Supporting Information

Zheng et al. 10.1073/pnas.1202630109

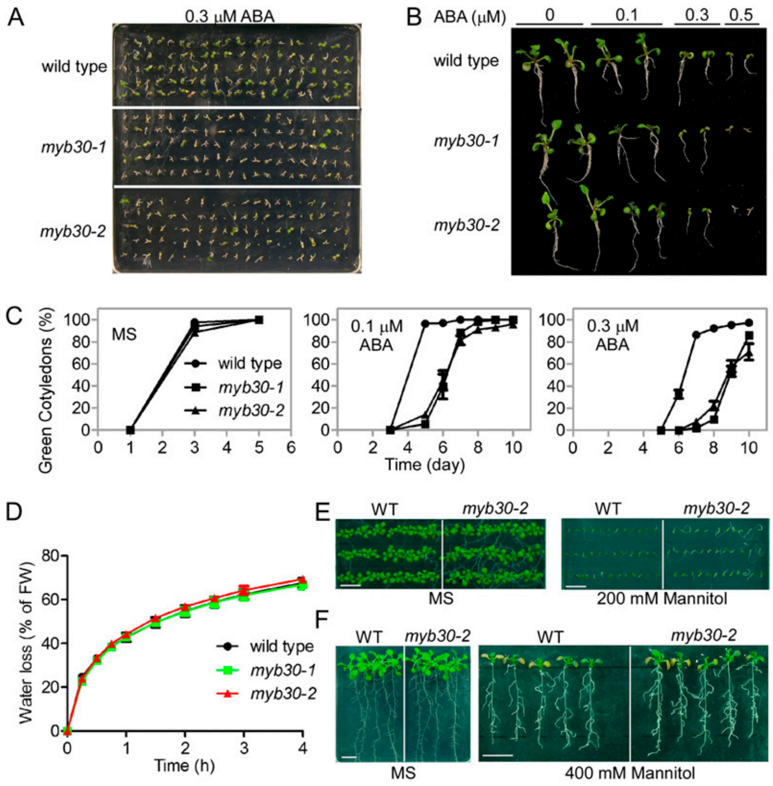

Fig. S1. *myb30-1* and *myb30-2* have similar responses to abscisic acid (ABA) and osmotic/drought stress. (*A*) *myb30-1* and *myb30-2* are hypersensitive to ABA. Seeds were sown on Murashige and Skoog (MS) medium containing 0.3 μM ABA; photographs were taken after 6 d. (*B*) Twelve-day-old seedlings of wild-type and the mutants grown without or with 0.1, 0.3, or 0.5 μM ABA. (*C*) Green cotyledons in wild-type and the *myb30-1* and *myb30-2* mutants were scored at the indicated times and represent an average of 100 seeds from three independent experiments ± SE. (*D*) Water loss from wild-type and the *myb30-1* and *myb30-2* mutants was measured using detached leaves. Water loss is expressed as a percentage of the initial fresh weight (FW). Data from one representative experiment of three. (*E*) Wild-type and *myb30-2* seeds were sown on MS medium (*Left*) or MS medium containing 200 mM mannitol (*Right*). Photographs were taken after 8 d. (Scale bars, 1 cm.) (*F*) Six-day-old wild-type and *myb30-2* seedlings were transferred from MS medium to MS medium without (*Left*) or with 400 mM mannitol (*Right*) and photographs were taken 8 d after transfer. (Scale bars, 1 cm.)

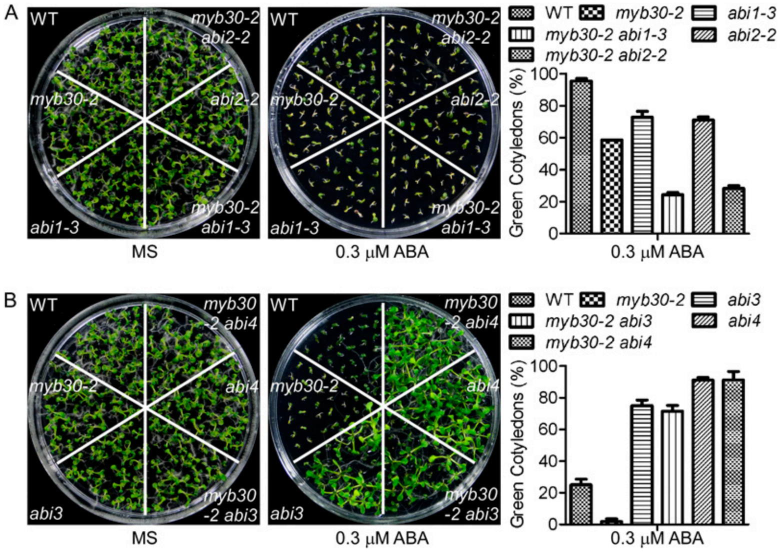

Fig. S2. ABA phenotypes of the *myb30-2 abi* double-mutants. (*A*) ABA phenotype of the *myb30-2 abi1-3* and *myb30-2 abi2-2* double-mutants. Seeds were sown on MS medium without (*Left*) or with 0.3 μM ABA (*Right*) and photographs were taken after 9 d. The mean germination value for wild-type and the *myb30-2*, *abi1-3*, *abi2-2*, and *myb30 abi1-3* and *myb30 abi2-2* double-mutants in response to 0.3 μM ABA is shown in the graph to the right of the images. Green cotyledons were scored after 6 d of growth and represent an average of 100 seeds from at least three independent experiments ± SE. (*B*) ABA phenotype of the *myb30-2 abi3* and *myb30-2 abi4* double-mutants. Seeds were sown on MS medium without (*Left*) or with 0.3 μM ABA (*Right*) and photographs were taken after 6 d. The mean germination value for wild-type and the *myb30-2*, *abi3*, *abi4*, and *myb30-2 abi3* and *myb30-2 abi4* double-mutants in response to 0.3 μM ABA is shown in the graph to the right of the images. Green cotyledons were scored after 6 d of growth and represent an average of 100 seeds from at least three independent experiments ± SE.

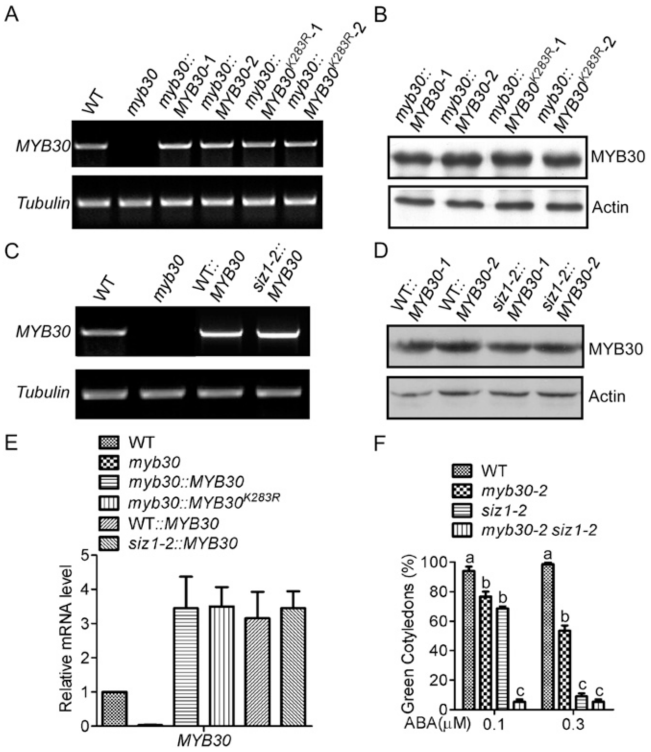

Fig. S3. Overexpression of *MYB30* and *MYB30*^{K283R} in wild-type and the *siz1-2* mutant. RNA and protein were extracted from 7-d-old seedlings without ABA treatment. (*A*) Transcript abundance of *MYB30* and *MYB30*^{K283R} in wild-type and *myb30-2* transgenic lines was monitored using RT-PCR. Shown are RT-PCR products after 30 cycles with *MYB30* gene-specific or *Tubulin* gene-specific primers as a loading control. (*B*) MYB30 and MYB30^{K283R} protein levels in the transgenic lines were detected by immunoblot analysis using an anti-Flag antibody. Actin was used as a loading control. (*C*) Transcript abundance of *MYB30* in wild-type and *siz1-2* transgenic lines was monitored by RT-RCR with *MYB30* gene-specific primers. *Tubulin* was included as a loading control. (*D*) MYB30 protein levels in wild-type and *siz1-2* transgenic lines were detected by immunoblot analysis using an anti-Flag antibody. (*E*) Transcript abundance of *MYB30* in wild-type, *myb30-2*, and different transgenic lines was determined by quantitative PCR. mRNA levels are expressed relative to the value of wild-type seedlings. Data represent means ± SD of three independent experiments. (*F*) Germination frequencies were determined for WT, the *myb30-2* and *siz1-2* single mutants and the *myb30-2 siz1*-2 double-mutant seeds sown on MS medium with 0.1 μM ABA or 0.3 μM ABA. Green cotyledons were scored after 7 (0.1 μM) or 9 d (0.3 μM) ABA. Data represent an average of 100 seeds from three independent experiments ± SE. Based on a Student *t* test, genotypes with different letters are statistically different; $P < 0.05$.

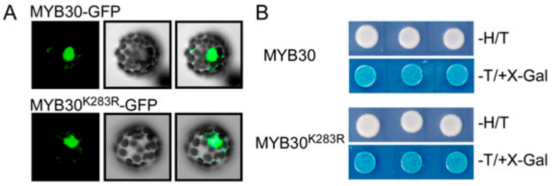

Fig. S4. Localization and transcriptional activity analysis of MYB30^{K283R}. (*A*) Nuclear localization of MYB30-GFP and MYB30^{K283R}-GFP in wild-type protoplasts. (*Left*) GFP fluorescence; (*Center*) bright field; (*Right*) merged image. One representative image of protoplasts from transiently transformed *Arabidopsis* leaves. (*B*) Transcriptional activity analysis of MYB30 and MYB30^{K283R} using the GAL4 transient expression assay in yeast (1). *Upper* panel for each represents growth on synthetic complete medium without His and Thr (–H/T). *Lower* panel for each represents growth without Thr in the presence of X-Gal (–H/+X-Gal).

1. Miura K, et al. (2007) SIZ1-mediated sumoylation of ICE1 controls *CBF3/DREB1A* expression and freezing tolerance in *Arabidopsis*. *Plant Cell* 19:1403–1414.

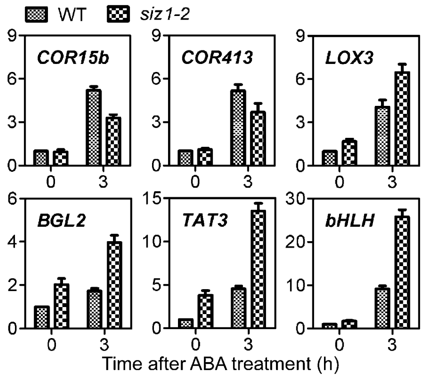

Fig. S5. ABA-responsive gene expression in wild-type and *siz1*. The transcript abundance of *TAT3*, *LOX3*, *BGL2*, *bHLH*, *COR15b*, and *COR413* in wild-type and *siz1-2* mutant was determined by quantitative PCR using 1-wk-old seedlings treated with 100 μM ABA for 3 h. mRNA levels are expressed relative to the value of wild-type seedlings. Data are mean ± SD of three independent experiments.

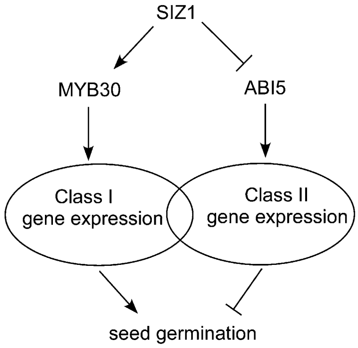

Fig. S6. MYB30, ABI5, and SIZ1 function in ABA signaling during seed germination. ABI5 and MYB30 regulate the expression of different sets of genes and share few common targets. SIZ1 actives MBY30 and inactivates ABI5 through sumoylation to regulate ABA signaling during seed germination.

Table S1. Changes in gene expression in the *myb30* mutant during ABA treatment

	Gene	WT	Mutant	Log(wt/mutant)	AA wt	ABA mutant	Log(wt/mutant)	Log(ABA wt/wt)	Log(ABA m/m)	Function
1	*AT1G64360*	29	40	−0.4441	76	31	1.2947	1.3678	−0.3710	Unknown protein
2	*AT1G73120*	54	75	−0.4620	145	67	1.1032	1.4107	−0.1545	Unknown protein
3	*AT1G15330*	52	47	0.1533	174	87	0.9951	1.7346	0.8928	Cystathionine β-synthase (CBS) protein
4	*AT2G42530*	638	903	−0.5009	4,209	2,220	0.9225	2.7214	1.2980	Cold regulated 15b (COR15B)
5	*AT4G21630*	13	3	2.1229	37	20	0.9098	1.5154	2.7286	Subtilase family protein
6	*AT4G25580*	15	5	1.6084	102	54	0.9080	2.7360	3.4364	CAP160 protein
7	*AT2G37900*	37	35	0.0811	133	73	0.8682	1.8458	1.0587	Major facilitator superfamily protein
8	*AT1G57590*	29	32	−0.1222	118	66	0.8310	2.0037	1.0505	Pectinacetylesterase family protein
9	*AT1G66390*	109	172	−0.6595	580	330	0.8128	2.4136	0.9413	myb domain protein 90 (MYB90)
10	*AT1G29395*	757	822	−0.1192	4,322	2,509	0.7847	2.5136	1.6097	COLD REGULATED 314 INNER MEMBRANE 1 (COR413IM1)
11	*AT5G42200*	27	20	0.4449	92	54	0.7688	1.7603	1.4364	RING/U-box superfamily protein
12	*AT1G01250*	42	18	1.2384	90	53	0.7615	1.0818	1.5586	Integrase-type DNA-binding superfamily protein
13	*AT1G23200*	21	23	−0.1527	169	101	0.7518	3.0323	2.1278	Plant invertase/pectin methylesterase inhibitor superfamily
14	*AT5G01595*	1,177	1,224	−0.0563	3,914	2,364	0.7276	1.7335	0.9496	Other RNA
15	*AT3G20340*	81	70	0.2031	184	112	0.7253	1.1947	0.6725	FUNCTIONS IN: molecular_function unknown
16	*AT1G74810*	42	30	0.5015	111	67	0.7188	1.3848	1.1674	BOR5
17	*AT2G19810*	118	89	0.4021	537	327	0.7158	2.1910	1.8773	CCCH-type zinc finger family protein
18	*AT5G24780*	462	732	−0.6648	3,123	1,931	0.6936	2.7578	1.3994	Vegetative storage protein 1 (VSP1)
19	*AT5G37300*	16	9	0.8599	169	105	0.6898	3.3734	3.5435	WSD1
20	*AT5G54585*	11	17	−0.6426	41	25	0.6854	1.9077	0.5797	Unknown protein
21	*AT3G21890*	39	53	−0.4350	198	124	0.6818	2.3398	1.2230	B-box type zinc-finger family protein
22	*AT1G10640*	98	73	0.4250	240	150	0.6788	1.2950	1.0412	Pectin lyase-like superfamily protein
23	*AT5G01600*	1,595	1,653	−0.0512	4,893	3,095	0.6606	1.6168	0.9050	Ferretin 1 (FER1)
24	*AT3G27660*	59	55	0.0965	120	76	0.6577	1.0320	0.4708	Oleosin 4 (OLEO4)
25	*AT1G51090*	62	55	0.1745	156	101	0.6380	1.3336	0.8700	Heavy metal transport/detoxification superfamily protein
26	*AT3G62740*	160	105	0.6084	358	232	0.6276	1.1628	1.1436	β-Glucosidase 7 (BGLU7)
27	*AT1G48100*	140	126	0.1569	703	462	0.6060	2.3228	1.8737	Pectin lyase-like superfamily protein
28	*AT2G37580*	36	31	0.2131	98	65	0.5894	1.4483	1.0720	RING/U-box superfamily protein
29	*AT1G02670*	25	24	0.0615	71	48	0.5842	1.5075	0.9849	P-loop containing nucleoside triphosphate hydrolases superfamily protein
30	*AT3G28220*	2,030	1821	0.1566	6,316	4,236	0.5761	1.6376	1.2181	TRAF-like family protein
31	*AT1G18810*	66	55	0.2723	263	177	0.5716	1.9834	1.6842	Phytochrome kinase substrate-related
32	*AT5G57790*	19	26	−0.4900	85	57	0.5691	2.2027	1.1436	Unknown protein
33	*AT1G67600*	24	54	−1.1725	57	39	0.5651	1.2556	−0.4820	Acid phosphatase/vanadium-dependent haloperoxidase-related protein
34	*AT4G12430*	22	23	−0.0787	62	42	0.5597	1.5064	0.8680	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
35	*AT4G12432*	22	23	−0.0787	62	42	0.5597	1.5064	0.8680	Conserved peptide upstream ORF 26 (CPuORF26)
36	*AT2G42540*	2,732	3,113	−0.1882	25,841 1	7,828	0.5355	3.2415	2.5178	Cold-regulated 15a (COR15A)
37	*AT1G22160*	30	23	0.4067	189	131	0.5248	2.6329	2.5149	Protein of unknown function (DUF581)
38	*AT5G10946*	23	23	−0.0083	67	46	0.5203	1.5409	1.0124	Unknown protein
39	*AT4G31330*	117	124	−0.0898	233	163	0.5141	1.0028	0.3989	Protein of unknown function, DUF599
40	*AT5G53870*	71	53	0.4174	262	183	0.5120	1.8854	1.7907	Early nodulin-like protein 1 (ENODL1)
41	*AT1G72490*	21	21	−0.0214	53	38	0.5041	1.3443	0.8387	Unknown protein
42	*AT4G11910*	35	37	−0.0865	162	230	−0.5018	2.2193	2.6346	INVOLVED IN: biological_process unknown
43	*AT1G63370*	38	42	−0.1401	202	286	−0.5025	2.4057	2.7681	Flavin-binding monooxygenase family protein
44	*AT4G37150*	383	561	−0.5495	1,028	1,457	−0.5025	1.4239	1.3770	Methyl esterase 9 (MES9)
45	*AT2G30362*	246	382	−0.6343	948	1,343	−0.5029	1.9455	1.8141	Other RNA
46	*AT1G52565*	24	38	−0.6655	226	321	−0.5052	3.2408	3.0805	Unknown protein
47	*AT3G22740*	57	99	−0.8060	191	272	−0.5052	1.7575	1.4568	Homocysteine S-methyltransferase 3 (HMT3)

Table S1. Cont.

	Gene	WT	Mutant	Log(wt/mutant)	AA wt	ABA mutant	Log(wt/mutant)	Log(ABA wt/wt)	Log(ABA m/m)	Function
48	*AT4G28085*	59	83	–0.4972	184	262	–0.5052	1.6493	1.6573	Unknown protein
49	*AT5G04390*	12	19	–0.6655	35	50	–0.5052	1.5478	1.3875	C2H2-type zinc finger family protein
50	*AT5G18270*	179	234	–0.3899	489	695	–0.5064	1.4536	1.5701	*Arabidopsis* NAC domain containing protein 87 (ANAC087)
51	*AT5G41040*	519	544	–0.0667	2,846	4,047	–0.5080	2.4540	2.8953	HXXXD-type acyl-transferase family protein
52	*AT1G56650*	64	80	–0.3163	360	511	–0.5084	2.4845	2.6765	Production of anthocyanin pigment 1 (PAP1)
53	*AT1G64610*	131	171	–0.3880	320	455	–0.5087	1.2915	1.4122	Transducin/WD40 repeat-like superfamily protein
54	*AT5G57550*	23	41	–0.8423	125	178	–0.5097	2.4495	2.1170	Xyloglucan endotransglucosylase/hydrolase 25 (XTH25)
55	*AT2G38750*	313	684	–1.1300	696	991	–0.5101	1.1546	0.5347	Annexin 4 (ANNAT4)
56	*AT3G02875*	265	323	–0.2876	621	886	–0.5125	1.2308	1.4557	IAA-LEUCINE RESISTANT 1 (ILR1)
57	*AT1G47510*	40	80	–0.9895	339	484	–0.5152	3.0708	2.5965	Inositol polyphosphate 5-phosphatase 11 (5PTASE11)
58	*AT5G26010*	37	57	–0.6225	86	124	–0.5182	1.2224	1.1181	Protein phosphatase 2C family protein
59	*AT1G69480*	74	103	–0.4761	1,020	1,461	–0.5184	3.7844	3.8267	EXS (ERD1/XPR1/SYG1) family protein
60	*AT3G22600*	977	1,119	–0.1961	5,643	8,094	–0.5203	2.5304	2.8546	Lipid-transfer protein/seed storage 2S albumin superfamily protein
61	*AT1G64380*	106	189	–0.8394	445	638	–0.5216	2.0741	1.7563	Integrase-type DNA-binding superfamily protein
62	*AT2G39030*	105	447	–2.0962	2,845	4,091	–0.5239	4.7663	3.1939	Acyl-CoA *N*-acyltransferases (NAT) superfamily protein
63	*AT2G23540*	128	145	–0.1743	357	514	–0.5240	1.4751	1.8248	GDSL-like Lipase/Acylhydrolase superfamily protein
64	*AT5G09980*	25	45	–0.8453	58	84	–0.5244	1.2207	0.8997	Elicitor peptide 4 precursor (PROPEP4)
65	*AT3G61190*	41	78	–0.9145	98	141	–0.5280	1.2448	0.8582	BON association protein 1 (BAP1)
66	*AT1G68620*	364	475	–0.3851	2,347	3,386	–0.5290	2.6896	2.8335	α/β-Hydrolases superfamily protein
67	*AT1G66830*	3	17	–2.3796	62	89	–0.5322	4.2433	2.3960	Leucine-rich repeat protein kinase family protein
68	*AT1G35910*	20	29	–0.5651	76	110	–0.5418	1.9528	1.9295	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
69	*AT2G01275*	11	17	–0.6426	30	44	–0.5418	1.4789	1.3781	RING/FYVE/PHD zinc finger superfamily protein
70	*AT4G39670*	144	360	–1.3245	739	1077	–0.5435	2.3620	1.5810	Glycolipid transfer protein (GLTP) family protein
71	*AT1G56320*	79	78	0.0274	300	437	–0.5440	1.9162	2.4876	BEST protein match is: Glycine-rich protein family (TAIR:AT5G49350)
72	*AT2G43570*	160	293	–0.8721	714	1044	–0.5471	2.1581	1.8330	Chitinase, putative (CHI)
73	*AT4G24130*	377	349	0.1105	1,973	2,883	–0.5473	2.3885	3.0463	Protein of unknown function, DUF538
74	*AT1G79450*	73	66	0.1446	167	244	–0.5483	1.1941	1.8871	ALA-interacting subunit 5 (ALIS5)
75	*AT4G20460*	119	204	–0.7813	270	394	–0.5483	1.1839	0.9510	NAD(P)-binding Rossmann-fold superfamily protein
76	*AT3G59930*	233	377	–0.6940	723	1,063	–0.5564	1.6327	1.4951	FUNCTIONS IN: molecular_function unknown
77	*AT4G25000*	10	45	–2.1990	229	337	–0.5582	4.5452	2.9044	α-Amylase-like (AMY1)
78	*AT1G23800*	390	436	–0.1614	1,833	2,717	–0.5682	2.2331	2.6399	Nuclear gene for mitochondrial product
79	*AT5G17450*	50	69	–0.4620	138	205	–0.5768	1.4594	1.5742	Heavy metal transport/detoxification superfamily protein
80	*AT1G09240*	174	349	–1.0022	355	530	–0.5792	1.0264	0.6034	Nicotianamine synthase 3 (NAS3)
81	*AT2G30360*	348	477	–0.4530	1,331	1,992	–0.5816	1.9333	2.0619	SOS3-interacting protein 4 (SIP4)
82	*AT3G48520*	611	855	–0.4850	3,514	5,288	–0.5896	2.5241	2.6287	Cytochrome P450, family 94, subfamily B, polypeptide 3 (CYP94B3)
83	*AT3G46660*	170	358	–1.0755	1,026	1,544	–0.5897	2.5947	2.1089	UDP-glucosyl transferase 76E12 (UGT76E12)
84	*AT1G02310*	11	43	–1.9814	116	176	–0.6038	3.4078	2.0302	Glycosyl hydrolase superfamily protein
85	*AT4G37432*	329	244	0.4306	1,031	1,569	–0.6057	1.6482	2.6845	Other RNA
86	*AT2G38760*	111	141	–0.3442	326	496	–0.6067	1.5521	1.8146	Annexin 3 (ANNAT3)
87	*AT2G34610*	42	34	0.3209	356	543	–0.6101	3.0676	3.9986	Unknown protein
88	*AT5G45070*	42	52	–0.2921	107	165	–0.6159	1.3385	1.6623	Phloem protein 2-A8 (PP2-A8)
89	*AT1G45145*	723	1,199	–0.7296	1,597	2,451	–0.6181	1.1432	1.0317	Thioredoxin H-type 5 (TRX5)
90	*AT5G33355*	72	119	–0.7275	221	339	–0.6201	1.6182	1.5109	Defensin-like (DEFL) family protein
91	*AT3G05630*	148	243	–0.7144	602	929	–0.6250	2.0241	1.9347	Phospholipase D P2 (PLDP2)
92	*AT3G60966*	17	32	–0.8771	71	110	–0.6334	2.0311	1.7875	RING/U-box superfamily protein
93	*AT2G22500*	267	490	–0.8771	872	1,354	–0.6351	1.7087	1.4667	Uncoupling protein 5 (UCP5)
94	*AT3G51440*	108	189	–0.8099	309	481	–0.6353	1.5209	1.3462	Calcium-dependent phosphotriesterase superfamily protein
95	*AT1G18100*	52	81	–0.6319	109	170	–0.6479	1.0546	1.0705	E12A11
96	*AT2G36770*	90	169	–0.9029	326	511	–0.6510	1.8494	1.5976	UDP-Glycosyltransferase superfamily protein

Table S1. Cont.

	Gene	WT	Mutant	Log(wt/mutant)	AA wt	ABA mutant	Log(wt/mutant)	Log(ABA wt/wt)	Log(ABA m/m)	Function
97	*AT3G44860*	152	642	−2.0742	386	609	−0.6555	1.3418	–0.0769	Farnesoic acid carboxyl-O-methyltransferase (FAMT)
98	*AT5G42510*	40	66	−0.7120	210	331	−0.6572	2.3828	2.3280	Disease resistance-responsive (dirigent-like protein) family protein
99	*AT1G19200*	42	98	−1.2064	285	451	−0.6620	2.7457	2.2013	Protein of unknown function (DUF581)
100	*AT2G43510*	1,079	1,629	−0.5941	2,162	3,421	−0.6621	1.0025	1.0705	Trypsin inhibitor protein 1 (TI1)
101	*AT4G34230*	2,762	5,039	−0.8676	11,694	18,562	−0.6665	2.0822	1.8811	Cinnamyl alcohol dehydrogenase 5 (CAD5)
102	*AT3G56730*	13	13	0.0075	29	46	−0.6687	1.1593	1.8355	Putative endonuclease or glycosyl hydrolase
103	*AT2G38340*	14	30	−1.0835	113	180	−0.6691	2.9998	2.5854	Integrase-type DNA-binding superfamily protein
104	*AT5G09470*	58	109	−0.9173	195	310	−0.6710	1.7562	1.5098	Dicarboxylate carrier 3 (DIC3)
105	*AT5G64190*	20	29	−0.5651	44	71	−0.6724	1.1784	1.2856	Unknown protein
106	*AT5G14700*	97	168	−0.7936	297	473	−0.6731	1.6133	1.4927	NAD(P)-binding Rossmann-fold superfamily protein
107	*AT1G09170*	16	19	−0.2181	53	84	−0.6764	1.6853	2.1436	P-loop nucleoside triphosphate hydrolases superfamily protein
108	*AT2G34810*	444	740	−0.7360	4,080	6,530	−0.6784	3.1990	3.1414	FAD-binding Berberine family protein
109	*AT4G00700*	49	89	−0.8609	130	208	−0.6805	1.4029	1.2225	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
110	*AT1G32350*	29	264	−3.1666	225	361	−0.6810	2.9379	0.4523	Alternative oxidase 1D (AOX1D)
111	*AT2G02990*	528	1,401	−1.4075	2,101	3,434	−0.7087	1.9923	1.2936	Ribonuclease 1 (RNS1)
112	*AT2G35585*	12	15	−0.3245	26	42	−0.7088	1.1004	1.4846	Unknown protein
113	*AT2G22930*	26	39	−0.5775	69	113	−0.7101	1.3980	1.5306	UDP-Glycosyltransferase superfamily protein
114	*AT4G33467*	17	42	−1.2694	1,578	2,583	−0.7105	6.5012	5.9423	Unknown protein
115	*AT3G43270*	420	816	−0.9570	1,452	2,385	−0.7157	1.7887	1.5473	Plant invertase/pectin methylesterase inhibitor superfamily
116	*AT4G30290*	75	215	−1.5167	231	380	−0.7172	1.6212	0.8217	Xyloglucan endotransglucosylase/hydrolase 19
117	*AT3G25180*	5	47	−3.1097	28	46	−0.7276	2.3634	–0.0187	Cytochrome P450, family 82, subfamily G, polypeptide 1 (CYP82G1)
118	*AT4G10500*	30	91	−1.5775	128	213	−0.7314	2.0744	1.2283	2-Oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
119	*AT5G23220*	48	50	−0.0615	153	255	−0.7386	1.6744	2.3515	Nicotinamidase 3 (NIC3)
120	*AT1G71520*	39	62	−0.6613	100	168	−0.7419	1.3567	1.4373	Integrase-type DNA-binding superfamily protein
121	*AT5G28237*	4	28	−2.6844	58	98	−0.7522	3.7442	1.8120	Pyridoxal-5′-phosphate-dependent enzyme family protein
122	*AT2G47190*	21	42	−1.0214	149	252	−0.7532	2.8524	2.5842	myb domain protein 2 (MYB2)
123	*AT4G35783*	14	14	0.0160	98	166	−0.7568	2.7922	3.5651	ROTUNDIFOLIA like 6 (RTFL6)
124	*AT5G02420*	23	38	−0.7327	103	175	−0.7646	2.1675	2.1995	Unknown protein
125	*AT5G02170*	28	38	−0.4245	69	117	−0.7656	1.2826	1.6236	Transmembrane amino acid transporter family protein
126	*AT5G05340*	63	90	−0.5109	263	447	−0.7683	2.0562	2.3135	Peroxidase superfamily protein
127	*AT4G11890*	100	227	−1.1800	209	358	−0.7763	1.0606	0.6569	Protein kinase superfamily protein
128	*AT1G61800*	103	268	−1.3733	390	672	−0.7845	1.9142	1.3254	Glucose-6-phosphate/phosphate translocator 2 (GPT2)
129	*AT4G37430*	325	276	0.2336	1,232	2,129	−0.7894	1.9242	2.9472	Cytochrome P450, family 91, subfamily A, polypeptide 2 (CYP91A2)
130	*AT5G13170*	28	33	−0.2210	2,077	3,604	−0.7954	6.1968	6.7712	Senescence-associated gene 29 (SAG29)
131	*AT5G67080*	11	75	−2.7839	78	136	−0.7967	2.8445	0.8573	Mitogen-activated protein kinase kinase kinase 19 (MAPKKK19)
132	*AT4G24380*	174	319	−0.8725	354	618	−0.8038	1.0216	0.9529	CONTAINS InterPro DOMAIN/s: Serine hydrolase (InterPro:IPR005645)
133	*AT2G14610*	180	761	−2.0825	522	926	−0.8270	1.5382	0.2827	Pathogenesis-related gene 1 (PR1)
134	*AT2G37670*	12	21	−0.8099	41	73	−0.8354	1.7702	1.7957	Transducin/WD40 repeat-like superfamily protein
135	*AT5G61890*	64	347	−2.4332	284	508	−0.8410	2.1425	0.5503	Integrase-type DNA-binding superfamily protein
136	*AT4G22470*	669	1,632	−1.2874	1,402	2,513	−0.8419	1.0683	0.6228	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
137	*AT3G03530*	28	44	−0.6360	124	222	−0.8434	2.1278	2.3352	Nonspecific phospholipase C4 (NPC4)
138	*AT3G43110*	61	145	−1.2496	126	226	−0.8449	1.0479	0.6432	Unknown protein
139	*AT1G62370*	101	109	−0.1061	358	648	−0.8554	1.8233	2.5726	RING/U-box superfamily protein
140	*AT1G73010*	408	1,184	−1.5358	880	1,595	−0.8577	1.1080	0.4300	Phosphate starvation-induced gene 2 (PS2)
141	*AT1G06520*	24	31	−0.3718	82	151	−0.8890	1.7702	2.2874	Glycerol-3-phosphate acyltransferase 1 (GPAT1)

Table S1. Cont.

	Gene	WT	Mutant	Log(wt/mutant)	AA wt	ABA mutant	Log(wt/mutant)	Log(ABA wt/wt)	Log(ABA m/m)	Function
142	*AT1G26390*	47	133	–1.5061	114	213	–0.8980	1.2888	0.6808	FAD-binding Berberine family protein
143	*AT3G21230*	185	453	–1.2910	410	764	–0.8996	1.1463	0.7549	4-Coumarate:CoA ligase 5 (4CL5)
144	*AT4G37990*	407	1,220	–1.5828	3,110	5,837	–0.9083	2.9329	2.2583	Elicitor-activated gene 3–2 (ELI3-2)
145	*AT3G45130*	8	40	–2.3916	36	68	–0.9203	2.2472	0.7759	lanosterol synthase 1 (LAS1)
146	*AT2G13810*	4	17	–1.9645	19	35	–0.9203	2.1004	1.0561	AGD2-like defense response protein 1 (ALD1)
147	*AT1G10585*	442	1,084	–1.2939	958	1,826	–0.9299	1.1163	0.7523	Basic helix–loop–helix (bHLH) DNA-binding superfamily protein
148	*AT3G57260*	237	1,270	–2.4195	551	1,056	–0.9385	1.2148	–0.2661	β-1,3-glucanase 2 (BGL2)
149	*AT2G18660*	37	153	–2.0470	90	172	–0.9389	1.2797	0.1716	Their biological role has remained elusive
150	*AT1G19250*	22	84	–1.9474	65	126	–0.9458	1.5858	0.5842	Flavin-dependent monooxygenase 1 (FMO1)
151	*AT2G45220*	674	1,145	–0.7644	2,037	3,930	–0.9481	1.5956	1.7793	Plant invertase/pectin methylesterase inhibitor superfamily
152	*AT5G46350*	58	108	–0.9040	120	238	–0.9820	1.0589	1.1369	WRKY DNA-binding protein 8
153	*AT3G52820*	27	17	0.6793	281	568	–1.0130	3.3694	5.0618	Purple acid phosphatase 22 (PAP22)
154	*AT2G14620*	19	37	–0.9990	53	106	–1.0134	1.5048	1.5191	Xyloglucan endotransglucosylase/hydrolase 10 (XTH10)
155	*AT1G69930*	10	59	–2.5898	48	97	–1.0222	2.2880	0.7204	GST tau 11 (GSTU11)
156	*AT2G29470*	27	117	–2.1036	225	476	–1.0794	3.0490	2.0248	GST tau 3 (GSTU3)
157	*AT1G17420*	258	499	–0.9512	643	1,371	–1.0917	1.3175	1.4580	Lipoxygenase 3 (LOX3)
158	*AT3G11480*	1	18	–4.0470	65	152	–1.2215	5.9077	3.0822	BSMT1
159	*AT4G32810*	28	40	–0.4985	127	324	–1.3469	2.1681	3.0164	Carotenoid cleavage dioxygenase 8 (CCD8)
160	*AT1G61120*	14	128	–3.1766	48	124	–1.3701	1.7575	–0.0490	Terpene synthase 04 (TPS04)
161	*AT2G24850*	292	2,039	–2.8046	818	2,249	–1.4585	1.4875	0.1415	Tyrosine aminotransferase 3 (TAT3)

The genes marked with red are used in the article.

Table S2. Primer sequences used in quantitative PCR

Gene	Sequence
TAT3	5′-CCTCCGCCCATTCCAACTTC-3′ 5′-ACACATCCTCGGCCTTCAGC-3′
LOX3	5′-TGCCGATCTAATTCGCAGAG-3′ 5′-GTTCGGGTTTGGATAGTAGC-3′
BGL2	5′-TGAACGTCTCGCCTCCAGTC-3′ 5′-CCGCGTTCTCGATGTTCTGC-3′
bHLH	5′-TCTCCCACTCGCAAGTTACC-3′ 5′-CGAATCCCGCGAACGAATAC-3′
COR15b	5′-AAAGTGACGGCAACATCCTC-3′ 5′-CTCAGTCGCAGTTTCATTGG-3′
COR413	5′-GTGGAGAAGCGGCGAAAGAG-3′ 5′-GGTGCGTGGAGAGCGAATAG-3′