

Table S1. The chemical component of the Hoagland solution.

	Chemical component	solution(mmol/L)
solution I	H3BO3	0.02
	ZnSO4 ·7H2O	0.001
	CuSO4 ·5H2O	0.0002
	MgSO4 ·H2O	0.001
	(NH4)6Mo7O24 ·4H2O	0.000005
solution II	Ca(NO3)2 ·4H2O	2.49841
solutionIII	KH2PO4	0.49967
	KNO3	2.5047
solutionIV	EDTA ·FeNa	0.1
solution V	MgSO4 ·7H2O	1.00012

Table S2. List of the primers.

Primer Name	Sequence	Experiment
Promoter-F	TTGAATAGATACGCTGACACGC	Cloning
GaJAZ1-F	ATGTTTGGTTCACCGGAATATACAT	Cloning
GaJAZ1-R	CTATCCCTTTCTCTTCTCG	Cloning
GaMYC2.1-AD-F	GCCATGGAGGCCAGTGAATTCATGAAGGACCATAGGTTAG	Yeast two hybrid assay
GaMYC2.1-AD-R	CGATTCATCTGCAGCTCGAGCTTATCTTGCATCTCCAAC	Yeast two hybrid assay
GaMYC2.2-AD-F	GCCATGGAGGCCAGTGAATTCATGACTGACTATCGATTTG	Yeast two hybrid assay
GaMYC2.2-AD-R	CGATTCATCTGCAGCTCGAGCCTATATCTCACTTCCGATTTTG	Yeast two hybrid assay
AtMYC2-AD-F	GCCATGGAGGCCAGTGAATTC ATGACTGATTACCGGCTAC	Yeast two hybrid assay
AtMYC2-AD-R	CGATTCATCTGCAGCTCGAG CTTAACCGATTTTTGAAATC	Yeast two hybrid assay
GaJAZ1-BD-F	ATGGAGGCCGAATTCATGTTTGGTTCACCGGAATATAC	Yeast two hybrid assay
GaJAZ1-BD-R	CAGGTCGACGGATCCCTACTGTAGTGATTCAACAG	Yeast two hybrid assay
GaJAZ1-△jas-BD-F	ATGGAGGCCGAATTCATGTTTGGTTCACCGGAATATAC	Yeast two hybrid assay
GaJAZ1-△jas-BD-R	TTATGCTAGTTATGCGGCCGCTAGATCGCCGGGAATGGGACG	Yeast two hybrid assay
AtJAZ1-BD-F	ATGGAGGCCGAATTCATGTCGAGTTCTATGGAATG	Yeast two hybrid assay
AtJAZ1-BD-R	CAGGTCGACGGATCCTCATATTCAGCTGCTAAAC	Yeast two hybrid assay
AtJAZ1-△jas-BD-F	ATGGAGGCCGAATTCATGTCGAGTTCTATGGAATG	Yeast two hybrid assay
AtJAZ1-△jas-BD-R	TTATGCTAGTTATGCGGCCGCAAGTTCTGTCAATGGTGTGGGGAG	Yeast two hybrid assay
nluc-GaJAZ1-F	CATTTTCATTTGGAGAGAACACGGGGGACGGGGGTACCATGTTTGGTTCACCGGAATATAC	Firefly luciferase complementation
nluc-GaJAZ1-R	GAGCCACCGCCCCGGGACGCGTACGAGATCTGGGG GTCGACCTACTGTAGTGATTCAACAG	Firefly luciferase complementation
nluc-GaJAZ1-△jas-F	CATTTTCATTTGGAGAGAACACGGGGGACGGGGGTACCATGTTTGGTTCACCGGAATATAC	Firefly luciferase complementation
nluc-GaJAZ1-△jas-R	GAGCCACCGCCCCGGGACGCGTACGAGATCTGGGGGTGCTAGATCGCCGGGAATGGGACG	Firefly luciferase complementation
cluc-GaMYC2.1-F	CGGAGGTCAGATCTCGTACGCGTCCCGGGGCGGGGTACCATGAAGGACCATAGGTTAG	Firefly luciferase complementation
cluc-GaMYC2.2-F	CGGAGGTCAGATCTCGTACGCGTCCCGGGGCGGG GGTACC ATGACTGACTATCGATTTG	Firefly luciferase complementation
cluc-GaMYC2.2-R	GTCGTCGTCGTCCTTGTAGTCCATTTGTTGGGGTGCACCCTATATCTCACTTCCGATTTTG	Firefly luciferase complementation

Primer Name	Sequence	Experiment
GaMYB59-F	TGCTTTGATCATATTCCTTGAAAAT	Reporter-effector
GaMYB59-R	GTTTCTTTCTCCTCTAAATCCG	Reporter-effector
GaJAZ1-F	GAGAACACGGGGGACTCTAGAATGTTTGGTTCACCGGAATATAC	Reporter-effector
GaJAZ1-R	GGACTGACCACCCGGGGATCCCTACTGTAGTGATTCAACAG	Reporter-effector
GaJAZ1-△jas-R	GGACTGACCACCCGGGGATCCTAGATCGCCGGGAATGGGACG	Reporter-effector
GaMYC2.1-F	GAGAACACGGGGGACTCTAGAATGAAGGACCATAGGTTAG	Reporter-effector
GaMYC2.1-R	GGACTGACCACCCGGGGATCCCTTATCTTGCATCTCCAAC	Reporter-effector
GaJAZ1-F	GGTAGTCCGAACGAATCCGGCC	Subcellular localization
GaJAZ1-R	TCGCCGGGAATGGAACGAACG	Subcellular localization
pYL156-GaJAZ1-F	GAATTCATGTTTGGTTCACCGG	Virus-induced gene silencing
pYL156-GaJAZ1-R	GGATCCCGGCGCTGCGGCGT	Virus-induced gene silencing
pYL156-GhMYB59-F	GAATTCATGAAACTTGTGCAA	Virus-induced gene silencing
pYL156-GhMYB59-R	GAATTCATGAAACTTGTGCAAGAAG	Virus-induced gene silencing
GaJAZ1-F	GGTAGTCCGAACGAATCCGGCC	qRT-PCR
GaJAZ1-R	TCGCCGGGAATGGAACGAACG	qRT-PCR
GaLOX3-F	AGAAAAGGAATGCCGATCCT	qRT-PCR
GaLOX3-R	AGGACCTGAGCTAGGTGCAA	qRT-PCR
GaAOS-F	CTTGACTGCCCATGACTGAA	qRT-PCR
GaAOS-R	GCACCACAAACCAAAGGACT	qRT-PCR
GaAOC4-F	AGAAGAGCTGCTTTGCAAGC	qRT-PCR
GaAOC4-R	CATGTGGCTCACAAGCCTTA	qRT-PCR
GaACS6-F	TGAAGAGCAATGCTGGATTG	qRT-PCR
GaACS6-R	ACTCGCCACAAGTCCATTTC	qRT-PCR
GaERF2-F	GGAGCCAGATCCAGTCAGAG	qRT-PCR
GaERF2-R	CTCCTTTTTTGGTGACGCATT	qRT-PCR
GaERF4-F	CGTCCTCGGTTGTTGATTTT	qRT-PCR
GaERF4-R	CAAACGGGGAAAAGAATTCA	qRT-PCR

Primer Name	Sequence	Experiment
GaABR1-F	CCTATGGTTTTTCCGCTTCA	qRT-PCR
GaABR1-R	CCAAGAATGCACCGAAAAAT	qRT-PCR
GaABA2-F	ATTTTGACCCCATTTGTTCCA	qRT-PCR
GaABA2-R	TTTCAACACTGCTGAAACCG	qRT-PCR
GaCBF4-F	GCTGACTCAGCTTGGAAGCT	qRT-PCR
GaCBF4-R	CAGCCGTTCTGAAAGTCTCC	qRT-PCR
GaRD26-F	AAAACGTGTTTGGTCGGCAAG	qRT-PCR
GaRD26-R	TCAATTGAGCCAATGGATCA	qRT-PCR
GaCIPK9-F	CTCAGGAGGCCGATCCTACCAA	qRT-PCR
GaCIPK9-R	CGGTGGCGCAAGAGTACCATAC	qRT-PCR
GaMYB13-F	GCTGCACAGTTACCTGGACGAA	qRT-PCR
GaMYB13-R	AAGTTGGTTGTGGGGATGCTGA	qRT-PCR
GaDFL2-F	AAGCAGAGCAAGACCAAAGGGG	qRT-PCR
GaDFL2-R	AGATTGCATTGCTGTCATCGCT	qRT-PCR
GhLOX3-F	ACGTCGACCTTATCCGAGACGA	qRT-PCR
GhLOX3-R	CTTCCGGCATCCACTGATCGTT	qRT-PCR
GhAOS-F	CTGGTGACTGCGGACATACGTT	qRT-PCR
GhAOS-R	CAACACGAGGGCAAGAGGCAAT	qRT-PCR
GhACS6-F	GACATTGAAGAGCATCGTGCAGT	qRT-PCR
GhACS6-R	AGGGTCTTTGAAGACTGTGGCG	qRT-PCR
GhERF2-F	GAAACCAAAGTCCGTTGCGAG	qRT-PCR
GhERF2-R	CTGTTCCGGCTGTTTCGAACGTG	qRT-PCR
GhERF4-F	CATCGGAGAGCGAAACGGAACA	qRT-PCR
GhERF4-R	CAGCTTCTTCAGCGGTGTCGTA	qRT-PCR
GhABR1-F	AAGCAGCCCTTGTTTCAGAGG	qRT-PCR
GhABR1-R	GAAAACGGGCAACAGGGTTGTG	qRT-PCR
GhABA2-F	CATTGCTTTACGTCGGCGTTCC	qRT-PCR

Primer Name	Sequence	Experiment
GhABA2-R	CATAGGAGTCGCAATGCCGTGA	qRT-PCR
GhCBF4-F	TCAGAACGGCTGAGCATTGAG	qRT-PCR
GhCBF4-R	CCCAAACAACGCTTCTTCGTCC	qRT-PCR
GhRD26-F	TCAAGCAGAGAGCAAAGCACGA	qRT-PCR
GhRD26-R	GAACGAGTTAATGCGCGGCAAA	qRT-PCR
GhGH3.6-F	ACCATTTGCTGCCATTTGGTGC	qRT-PCR
GhGH3.6-R	GCCCTTGGCGGTATACACTGTT	qRT-PCR
GhCIPK9-F	AGAATGTTGAGACCGGCGAGTG	qRT-PCR
GhCIPK9-R	ACTGTTCGACCATTCGGTGACG	qRT-PCR
GhMYB13-F	AGCATCCCCACAACCAACTTCA	qRT-PCR
GhMYB13-R	CCACTATTTGCCTCGTACCCGT	qRT-PCR
GhDFL2-F	AATGTGGACGTATCGGCTGACC	qRT-PCR
GhDFL2-R	TCCCTTCCAAACAACTCGGAGC	qRT-PCR
GhMYB59-F	GAATTCATGAAAATGATGCAAGAGG	qRT-PCR
GhMYB59-R	GGATCCCCTGTTTCCCCACTTAG	qRT-PCR
Gossypium hirsutum histone 3Forward Primer	CCTTGTGGGTCTTTTGTAA	qRT-PCR
Gossypium hirsutum histone 3 Reverse Primer	AACTGGATGTCCTTGGGC	qRT-PCR

Table S3. Fiber quality in transgenic cotton and the control (CCRI24) .

Line	Fiber length (mm)	Length uniformity (%)	Micronaire value	Fiber strength (cN/tex)
L2	28.2	85.3	4.3	26.6
L4	30.0	85.7	4.3	27.5
L5	31.3	86.1	4.0	26.7
control	29.7	87.1	4.4	27.9

The plot mean values were based on the average over 15 individual plants.

Table S4. Summary of sequencing results.

Samples	Clean reads	clean bases	Total mapped	Q30 (%)	GC content (%)
WT-0h	5.47E+07	8.20G	4.76E+07	93.28	43.92
<i>GaJAZ1</i> -OE-0h	5.36E+07	8.05G	4.72E+07	93.29	43.76
WT-6h	5.53E+07	8.29G	4.29E+07	93.65	43.86
<i>GaJAZ1</i> -OE-6h	5.02E+07	7.52G	4.42E+07	93.37	43.68
WT-12h	5.17E+07	7.75G	4.42E+07	92.96	43.62
<i>GaJAZ1</i> -OE-12h	5.26E+07	7.89G	4.60E+07	93.51	43.66
WT-24h	5.27E+07	7.91G	4.61E+07	93.08	43.78
<i>GaJAZ1</i> -OE-24h	4.92E+07	7.38G	4.29E+07	94.60	43.66

Table S5. Distribution of FPKM interval in *GaJAZ1*-OE and WT plants at different times.

FPKM Interval	0~1	Percent	1~3	Percent	3~15	Percent	15~60	Percent	>60	Percent
WT-0h	26605	34.34%	11209	14.47%	25295	32.65%	11592	14.96%	2783	3.59%
<i>GAJAZ1</i> -OE-0h	27175	35.07%	11395	14.71%	25114	32.41%	10985	14.18%	2814	3.63%
WT-6h	26687	34.44%	11179	14.43%	24681	31.85%	11817	15.25%	3120	4.03%
<i>GAJAZ1</i> -OE-6h	27384	35.34%	11241	14.51%	24405	31.50%	11581	14.95%	2873	3.71%
WT-12h	25980	33.53%	10778	13.91%	25106	32.40%	12623	16.29%	2997	3.87%
<i>GAJAZ1</i> -OE-12h	26332	33.98%	10750	13.88%	24900	32.13%	12493	16.13%	3008	3.88%
WT-24h	27480	35.47%	11075	14.29%	24456	31.56%	11510	14.86%	2963	3.82%
<i>GAJAZ1</i> -OE-24h	26822	34.62%	11152	14.39%	24721	31.91%	11785	15.21%	3003	3.87%

Table S6. Differentially expressed genes in different groups.

sample	sample	log2FoldChange $\geq$ 2	up	down
WT_6h	WT_0h	4761	2532	2229
WT_12h	WT_6h	1413	425	988
WT_24h	WT_12h	2580	1456	1124
<i>GaJAZ1</i> -OE_6h	<i>GaJAZ1</i> -OE_0h	5886	2582	3304
<i>GaJAZ1</i> -OE_12h	<i>GaJAZ1</i> -OE_6h	1459	599	860
<i>GaJAZ1</i> -OE_24h	<i>GaJAZ1</i> -OE_12h	1934	1194	740
<i>GaJAZ1</i> -OE_0h	WT_0h	1146	377	769
<i>GaJAZ1</i> -OE_6h	WT_6h	520	146	374
<i>GaJAZ1</i> -OE_12h	WT_12h	576	240	336

Table S7. Genes exclusively by salt stress between *GaJAZ1*-OE and WT plants.

Gene ID	log2 (<i>GaJAZ1</i> /WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A01G0055	-2.2709	AT3G19000	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein
Gh_A01G0347	-2.0502	AT2G21110	Disease resistance-responsive (dirigent-like protein) family protein
Gh_A01G0382	-5.105	AT5G46330	Leucine-rich receptor-like protein kinase family protein
Gh_A01G0384	-2.0615	AT4G20140	Leucine-rich repeat transmembrane protein kinase
Gh_A01G0467	-2.8541	AT4G21700	Protein of unknown function
Gh_A01G0526	-2.4629	AT4G21440	MYB-like 102
Gh_A01G0547	-2.5331	AT5G54510	Auxin-responsive GH3 family protein
Gh_A01G0613	-2.1755	AT5G36110	cytochrome P450, family 716, subfamily A, polypeptide 1
Gh_A01G0767	-2.3773	AT5G07280	Leucine-rich repeat transmembrane protein kinase
Gh_A01G0966	-2.5167	AT2G26530	Protein of unknown function
Gh_A01G1477	-3.0019	AT1G68150	WRKY DNA-binding protein 9
Gh_A01G1655	-2.2389	AT5G06839	bZIP transcription factor family protein
Gh_A01G1658	-2.7324	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_A01G1659	-3.0697	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_A01G1660	-2.4235	AT2G42250	cytochrome P450, family 712, subfamily A, polypeptide 1
Gh_A01G1887	-2.1581	AT3G06880	Transducin/WD40 repeat-like superfamily protein
Gh_A01G2141	3.2525	AT1G52340	NAD(P)-binding Rossmann-fold superfamily protein
Gh_A02G0011	2.3637	AT5G01990	Auxin efflux carrier family protein
Gh_A02G0050	-2.7755	AT4G36220	ferulic acid 5-hydroxylase 1
Gh_A02G0330	-2.1027	AT1G60680	NAD(P)-linked oxidoreductase superfamily protein
Gh_A02G0741	-3.368	AT1G77330	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A02G0866	2.1881	AT4G25810	xyloglucan endotransglycosylase 6
Gh_A02G1014	-3.0695	AT5G41610	cation/H ⁺ exchanger 18

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A02G1017	-2.7688	AT5G41610	cation/H ⁺ exchanger 18
Gh_A02G1175	2.7957	AT3G15990	sulfate transporter 3;4
Gh_A02G1197	-2.6326	AT1G52800	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A02G1241	4.3938	AT1G72210	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A02G1604	-2.0935	AT1G27660	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A02G1734	-2.5021	AT1G06620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A03G0401	2.077	AT1G12740	cytochrome P450, family 87, subfamily A, polypeptide 2
Gh_A03G0507	2.0413	AT1G12240	Glycosyl hydrolases family 32 protein
Gh_A03G0991	-2.3202	AT2G01900	DNAse I-like superfamily protein
Gh_A03G1411	3.0364	AT4G10265	Wound-responsive family protein
Gh_A03G1412	3.3112	AT4G10265	Wound-responsive family protein
Gh_A03G1493	-2.353	AT4G38140	RING/U-box superfamily protein
Gh_A03G1537	2.371	AT1G17840	white-brown complex homolog protein 11
Gh_A03G1776	Inf	AT4G38840	SAUR-like auxin-responsive protein family
Gh_A03G1935	-2.3817	AT2G35060	K ⁺ uptake permease 11
Gh_A03G2015	-2.7674	AT4G23030	MATE efflux family protein
Gh_A03G2044	-2.0772	AT4G11650	osmotin 34
Gh_A03G2148	-4.9216	AT4G35150	O-methyltransferase family protein
Gh_A03G2159	2.8321	AT5G02600	Heavy metal transport/detoxification superfamily protein
Gh_A04G0071	2.6514	AT2G21110	Disease resistance-responsive (dirigent-like protein) family protein
Gh_A04G0284	-2.3029	AT4G27220	NB-ARC domain-containing disease resistance protein
Gh_A04G0392	-2.4893	AT1G55020	lipoxygenase 1
Gh_A04G0485	-3.3172	AT5G06200	Uncharacterised protein family
Gh_A04G0558	-2.2082	AT3G52970	cytochrome P450, family 76, subfamily G, polypeptide 1
Gh_A04G0578	-2.8724	AT4G40070	RING/U-box superfamily protein
Gh_A04G0634	-2.3846	AT1G61110	NAC domain containing protein 25

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A04G0810	-2.3143	AT5G66770	GRAS family transcription factor
Gh_A04G0848	2.829	AT5G56660	IAA-leucine resistant (ILR)-like 2
Gh_A04G0921	2.2106	AT2G31180	myb domain protein 14
Gh_A04G0996	-2.3895	AT5G42500	Disease resistance-responsive (dirigent-like protein) family protein
Gh_A04G1209	-2.7992	AT1G74110	cytochrome P450, family 78, subfamily A, polypeptide 10
Gh_A04G1216	-2.64	AT4G10310	high-affinity K ⁺ transporter 1
Gh_A04G1361	-3.2167	AT2G24130	Leucine-rich receptor-like protein kinase family protein
Gh_A05G0014	2.0168	AT5G57090	Auxin efflux carrier family protein
Gh_A05G0164	-2.2544	AT3G24520	heat shock transcription factor C1
Gh_A05G0423	-3.9333	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_A05G0834	-2.0534	AT4G01470	tonoplast intrinsic protein 1;3
Gh_A05G0889	-2.1871	AT5G60660	plasma membrane intrinsic protein 2;4
Gh_A05G1449	-2.3992	AT3G21690	MATE efflux family protein
Gh_A05G1467	2.4921	AT4G22030	F-box family protein with a domain of unknown function
Gh_A05G1468	3.8079	AT4G22030	F-box family protein with a domain of unknown function
Gh_A05G1469	2.6281	AT4G22030	F-box family protein with a domain of unknown function
Gh_A05G1576	2.2426	AT1G20190	expansin 11
Gh_A05G1741	-2.14	AT2G26570	Plant protein of unknown function
Gh_A05G1779	2.0831	AT4G34150	Calcium-dependent lipid-binding (CaLB domain) family protein
Gh_A05G2391	-3.0587	AT1G11300	protein serine/threonine kinases
Gh_A05G2501	2.0271	AT5G04460	RING/U-box superfamily protein
Gh_A05G2516	-2.3526	AT4G36220	ferulic acid 5-hydroxylase 1
Gh_A05G2682	-2.0144	AT2G01430	homeobox-leucine zipper protein 17
Gh_A05G2878	-2.4283	AT5G05600	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A05G2921	2.1169	AT1G28050	B-box type zinc finger protein with CCT domain
Gh_A05G3413	-2.3506	AT4G23920	UDP-D-glucose/UDP-D-galactose 4-epimerase 2

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A05G3493	2.6775	AT2G40610	expansin A8
Gh_A05G3748	-2.8209	AT4G08250	GRAS family transcription factor
Gh_A05G3945	-2.5551	AT3G14690	cytochrome P450, family 72, subfamily A, polypeptide 15
Gh_A05G3970	-2.5183	AT5G43470	Disease resistance protein (CC-NBS-LRR class) family
Gh_A06G0018	3.1123	AT1G20190	expansin 11
Gh_A06G0187	-2.0365	AT3G53010	Domain of unknown function
Gh_A06G0228	-2.0588	AT3G24240	Leucine-rich repeat receptor-like protein kinase family protein
Gh_A06G0358	-2.8822	AT4G08250	GRAS family transcription factor
Gh_A06G0497	-2.0682	AT2G26650	K ⁺ transporter 1
Gh_A06G0563	-2.0635	AT4G28890	RING/U-box superfamily protein
Gh_A06G0829	-3.8829	AT4G32860	unknown protein
Gh_A06G0972	-4.5314	AT5G24800	basic leucine zipper 9
Gh_A06G0999	-2.1845	AT5G09970	cytochrome P450, family 78, subfamily A, polypeptide 7
Gh_A06G1070	2.205	AT4G23250	kinases;protein kinases
Gh_A06G1542	6.0878	AT2G02990	ribonuclease 1
Gh_A06G1600	-3.0978	AT1G11300	protein serine/threonine kinases
Gh_A06G1649	-3.6225	AT5G46330	Leucine-rich receptor-like protein kinase family protein
Gh_A06G1699	-2.6378	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_A06G1701	-2.3036	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_A06G1730	-2.8769	AT5G47740	Adenine nucleotide alpha hydrolases-like superfamily protein
Gh_A06G1755	-2.2349	AT1G12030	Protein of unknown function
Gh_A06G1765	3.7816	AT4G22030	F-box family protein with a domain of unknown function
Gh_A06G1802	3.0018	AT1G17420	lipoxygenase 3
Gh_A06G1803	2.149	AT1G17420	lipoxygenase 3
Gh_A07G0229	-2.7448	AT5G44700	Leucine-rich repeat transmembrane protein kinase
Gh_A07G0328	-2.2198	AT1G15550	gibberellin 3-oxidase 1

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A07G0450	-3.2086	AT1G12740	cytochrome P450, family 87, subfamily A, polypeptide 2
Gh_A07G0553	-2.2014	AT1G63800	ubiquitin-conjugating enzyme 5
Gh_A07G0723	-3.5072	AT3G30210	myb domain protein 121
Gh_A07G1349	-2.2321	AT2G45430	AT-hook motif nuclear-localized protein 22
Gh_A07G1547	-2.3409	AT1G66140	zinc finger protein 4
Gh_A07G1611	2.7109	AT5G15780	Pollen Ole e 1 allergen and extensin family protein
Gh_A07G2016	-2.1583	AT1G23740	Oxidoreductase, zinc-binding dehydrogenase family protein
Gh_A07G2033	2.8896	AT5G14650	Pectin lyase-like superfamily protein
Gh_A08G0064	-2.1085	AT2G27370	Uncharacterised protein family
Gh_A08G0179	Inf	AT4G27350	Protein of unknown function
Gh_A08G0182	Inf	AT1G53050	Protein kinase superfamily protein
Gh_A08G0346	3.1213	AT4G11290	Peroxidase superfamily protein
Gh_A08G0347	2.688	AT3G01190	Peroxidase superfamily protein
Gh_A08G0417	-2.4695	AT3G23240	ethylene response factor 1
Gh_A08G0580	-2.1428	AT2G41100	Calcium-binding EF hand family protein
Gh_A08G0962	2.0744	AT1G32640	Basic helix-loop-helix (bHLH) DNA-binding family protein
Gh_A08G0990	-2.6352	AT1G01490	Heavy metal transport/detoxification superfamily protein
Gh_A08G1196	-2.1432	AT2G45430	AT-hook motif nuclear-localized protein 22
Gh_A08G1210	-2.6065	AT2G45360	Protein of unknown function
Gh_A08G1400	-2.1714	AT5G16770	myb domain protein 9
Gh_A08G1572	-2.1181	AT4G12110	sterol-4alpha-methyl oxidase 1-1
Gh_A08G1613	2.2937	AT4G23030	MATE efflux family protein
Gh_A08G1684	-2.3102	AT3G28730	high mobility group
Gh_A08G1778	-2.1873	AT1G08090	nitrate transporter 2:1
Gh_A08G1885	-2.062	AT1G54740	Protein of unknown function
Gh_A08G1950	2.7909	AT5G17820	Peroxidase superfamily protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A08G2059	-4.0565	AT4G27190	NB-ARC domain-containing disease resistance protein
Gh_A08G2199	4.2063	AT1G19180	jasmonate-zim-domain protein 1
Gh_A08G2362	Inf	AT2G42430	lateral organ boundaries-domain 16
Gh_A08G2388	-2.6857	AT1G63440	heavy metal atpase 5
Gh_A08G2500	-2.3885	AT2G18960	H(+)-ATPase 1
Gh_A08G2559	-2.1412	AT2G37170	plasma membrane intrinsic protein 2
Gh_A09G0142	-2.582	AT1G26800	RING/U-box superfamily protein
Gh_A09G0159	-2.238	AT1G26870	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
Gh_A09G0474	-2.2588	AT3G18400	NAC domain containing protein 58
Gh_A09G0566	-2.2447	AT3G54700	phosphate transporter 1;7
Gh_A09G0903	-2.1256	AT1G08320	bZIP transcription factor family protein
Gh_A09G1165	2.6971	AT3G57670	C2H2-type zinc finger family protein
Gh_A09G1179	-2.248	AT5G06905	cytochrome P450, family 712, subfamily A, polypeptide 2
Gh_A09G1181	-2.6631	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_A09G1261	2.1151	AT3G52450	plant U-box 22
Gh_A09G1353	-2.8609	AT4G18250	receptor serine/threonine kinase, putative
Gh_A09G1359	-3.8969	AT2G39210	Major facilitator superfamily protein
Gh_A09G1486	3.7677	AT2G37430	C2H2 and C2HC zinc fingers superfamily protein
Gh_A09G1649	-2.7472	AT1G07430	highly ABA-induced PP2C gene 2
Gh_A09G1775	-2.747	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_A09G1848	-2.0217	AT5G07990	Cytochrome P450 superfamily protein
Gh_A09G1849	-2.7106	AT5G07990	Cytochrome P450 superfamily protein
Gh_A09G2283	-2.4721	AT1G06000	UDP-Glycosyltransferase superfamily protein
Gh_A09G2284	-2.1314	AT1G06000	UDP-Glycosyltransferase superfamily protein
Gh_A09G2474	-2.1262	AT2G28160	FER-like regulator of iron uptake
Gh_A10G0054	-2.1453	AT1G30650	WRKY DNA-binding protein 14

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A10G0156	-2.1596	AT1G11300	protein serine/threonine kinases
Gh_A10G0292	-2.0068	AT1G68810	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A10G0340	3.1899	AT2G40330	PYR1-like 6
Gh_A10G0436	-2.2037	AT1G31320	LOB domain-containing protein 4
Gh_A10G0493	-2.3516	AT3G13840	GRAS family transcription factor
Gh_A10G0697	-2.9339	AT1G52790	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A10G1055	-3.0586	AT1G11300	protein serine/threonine kinases
Gh_A10G1124	-2.2207	AT2G32830	phosphate transporter 1;5
Gh_A10G1129	-3.8199	AT3G11080	receptor like protein 35
Gh_A10G1332	2.2328	AT5G59320	lipid transfer protein 3
Gh_A10G1537	3.9923	AT3G17070	Peroxidase family protein
Gh_A10G2073	-2.4607	AT1G69550	disease resistance protein (TIR-NBS-LRR class)
Gh_A10G2081	-3.0276	AT3G25510	disease resistance protein (TIR-NBS-LRR class), putative
Gh_A10G2089	-2.2808	AT4G00430	plasma membrane intrinsic protein 1;4
Gh_A10G2101	-2.2348	AT4G20140	Leucine-rich repeat transmembrane protein kinase
Gh_A10G2148	-2.7922	AT4G20140	Leucine-rich repeat transmembrane protein kinase
Gh_A10G2231	-2.2955	AT2G47000	ATP binding cassette subfamily B4
Gh_A11G0234	4.0773	AT1G62510	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Gh_A11G0378	-2.617	AT1G48480	receptor-like kinase 1
Gh_A11G0410	-2.8317	AT4G36740	homeobox protein 40
Gh_A11G0743	-2.0484	AT2G45430	AT-hook motif nuclear-localized protein 22
Gh_A11G0750	-2.2767	AT2G45510	cytochrome P450, family 704, subfamily A, polypeptide 2
Gh_A11G0773	-2.4617	AT3G61060	phloem protein 2-A13
Gh_A11G0906	-2.0019	AT2G46680	homeobox 7
Gh_A11G0942	-2.7402	AT3G53480	pleiotropic drug resistance 9
Gh_A11G1177	-2.0585	AT5G43580	Serine protease inhibitor, potato inhibitor I-type family protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A11G1197	-2.1716	AT4G10500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A11G1397	-2.7966	AT3G07870	F-box and associated interaction domains-containing protein
Gh_A11G1398	-2.8148	AT3G07870	F-box and associated interaction domains-containing protein
Gh_A11G1521	-2.2062	AT5G38280	PR5-like receptor kinase
Gh_A11G1897	-2.7274	AT4G37850	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A11G2144	-2.4735	AT1G52820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A11G2463	-3.298	AT5G02070	Protein kinase family protein
Gh_A11G2482	-2.3294	AT3G05725	Protein of unknown function
Gh_A11G2552	-2.6106	AT1G11300	protein serine/threonine kinases
Gh_A11G2576	-2.8006	AT1G28130	Auxin-responsive GH3 family protein
Gh_A11G2620	5.1933	AT4G38700	Disease resistance-responsive (dirigent-like protein) family protein
Gh_A11G2752	-2.6499	AT3G56970	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A11G2836	-2.3271	AT3G14470	NB-ARC domain-containing disease resistance protein
Gh_A11G3000	3.9139	AT1G74500	activation-tagged BRI1(brassinosteroid-insensitive 1)-suppressor 1
Gh_A11G3009	-2.2417	AT2G47140	NAD(P)-binding Rossmann-fold superfamily protein
Gh_A12G0320	2.1163	AT1G20440	cold-regulated 47
Gh_A12G0375	-4.4277	AT4G34760	SAUR-like auxin-responsive protein family
Gh_A12G0581	-2.3089	AT1G19630	cytochrome P450, family 722, subfamily A, polypeptide 1
Gh_A12G0584	2.675	AT3G11480	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Gh_A12G0736	3.8148	AT2G22760	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A12G0841	2.354	AT5G10130	Pollen Ole e 1 allergen and extensin family protein
Gh_A12G0842	-2.2831	AT5G65090	DNAse I-like superfamily protein
Gh_A12G0875	2.3532	AT2G44840	ethylene-responsive element binding factor 13
Gh_A12G0876	Inf	AT2G44840	ethylene-responsive element binding factor 13
Gh_A12G0949	-2.0901	AT4G10160	RING/U-box superfamily protein
Gh_A12G1006	-2.1096	AT2G46495	RING/U-box superfamily protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A12G1029	-2.5287	AT2G46660	cytochrome P450, family 78, subfamily A, polypeptide 6
Gh_A12G1033	-2.2973	AT2G46680	homeobox 7
Gh_A12G1034	-2.1847	AT2G46690	SAUR-like auxin-responsive protein family
Gh_A12G1508	Inf	AT5G15290	Uncharacterised protein family
Gh_A12G1680	-3.9522	AT4G20240	cytochrome P450, family 71, subfamily A, polypeptide 27
Gh_A12G1681	-2.4263	AT3G26310	cytochrome P450, family 71, subfamily B, polypeptide 35
Gh_A12G1830	2.2242	AT5G45340	cytochrome P450, family 707, subfamily A, polypeptide 3
Gh_A12G2247	-2.1222	AT3G61850	Dof-type zinc finger DNA-binding family protein
Gh_A12G2286	-2.5953	AT1G64065	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Gh_A12G2377	3.1624	AT5G51790	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_A12G2397	-2.3417	AT4G12300	cytochrome P450, family 706, subfamily A, polypeptide 4
Gh_A12G2445	3.3093	AT2G40540	potassium transporter 2
Gh_A12G2449	3.5709	AT5G37490	ARM repeat superfamily protein
Gh_A12G2619	-2.5065	AT5G50760	SAUR-like auxin-responsive protein family
Gh_A12G2643	2.5621	AT1G18870	isochorismate synthase 2
Gh_A13G0175	-3.134	AT5G49690	UDP-Glycosyltransferase superfamily protein
Gh_A13G0183	-3.0315	AT4G17810	C2H2 and C2HC zinc fingers superfamily protein
Gh_A13G0249	-2.7081	AT1G68040	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Gh_A13G0256	2.1589	AT5G37490	ARM repeat superfamily protein
Gh_A13G0411	2.275	AT5G48490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Gh_A13G0713	2.0587	AT3G29320	Glycosyl transferase, family 35
Gh_A13G0783	-2.4303	AT2G26710	Cytochrome P450 superfamily protein
Gh_A13G0844	-2.5439	AT1G06620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_A13G0935	-2.1123	AT1G56600	galactinol synthase 2
Gh_A13G1025	-2.7636	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_A13G1043	2.1719	AT4G05100	myb domain protein 74

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_A13G1388	-2.6434	AT3G60470	Plant protein of unknown function
Gh_A13G1611	-2.0011	AT2G18660	plant natriuretic peptide A
Gh_A13G1634	-3.4495	AT4G32650	potassium channel in Arabidopsis thaliana 3
Gh_A13G1852	-2.2624	AT5G19640	Major facilitator superfamily protein
Gh_A13G2059	2.0697	AT2G40610	expansin A8
Gh_A13G2173	4.7186	AT3G53990	Adenine nucleotide alpha hydrolases-like superfamily protein
Gh_A13G2193	-2.2077	AT5G06060	NAD(P)-binding Rossmann-fold superfamily protein
Gh_A13G2339	-2.1764	AT1G52820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D01G0156	4.2775	AT2G20340	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
Gh_D01G0168	-2.2059	AT4G03510	RING membrane-anchor 1
Gh_D01G0169	Inf	AT1G53025	Ubiquitin-conjugating enzyme family protein
Gh_D01G0180	-2.7109	AT1G03790	Zinc finger C-x8-C-x5-C-x3-H type family protein
Gh_D01G0253	-2.0388	AT1G11300	protein serine/threonine kinases
Gh_D01G0263	-2.2415	AT1G11300	protein serine/threonine kinases
Gh_D01G0280	2.6623	AT3G12900	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D01G0517	2.5652	AT5G54370	Late embryogenesis abundant (LEA) protein-related
Gh_D01G0787	-2.0437	AT5G07280	Leucine-rich repeat transmembrane protein kinase
Gh_D01G1015	-2.0638	AT2G26530	Protein of unknown function
Gh_D01G1714	-2.6442	AT1G68150	WRKY DNA-binding protein 9
Gh_D01G1748	2.3991	AT4G37850	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_D01G1760	-2.2616	AT4G13420	high affinity K ⁺ transporter 5
Gh_D01G1763	-2.1762	AT4G13420	high affinity K ⁺ transporter 5
Gh_D01G1908	-2.4534	AT5G06900	cytochrome P450, family 93, subfamily D, polypeptide 1
Gh_D01G1909	-3.1659	AT2G42250	cytochrome P450, family 712, subfamily A, polypeptide 1
Gh_D01G2145	-2.3031	AT3G06880	Transducin/WD40 repeat-like superfamily protein
Gh_D02G0598	2.2081	AT1G60360	RING/U-box superfamily protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D02G0712	-3.675	AT5G45340	cytochrome P450, family 707, subfamily A, polypeptide 3
Gh_D02G0783	-2.2705	AT1G77330	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D02G1236	-2.5238	AT4G31330	Protein of unknown function
Gh_D02G1405	-2.2174	AT1G31050	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_D02G1664	-2.1441	AT1G10560	plant U-box 18
Gh_D02G1728	Inf	AT1G68510	LOB domain-containing protein 42
Gh_D02G1798	-4.0484	AT1G03840	C2H2 and C2HC zinc fingers superfamily protein
Gh_D02G1848	-2.7304	AT4G35160	O-methyltransferase family protein
Gh_D02G1872	3.6258	AT4G10265	Wound-responsive family protein
Gh_D02G1873	3.3079	AT4G10265	Wound-responsive family protein
Gh_D02G1998	2.0137	AT5G64120	Peroxidase superfamily protein
Gh_D02G2374	-2.3212	AT2G35060	K ⁺ uptake permease 11
Gh_D02G2446	-2.3909	AT1G30330	auxin response factor 6
Gh_D03G0206	-2.0009	AT4G31500	cytochrome P450, family 83, subfamily B, polypeptide 1
Gh_D03G0239	2.3621	AT2G14900	Gibberellin-regulated family protein
Gh_D03G0747	-2.7352	AT5G53110	RING/U-box superfamily protein
Gh_D03G0754	-2.1619	AT5G08590	SNF1-related protein kinase 2.1
Gh_D03G1207	-2.4473	AT1G07620	GTP-binding protein Obg/CgtA
Gh_D03G1484	-2.3988	AT4G23030	MATE efflux family protein
Gh_D03G1533	4.6961	AT1G62790	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Gh_D03G1568	-2.7336	AT5G47450	tonoplast intrinsic protein 2;3
Gh_D03G1604	-2.4419	AT1G61590	Protein kinase superfamily protein
Gh_D03G1706	-2.2533	AT1G52800	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D03G1794	-2.2656	AT1G52820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D04G0262	2.8011	AT1G28130	Auxin-responsive GH3 family protein
Gh_D04G0470	2.2097	AT5G15130	WRKY DNA-binding protein 72

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D04G0732	-2.3664	AT5G40960	Protein of unknown function
Gh_D04G0816	-2.3263	AT1G11300	protein serine/threonine kinases
Gh_D04G1016	-2.0636	AT3G52970	cytochrome P450, family 76, subfamily G, polypeptide 1
Gh_D04G1303	-2.2477	AT2G01570	GRAS family transcription factor family protein
Gh_D04G1304	-2.8865		Nodulation-signaling pathway 2 protein
Gh_D04G1434	-2.147	AT4G28110	myb domain protein 41
Gh_D04G1494	-2.3841	AT3G43660	Vacuolar iron transporter (VIT) family protein
Gh_D04G1548	-2.7928	AT5G49040	Disease resistance-responsive (dirigent-like protein) family protein
Gh_D04G1853	-3.7419	AT4G10310	high-affinity K ⁺ transporter 1
Gh_D05G0054	-2.2809	AT3G46530	NB-ARC domain-containing disease resistance protein
Gh_D05G0541	-2.0048	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_D05G0858	-2.2028	AT2G28160	FER-like regulator of iron uptake
Gh_D05G0956	-3.2455	AT2G36830	gamma tonoplast intrinsic protein
Gh_D05G1022	-2.1879	AT2G38300	myb-like HTH transcriptional regulator family protein
Gh_D05G1036	-2.2869	AT3G51680	NAD(P)-binding Rossmann-fold superfamily protein
Gh_D05G1137	2.5328	AT1G80840	WRKY DNA-binding protein 40
Gh_D05G1582	2.8212	AT4G28240	Wound-responsive family protein
Gh_D05G1642	5.4778	AT4G22030	F-box family protein with a domain of unknown function
Gh_D05G1754	2.6457	AT1G20190	expansin 11
Gh_D05G1780	-2.4309	AT1G75750	GAST1 protein homolog 1
Gh_D05G1896	-2.0727	AT4G31940	cytochrome P450, family 82, subfamily C, polypeptide 4
Gh_D05G1897	-3.6758	AT4G31940	cytochrome P450, family 82, subfamily C, polypeptide 4
Gh_D05G1973	2.0238	AT4G34150	Calcium-dependent lipid-binding (CaLB domain) family protein
Gh_D05G1997	3.9908	AT2G14900	Gibberellin-regulated family protein
Gh_D05G2218	-4.1551	AT4G08250	GRAS family transcription factor
Gh_D05G2433	Inf	AT1G20190	expansin 11

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D05G2505	2.4411	AT5G59845	Gibberellin-regulated family protein
Gh_D05G2912	-2.2868	AT2G38080	Laccase/Diphenol oxidase family protein
Gh_D05G2949	-2.379	AT1G18650	plasmodesmata callose-binding protein 3
Gh_D05G3827	-2.0162	AT1G29280	WRKY DNA-binding protein 65
Gh_D06G0152	-3.5577	AT3G50330	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_D06G0177	2.0503	AT4G34150	Calcium-dependent lipid-binding (CaLB domain) family protein
Gh_D06G0183	-3.344	AT3G53010	Domain of unknown function
Gh_D06G0388	-3.2249	AT4G08250	GRAS family transcription factor
Gh_D06G0637	-2.3914	AT4G28890	RING/U-box superfamily protein
Gh_D06G0842	-2.2531	AT2G26290	root-specific kinase 1
Gh_D06G1673	-2.2825	AT4G03965	RING/U-box superfamily protein
Gh_D06G2051	-2.1872	AT1G17620	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Gh_D06G2071	-2.0807	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_D06G2077	-2.7209	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_D06G2078	-2.0549	AT5G48930	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Gh_D06G2222	-2.8934	AT1G12030	Protein of unknown function
Gh_D07G0079	-2.1237	AT2G20030	RING/U-box superfamily protein
Gh_D07G0265	-2.13	AT4G30960	SOS3-interacting protein 3
Gh_D07G0385	-2.2939	AT1G15550	gibberellin 3-oxidase 1
Gh_D07G0404	-3.3623	AT5G51800	Protein kinase superfamily protein
Gh_D07G0781	-3.3427	AT3G30210	myb domain protein 121
Gh_D07G1078	-2.0493	AT1G08320	bZIP transcription factor family protein
Gh_D07G1169	2.7072	AT5G60520	Late embryogenesis abundant (LEA) protein-related
Gh_D07G1527	2.2872	AT5G44700	Leucine-rich repeat transmembrane protein kinase
Gh_D07G1641	3.0099	AT5G03795	Exostosin family protein
Gh_D07G1705	-2.41	AT1G66140	zinc finger protein 4

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D07G1809	2.4975	AT5G15780	Pollen Ole e 1 allergen and extensin family protein
Gh_D07G1898	-2.4363	AT3G14630	cytochrome P450, family 72, subfamily A, polypeptide 9
Gh_D07G1902	-2.9714	AT5G14180	Myzus persicae-induced lipase 1
Gh_D07G1920	-8.0056	AT3G07810	RNA-binding (RRM/RBD/RNP motifs) family protein
Gh_D07G1930	4.2189	AT3G63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
Gh_D07G1947	-2.207	AT4G39950	cytochrome P450, family 79, subfamily B, polypeptide 2
Gh_D07G2208	-2.2829	AT2G36910	ATP binding cassette subfamily B1
Gh_D07G2239	-2.0525	AT1G23740	Oxidoreductase, zinc-binding dehydrogenase family protein
Gh_D07G2291	-3.3757	AT5G14340	myb domain protein 40
Gh_D07G2498	-3.0089	AT3G23240	ethylene response factor 1
Gh_D08G0007	-2.3199	AT2G37170	plasma membrane intrinsic protein 2
Gh_D08G0103	-2.0352	AT2G27370	Uncharacterised protein family
Gh_D08G0238	-2.2791	AT2G18960	H(+)-ATPase 1
Gh_D08G0442	4.0783	AT1G05260	Peroxidase superfamily protein
Gh_D08G0443	Inf	AT1G05260	Peroxidase superfamily protein
Gh_D08G0451	-2.1501	AT1G02400	gibberellin 2-oxidase 6
Gh_D08G0487	-2.0187	AT5G18840	Major facilitator superfamily protein
Gh_D08G0629	2.3523	AT2G44840	ethylene-responsive element binding factor 13
Gh_D08G0650	-3.1873	AT2G42440	Lateral organ boundaries (LOB) domain family protein
Gh_D08G0925	-2.3182	AT1G11300	protein serine/threonine kinases
Gh_D08G1222	-2.6261	AT5G53110	RING/U-box superfamily protein
Gh_D08G1534	4.1949	AT2G44840	ethylene-responsive element binding factor 13
Gh_D08G1535	4.1623	AT2G44840	ethylene-responsive element binding factor 13
Gh_D08G1696	-2.3895	AT4G17785	myb domain protein 39
Gh_D08G1697	-2.3251	AT5G16770	myb domain protein 9
Gh_D08G1799	5.4095	AT4G17500	ethylene responsive element binding factor 1

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D08G1879	-3.115	AT4G12110	sterol-4alpha-methyl oxidase 1-1
Gh_D08G1950	-2.142	AT1G63440	heavy metal atpase 5
Gh_D08G2042	-2.2891	AT5G24530	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D08G2048	-2.6246	AT2G31160	Protein of unknown function
Gh_D08G2330	3.0716	AT5G17820	Peroxidase superfamily protein
Gh_D08G2656	-2.4765	AT2G42610	Protein of unknown function
Gh_D09G0151	-3.5098	AT1G26870	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
Gh_D09G0567	-2.7184	AT3G54700	phosphate transporter 1;7
Gh_D09G0856	-2.9325	AT5G22890	C2H2 and C2HC zinc fingers superfamily protein
Gh_D09G0859	-2.4953	AT2G28160	FER-like regulator of iron uptake
Gh_D09G0928	-2.5101	AT1G08320	bZIP transcription factor family protein
Gh_D09G1019	2.0635	AT5G60520	Late embryogenesis abundant (LEA) protein-related
Gh_D09G1261	2.3139	AT2G35930	plant U-box 23
Gh_D09G1579	-2.3294	AT5G66770	GRAS family transcription factor
Gh_D09G1631	2.3016	AT3G17730	NAC domain containing protein 57
Gh_D09G1714	2.7474	AT5G52400	cytochrome P450, family 715, subfamily A, polypeptide 1
Gh_D09G1743	-3.2574	AT5G59220	highly ABA-induced PP2C gene 1
Gh_D09G1969	-2.1035	AT5G07990	Cytochrome P450 superfamily protein
Gh_D09G1999	-2.2571	AT1G06000	UDP-Glycosyltransferase superfamily protein
Gh_D09G2000	-3.1718	AT1G06000	UDP-Glycosyltransferase superfamily protein
Gh_D10G0061	-2.6617	AT1G30650	WRKY DNA-binding protein 14
Gh_D10G0086	-2.1599	AT5G47560	tonoplast dicarboxylate transporter
Gh_D10G0452	-2.0576	AT1G31320	LOB domain-containing protein 4
Gh_D10G0689	-2.5424	AT1G52820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D10G1381	-3.2589	AT2G15080	receptor like protein 19
Gh_D10G1462	-2.5221	AT1G11300	protein serine/threonine kinases

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D10G1706	-2.6234	AT3G16660	Pollen Ole e 1 allergen and extensin family protein
Gh_D10G1784	2.4402	AT3G17070	Peroxidase family protein
Gh_D10G1865	3.1968	AT5G05260	cytochrome p450 79a2
Gh_D10G2000	-3.6013	AT4G31500	cytochrome P450, family 83, subfamily B, polypeptide 1
Gh_D10G2050	-2.1062	AT5G24910	cytochrome P450, family 714, subfamily A, polypeptide 1
Gh_D10G2235	-3.2976	AT1G74170	receptor like protein 13
Gh_D10G2258	-4.0747	AT4G31500	cytochrome P450, family 83, subfamily B, polypeptide 1
Gh_D10G2359	-2.4141	AT4G00430	plasma membrane intrinsic protein 1;4
Gh_D10G2360	-2.1178	AT4G00430	plasma membrane intrinsic protein 1;4
Gh_D10G2380	-3.973	AT4G20140	Leucine-rich repeat transmembrane protein kinase
Gh_D11G0124	-2.0777	AT5G24030	SLAC1 homologue 3
Gh_D11G0275	2.8058	AT3G10600	cationic amino acid transporter 7
Gh_D11G0316	-2.0956	AT2G47140	NAD(P)-binding Rossmann-fold superfamily protein
Gh_D11G0439	-3.1213	AT3G02880	Leucine-rich repeat protein kinase family protein
Gh_D11G0479	-2.5899	AT2G33580	Protein kinase superfamily protein
Gh_D11G0495	-2.2205	AT4G37050	PATATIN-like protein 4
Gh_D11G0704	-2.6645	AT5G63090	Lateral organ boundaries (LOB) domain family protein
Gh_D11G0743	-2.001	AT5G61430	NAC domain containing protein 100
Gh_D11G0746	-2.2832	AT3G01090	SNF1 kinase homolog 10
Gh_D11G0802	2.1581	AT2G44840	ethylene-responsive element binding factor 13
Gh_D11G0871	-2.3442	AT2G45510	cytochrome P450, family 704, subfamily A, polypeptide 2
Gh_D11G1188	-2.1831	AT1G02810	Plant invertase/pectin methylesterase inhibitor superfamily
Gh_D11G1339	-2.9414	AT4G17810	C2H2 and C2HC zinc fingers superfamily protein
Gh_D11G1353	-2.555	AT4G10500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D11G1542	-2.4411	AT3G07870	F-box and associated interaction domains-containing protein
Gh_D11G1989	-2.3114	AT2G14960	Auxin-responsive GH3 family protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D11G2073	-2.3082	AT4G37850	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_D11G2781	-2.2865	AT5G02070	Protein kinase family protein
Gh_D11G2926	4.956	AT4G38700	Disease resistance-responsive (dirigent-like protein) family protein
Gh_D11G2943	-2.1175	AT1G28130	Auxin-responsive GH3 family protein
Gh_D11G3081	-2.2958	AT3G56970	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Gh_D11G3107	-2.0258	AT4G27220	NB-ARC domain-containing disease resistance protein
Gh_D11G3156	-2.052	AT3G14470	NB-ARC domain-containing disease resistance protein
Gh_D11G3200	-2.7544	AT3G14470	NB-ARC domain-containing disease resistance protein
Gh_D11G3217	-2.1908	AT1G52340	NAD(P)-binding Rossmann-fold superfamily protein
Gh_D11G3255	-5.2797	AT3G52970	cytochrome P450, family 76, subfamily G, polypeptide 1
Gh_D11G3268	-2.3296	AT2G36830	gamma tonoplast intrinsic protein
Gh_D11G3390	-2.3306	AT3G14470	NB-ARC domain-containing disease resistance protein
Gh_D11G3457	-3.208	AT5G67150	HXXXD-type acyl-transferase family protein
Gh_D12G0121	-2.0056	AT2G17290	Calcium-dependent protein kinase family protein
Gh_D12G0234	-2.8666	AT2G23610	methyl esterase 3
Gh_D12G0346	2.8462	AT1G20450	Dehydrin family protein
Gh_D12G0567	2.5974	AT1G75750	GAST1 protein homolog 1
Gh_D12G0671	Inf	AT5G42940	RING/U-box superfamily protein
Gh_D12G0699	2.0894	AT4G37530	Peroxidase superfamily protein
Gh_D12G0899	-2.071	AT2G21990	Protein of unknown function
Gh_D12G0918	2.9732	AT5G10130	Pollen Ole e 1 allergen and extensin family protein
Gh_D12G0958	3.2389	AT2G44840	ethylene-responsive element binding factor 13
Gh_D12G0959	3.2313	AT2G44840	ethylene-responsive element binding factor 13
Gh_D12G1152	-3.1672	AT2G46680	homeobox 7
Gh_D12G1632	-2.2357	AT5G15290	Uncharacterised protein family
Gh_D12G1793	-2.2656	AT3G02100	UDP-Glycosyltransferase superfamily protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Gh_D12G1840	-2.5758	AT3G26310	cytochrome P450, family 71, subfamily B, polypeptide 35
Gh_D12G2243	-2.0659	AT4G11655	Uncharacterised protein family
Gh_D12G2370	-2.0279	AT1G33030	O-methyltransferase family protein
Gh_D12G2561	-2.0757	AT3G24020	Disease resistance-responsive (dirigent-like protein) family protein
Gh_D12G2576	4.336	AT5G37490	ARM repeat superfamily protein
Gh_D12G2605	2.4121	AT5G14740	carbonic anhydrase 2
Gh_D13G0266	-2.403	AT1G68040	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Gh_D13G0791	-2.9487		rRNA N-glycosidase (Fragment)
Gh_D13G0883	-3.7541	AT3G51550	Malectin/receptor-like protein kinase family protein
Gh_D13G0962	-3.1692	AT2G21210	SAUR-like auxin-responsive protein family
Gh_D13G0971	-2.1694	AT5G06060	NAD(P)-binding Rossmann-fold superfamily protein
Gh_D13G0980	2.0244	AT3G53990	Adenine nucleotide alpha hydrolases-like superfamily protein
Gh_D13G1271	-2.2182	AT1G71930	vascular related NAC-domain protein 7
Gh_D13G1294	3.1484	AT4G21440	MYB-like 102
Gh_D13G1655	-3.4943	AT3G13610	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_D13G1900	-2.2548	AT1G09380	nodulin MtN21 /EamA-like transporter family protein
Gh_D13G2317	-2.0965	AT5G22220	E2F transcription factor 1
Gh_D13G2460	2.0773	AT2G40610	expansin A8
Gh_D13G2465	-2.0002	AT1G52820	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Gh_Sca005458G01	4.0805	AT3G48270	cytochrome P450, family 71, subfamily A, polypeptide 26
Gh_Sca005510G01	-2.7631	AT2G26710	Cytochrome P450 superfamily protein
Gh_Sca007264G01	-2.6294	AT1G09155	phloem protein 2-B15
Gh_Sca010862G01	-2.3571	AT4G21700	Protein of unknown function
Novel00107	-2.3809	--	hypothetical protein F383_20901
Novel00838	-3.1975	--	PREDICTED: cytochrome P450 CYP749A22-like
Novel00877	-2.1451	--	Cytochrome P450 protein

Gene ID	log2 (GaJAZ1/WT)	Arabidopsis ID	Annotation (acc. To TAIR)
Novel01012	-3.6931	--	PREDICTED: putative receptor-like protein kinase At4g00960 isoform X2
Novel01626	5.8859	--	PREDICTED: auxin-responsive protein IAA29
Novel01663	-2.1177	--	auxin response factor, partial
Novel02264	-2.8278	--	putative WRKY transcription factor 16 -like protein
Novel02986	4.499	--	Homeobox prospero
Novel03310	-2.8644	--	PREDICTED: LRR receptor-like serine/threonine-protein kinase EFR
Novel03492	-2.4159	--	PREDICTED: cytochrome P450 CYP749A22-like
Novel03493	-2.7515	--	PREDICTED: cytochrome P450 CYP749A22-like
Novel03664	6.7947	--	PREDICTED: F-box/kelch-repeat protein At5g60570-like isoform X1
Novel03971	-2.316	--	Cytochrome P450 protein
Novel05745	-2.1509	--	PREDICTED: cytochrome P450 CYP749A22-like
Novel05750	-5.8342	--	PREDICTED: auxin-induced protein 15A-like
Novel06076	-2.8456	--	Gibberellin 20 oxidase 1 -like protein
Novel06255	-3.1009	--	PREDICTED: putative RING-H2 finger protein ATL21B
Novel06283	-3.3245	--	NADH-ubiquinone oxidoreductase chain 4L
Novel06462	-2.8766	--	PREDICTED: receptor-like protein 12