein family
response to phosphate, salt				
GRMZM2G112377	1.82	AT3G54700.1	PHT1;7	Encodes Pht1;7, a member of the Pht1 family of phosphate transporters.
GRMZM2G070087	-1.53	AT3G54700.1	PHT1;7	
GRMZM2G009045	2.11	AT5G14040.1	PHT3;1	Encodes a mitochondrial phosphate transporter. Modulates plant responses to salt stress.
GRMZM2G073860	1.57	AT2G16430.2	ATPAP10,PAP10	A major root-associated acid phosphatase, is regulated by local and systemic phosphate signals.
GRMZM2G097704	3.72	AT4G16820.1	PLA-I[β]2	Encodes a lipase that hydrolyzes phosphatidylcholine, glycolipids as well as triacylglycerols.
GRMZM2G106026	9.12	AT1G27730.1	STZ,ZAT10	Salt tolerance zinc finger. Salt tolerance produced by ZAT10 appeared to be partially dependent on ENA1/PMR2, a P-type ATPase required for Li ⁺ and Na ⁺ efflux in yeast. Acts as a transcriptional repressor and is responsive to chitin oligomers and photooxidative stress.
GRMZM2G400714	3.00	AT1G27730.1	STZ,ZAT10	
GRMZM2G035103	2.78	AT1G27730.1	STZ,ZAT10	

The criterion "FDR \leq 0.001 and the absolute value of $\log_2\text{Ratio}(L+4/WT) \geq 1$ " was used as the threshold to judge the significance of gene expression differences.

Table S6

Table S8 Real-time RT-PCR to validate the results in the RNAseq analysis in *ZmPTF1* overexpression lines L+3, L+4 and WT

ID_maize	Name	L+4/WT (DGE)	L+3/WT (qPCR)	L+4/WT (qPCR)	Forward primer (5' to 3')	Reverse primer (5' to 3')
GRMZM2G442000	SAUR53	0.37	0.25±0.02	0.34±0.03	CAGGCGGAGGAGGAGTACGGGTTC	CGCTCTGGAGGTCGTCGAGGGT
GRMZM2G130149	ATMYB59,ATMYB59-1,A	0.34	0.40±0.03	0.27±0.02	GATTTTCATTGCCAAAGTATCAGG	TGGTAAGTCAGCGAAGACGAG
GRMZM2G081158	ARF6	0.44	0.41±0.03	0.36±0.04	AGATTCGGCAGCTACTACGA	TATGCACCTACGCTATTCA
GRMZM2G461447	ORTH2,VIM1	0.46	0.41±0.03	0.36±0.04	TGCCCTACTGACATCTGCGACTT	GCACCTCCATTTCAACCAC
GRMZM2G033413	ABF4,AREB2	2.19	2.44±0.12	3.13±0.32	TGGAGCGTATCAACAGCCAACA	CGCAGACTACCCACGTCACAGA
GRMZM2G430052	SAUR55	2.26	2.61±0.13	5.62±0.25	TCGTGGTGGGACGGAGTGC	TACGCGGAGTGGCCCCGGACAAG
GRMZM2G001930	ATMYC2,JAI1,JIN1,MYC2	2.47	2.61±0.24	5.24±0.11	CGCCGTTCTTCAAGCCCGAGTC	CGGGTGGTGGTTGGTGTGCTC
AC212859.3_FG008	ANAC030,VND7	257.00	234.51±5.67	245.21±7.91	CGGCTACTACGACCACAACCTC	CAGCGGGGGATACTCAACA
GRMZM2G063522	anac021,ANAC022,NAC1	2.39	3.52±0.63	7.14±0.54	GTGGTGGTGAGCATCTACGG	CGGCTATTGGACGGTCTTT
GRMZM2G414727	SAUR32	3.91	3.62±0.30	4.44±0.44	CCCAAGGGGTGCGTGACGGT	CGGCAGGTGGAGGTGGTGCT
GRMZM2G162739	anac081,ATAF2	3.89	3.62±0.72	6.27±0.62	CAGGTTGGATGACTGGGTGCTCTG	GCCCAAGTCTCCACCTCCTCCTT
GRMZM2G146108	SAUR71	364.00	381±11.21	404±12.43	GGCTTGGACGAAGAGGAAGACTGG	GATCCCGCATCTGTGCATAGCG
GRMZM2G347043	anac081,ATAF2	4.20	4.19±0.23	3.96±0.24	CTTAGGTTGGATGACTGGGTGCTG	GATTGGGAGTGGGAGTGC GTGT
GRMZM2G009045	PHT3;1	4.32	5.51±0.13	6.17±0.52	CTCTTTGGGGGCGACAGATT	CGACCATCAGGATGCGAAGA
GRMZM2G045820	VFB1	0.46	5.62±0.32	6.24±0.41	GTGGCATCCTCACCAGAACTCC	CCAGATTGGCACAGGCAGAAA
GRMZM2G115357	IAA3,SHY2	5.34	5.62±0.32	6.24±0.41	CCTCCCAAGGCGCAAGTGGT	TCGTAGGCGATGGCGTGCTG
GRMZM2G059562	ATWRKY46,WRKY46	9.03	6.32±0.12	10.21±0.14	CGCACAAGGACCAGGGATGCA	ACTGAGACCGCCGAAGTCAAAGC
GRMZM2G010251	ACH1,ATNRT2.1,ATNRT2	5.82	7.40±0.73	8.63±0.34	CGGAGCACAAGGCGAAGAGC	GATGAGCGACATGCAGAACACG
GRMZM2G068973	anac081,ATAF2	4.85	7.62±0.51	4.04±0.11	GCAAGTACCCAAACGGCTCG	GCACAACCCCACTCATCCAAC
GRMZM2G012724	ATWRKY33,WRKY33	8.88	9.01±1.01	10.4±1.42	GCCGTGTGTTTCTGTGTTT	GATGTCGCTCAGCGTCTGTA
GRMZM2G014392	ATNCED9,NCED9	6.19	7.19±0.21	6.76±0.22	CGGAGGAGGAACAGAGGAGCCA	GCAACCAAGATCCCAGACACCC
GRMZM2G052948	Protein kinase	0.36	0.32±0.13	2.17±0.12	ATTGTGCTGGTGGTTCTGTT	CCTCTGTAGGATGATTTGGGTC
GRMZM2G057506	unknown protein	1241.00	1500.62±13.42	1702.25±15.33	CAGCAAAATGCTGCAAAGCG	CCCCACTACACCAAGAGACG
GRMZM2G057959	PYL5,RCAR8	0.27	0.62±0.02	0.24±0.11	GCACCGGCTCCAGAACTACCT	CATCCCTGATCCCTCCTCCC
GRMZM2G069082	CBF4,DREB1D	2119.00	1897.34±15.12	2433.43±20.14	CAGACTCAGCTCAATCCCGA	TTCTTGGGACCAGAGCAGCA
GRMZM2G112377	PHT1;7	3.54	3.40±0.33	5.33±0.44	TCCTTCGGGTTCTGTACTT	GCACTGTGCGGTTGTTGTAG
GRMZM2G123667	anac081,ATAF2	0.39	0.62±0.01	0.14±0.02	GAAGAACCCGCGTGCCAGTG	ACGGCGTCTCCAGGTCGTCGA
GRMZM2G124037	CBF4,DREB1D	1091.00	1381±15.20	1404±19.47	CACCTCCCACAAAACACAC	GCTGTGACTGTGACCCTGAC
GRMZM2G129375	ATCNGC1,CNGC1	2.34	5.19±0.13	3.85±0.28	ACGACGAATGGTGGAAAGAAC	CTGCGAGTAGAACCTGAAAGTG
GRMZM2G369472	ATEBP,EBP,ERF72,RAP2.1	1263.00	1475.51±16.13	1456.17±21.52	CACGTTTACTTTGCGCTGCT	GGCTGTAGCGATCTGTGTGT
GRMZM2G417954	ATNCED9,NCED9	385.00	400.60±8.32	456.22±10.41	TGTCGTGTCCAAGCCGTTCT	CGGGATGATGGCGTGGTTCT
GRMZM2G436299	ATCSLD3,CSLD3,KJK	2.21	2.62±0.12	4.24±0.31	TTGTGGCAGAAGCGATCAGTG	CCTTTGGAGCACCTTCATCTTG
GRMZM2G436583	ATCNGC14,CNGC14	0.12	0.09±0.02	0.21±0.04	GAGCACAGAGGGCACATACATT	GGTGGACAGTGGCAGGTTGA
GRMZM2G474194	ATEXPB2,ATHEXP BETA 1	0.48	0.40±0.03	0.63±0.01	AGCAGCAAGAGCCAAGCAA	CGTCATCGCCGAGAAAGGTG
GRMZM2G474755	calcium-binding protein	42.80	36.62±0.71	4.84±3.11	CCAGGCTTGTGCTCCTCGTCTC	CGAACTCGGGCAGGCTGATGT

Table S8