

Table 2. Genes up-regulated in leaves of *Arabidopsis ada2b-1* or *gcn5-1* mutant plants as assayed by Affymetrix microarray.^a

Gene groups ^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					
Transcription Factors	13015	At2g46680	ZAT12	4.7	7.9
	13273	AT4g36990	AtHSF4	11	16
	13432	At2g25000	WRKY60	4.3	6.8
	13806	At2g17040	putative NAM/no apical meristem protein	4.0	7.3
	13933	AT4g17230	scarecrow-like 13 (SCL13)	4.2	4.6
	14431	AT4g23810	WRKY53	4.6	7.7
	14711	At2g40140	Cys-3-His zinc finger protein	29	30
	15779	AT3g46090	ZAT7	8.5	10
	15665	AT5g04340	putative c2h2 zinc finger	6.5	9.4
	16063	At4g17500	AtERF-1	15	21
	16130	AT4g11370	RING-H2 finger protein RHA1a	4.2	5.5
	16536	At5g47230	AtERF5	6.0	5.5
	16609	AT5g47220	AtERF2	11	16
	16945	AT4g27900	unknown, similarity to Zn finger from rice	3.9	4.8
	17303	At2g38470	WRKY33	12	13
	18216	At1g27730	ZAT10, Salt tolerance zing finger	10	13
	18591	At5g63790	ATAF2	5.2	6.4
	19646	At2g46680	homeodomain transcription factor (ATHB-7)	4.7	5.1
	19936	At1g70000	DNA binding protein MybSt1, putative	6.1	12
	20382	At2g30250	WRKY25	4.0	6.1
	12643	At1g34180	putative NAM/no apical meristem protein	3.4 ^f	5.7
	12712	At1g18570	myb factor, putative	3.2 ^f	4.0
	13115	At1g62300	WRKY6	8.3 ^f	14
	18590	At1g69490	NAP (NAC-like, activated by AP3/PI)	2.1	3.1
	13381	At2g43000	Putative NAM/no apical meristem protein	2.9	6.0
	14553	At3g54810	GATA transcription factor putative	7.3 ^f	11
	16829	AT4g01920	CHP-rich zinc finger	2.2	5.0
	17052	At1g52880	NAC domain protein NAM	2.9	3.6
	17180	AT5g26920	GATA-type zinc fingers	A	5.4
	17881	At2g23320	WRKY15	2.2	3.8
	18600	AT3g16720	RING-H2 Zn finger at12 protein	3 ^f	4.9
	19202	At2g45680	PCF2-like DNA binding protein	2.3	3.7
	19696	At4g24240	WRKY7	3.1 ^f	4.0
	16638	At4g24240	putative zinc finger protein PMZ	4.2	3.3 ^f
16539	AT4g17490	AtERF6	4.8	1.8	
13271	At4g18880	heat shock transcription factor 21	3.0	2.3	

HATs mRNA splicing	19537	At1g67220	CBP related protein (pCAT1)	A	4.3	
	12390	At2g42270	putative U5 small nuclear ribonucleoprotein-specific protein.	3.1	4.2	
	18242	At2g42890	putative RNA-binding protein mei2	3.6	3.6	
	18001	At1g01040	CAF RNA helicase/RNaseIII	2.2	3.5	
Signal Transduction						
Receptor-like kinases	12497	At2g31880	Receptor-like kinase, LRR VII	7.7	10	
	12958	At2g33580	Receptor-like kinase Lys M	9.5	13	
	13659	AT4g23150	serine/threonine kinase-like protein, KIK1 (DUF26)	4	5.8	
	14763	AT3g09010	AK13 gene RECEPTOR-LIKE kinase LRRVIII-2	7.4	10	
	15616	At1g21250	wak1	10	8.4	
	16059	At1g14370	APK2a mRNA for protein kinase, RLCK VII	4.1	5.8	
	16348	At1g65790	receptor kinase (Ark1) gene, S-domain	4.7	5.3	
	16360	AT4g21380	Receptor-like serine/threonine protein kinase S-domain, ark3	4.6	5	
	16393	At2g13790	Receptor-like kinase, LRR II	9.3	9.4	
	16781	At2g19130	Receptor-like kinase, S-RECEPTOR KINASE	6.5	8.4	
	19092	AT4g11890	protein kinase-like (KIK1) SUBFAMILY duf26	7.3	13	
	19433	AT4g23270	Receptor-like serine/threonine kinase (duf26)	3.9	5.7	
	20232	AT4g23130	RECEPTOR LIKE KINASE (RLK6, DUF26)	6.6	9.7	
	12305	AT4g23260	similar to receptor protein kinase (S-domain), <i>Ipomoea trifida</i>	2.8	4.2	
		12307	At2g19190	Receptor-like kinase, LRR I (FRK1)	4 ^f	5.9
		12354	At2g37710	Receptor-like kinase, L-lectin (LRK1)	3 ^f	3.7
		16357	AT5g25930	Receptor-like kinase, LRK5 (LRR XI)	3.7 ^f	5.1
		16363	At1g61370	receptor protein kinase IRK1 S-domain	2.1	3.3
		17068	At5g60900	S-receptor kinase homolog 2	3.5 ^f	5.4
		17464	At1g09970	Receptor-like kinase, LRR XI	2.6	3.5
		19462	AT3g59700	serine/threonine-specific kinase lecRK1 precursor, lectin receptor-like	3.9 ^f	5
	Kinases	16061	AT4g26070	MEK1 (MAPKK)	8.2	9.3
		15680	At3g08720	ATPK19 mRNA for ribosomal-protein S6 kinase homolog	7.8	11
16412		At4g21400	serine/threonine protein kinase	5.4	3.8	
15005		At2g30040	kinase	4.8	5.7	
16151		AT5g02290	NAK S/T kinase	4.4	4.2	
18952		At4g23900	nucleoside diphosphate kinase 4	A	5.2	
17354		At4g35500	SRPK1	2.3	3	
Phosphatases	13022	At1g34750	Phosphatase type 2C	3.6 ^f	5.8	
	16203	At1g47510	inositol polyphosphate 5-phosphatase	A	5.3	
	20107	At1g05630	inositol 1,4,5-trisphosphate- 5-phosphatase	1.3	4.3	
Lipases	16493	At1g54010	lipase-like	12	13	
	20590	AT4g38550	Phospholipase like, pEARLI 4	3.4 ^f	4.1	

Others	14250	AT3g52430	pad4, SA signaling	8.8	8.3 ^f	
	19435	AT4g00240	phospholipase D	4	2.4	
	20142	AT4g34390	extra-large G-protein-like	4.3	4.5	
	16995	At2g23170	auxin-responsive GH3 - like	4.3	9.6	
	12772	At1g03220	glycoprotein	3.9	4.7	
	12760	At1g03230	Strong similarity extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> .	3.1	3.5	
	15965	AT3g16460	Putative lectin	3.2 ^f	4	
	16952	At2g41410	calmodulin-like	2.5	4.5	
Cell Rescue, Defense						
Peroxidases	17930	AT4g37520	Peroxidase, PRXR2	12	16	
	17413	AT5g64120	peroxidase	7.8	8.1	
	16963	At2g38390	peroxidase C3 precursor	7.3	4.1	
	15982	At2g37130	peroxidase ATP2a	4.2	4.6	
	14638	AT3g49120	peroxidase prxCb	3.4	4.8	
	17102	At1g05260	peroxidase precursor RC13A	6.1	3.2 ^f	
	12324	At2g18150	class III peroxidase ATP36	4.5	1.3	
GST	16462	At2g38380	class III peroxidase ATPEa	3.9	1.8	
	16054	At1g02920	GST11 (GSTF8)	170	250	
	19640	At2g29460	GST22	9.9	23	
	20356	At2g29470	GST21	8.3	20	
	12764	At2g02930	GST16 (GSTZ1)	6.7	10	
	Thioredoxin	13189	At1g45145	thioredoxin	10	8.8
		12623	At1g60420	red-1 (related to thioredoxin) gene	3.5 ^f	5.7
Copper amine oxidase	20585	At2g47880	putative glutaredoxin	A	14	
Defense related genes	20555	At4g12280	copper amine oxidase like	2.3	4.3	
	13212	AT3g57260	beta-1,3-glucanase (BG-2, PR-2)	75	120	
	17485	AT4g16260	beta-1, 3-glucanase class I precursor	8	52	
	12364	AT3g57240	beta-1,3-glucanase (BG3)	2.1	6.9	
	12574	AT3g60140	beta-glucosidase like	21	56	
	19451	At1g61820	beta-glucosidase	4.4	7.7	
	17840	At2g43570	endochitinase, class IV	70	110	
	20287	AT3g54420	Chitinase class IV	7.3	9	
	20420	AT4g19810	chitinase , class V?	6.4	9.5	
	12332	AT3g12500	Basic chitinase	4.2	17	
	14635	At2g14610	PR-1-like (PR-1)	16	40	
	14636	At1g75040	thaumatin-like, PR5	8.7	21	
	19171	At2g43510	trypsin inhibitor	5.5	16	
	12530	AT4g37150	hydroxynitrile lyase-like	2	4.4	
	17012	At1g72260	thionin (Thi2.1)	A	12	

R genes	16702	At2g02360	phloem-specific lectin	5.4	5.6	
	16440	At2g40000	nematode resistant protein-like	5.9	11	
	16365	At2g32680	disease resistant protein, LRR?	62	68	
	16347	At2g24160	disease resistant protein	5.4	7.9	
	12251	At2g34930	disease resistant protein	4.6	5.1	
	13641	At4g33300	disease resistant protein, RFL1 R gene	3.6	4.1	
	19423	At3g25510	disease resistance protein RPP1-WsB	2.4	3.4	
	14640	At2g39200	Mlo 12	3.2 ^f	3.7	
	14111	At4g13900	disease resistance protein, similarity to Hcr9-9A, <i>Lycopersicon pimpinellifolium</i>	5.3	4.3 ^f	
	14649	At1g12220	NBS/LRR disease resistance protein, RPS5	8.4	A	
Senescence	20491	At2g29350	tropinone reductase (SAG13-1)	17	29	
	19178	AT5g20230	blue copper binding-like (SAG14)	8.2	12	
	19181	At4g02380	late embryogenesis abundant protein homolog (SAG21)	7.6	11	
	19946	At2g23810	SAG5	4	3.7	
	19614	At1g09500	cinnamyl alcohol dehydrogenase (SAG26)	4	12	
	13243	AT4g37990	cinnamyl-alcohol dehydrogenase ELI3-2 (SAG25)	3.7	3.4	
	13004	At2g17840	SAG12/erd7 (cysteine protease)	3.5	4.1	
	20017	At2g44290	Unknown, lipid transfer protein (YLS3)	30	38	
	18255	At2g38860	YLS5, protease pfrp1	4.5	8.1	
	16632	AT5g13170	SAG29-MtN3-like	2.6	6.4	
Stress related	15137	At2g44790	blue copper-binding protein II	33	32	
	16150	AT4g12480	pEARLI 1	15	18	
	16914	AT4g11650	osmotin like (OSL3)	13	20	
	20421	AT4g14630	Oxalate oxidase	10	11	
	20641	At1g52690	LEA76 type1	7.5	6.8	
	13842	At1g24140	zn-metalloproteinase	6.8	9	
	14083	At2g41380	embryo-abundant protein	4.6	6.8	
	12801	At1g55450	embryonic abundant protein	3.1	3.7	
	15162	At3g04720	hevein-like protein precursor	3.4	5.3	
	13491	At1g48610	HAL3B F186	3.7 ^t	5	
	15967	AT4g01610	putative cathepsin B-like cysteine protease	2.9	3.7	
	16439	At1g31580	CXc750	6.6 ^f	7.7	
	19046	At2g44240	peptidase?	3.1 ^f	5.5	
	19152	At5g06760	late embryogenesis abundant protein	2.9	4.9	
	14800	At2g18370	putative lipid transfer	3.4	2.4	
Metabolism						
	Trp biosynthesis	19555	AT4g00700	phosphoribosylanthranilate transferase-like	9	13
		14673	AT4g27070	tryptophan synthase beta-subunit (TSB2)	3.1	3.7
14672		At4g02610	tryptophan synthase alpha chain TSA1	2.3	3.8	

Nitrogen & Carbon	13818	At2g13810	aspartate aminotransferase (ASP1), mitochondrial?	23	21	
	15594	At5g07440	glutamate dehydrogenase 2 (gdh2)	4.4	1.8	
Tyr	17008	At2g24850	tyrosine aminotransferase (similarity with <i>rooty</i>)	18	19	
Auxin	12500	At1g51760	IAA-Ala hydrolase (IAR3)	5.9	8.7	
Lys catabolism	15161	AT4g33150	lysine-ketoglutarate reductase/saccharopine dehydrogenase	4.5	8.9	
	15120	At5g17330	glutamate decarboxylase 1 (GAD 1)	A	9.2	
Asn biosynthesis	15154	AT3g47340	At-ASN1, glutamine-dependent asparagine synthetase	2.9	6.7	
Ethylene	16817	AT4g11280	ACC synthase (AtACS-6)	3.2 ^f	3.9	
TCA cycle	19225	AT5g65750	2-oxoglutarate dehydrogenase E1 subunit	2.4	3.9	
sulfate assimilation	16029	AT5g43780	ATP sulfurylase precursor (APS4)	5.3	2.5	
Cell Wall	20269	At2g45220	Pectinesterase	14	22	
	20239	AT3g13790	beta-fructofuranosidase 1	7.7	15	
	12642	At2g15390	xyloglucan fucosyl transferase-like (FUT4)	6.8	12	
	20432	At1g32170	xyloglucan endotransglycosylase (XTR4)	6.5	6.9	
	13900	AT3g47380	Pectinesterase	3.5	6.5	
	12449	At4g24000	cellulose synthase	1.5	6.6	
	17748	At4g20460	UDP-glucose 4-epimerase - like	A	3.4	
	18544	At1g30620	UDP-galactose-4-epimerase	2.6	3.8	
	19546	At2g14620	putative endoxyloglucan	A	3.6	
	19747	At1g10050	Endoxylanase	3.5 ^f	4	
	Alkaloid	14016	At1g30700	reticuline oxidase-like	11	18
		13908	AT4g20860	berberine bridge enzyme	8.3	10
		17422	AT4g13660	isoflavone reductase-like protein	2.7	3.4
		20096	At2g34810	berberine bridge enzyme	A	5.6
		19840	At1g30720	putative reticuline oxidase-like	5.1	A
	Steroids	18567	At2g47130	alcohol dehydrogenase (similarity to 3-beta-hydroxysteroiddehydrogenase)	11	21
16888		At2g37770	alcohol dehydrogenase (aldose reductase, steroids)	5.4	7	
17744		At2g37760	alcohol dehydrogenase (aldose reductase, steroids)	3.4	4.4	
Carbohydrates	20446	At1g05570	callose synthase 1 catalytic subunit (CalS1)	3.3	3.8	
	12998	AT3g47800	aldose 1-epimerase-like protein	2.2	4	
Cytochrome P450	14609	At2g30770	CYP71A13	22	58	
	12989	At2g34490	putative cytochrome P450 (weak similarity to C-22 sterol desaturase, ergosterol biosynthesis yeast)	13	18	
	12482	At2g44890	putative cytochrome P450	11	12	
	20479	AT4g39950	CYP79B2 (Converts Trp to aldoxime in IAA biosynthesis)	9.5	17	
	14032	AT4g37370	CYP81D8 (weak similarity to isoflavone 2'-hydroxylase)	6.3	8.8	
	13100	At2g45570	CYP76C2, YLS6 (similarity to geraniol 10-hydroxylase)	4.2	7.2	
	17522	AT5g36220	CYP91A1 (weak similarity to isoflavone 2'-hydroxylase)	3.5	6.8	
	17039	AT3g26220	CYP71B3	3.2 ^f	7.5	

Others	20290	At5g25130	CYP71B12	1.8	4.8	
	16993	At5g58860	CYP86A1	3.6	A	
	18753	AT4g10500	putative Fe(II)/ascorbate oxidase	5.4	11	
	16721	At2g31870	poly(ADP-ribose) glycohydrolase	4.7	8.9	
	13215	At1g67980	S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase	2.2	7.1	
	13351	At4g20320	cytidine 5'-triphosphate synthase	A	3.9	
	15496	At2g36800	UDP-glucosyl transferase	3.6 ^f	5.8	
	16791	AT4g39830	L-ascorbate oxidase	2.6	4.3	
	16968	At4g34131	glucosyltransferase -like	A	4.1	
	17051	At2g29720	CTF2B, monooxygenase	3.1 ^f	3.6	
	17481	At1g03400	E8 homolog	7.6 ^f	7	
	17548	At1g09500	putative cinnamyl alcohol dehydrogenase	3.3 ^f	8.4	
	17595	At2g38400	b-alanine-pyruvate aminotransferase	2.2	4.2	
	18888	At1g15380	Glyoxalase	2.5	14	
	16288	At2g17720	putative prolyl 4-hydroxylase, alpha subunit	4	2.1	
	18920	At2g30210	laccase putative	3.3	1.8	
	16784	At4g00040	putative chalcone synthase	3.3	2.6	
	Transporters	17899	AT4g15610	unknown, similarity to sodium channel protein	38	75
		14731	At2g34660	multidrug resistance-associated protein 2; AtMRP2	12	12
12521		AT3g51860	Ca ²⁺ /H ⁺ exchanging protein (CAX3)	8.6	14	
17499		At2g46430	cyclic nucleotide gated channel (CNGC3)	7.3	4.7	
14116		AT5g26340	hexose-transporter like (SPT13, MSS1, similar to HT2 tomato)	6.2	7.2	
15338		At1g23840	unknown, Sodium transporter?	4.3	6.6	
17653		AT4g39030	EDS5, MATE-transporter	3.8	4.4	
13627		At4g23700	putative Na ⁺ /H ⁺ -exchanging	A	8.2	
13834		At4g01010	cyclic nucleotide gated channel (CNGC4)	A	3.9	
12347		At1g59820	chromaffin granule ATPase II, phospholipid-transporting ATPase 3 (ALA3)	A	5.9	
16003		AT4g28390	ADP, ATP carrier-like	2.7	5.5	
17775		At1g61800	glucose-6-phosphate/phosphate-translocator (GPT)	4.4 ^f	6.3	
18328		At3g19930	monosaccharide transport protein STP4	2.6	4.8	
19581	At2g46450	cyclic nucleotide-regulated ion channel protein (cngc12)	2.5	4.3		
Cellular transport and Cellular organization	18720	AT5g61210	SNAP25A	2.8	3.5	
	16939	At2g33110	Synaptobrevin	4.2	5.1	
	12247	AT4g28710	myosin heavy chain-like	4.2	4.6	
Protein destination	12341	AT4g20110	vacuolar sorting receptor-like	19	23	

	12434	At2g36130	cyclophilin (peptidylprolyl isomerase) like	11	10
	16916	AT5g02490	Hsc70-2	7.1	14
	13285	AT5g52640	AtHSP90-1	5.3	11
	17278	At1g30900	vacuolar sorting receptor putative	4.3	7.2
	16043	At1g10290	ADL6 (dynamin-like protein 6)	6	9.8
	17097	At1g08450	calreticulin (Crt3), also binds to Calcium	3.2	4.7
	18783	At2g45500	unknown (similarity to human spastin)	2.4	3.1
	13284	At3g12580	heat shock protein 70	2.1	4.4
	13238	At1g28210	mitochondrial protein (AtJ1), Homolog of DnaJ	A	7.3
	15508	At2g29070	ubiquitin fusion-degradation protein	3 ^f	4.2
	20140	At4g31670	Similarity to deubiquitinating enzyme (DUB-1)	3.6 ^f	4.7
	18909	At2g04160	subtilisin-like protease (AIR3)	3.8	2.8
	17138	At1g03550	putative secretory carrier-associated membrane protein	4.4	2.9
Energy	15424	At3g50930	BCS1 protein-like protein (Mitochondrial protein)	A	7.3
	12562	At4g21090	MFDX2, adrenodoxin – like	3.5	3 ^f
Ionic homeostasis	16031	AT5g01600	ferritin 1 precursor	3.5	4.7
Cell Growth, Cell Division	15431	AT4g27280	unknown, centrin?	6.6	7.8
	16846	At3g22880	Meiotic Recombination protein DMC1	2.5	4.1
	19257	At1g04280	Histone 1flk	1.8	4.3
	17854	AT4g37010	centrin-like	2.7	4.8
Unclassified	13177	AT4g12720	growth factor like (NUDIX Hydrolase family)	7.3	6
	13880	AT4g25900	apospory-associated like	3.1 ^f	3.6
	13110	AT4g04620	symbiosis-related, Microtubule associated protein 1A/1B, light chain 3	2.1	3.8
	18069	BAC F4C21	small nucleolar RNA R30	A	3.3
	20051	At1g08940	Similarity to Saccharomyces hypothetical protein YDR051c (phosphoglycerate mutase)	1.9	4.2
Unknowns	13645	At1g05340		4.8	12
	15526	At1g10040		3.9	4.2
	12136	At1g15350		4.5	5.1
	14964	At1g65500		19	28
	15846	At2g14560		5.7	6.8
	17894	At2g18690		8.1	9.6
	17907	At2g37750		4.6	6.9
	13656	AT4g01870		9.4	9.9
	19247	AT4g03450		4.6	6.4
	19182	AT4g33050		17	24
	14278	AT4g36090		4.3	4.7
	13059	At4g36550		3.9	4.4

14882	AT4g39670	Similarity to a gene induced by high salinity	6.8	11	
19977	At1g02150		2	6.3	
14130	At1g03080		2.6	3.1	
15477	At1g10690		A	6.3	
12227	At1g13990		2.8	4.3	
18415	At1g27560		A	11	
13582	At1g60200		RNA metabolism (splicing?)	4.5 ^f	3.7
19230	At1g62420			2.5	4.7
14959	At1g79450			2.8	6
13865	At2g21850			A	3.9
12765	At2g22660	2.5		3.3	
13985	At2g25930	3.2 ^f		4.7	
17886	At2g26190	2.7		3.6	
15485	At2g27310	2.6		3.4	
14924	At2g28400	2.9		4.4	
14462	At2g32130	A		3.3	
18631	At2g41640	3.1 ^f		3.7	
15815	AT4g17070	2.3		4	
13971	AT4g17120	3 ^f		3.5	
18660	AT4g17670	A		5.2	
16299	AT4g19880	3 ^f		4.6	
20554	AT4g21670	2.1		3.4	
18224	At4g21830	2.8		6.2	
17376	At4g21970	2.6	4		
15076	At4g23530	A	5.8		
12995	AT4g24970	2.7	3.3		
12240	At4g27860	A	6.6		
18409	At1g03260	4.7	A		
12062	At2g01650	3.4	3.2 ^f		
18263	At2g18680	6.9	6.6 ^f		
15865	At2g20480	3.3	3.3 ^f		
19386	At2g22510	3.7	1.1		
16514	At4g38080	3.4	1.4		

Notes for Table 2.

- a. Genes designated as up-regulated satisfy three criteria: signals are designated as “present” in mutant 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). A = absent in both wildtype and mutant samples. Entries highlighted in yellow are up-regulated in *ada2b-1* leaves; entries highlighted in blue are up-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.