

**Supplementary Table 4. ABA-Repressed Genes in Mesophyll Cells.**

Affy probe <sup>a</sup>	Description	AGI number <sup>b</sup>	Cluster <sup>c</sup>	Experiment 1			Experiment 2			Seki et al. <sup>g</sup>	Hoth et al. <sup>h</sup>
				Ratio <sup>d</sup>	p-value <sup>e</sup>	Fold chge <sup>f</sup>	Ratio	p-value	Fold chge		
15194_s_at	GASA4	At5g15230	VI	-1.9	0.99885	-3.7	-2	0.99997	-4.0		
15624_s_at	ADPG pyrophosphorylase small subunit	At5g48300	VI	-0.6	1.00000	-1.5	-1.2	1.00000	-2.3		
17957_at	acetone-cyanohydrin lyase	At2g23600	VI	-0.9	1.00000	-1.9	-2.8	1.00000	-7.0		
12233_at	succinyl-CoA-ligase alpha subunit	At5g08300	VI	-0.6	0.99997	-1.5	-2.7	0.99898	-6.5		
12337_at	putative protein kinase	At2g21480	VI	-1.4	0.99823	-2.6	-0.7	0.99978	-1.6		
12393_at	alcohol dehydrogenase	At2g47140	VI	-1.1	0.99999	-2.1	-1.3	0.99971	-2.5		
12566_at	AP2 domain transcription factor	At2g20880	VI	-0.6	0.99953	-1.5	-2.3	0.99870	-4.9		
12740_s_at	myrosinase	At5g25980	VI	-0.6	1.00000	-1.5	-0.7	0.99861	-1.6		
12752_s_at	peroxidase	At4g21960	VI	-2.9	1.00000	-7.5	-0.9	0.99999	-1.9		
12761_s_at	jasmonate inducible protein	At1g54040	VI	-1.4	0.99870	-2.6	-2.6	1.00000	-6.1		
12785_at	P-Protein	At4g33010	VI	-0.7	0.99999	-1.6	-1.1	1.00000	-2.1		
12787_at	fasciclin-like arabinogalactan-protein (FLA8)	At2g45470	VI	-1.5	0.99885	-2.8	-0.8	0.99870	-1.7		
13124_at	phosphoenolpyruvate carboxylase	At2g42600	VI	-0.7	1.00000	-1.6	-1.1	0.99995	-2.1		
13150_at	rubisco subunit binding-prot. alpha subunit	At2g28000	VI	-1.3	1.00000	-2.5	-3.8	1.00000	-13.9		
13151_g_at	putative rubisco subunit binding-protein alpha subunit	At2g28000	VI	-0.8	0.99994	-1.7	-5.4	1.00000	-42.2		
13212_s_at	beta-1,3-glucanase 2	At3g57260	VI	-1.1	1.00000	-2.1	-0.6	0.99999	-1.5		
13218_s_at	catalase 3	At1g20620	VI	-1.1	1.00000	-2.1	-3.1	1.00000	-8.6		
13219_at	class IV chitinase	At3g54420	VI	-1.1	0.99996	-2.1	-2.5	0.99988	-5.7		
13229_s_at	no hits		VI	-1	0.99987	-2.0	-0.7	0.99997	-1.6		
13247_f_at	omega-3 fatty acid desaturase	At3g11170	VI	-1	0.99999	-2.0	-2.7	1.00000	-6.5		
13269_s_at	dnaK-type molecular chaperone hsc70	At5g02500	VI	-1.1	1.00000	-2.1	-1.8	1.00000	-3.5		
13283_at	mitochondrial chaperonin hsp60	At3g23990	VI	-3.5	0.99947	-11.3	-0.7	0.99971	-1.6		
13320_at	unknown protein	At4g23350	VI	-2	0.99718	-4.0	-2.7	0.99995	-6.5		
13607_at	hsp 70-like protein	At4g24280	VI	-0.7	0.99982	-1.6	-1.7	0.99995	-3.2		
13659_at	serine/threonine kinase	At4g23150	VI	-2.9	0.99978	-7.5	-0.7	0.99959	-1.6		
13850_i_at	no hits		VI	-1.2	0.99766	-2.3	-1.3	0.99734	-2.5		
14056_at	phenylalanyl-trna synthetase	At4g39280	VI	-3.3	0.99921	-9.8	-2.3	0.99967	-4.9		
14057_at	putative aconitase	At4g26970	VI	-0.6	0.99939	-1.5	-1.1	0.99999	-2.1		
14383_at	unknown protein	At1g09460	VI	-1.8	0.99718	-3.5	-1.7	1.00000	-3.2		
14384_at	putative phosphoribosylaminoimidazolecarboxamid	At2g35040	VI	-0.9	0.99950	-1.9	-5	0.99980	-32.0		
14642_f_at	Ran-binding protein (atranbp1a)	At1g07140	VI	-0.6	1.00000	-1.5	-2.7	0.99989	-6.5		
14662_f_at	no hits		VI	-0.6	0.99870	-1.5	-1.3	0.99994	-2.5		
14679_at	WRKY DNA-binding protein	At2g03340	VI	-3.1	0.99943	-8.6	-2.8	0.99943	-7.0		
14883_at	unknown protein	At4g27380	VI	-3.5	0.99935	-11.3	-1.2	0.99947	-2.3		
15012_g_at	unknown protein	At2g44525	VI	-3.3	0.99905	-9.8	-2.8	0.99988	-7.0		
15144_s_at	Carbonic anhydrase	At5g14740	VI	-0.6	0.99999	-1.5	-1.9	1.00000	-3.7		
15160_s_at	germin-like protein	At5g20630	VI	-1	0.99984	-2.0	-1.3	0.99988	-2.5	0.2	
15168_at	histone deacetylase-like protein	At5g22650	VI	-0.9	0.99988	-1.9	-2.7	1.00000	-6.5		
15172_s_at	luminal binding protein	At5g42020	VI	-1	0.99921	-2.0	-2.8	0.99834	-7.0		

15278_at	unknown protein	At2g45930	VI	-3.3	0.99916	-9.8	-4.4	0.99993	-21.1		
15299_s_at	unknown protein	At1g30660	VI	-3.9	0.99943	-14.9	-1.5	0.99812	-2.8		
15411_at	unknown protein	At2g17240	VI	-0.6	0.99985	-1.5	-1.3	0.99998	-2.5		
15463_at	unknown protein	At4g23480	VI	-0.6	0.99999	-1.5	-1.1	1.00000	-2.1		
15523_s_at	Storage protein	At4g24360	VI	-0.6	0.99939	-1.5	-1.2	0.99877	-2.3		
15620_s_at	4-coumarate:CoA ligase	At1g51680	VI	-0.8	0.99953	-1.7	-0.8	0.99998	-1.7		
15953_s_at	dnaK-type molecular chaperone	At5g02500	VI	-1.1	1.00000	-2.1	-1.9	1.00000	-3.7		
15992_s_at	translation elongation factor eEF	At5g60390	VI	-0.7	1.00000	-1.6	-3.1	1.00000	-8.6		
15993_at	no hits		VI	-0.8	0.99994	-1.7	-0.7	0.99998	-1.6		
16049_s_at	no hits		VI	-1.3	1.00000	-2.5	-1.9	0.99999	-3.7		
16053_i_at	glutathione transferase	At1g02920	VI	-2	0.99999	-4.0	-0.7	0.99999	-1.6		
16060_at	zinc finger protein ATZF1	At1g08930	VI	-1	1.00000	-2.0	-0.6	0.99931	-1.5	0.41	6.5
16120_at	nonphototropic hypocotyl	At3g45780	VI	-0.8	0.99994	-1.7	-0.6	0.99939	-1.5		
16288_at	putative prolyl 4-hydroxylase	At2g17720	VI	-1.3	0.99992	-2.5	-0.6	0.99910	-1.5		
16333_i_at	xanthine dehydrogenase	At4g34900	VI	-2	0.99973	-4.0	-2.5	0.99978	-5.7		
16382_at	similar to UMP synthase	At3g54470	VI	-1.2	0.99763	-2.3	-3	0.99999	-8.0		
16435_at	RNA binding protein 45	At1g11650	VI	-0.7	0.99999	-1.6	-1.7	1.00000	-3.2		
16672_at	no hits		VI	-1.9	0.99998	-3.7	-3	0.99964	-8.0		
16916_s_at	dnaK-type molecular chaperone	At5g02490	VI	-2	0.99999	-4.0	-1.9	0.99733	-3.7		
16922_i_at	Putative S-phase-specific ribosomal protein	At4g34670	VI	-1.2	1.00000	-2.3	-0.6	0.99809	-1.5		
16923_s_at	Putative S-phase-specific ribosomal protein	At4g34670	VI	-0.8	0.99995	-1.7	-0.8	1.00000	-1.7		
16942_at	putative ribosomal protein	At4g25740	VI	-0.6	0.99984	-1.5	-1.9	0.99998	-3.7		
17102_s_at	putative peroxidase	At1g05260	VI	-3.9	0.99959	-14.9	-2.8	0.99962	-7.0		
17178_at	unknown protein	At1g20910	VI	-3.5	0.99935	-11.3	-1.4	0.99931	-2.6		41
17292_at	amino acid permease	At5g49630	VI	-1.6	0.99776	-3.0	-1	0.99977	-2.0		
17392_at	phenylalanine ammonia-lyase	At3g53260	VI	-0.9	0.99978	-1.9	-1.6	0.99993	-3.0		
17393_at	Rubisco subunit binding-protein	At1g55490	VI	-1.4	1.00000	-2.6	-3.2	0.99999	-9.2		
17413_s_at	peroxidase	At5g64120	VI	-2.2	1.00000	-4.6	-4.1	1.00000	-17.1		
18002_at	fibrillarlin 1	At5g52470	VI	-0.6	0.99748	-1.5	-1.3	1.00000	-2.5		
18005_at	exonuclease	At3g61620	VI	-2.9	0.99975	-7.5	-1.8	0.99748	-3.5		
18251_at	nuclear antigen homolog	At4g16830	VI	-1	0.99988	-2.0	-0.9	0.99801	-1.9		
18255_at	unknown protein	At2g38860	VI	-3.3	0.99973	-9.8	-0.7	0.99994	-1.6		
18284_at	putative hydroxyproline-rich glycoprotein precursor	At4g34150	VI	-0.6	0.99984	-1.5	-0.8	0.99969	-1.7		
18351_at	unknown protein	At4g23060	VI	-4.4	0.99997	-21.1	-1.1	0.99997	-2.1		
18826_at	glucan synthase	At2g31960	VI	-1.5	0.99989	-2.8	-2.3	0.99993	-4.9		
18928_at	endochitinase	At2g43620	VI	-1.8	1.00000	-3.5	-1.1	0.99877	-2.1		
18972_at	unknown protein	At4g29060	VI	-0.7	0.99843	-1.6	-1.3	0.99892	-2.5		
19422_at	putative heat shock protein	At2g04030	VI	-0.7	0.99977	-1.6	-2.2	0.99999	-4.6		
19426_s_at	no hits		VI	-0.7	0.99994	-1.6	-1.9	1.00000	-3.7		
19463_s_at	2-dehydro-3-deoxyphosphoheptonate aldolase	At4g39980	VI	-0.7	0.99992	-1.6	-2.3	0.99999	-4.9		
20156_at	hairpin-induced protein	At3g52470	VI	-0.8	0.99999	-1.7	-0.8	0.99939	-1.7		
20285_s_at	putative protein kinase	At2g39660	VI	-0.7	0.99853	-1.6	-1.1	0.99885	-2.1		
20429_at	unknown protein	At4g14400	VI	-3.2	0.99989	-9.2	-0.6	0.99877	-1.5		
20462_at	brassinosteroid receptor kinase	At3g13380	VI	-2.3	0.99905	-4.9	-3.3	0.99996	-9.8		

20640_s_at	glyceraldehyde-3-phosphate dehydrogenase	At1g42970	VI	-0.6	1.00000	-1.5	-3.3	1.00000	-9.8		
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<sup>a</sup>Describes names of probe set on Affymetrix chip.

<sup>b</sup>Arabidopsis Genome Initiative locus numbers.

<sup>c</sup>Indicates clusters in Figure 5.

<sup>d</sup>Signal Log ratio value, which measures the change in expression level for a transcript between two arrays. This change is expressed as the log<sub>2</sub> ratio.

A log<sub>2</sub> ratio of 1 is the same as a Fold change of 2 (see Materials and Methods).

<sup>e</sup>Change P-value which measures the probability that the expression levels of a probe set in two different arrays are the same or not. Change P-value of 1.0000 corresponds to P-value > 0.99995.

<sup>f</sup>Fold changes were calculated using the signal log ratio.

<sup>g</sup>Fold changes obtained from Supplemental Table 5 online (column for 5-h ABA treatment; Seki et al., 2002).

<sup>h</sup>Fold changes obtained from Supplemental Table Repressed.xls online (Hoth et al., 2002).

This table contains genes that have a change P-value  $\geq 0.997$  (Decrease or Marginal Decrease in Affymetrix nomenclature) in the 2 independent comparison analyses and a signal log ratio < -0.6 in the 2 independent comparison analyses.