

Table 3. Genes down-regulated in leaves of *Arabidopsis ada2b-1* or *gcn5-1* mutant plants as assayed by Affymetrix microarray.^a

Gene functional group ^b	Probe set ^c	Gene number ^d	Gene description	Fold change in <i>ada2b-1</i> ^e	Fold change in <i>gcn5-1</i> ^e
Transcription	13301	At1g04240	IAA3	-7.6	-13
	13662	AT3g23050	IAA7 (<i>axr2</i>)	-5.3	-9.9
	17032	At2g03710	MADS-box protein (<i>AGL3</i>)	-6.1	-3.6
	18036	At2g33810	SPL3	-25	-6.8
	20044	AT4g27310	similarity to zinc-finger protein S3574, <i>Oryza</i>	-2.9	-5.6
	20362	At1g71030	myb-related transcription factor	-2.1	-3.3
	12876	At1g69120	agamous-like 8 (<i>AGL8</i> , <i>FUL</i>)	-11	-1.8
	13023	At4g00050	putative transcriptional regulator	-4	-4 ^f
	18026	AT3g15270	SPL5	-4.9	-1.2
Signal Transduction					
Receptor-like kinases	12299	AT4g23290	Receptor like serine/threonine kinase, DUF26	-4.8	-8.6
	14048	At2g18890	Kinase RLCK VI, domain K	-13	-12
	18543	At2g36570	receptor-like kinase, LRRIII, LRR5	-12	-5.8
Lipases	18115	At1g54820	Receptor-like kinase EXTENSIN	-7.3	-3.1 ^f
	17113	AT5g58670	PI-PLC (PLC1)	-5.3	-7.2
	18890	AT4g38690	putative PI-PLC	-5.4	-4
	12777	At1g54000	myrosinase-associated protein Lipase/Acylhydrolase	-13	-11
	13793	At4g26790	putative APG protein (lipase)	-2.4	-3.7
	16434	AT4g18970	unknown, lipase domain	-3.6	-2.2
Phosphatases	13587	At1g04040	putative acid phosphatase	-4.4	-3.1 ^f
Others	13085	At1g78820	putative glycoprotein ep1	-10	-7.5
	15202	At5g39340	His-Asp Phosphotransfer Signal Transducer AHP3	0	-10
Cell Rescue, Defense					
Defense related genes	14606	At2g32990	putative glucanase (similarity to β -1,4 glucanase from <i>fragaria</i>)	-7.7	-7.1
	15190	At2g26740	epoxide hydrolase	-6.3	-5.8
	12788	At1g23130	ripening-induced protein	-3.2	-3 ^f
	14803	At1g03020	Glutaredoxin	-2.8	-3.2
	20440	AT4g38660	thaumatin-like protein	-3.9	-2.7
	13242	AT4g37980	Eli3-1 cinnamyl alcohol dehydrogenases	-5.3	-3.1 ^f
Stress related	18699	AT5g15960	<i>cor6.6</i>	-6.4	-5
	20391	At2g23560	acetone-cyanohydrin lyase	-7.2	-5
	13160	At2g23610	acetone-cyanohydrin lyase	-3.2 ^f	-9.8
	13546	At2g22170	unknown, similarity to bn116 dehydration induced	-3.9	-2.6

	16048	At1g73330	Dr4 (protease inhibitor)	-6.3	-0.7
Metabolism					
Cell Wall	15178	AT4g14130	xyloglucan endotransglycosylase-related protein (XTR7)	-7.5	-7.7
	17305	At1g53830	Pectin methylesterase (ATPME2), pectinesterase2	-4	-3.2
	18265	AT4g12730	fasciclin-like arabinogalactan-protein 2	-13	-9.6
	18533	AT5g65730	endoxyloglucan tranferase-like	-9.1	-7.5
	20675	At2g20750	b-expasin B1	-12	-11
	12787	At2g45470	fasciclin-like arabinogalactan-protein 8	-2.8	-3.4
	12097	At2g20870	gibberellin induced cell wall protein	-13	0
	13628	AT4g23820	Polygalacturonase	-5.8	-2.6
	16438	At1g03870	fasciclin-like arabinogalactan-protein 9	-4.9	-2.9
	17494	AT3g29030	expansin At-EXP5 (At-EXP5)	-4.2	-2.6
	18911	At1g04680	pectate lyase	-3.6	-0.8
	20316	At4g23990	cellulose synthase catalytic	-3.4	-2.1
Alkaloid	13622	AT4g20820	reticuline oxidase-like	-4.5	-4.6
	18635	At2g43920	Thio methyltransferase (sulfur volatiles)	-7.2	-2.8
Cytochrome P450	19502	At4g39510	cytochrome P450 -like	-4.1	-2.1
Flavonoid biosynthesis	17089	AT4g36220	ferulate-5-hydroxylase (FAH1)	-3.5	-3.1 ^f
	17123	At1g65060	4-coumarate:CoA ligase 3	-3.3	-2.7
Others	12269	AT4g34650	squalene synthase 2	-7.4	-4.7
	13561	F5I14.13	unknown N-acetyl-beta-glucosaminidase-like, Glycosyl hydrolase family 20	-4.2	-5.4
	16629	AT4g15440	hydroperoxide lyase (HPL1)	-7.8	-5.1
	17187	AT4g08870	arginase (arg2)	-24	-29
	13463	AT4g33790	male sterility 2-like, Fatty acid -Coenzyme A reductase	-29	-8.8
	14062	At2g47780	Similarity to small rubber particle protein	-3.3	-2.8
	14497	At4g02850	Phenazine biosynthesis-like protein	-2.4	-3.6
	13245	At5g40280	beta subunit of protein farnesyl transferase ERA1	-1.1	-7.3
Lipid biosynthesis	13618	At2g05990	enoyl-ACP reductase (enr-A)	-1.8	-6.9
Transporters					
	17642	AT4g04750	sugar transporter	-10	-3.9
	15607	AT5g15410	cyclic nucleotide-gated cation channel (CNGC2 or DND1)	-3.7 ^f	-4.1
Aquaporins	14714	AT3g26520	salt-stress induced tonoplast intrinsic protein (gamma TIP2 OR TIP1;2)	-2.4	-7.8
	15100	AT4g35100	plasma membrane intrinsic protein PIP3	-3.2 ^f	-3.3
	15977	At2g45960	aquaporin (plasma membrane intrinsic)	-1.6	-4.4
	15122	At3g16240	delta tonoplast integral protein	-4.2	-3.3 ^f
	15962	At2g36830	aquaporin (tonoplast intrinsic protein gamma 1, TIP1;1)	-4.4	-3.4 ^f

Other	16030	At1g01620	transmembrane protein TMP-B (PIP1;3)	-3.8	-2.3
	13784	At2g13610	ABC transporter [AtWBC5]	-3.6	-1.9
	19717	AT4g10770	sc icp4, oligopeptide transporter	-3.8	-3.1 ^f
Cellular transport and Cellular organization	20212	At2g31900	Putative unconventional myosin	-3.2	-2.3
	13032	At2g46710	Putative rac GTPase activating	-5	-1.9
	20330	At1g22740	GTP-binding protein Rab7	-7.4	-3.5 ^f
	17567	At5g03540	AT4 (Exo70 exocyst complex subuni)	-17	-3.4
Protein destination	14114	AT4g21640	subtilisin proteinase-like	-13	-7.8
	19453	At2g22980	serine carboxypeptidase I	-8.3	-6
	13603	At4g21650	subtilisin proteinase-like	-35	-6.2 ^f
Energy	12738	At2g34420	type I chlorophyll a/b binding protein Lhb1B2	-2.2	-3.8
	14484	At3g52720	carbonic anhydrase (CAH1)	-2.7	-4.4
	15097	At1g15820	Lhcb6	-1.9	-4.3
	15153	AT3g27690	Lhcb2:4	-2.7	-8.7
	15170	AT5g54270	LHCB3*1	-1.9	-5.3
	15659	At1g61520	Lhca3*1	-1.2	-4.9
	17087	AT5g64040	photosystem I PSI-N	-2	-3.8
	18088	AT4g28750	Subunit PSI-E-like (psaE1)	-2.5	-4.2
	16540	At2g26670	HY1 heme oxygenase	-0.7	-4.3
	13213	AT3g54890	CAB1	-1.7	-5.1
	17054	At2g40100	Lhcb4:3 protein (Lhcb4.3) CP29 antenna protein of PS II	-6.1	-3.4 ^f
Cell Growth, Cell Division	19187	At3g12110	actin-11 (ACT11)	-7.2	-5.2
	13228	At1g70210	cyclin delta-1	-7.4	-2.9
Unclassified	16214	F6H11.200	retrotransposon - like protein	-3 ^f	-4.6
	18342	At4g18570	pherophorin – like	-4.7	-2
	19863	At2g14900	GA-regulated protein GAST1/GASA-like protein	-16	-3.5 ^f
Unknowns	14401	AT4g15630		-13	-8
	15896	At1g11850		-3.5	-3.8
	19184	At1g27030		-5.5	-3.7
	19889	At2g32870		-14	-7.2
	19901	At2g32880		-12	-3.7
	20054	At1g03420		-9.2	-9.1
	20061	At1g26920	unknown, lea?	-6.4	-4.5
	12095	At2g32100		-2.2	-3.4

13568	At2g43010		-2.1	-3.9
13144	At2g35860		-4	-2.2
14469	AT4g00400		-3.4	-1.4
14582	At2g38800		-3.2	-2.1
15901	At1g54740	hypothetical protein	-3.8	-2.1
18270	At2g30930		-5.7	-1.6
18881	At1g12080		-6.8	-3.1 ^f
19867	AT3g24180		-3.3	-1.8
20558	AT4g36850	unknown, probable membrane protein YBR147w	-7.2	-2.5

Notes for Table 3.

- a. Genes designated as down-regulated satisfy three criteria: signals are designated as “present” in wildtype samples; signals have an average difference in expression level of at least 100; and the difference between mutant and wildtype signals is at least three-fold in three out of four comparisons.
- b. Gene functional groups are based on the classification scheme of Schoof, *et al.* (Nucleic Acids Res, 30:91-93, 2002; see <http://mips.gsf.de/proj/that/db>).
- c. Probe set numbers as assigned by Affymetrix for the GeneChip® Arabidopsis Genome Array.
- d. Arabidopsis gene numbers as assigned by the Arabidopsis Genome Initiative (<http://www.arabidopsis.org/info/agi.html>).
- e. Values represent the mean of four comparisons (two mutant samples v. two wildtype samples). Entries highlighted in yellow are down-regulated in *ada2b-1* leaves; entries highlighted in blue are down-regulated in *gcn5-1* leaves.
- f. Mean value is greater than three-fold, but the difference between mutant and wildtype signals was less than three-fold in at least two of the comparisons.