

Supplementary Table 3. ABA-Induced Genes in Mesophyll Cells.

Affy probe ^a	Description	AGI number ^b	Cluster ^c	Experiment 1			Experiment 2			Seki et al. ^g	Hoth et al. ^h
				Ratio ^d	p-value ^e	Fold chge ^f	Ratio	p-value	Fold chge		
12156_at	unknown protein	At2g29020	III	0.4	0.00108	1.32	1.2	0.00001	2.30		
12186_at	unknown protein	At2g46100	III	1.4	0.00038	2.64	2	0.00027	4.00		
12212_at	unknown protein	At3g52070	III	1.5	0.00004	2.83	1.1	0.00001	2.14		
12340_at	unknown protein	At1g10450	III	2.6	0.00166	6.06	3.3	0.00053	9.85		
12457_at	nitrate transporter	At3g21670	III	0.8	0.00166	1.74	2.5	0.00000	5.66		
12645_at	fibrillin precursor-like protein	At4g22240	I	0.7	0.00000	1.62	1.6	0.00000	3.03		
12698_at	sugar transport protein	At1g08920	III	1.3	0.00000	2.46	1.7	0.00002	3.25	3.26	10.4
12749_at	cold acclimation protein	At2g15970	I	1.8	0.00000	3.48	2.8	0.00000	6.96	6.69	6.2
12753_at	nonspecific lipid-transfer protein	At2g38540	I	1.1	0.00000	2.14	0.7	0.00000	1.62		
12788_at	unknown protein	At1g23130	III	1.1	0.00000	2.14	0.7	0.00004	1.62		
12791_r_at	unknown protein	At2g45180	III	0.9	0.00000	1.87	0.9	0.00001	1.87	0.83	
12793_at	gamma glutamyl hydrolase	At1g78670	III	0.8	0.00007	1.74	1.5	0.00000	2.83		
12803_s_at	protein induced upon wounding	At4g24220	III	0.7	0.00001	1.62	1	0.00001	2.00		
12860_s_at	thioredoxin h	At1g11530	III	0.8	0.00012	1.74	1.8	0.00000	3.48		
12886_s_at	thylakoid-bound ascorbate peroxidase	At1g77490	III	0.5	0.00036	1.41	1.2	0.00057	2.30		
12920_at	no hits		III	0.7	0.00001	1.62	1.2	0.00000	2.30		
13158_at	cinnamoyl-CoA reductase	At2g33590	I	1.1	0.00000	2.14	2	0.00000	4.00	2.65	
13182_i_at	thioredoxin	At5g42980	III	0.8	0.00001	1.74	2.3	0.00001	4.92		
13183_r_at	thioredoxin	At5g42980	III	0.9	0.00000	1.87	2.6	0.00000	6.06		
13184_s_at	thioredoxin	At5g42980	III	1.2	0.00000	2.30	1.8	0.00000	3.48		
13214_at	chlorophyll a/b binding protein	At3g47470	III	0.4	0.00001	1.32	1.2	0.00000	2.30	1.70	
13242_at	no hits		III	0.8	0.00000	1.74	2.6	0.00000	6.06		
13293_s_at	auxin regulated protein	At2g33310	III	4.9	0.00003	29.86	0.7	0.00004	1.62		
13426_at	unknown protein	At2g41190	I	3.1	0.00005	8.57	4.8	0.00000	27.86	10.19	28.6
13590_at	unknown protein	At2g21240	III	0.6	0.00003	1.52	1	0.00009	2.00		
13785_at	cold-regulated protein cor15b	At2g42530	III	0.6	0.00000	1.52	1.9	0.00000	3.73	2.28	8.5
14037_at	cinnamyl alcohol dehydrogenase	At1g09490	III	0.5	0.00267	1.41	2.1	0.00000	4.29	3.12	
14073_at	water stress-induced protein	At1g54410	III	1	0.00000	2.00	0.4	0.00238	1.32		
14088_at	unknown protein	At1g51160	III	0.5	0.00033	1.41	1	0.00003	2.00		
14089_at	putative hydrolase	At2g32150	III	1.4	0.00002	2.64	2.5	0.00000	5.66		

14097_at	unknown protein	At2g47770	III	1.6	0.00000	3.03	2.1	0.00001	4.29	10.1	205
14108_at	putative protein	At4g30010	III	0.6	0.00004	1.52	0.7	0.00001	1.62		
14123_at	MADS-box protein	At2g45660	III	1.5	0.00004	2.83	1.7	0.00000	3.25		
14245_at	no hits		III	0.7	0.00000	1.62	2.1	0.00000	4.29		
14658_s_at	cysteine proteinase RD19A	At4g39090	III	1.2	0.00000	2.30	1	0.00000	2.00		
14689_at	unknown protein	At5g67490	III	0.5	0.00000	1.41	0.8	0.00139	1.74		
14733_s_at	synthetase	At2g39800	III	2.4	0.00000	5.28	4	0.00000	16.00	3.57	22.3
14737_s_at	alanine-glyoxylate aminotransferase	At2g13360	III	0.6	0.00004	1.52	0.6	0.00079	1.52		
14832_at	tyrosine transaminase	At4g23600	III	1	0.00000	2.00	1.7	0.00000	3.25		
15003_at	clathrin assembly protein	At2g19790	III	0.9	0.00001	1.87	0.7	0.00027	1.62		
15018_at	unknown protein	At1g79520	III	3.5	0.00065	11.31	2.1	0.00013	4.29		4.2
15052_at	calcium-binding EF-hand protein	At2g33380	I	1.3	0.00005	2.46	4.8	0.00000	27.86	24.09	18
15058_s_at	cinnamyl-alcohol dehydrogenase	At4g37980	III	0.8	0.00000	1.74	2.6	0.00000	6.06	4.24	
15098_s_at	senescence-associated protein	At4g35770	III	1.1	0.00001	2.14	1.3	0.00000	2.46	5.48	
15100_f_at	plasma membrane intrinsic protein	At4g35100	III	0.5	0.00044	1.41	1.2	0.00006	2.30		
15103_s_at	unknown protein	At1g20450	III	1	0.00000	2.00	1.9	0.00000	3.73	3.58	
15110_s_at	dehydrin	At1g76180	I	0.3	0.00024	1.23	1.4	0.00000	2.64		
15147_s_at	plasma membrane intrinsic protein	At4g00430	III	0.3	0.00074	1.23	1.3	0.00000	2.46		
15154_at	synthetase	At3g47340	III	2.4	0.00000	5.28	2.7	0.00000	6.50	14.04	
15161_s_at	reductase/saccharopine	At4g33150	III	2.5	0.00267	5.66	3.5	0.00004	11.31	5.49	11.2
15164_s_at	acyl-coA dehydrogenase	At3g51840	III	0.8	0.00053	1.74	1.5	0.00000	2.83		
15191_at	vacuolar H ⁺ -transporting ATPase	At4g34720	III	1.3	0.00000	2.46	1.4	0.00000	2.64		
15202_s_at	Transducer	At5g39340	III	0.6	0.00053	1.52	1	0.00009	2.00		
15206_s_at	K ⁺ channel	At1g04690	III	0.5	0.00005	1.41	0.7	0.00252	1.62		
15207_s_at	gamma glutamyl hydrolase	At1g78680	III	3.1	0.00053	8.57	0.9	0.00003	1.87		
15356_at	zinc finger protein	At4g23450	III	3.6	0.00003	12.13	1.9	0.00022	3.73		26
15497_at	serine/threonine protein kinase	At4g30960	III	0.8	0.00283	1.74	2.7	0.00004	6.50	3.27	3.2
15586_s_at	protein phosphatase ABI1	At4g26080	III	0.6	0.00006	1.52	3.7	0.00000	13.00		16.4
15607_s_at	cyclic nucleotide-regulated ion channel	At5g15410	III	0.8	0.00024	1.74	2.3	0.00000	4.92		
15614_s_at	xyloglucan endotransglycosylase	At4g30270	III	2.2	0.00000	4.59	3.2	0.00000	9.19	5.03	
15621_f_at	myo-inositol 1-phosphate synthase	At2g22240	III	1.2	0.00050	2.30	2.4	0.00014	5.28	1.21	
15625_at	glyoxalase II	At1g53580	I	1.5	0.00000	2.83	2.6	0.00000	6.06	5.63	
15629_s_at	unknown protein	At1g17745	III	1.6	0.00001	3.03	1.3	0.00005	2.46		
15659_at	chlorophyll a/b binding protein	At1g61520	III	0.4	0.00000	1.32	0.7	0.00006	1.62		
15669_s_at	4-hydroxyphenylpyruvate dioxygenase	At1g06570	III	0.9	0.00001	1.87	2.7	0.00003	6.50	6.37	

15681_s_at	farnesyltransferase	At4g34640	III	2.3	0.00047	4.92	2.3	0.00001	4.92		
15909_at	unknown protein	At1g64850	III	1.2	0.00001	2.30	1.3	0.00001	2.46		
15967_at	cathepsin B-like cysteine protease	At4g01610	III	0.4	0.00115	1.32	2	0.00000	4.00		
15973_at	cysteine proteinase RD21A	At1g47128	III	0.6	0.00001	1.52	0.9	0.00000	1.87		
15987_at	putative aquaporin	At2g39010	III	1.1	0.00000	2.14	0.9	0.00000	1.87		
15997_s_at	unknown protein	At1g20440	I	0.9	0.00000	1.87	2.2	0.00000	4.59	6.28	18.4
16014_at	unknown protein	At1g75750	III	1.9	0.00000	3.73	0.9	0.00002	1.87		
16030_s_at	plasma membrane intrinsic protein	At1g01620	III	1	0.00000	2.00	0.7	0.00019	1.62		
16031_at	ferritin 1 precursor	At5g01600	I	0.5	0.00000	1.41	3.2	0.00000	9.19	2.77	
16032_s_at	thioredoxin	At5g42980	III	0.6	0.00000	1.52	1.1	0.00000	2.14		
16036_i_at	no hits		III	0.5	0.00000	1.41	1	0.00000	2.00		
16038_s_at	dehydrin	At5g66400	I	3	0.00000	8.00	4.3	0.00000	19.70	6.83	77.6
16046_s_at	light regulated protein	At3g26740	III	1	0.00000	2.00	0.7	0.00001	1.62		
16047_at	unknown protein	At2g25510	III	0.4	0.00009	1.32	0.6	0.00003	1.52		
16057_s_at	acetyl-CoA carboxylase	At5g35360	III	0.7	0.00036	1.62	0.7	0.00007	1.62		
16115_at	homeobox protein ATHB-12	At3g61890	I	1	0.00096	2.00	3.7	0.00002	13.00	9.11	58
16136_at	thioredoxin	At5g16400	III	0.6	0.00025	1.52	0.7	0.00283	1.62		
16172_at	cytochrome P450 monooxygenase	At3g26280	III	1.2	0.00238	2.30	2.1	0.00036	4.29		3.1
16306_at	unknown protein	At4g13250	III	1	0.00002	2.00	2.4	0.00065	5.28		
16427_at	amino acid transport protein AAP2	At5g09220	III	1.2	0.00006	2.30	1.7	0.00013	3.25		
16436_at	unknown protein	At3g15353	III	1	0.00000	2.00	0.6	0.00005	1.52		
16446_at	plasma membrane intrinsic protein	At3g61430	III	1.1	0.00001	2.14	1.7	0.00000	3.25		
16524_at	aldehyde dehydrogenase	At1g54100	I	1.9	0.00000	3.73	3.4	0.00000	10.56	6.61	
16540_s_at	heme oxygenase 1	At2g26670	III	0.3	0.00115	1.23	0.8	0.00000	1.74		
16620_s_at	TCH4 protein	At5g57560	III	0.7	0.00001	1.62	1	0.00000	2.00		
16899_at	photosystem II 5 KD protein	At1g51400	III	0.9	0.00009	1.87	0.6	0.00013	1.52		
16927_s_at	xyloglucan endo-1,4-beta-D-glucanase	At4g30270	III	2.3	0.00000	4.92	1.6	0.00000	3.03		
17187_at	putative arginase	At4g08870	III	0.6	0.00019	1.52	0.9	0.00000	1.87		
17421_s_at	ubiquitin-conjugating enzyme	At2g46030	III	0.7	0.00001	1.62	1.8	0.00000	3.48		
17548_s_at	cinnamyl alcohol dehydrogenase	At1g09500	III	1.1	0.00000	2.14	2.7	0.00000	6.50	8.09	5.4
17913_at	unknown protein	At4g37300	III	0.8	0.00065	1.74	0.4	0.00199	1.32		
17994_r_at	no hits		III	0.3	0.00061	1.23	1.1	0.00000	2.14		
18273_at	cold acclimation protein	At3g50830	III	0.8	0.00013	1.74	1.3	0.00015	2.46		
18280_at	unknown protein	At1g21000	III	0.8	0.00096	1.74	1.3	0.00001	2.46		
18290_at	unknown protein	At1g49500	III	1.2	0.00000	2.30	1.4	0.00009	2.64		

18560_at	proline-rich protein	At1g62510	III	2.7	0.00000	6.50	2.8	0.00000	6.96		
18594_at	unknown protein	At1g01470	I	0.4	0.00003	1.32	0.8	0.00001	1.74	4.01	4.6
18601_s_at	microtubule-associated protein	At2g45170	III	0.8	0.00005	1.74	2.1	0.00000	4.29		
18661_at	unknown protein	At4g26710	III	0.6	0.00018	1.52	0.7	0.00001	1.62		
18679_s_at	metallothionein	At1g07600	III	0.4	0.00010	1.32	2.1	0.00000	4.29		
18682_s_at	GTP-binding protein	At2g44610	III	0.9	0.00090	1.87	0.7	0.00238	1.62		
18699_i_at	cold-regulated protein COR6.6 (KIN2)	At5g15970	III	0.6	0.00002	1.52	2	0.00002	4.00	8.76	17.7
18700_r_at	cold-regulated protein COR6.6 (KIN2)	At5g15970	III	0.7	0.00000	1.62	2	0.00000	4.00	8.76	
18701_s_at	cold and ABA inducible protein kin1	At5g15960	III	0.8	0.00000	1.74	2	0.00000	4.00	9.22	24
18936_at	protein phosphatase 2C (AtP2C-HA)	At1g72770	I	0.8	0.00157	1.74	3.5	0.00012	11.31		3.5
18953_at	alpha keto-acid dehydrogenase	At1g21400	III	1.4	0.00036	2.64	3.1	0.00000	8.57		
18962_s_at	Protein similar to nodulin-35	At2g26230	III	0.6	0.00188	1.52	1	0.00000	2.00		
19139_at	RUB1-conjugating enzyme RCE1	At4g36800	III	0.5	0.00002	1.41	1.3	0.00000	2.46		
19152_at	late embryogenesis abundant protein	At5g06760	I	2.9	0.00000	7.46	4	0.00000	16.00	13.29	328
19177_at	male sterility 2-like protein	At5g22500	III	2.1	0.00267	4.29	1.5	0.00005	2.83		4.5
19186_s_at	dehydrin Xero2	At3g50970	I	3	0.00000	8.00	2.4	0.00000	5.28		
19421_at	no hits		III	1.7	0.00000	3.25	2.1	0.00188	4.29		
19638_at	protein phosphatase 2C	At3g11410	I	2	0.00000	4.00	3.4	0.00000	10.56	7.58	4.6
19646_at	homeodomain transcription factor	At2g46680	I	2.5	0.00001	5.66	4	0.00000	16.00	8.84	27.7
19656_s_at	nitrate transporter	At2g26690	III	1.7	0.00007	3.25	3.1	0.00000	8.57	3.08	
19982_at	unknown protein	At1g79270	I	1.3	0.00050	2.46	1.1	0.00166	2.14		
20024_s_at	unknown protein	At2g35810	III	0.9	0.00002	1.87	0.6	0.00017	1.52		
20149_at	sugar transport protein	At1g08890	III	1.2	0.00047	2.30	2.7	0.00267	6.50		
20256_s_at	serine carboxypeptidase I	At2g22990	III	0.4	0.00224	1.32	1.1	0.00000	2.14		
20491_at	tropinone reductase	At2g29350	III	0.5	0.00177	1.41	2.3	0.00000	4.92		
20641_at	late embryogenesis-abundant protein	At1g52690	I	2.8	0.00000	6.96	7.1	0.00000	137.19	30.75	1799

^aDescribes names of probe set on Affymetrix chip. ^bArabidopsis Genome Initiative locus numbers. ^cIndicates clusters in Figure 5. ^dSignal Log value which measures the change in expression level for a transcript between two arrays. This change is expressed as the log₂ ratio. A log₂ ratio of 1 is the same as a Fold change of 2. ^eChange p-value which measures the probability that the expression levels of a probe in two different arrays are the same or not. Change p-values of 0.00000 correspond to p < 0.000005. ^fFold changes is calculated using the signal log ratio. ^gObtained from supplemental Table 1 (column for 5 hr ABA treatment), Seki et al., 2002. ^hObtained from supplemental Table Induced, Hoth et al., 2002.