

Supplementary Table S1. *jaz* double and triple mutant lines screened in *F. oxysporum* disease assays.

Insertion lines used for double and triple mutants are *jaz1* (SALK_011957), *jaz2* (SALK_025279), *jaz3* (SALK_139337), *jaz4* (SALK_026633), *jaz5* (SALK_053775), *jaz6*

<i>jaz</i> double mutants	<i>jaz</i> triple mutants
<i>jaz2/7</i>	<i>jaz2/5/10</i>
<i>jaz5/7</i>	<i>jaz3/5/10</i>
<i>jaz6/7</i>	<i>jaz5/6/10</i>
<i>jaz3/10</i>	<i>jaz5/7/10</i>
<i>jaz5/10</i>	
<i>jaz7/10</i>	
<i>jaz1/3</i>	
<i>jaz2/5</i>	
<i>jaz3/5</i>	

(SAIL_1156_C06), jaz7 (WiscDsLox7H11), jaz10 (SAIL_92_D08).

Supplementary Table S2. Primers used for the generation of transgenic plants and Y2-H and Co-IP constructs.

Primer ID	Primer sequence (5'-3')
JAZ7- <i>HindIII</i> -F	TGACAAGCTTAACAATGATCATCATCAAA
JAZ7- <i>EcoRI</i> -R	ATAGGAATTCCTATCGGTAACGGTGGTA
JAZ7-EAR- <i>HIII</i> - <i>Sma</i> -F	CAAAAAGCTTGAGCCCGGACAAAATGCGACTTGGAACCTTCGCC
JAZ7_EAR_STOP- <i>EcoRI</i> -R	CAGAGAATTCTCAAGAAGTAAGAAGGCGAAGTTCCAAGTCGCAT
CUC1- <i>HIII</i> -F	TTCTAAGCTTAACAATGGATGTTGATGTGTTTAACGGTTG
CUC1-STOPdel- <i>Sma</i> -R	CATGGCCCGGGGAGAGTAAACGGCCACACTCACGGCGG
TPL-F	AAAAAGCAGGCTTCACCATGTCTTCTTAGTAGAGAGCTCG
TPL-R	CAAGAAAGCTGGGTTTCATCTCTGAGGCTGATCAGATGC
JAM1-F	AAAAAGCAGGCTTCACCATGAATATGAGTGATTTAGGTTGG
JAM1-R	CAAGAAAGCTGGGTTTATATATACCAGAGACCTGTG
MYC2-F	AAAAAGCAGGCTTCACCATGACTGATTACCGGCTACAAC
MYC2-R	CAAGAAAGCTGGGTACCGATTTTTGAAATCAAATTGC
MYC3-F	AAAAAGCAGGCTTCACCATGAACGGCACAACATCATCAATC
MYC3-R	CAAGAAAGCTGGGTATAGTTTTCTCCGACTTTTCGTC
MYC4-F	AAAAAGCAGGCTTCACCATGTCTCCGACGAATGTTCAAG
MYC4-R	CAAGAAAGCTGGGTTGGACATTCTCCAACCTTCTCC
JAZ7-F	AAAAAGCAGGCTTCACCATGATCATCATCAAAAAGCTG
JAZ7-R	CAAGAAAGCTGGGTCTATCGGTAACGGTGGTA
JAZ7-R2	CAAGAAAGCTGGGTCTCGGTAACGGTGGTAAGG
JAZ8-F	AAAAAGCAGGCTTCACCATGAAGCTACAGCAAATTGTG
JAZ8-R	CAAGAAAGCTGGGTTTATCGTCGTGAATGGTAC
JAZ8-R2	CAAGAAAGCTGGGTCTCGTCGTGAATGGTACGG
JAZ5-F	AAAAAGCAGGCTTCACCATGTCTCGTCGAGCAATGAAAATGC
JAZ5-R	CAAGAAAGCTGGGTCTATAGCCTTAGATCGAGATCT
JAZ5-R2	CAAGAAAGCTGGGTCTAGCCTTAGATCGAGATCT
pAttB1	GGGGACAAGTTTGTACAAAAAAGCAGGCT
pAttB2	GGGGACCACTTTGTACAAGAAAGCTGGGT

Supplementary Table S3. Primers used for qRT-PCR.

Primer ID	Gene Locus (AGI)	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
<i>ACT-8</i>	At1g49240		GAGGATAGCATGTGGAAGTCTGAGAA
<i>ACT-2</i>	At3g18780		GATGGCATGGAGGAAGAGAGAAAAC
<i>ACT-7</i>	At5g09810		GAGGAAGAGCATTCCCCTCGTA
<i>ACTuni</i>		AGTGGTCGTACAACCGGTATTGT	
<i>JAZ1</i>	At1g19180	CGGTAGCTTTGGAGATCTGAG	TCACAAGGGAATAAACTCATGG
<i>JAZ2</i>	At1g74950	CCTCTGGGACCAAAGAAGAT	CCATAACTCGACCACCGTAG
<i>JAZ3</i>	At3g17860	TTTATGATTCAACCCGCAAA	CGACATGGAAACTGCGTTAG
<i>JAZ4</i>	At1g48500	CAATCTTTTATGCCGTTCA	CGGTTTAGCATGAGGTCCAT
<i>JAZ5</i>	At1g17380	CACGTAGAGCTTCCCTCCAT	TGGGAGGATAACGATGATGA
<i>JAZ6</i>	At1g72450	GGAACGCATTGCAAGAAGA	GGAAGATGACTACCGTGTG
<i>JAZ7</i>	At2g34600	GACTTGGAAGTTCGCCTTCTT	TCTGAGATTCTTGCTTTGGTTG
<i>JAZ7 exon1 specific</i>	At2g34600	CATCATCAAAAAGTTCGACAA	GAAGTAAGAAGGCGAAGTTCCA
<i>JAZ7 exon2 specific</i>	At2g34600	CAACAATCCCAACAATTTCG	GAAGTTGCTTGAATCCGAAGA
<i>JAZ8</i>	At1g30135	CAGCAAAATTGTGACTTGAA	TGGATTTCCAGAACTGGTTG
<i>JAZ9</i>	At1g70700	CACAATCTTTTATGGCGAAC	TCCAGTTTACCTTTCAAACC
<i>JAZ10</i>	At5g13220	ATCTCGTTTCGGTCCGTCTA	ACAGTTCGAAACGAGTTC
<i>JAZ11</i>	At3g43440	TTTGGTGGGAGTTTATAGCGTA	TTGTCTCAGTGGCTTTAGCTG
<i>JAZ12</i>	At5g20900	GCTGCACAGCCATTTCTA	CTCGAGGAATCGTTGAAGC
<i>MYC2</i>	At1g32640	TCATACGACGGTTGCCAGAA	AGCAACGTTTACAAGCTTTGATTG
<i>ERF1</i>	At3g23240	TCAGAAGACCCCAAAAGCTCCTCA	TTGATCACCGCTCCGTGAAGTTAG
<i>LOX3</i>	At1G17420	TAACGATGCTGGTGTCCATC	AATTGCCTGTGTGCAGCTAA
<i>PDF1.2</i>	At5g44420	TTTGCTGCTTTTCGACGCAC	CGCAAACCCCTGACCATG
<i>Thi2.1</i>	At1g72260	CTCAGCTGATGCTACCAATGAGC	GCTCCATTACAATTTCACTTGC
<i>PR3-F</i>	At3g12500	ATCAGCGCTGCAAAGTCCTTC	GTGCTGTAGCCATCCACCTG
<i>VSP2</i>	At5g24770	CCTAAAGAACGACACCGTCA	TCGGTCTTCTCTGTTCCGTA
<i>SAG12</i>	At5g45890	AAAGGCGAAGACGCTACTTG	TCATCAGTGCTTGCTCATCA
<i>GSTF6</i>	At1g02930	GTCGACTTTGAATTCGTTTCATG	CCTTGCCAGTTGAGAGAAGG
<i>DHAR1</i>	At1g19570	CTCTGACAAAACCCAGTGGTTC	CAACGATGACGTCGGAATCA
<i>PR1</i>	AT2G14610	AAGAGGCAACTGCAGACTCA	TCTCGCTAACCCACATGTTC
<i>PR2</i>	At3g57260	AGCTTAGCCTCACCACCAAT	CCCGTAGCATACTCCGATTT
<i>NATA1</i>	AT2G39030	TTCTTCCCGAACTACCCAAG	GCGGTACAGTAGCAGTTTCC

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Supplementary Table S5. Genes differentially expressed ≥ 2 -fold in the *jaz7-1D* line relative to wild-type.

AGI	TAIR description	<i>jaz7-1D</i> / WT	P-value
AT2G39030	N-acetyltransferase Activity1 (NATA1)	9.53	8.10E-05
AT1G72260	thionin (THI2.1)	7.52	1.50E-04
AT3G49620	2-oxoacid-dependent oxidase (DIN11)	6.18	1.50E-03
AT2G18050	histone H1-3 (HIS1-3)	6.02	2.70E-05
AT1G26380	FAD-binding domain-containing protein	4.14	1.80E-03
AT3G23550	MATE efflux	4.03	6.00E-04
AT5G48540	33 kDa secretory protein-related	3.79	3.00E-05
AT5G61160	transferase family protein similar to anthocyanin 5-aromatic acyltransferase	3.62	3.20E-02
AT2G38860	protease1 (pfpl)-like protein (YLS5)	3.52	3.80E-05
AT1G21120	O-methyltransferase	3.46	1.00E-03
AT2G44480	glycosyl hydrolase family 1 protein	3.45	6.20E-05
AT5G24110	WRKY family transcription factor	3.4	8.90E-03
AT3G26830	cytochrome P450 (CYP71B15), PHYTOALEXIN DEFICIENT 3 (PAD3)	3.24	1.00E-02
AT1G05310	pectinesterase	3.22	3.00E-04
AT2G37710	lectin protein kinase	3.15	3.10E-04
AT2G37430	zinc finger (C2H2 type) family protein (ZAT11)	3.14	3.50E-02
AT2G46430	cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC3)	3.08	2.90E-04
AT2G46450	cyclic nucleotide-regulated ion channel, putative (CNGC12)	3.08	3.40E-05
AT2G39210	nodulin family protein	3.05	1.80E-05
AT2G39420	esterase/lipase/thioesterase	3.02	5.80E-04
AT1G21100	O-methyltransferase	2.93	7.20E-04
AT3G16530	legume lectin	2.88	3.00E-04
AT2G35980	harpin-induced family protein (YLS9) / HIN1	2.84	9.80E-03
AT2G47130	short-chain dehydrogenase/reductase (SDR)	2.82	7.90E-05
AT2G35930	U-box domain-containing protein similar to immediate-early fungal elicitor protein	2.8	1.10E-02
AT2G36970	UDP-glucuronosyl/UDP-glucosyl transferase	2.75	8.20E-05
AT2G46650	cytochrome b5	2.64	7.00E-03
AT1G66690	S-adenosyl-L-methionine:carboxyl methyltransferase	2.64	2.40E-02
AT4G16260	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase	2.63	3.40E-02
AT2G39660	protein kinase	2.57	9.40E-04

AT2G39200	seven transmembrane MLO family protein / MLO-like protein 12 (MLO12)	2.56	1.60E-04
AT1G21120	O-methyltransferase	2.56	3.90E-03
AT2G37950	zinc finger (C3HC4-type RING finger)	2.51	4.60E-04
AT2G40460	proton-dependent oligopeptide transport (POT) family protein	2.5	9.70E-05
AT2G37040	phenylalanine ammonia-lyase 1 (PAL1)	2.48	4.20E-04
AT5G57220	cytochrome P450	2.47	1.80E-02
AT1G79680	wall-associated kinase	2.47	2.20E-02
AT2G29720	monooxygenase	2.47	1.00E-03
AT2G37940	expressed protein	2.47	6.90E-04
AT2G41180	sigA-binding protein-related	2.44	2.80E-03
AT2G40150	expressed protein	2.43	9.80E-05
AT1G26420	FAD-binding domain-containing protein	2.43	1.60E-04
AT2G40110	yippee family protein	2.4	2.30E-03
AT2G47490	NAD ⁺ TRANSPORTER 1 (NDT1)	2.39	7.30E-06
AT2G38640	expressed protein contains	2.38	6.50E-04
AT2G38020	vacuoleless1 (VCL1), mangled (MAN)	2.37	6.50E-05
AT5G24420	glucosamine/galactosamine-6-phosphate isomerase	2.37	2.80E-02
AT4G19430	expressed protein	2.37	2.20E-02
AT3G05360	disease resistance family protein / LRR family protein	2.36	2.10E-02
AT2G46620	AAA-type ATPase	2.36	5.40E-04
AT2G38290	ammonium transporter 2 (AMT2)	2.36	1.80E-05
AT1G67980	caffeoyl-CoA 3-O-methyltransferase	2.33	3.50E-02
AT2G41250	haloacid dehalogenase-like hydrolase	2.3	5.40E-04
AT4G19370	hypothetical protein	2.29	1.30E-02
AT2G43200	dehydration-responsive family protein	2.28	3.80E-04
AT2G35060	potassium transporter	2.27	1.70E-05
AT4G21390	S-locus lectin protein kinase	2.27	5.40E-03
AT1G80130	expressed protein	2.27	7.20E-03
AT3G18710	U-box domain-containing protein similar to immediate-early fungal elicitor protein	2.24	4.40E-02
AT2G35710	glycogenin glucosyltransferase (glycogenin)	2.24	4.70E-02
AT2G38790	expressed protein	2.22	8.90E-03
AT2G46690	SMALL AUXIN UPREGULATED RNA 32 (SAUR32)	2.21	7.50E-03
AT2G43590	chitinase	2.21	1.50E-04

AT2G40010	60S acidic ribosomal protein P0 (RPP0A)	2.21	2.70E-05
AT2G43520	trypsin inhibitor	2.19	4.90E-02
AT2G45920	U-box domain-containing protein	2.18	2.20E-05
AT1G02360	chitinase	2.18	4.10E-03
AT2G36840	ACT domain-containing protein	2.18	1.80E-05
AT2G45280	DNA repair family protein	2.17	4.50E-05
AT2G41870	remorin family protein	2.15	1.20E-05
AT2G40270	protein kinase	2.15	4.00E-03
AT2G42690	lipase	2.15	4.20E-05
AT2G39690	expressed protein	2.14	1.20E-04
AT2G39480	ABC transporter family protein related to multi drug resistance proteins and P-glycoproteins	2.14	5.10E-04
AT2G38410	VHS domain-containing protein	2.13	5.70E-05
AT2G41890	curculin-like (mannose-binding)	2.13	2.70E-04
AT2G26440	pectinesterase	2.12	2.30E-03
AT3G09410	pectinacetylerase	2.12	1.10E-03
AT2G41700	ABC transporter family protein related to multi drug resistance proteins and P-glycoproteins	2.12	3.10E-04
AT2G41980	seven in absentia (SINA) family protein	2.12	2.00E-04
AT2G39870	expressed protein	2.1	7.10E-05
AT2G36400	expressed protein	2.1	7.10E-05
AT2G36470	expressed protein	2.09	3.20E-05
AT2G43800	formin homology 2 domain-containing protein	2.09	1.10E-04
AT4G39950	cytochrome P450 (CYP79B2)	2.08	7.60E-03
AT2G44790	uclacyanin II	2.07	3.90E-02
AT1G51280	disease resistance protein (TIR class)	2.07	2.90E-04
AT2G39360	protein kinase	2.07	3.60E-03
AT2G46530	transcriptional factor B3 family protein / auxin-responsive factor 11 (ARF11)	2.07	4.30E-05
AT2G42760	expressed protein	2.07	1.80E-02
AT1G74590	glutathione S-transferase	2.06	6.70E-03
AT2G38050	3-oxo-5-alpha-steroid 4-dehydrogenase, de-etiolated 2 (DET2), dwarf6 (DWF6)	2.06	5.10E-04
AT2G36220	expressed protein	2.06	3.20E-03
AT2G21890	CINNAMYL ALCOHOL DEHYDROGENASE HOMOLOG 3 (CAD3)	2.05	2.20E-05
AT2G46720	fatty acid elongase 3-ketoacyl-CoA synthase, 3-KETOACYL-COA SYNTHASE 13 (KCS13)	2.05	2.60E-05
AT2G37970	SOUL heme-binding family protein, SOUL-1	2.05	8.30E-03

AT2G41640	expressed protein	2.05	3.00E-02
AT2G44660	ALG6, ALG8 glycosyltransferase	2.03	5.40E-04
AT3G04720	hevein-like protein (HEL), pathogenesis-related 4 (PR4)	2.02	3.10E-03
AT2G34810	FAD-binding domain-containing protein	2.02	2.80E-02
AT2G38280	AMP deaminase, putative / myoadenylate deaminase	2.02	1.10E-03
AT2G37240	expressed protein	2.02	3.70E-04
AT2G43130	Ras-related protein (ARA-4) / small GTP-binding protein	2.01	6.80E-04
AT2G34640	expressed protein	2.01	2.60E-05
AT2G38870	protease inhibitor	2.01	6.50E-03
AT3G22060	receptor protein kinase	2.01	1.30E-03
AT2G41990	expressed protein	2.01	5.90E-04
AT3G12910	expressed protein	2.01	1.10E-03
AT2G34620	mitochondrial transcription termination factor-related	2.01	6.20E-03
AT2G45010	expressed protein	2	6.20E-05
AT1G63530	hypothetical protein	2	2.30E-03
AT2G38740	haloacid dehalogenase-like hydrolase	2	7.50E-04
AT2G46420	expressed protein	2	4.20E-04

Supplementary Table S6. Genes differentially expressed ≤ 2 -fold in the *jaz7-1D* line relative to wild-type.

AGI	TAIR description	<i>jaz7-1D</i> / WT	P-value
AT4G34135	UDP-glucuronosyl/UDP-glucosyl transferase	0.24	1.90E-03
AT2G29490	glutathione S-transferase	0.27	9.60E-03
AT4G32770	tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1)	0.28	7.30E-06
AT1G05680	UDP-glucuronosyl/UDP-glucosyl transferase	0.34	2.40E-02
AT5G65080	MADS-box family protein, mads affecting flowering 5 (MAF5)	0.37	1.10E-04
AT1G62770	invertase/pectin methylesterase inhibitor	0.38	7.90E-05
AT1G05560	UDP-glucose transferase (UGT75B2)	0.38	4.00E-03
AT1G17170	glutathione S-transferase	0.41	1.60E-03
AT5G16990	NADP-dependent oxidoreductase	0.41	4.40E-03
AT1G24575	expressed protein	0.42	8.80E-04
AT4G37220	stress-responsive protein, similar to cold acclimation WCOR413-like protein	0.42	2.30E-03
AT3G29810	phytochelatin synthetase family protein / COBRA cell expansion protein COBL2	0.43	2.00E-05
AT5G62360	invertase/pectin methylesterase inhibitor	0.43	9.00E-05
AT5G09220	amino acid permease 2 (AAP2)	0.43	6.10E-05
AT1G09500	cinnamyl-alcohol dehydrogenase	0.44	2.10E-02
AT1G09240	nicotianamine synthase	0.46	1.40E-02
AT4G12470	protease inhibitor/seed storage/lipid transfer protein (LTP)	0.46	1.50E-03
AT4G14130	xyloglucan:xyloglucosyl transferase	0.47	2.60E-02
AT3G28310	expressed protein	0.47	3.60E-03
AT1G27590	expressed protein	0.47	2.90E-05
AT1G53100	glycosyltransferase family 14	0.49	3.20E-04
AT4G30140	GDSL-motif lipase/hydrolase	0.49	1.30E-02
AT1G34760	14-3-3 protein GF14 omicron (GRF11)	0.5	1.60E-04
AT2G29420	glutathione S-transferase	0.5	3.10E-02
AT1G64950	cytochrome P450 (CYP89A)	0.5	2.90E-02

2025-10-10 10:10:10 [INFO] Application started successfully. Version 1.0.0

2025-10-10 10:10:15 [INFO] User 'admin' logged in from 192.168.1.100

2025-10-10 10:10:20 [INFO] Request received for /api/users/1

2025-10-10 10:10:25 [INFO] Database connection established

2025-10-10 10:10:30 [INFO] Cache hit for key 'user:1'

2025-10-10 10:10:35 [INFO] Response sent to client

2025-10-10 10:10:40 [INFO] Session expired for user 'admin'

2025-10-10 10:10:45 [INFO] Error: Database connection failed

2025-10-10 10:10:50 [INFO] Request received for /api/users/2

2025-10-10 10:10:55 [INFO] Cache miss for key 'user:2'

2025-10-10 10:11:00 [INFO] Database query executed

2025-10-10 10:11:05 [INFO] Response sent to client

2025-10-10 10:11:10 [INFO] Application shutdown initiated

2025-10-10 10:11:15 [INFO] All resources released

2025-10-10 10:11:20 [INFO] Application stopped successfully

2025-10-10 10:10:10 [INFO] Application started successfully. Version 1.0.0

2025-10-10 10:10:15 [INFO] User 'admin' logged in from 192.168.1.100

2025-10-10 10:10:20 [INFO] Request received for /api/users/1

2025-10-10 10:10:25 [INFO] Database connection established

2025-10-10 10:10:30 [INFO] Cache hit for key 'user:1'

2025-10-10 10:10:35 [INFO] Response sent to client

2025-10-10 10:10:40 [INFO] Session expired for user 'admin'

2025-10-10 10:10:45 [INFO] Error: Database connection failed

2025-10-10 10:10:50 [INFO] Request received for /api/users/2

2025-10-10 10:10:55 [INFO] Cache miss for key 'user:2'

2025-10-10 10:11:00 [INFO] Database query executed

2025-10-10 10:11:05 [INFO] Response sent to client

2025-10-10 10:11:10 [INFO] Application shutdown initiated

2025-10-10 10:11:15 [INFO] All resources released

2025-10-10 10:11:20 [INFO] Application stopped successfully

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Supplementary Table S8. Genes differentially expressed ≥ 2 -fold in the *jaz7-1D* line relative to wild-type under MeJA treatment.

AGI	P-value	MeJA		MeJA inducibility		TAIR description
		<i>jaz7-1D</i> / WT	WT MeJA / control	<i>jaz7-1D</i> MeJA / control		
AT2G39030	4.37E-04	5.26	7.36	4.06	N-acetyltransferase (NATA1)	
AT3G26830	1.47E-02	4.87	2.82	4.24	cytochrome P450 (CYP71B15)	
AT2G24210	2.23E-02	3.9	1.56	6.17	myrcene/ocimene synthase (TPS10)	
AT2G43590	1.07E-03	3.56	1.73	2.79	chitinase	
AT2G35060	1.10E-02	3.23	0.61	0.87	potassium transporter	
AT2G38290	1.83E-02	2.99	1.18	1.5	ammonium transporter 2 (AMT2)	
AT3G09410	1.18E-02	2.78	1.61	2.1	pectinacetyltransferase	
AT2G46340	4.71E-03	2.77	0.42	0.68	phytochrome A suppressor spa1 (SPA1)	
AT2G38860	1.94E-03	2.69	2.15	1.64	protease1 (pfpl)-like protein (YLS5)	
AT4G39950	4.56E-03	2.66	2.13	2.72	cytochrome P450 (CYP79B2)	
AT1G59950	2.13E-02	2.57	1.74	4.12	aldo/keto reductase	
AT4G02410	1.09E-02	2.48	0.39	0.63	lectin protein kinase family protein	
AT1G61120	7.78E-05	2.43	6.16	9.74	terpene synthase/cyclase family protein	
AT3G18710	1.58E-02	2.39	0.42	0.45	U-box domain-containing protein	
AT2G47680	2.10E-02	2.39	1.29	1.61	zinc finger (CCCH type) helicase	
AT2G26440	1.02E-02	2.34	1.77	1.95	pectinesterase	
AT2G46520	8.37E-03	2.34	1.39	1.82	cellular apoptosis susceptibility protein	
AT5G55930	1.14E-02	2.3	1.42	2.24	oligopeptide transporter OPT family protein	
AT2G46710	1.46E-03	2.29	0.66	0.76	rac GTPase activating protein	
AT4G37370	1.95E-02	2.28	0.45	0.7	cytochrome P450	
AT3G47420	2.11E-02	2.27	0.48	0.68	glycerol-3-phosphate transporter	
AT2G39340	2.22E-02	2.27	1.23	1.7	SAC3/GANP family protein	
AT2G35260	8.90E-03	2.26	0.65	0.75	expressed protein	
AT2G47600	1.20E-04	2.24	2.55	2.89	magnesium/proton exchanger (MHX1)	
AT2G43160	2.30E-02	2.24	1.22	1.68	epsin N-terminal homology (ENTH)	
AT2G46530	2.09E-02	2.21	0.74	0.8	transcriptional factor B3 family protein	
AT3G48850	3.30E-02	2.2	1.31	1.69	mitochondrial phosphate transporter	
AT2G42690	3.40E-03	2.2	0.67	0.69	lipase	
AT2G35040	4.98E-02	2.19	1.16	1.34	AICARFT/IMPCHase bienzyme	
AT2G39710	3.06E-02	2.19	0.63	0.85	aspartyl protease	
AT2G42490	2.94E-02	2.19	1.27	1.46	copper amine oxidase	
AT5G24160	4.67E-02	2.18	1.08	1.5	squalene monooxygenase 1,2	
AT1G19640	1.12E-04	2.18	1.94	3.56	S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (JMT)	
AT2G35610	1.23E-02	2.16	1.25	1.45	expressed protein	
AT2G41880	1.09E-02	2.14	1.27	1.46	guanylate kinase 1 (GK-1)	
AT2G37690	2.59E-02	2.14	1.32	1.63	phosphoribosylaminoimidazole carboxylase	
AT2G45560	6.09E-03	2.13	0.51	0.61	cytochrome P450 family protein	
AT2G35230	4.43E-02	2.12	1.19	1.36	VQ motif-containing protein	
AT5G65600	4.64E-02	2.12	1.3	1.7	legume lectin family protein	
AT2G38050	1.53E-02	2.11	1.51	1.55	3-oxo-5-alpha-steroid 4-dehydrogenase	
AT2G45290	1.27E-02	2.11	1.38	1.85	transketolase	
AT2G47490	2.45E-03	2.09	0.84	0.74	mitochondrial substrate carrier family protein	
AT2G46380	1.96E-02	2.09	0.73	0.82	hypothetical protein	
AT2G47760	9.19E-03	2.08	1.18	1.27	ALG3 family protein	
AT2G46020	4.54E-02	2.08	1.07	1.4	transcription regulatory protein SNF2	
AT2G41540	1.06E-02	2.07	0.61	0.84	NAD-dependent glycerol-3-phosphate dehydrogenase	
AT2G43500	3.99E-02	2.07	0.73	0.89	RWP-RK domain-containing protein low	
AT2G39890	1.63E-02	2.06	0.71	0.88	proline transporter 1 (ProT1)	
AT4G19170	7.66E-04	2.06	0.21	0.32	9-cis-epoxycarotenoid dioxygenase	
AT2G40540	4.63E-02	2.04	0.68	0.84	potassium transporter (KT2)	
AT2G36380	3.18E-04	2.03	2.23	3.31	ABC transporter family protein	
AT1G21100	1.74E-02	2.01	1.98	1.36	O-methyltransferase	
AT4G19430	3.33E-02	2.01	0.59	0.5	expressed protein	
AT2G45590	2.01E-02	2.01	0.72	0.85	protein kinase	
AT3G49620	5.96E-04	2	8.08	2.62	2-oxoacid-dependent oxidase (DIN11)	
AT2G40090	8.39E-03	2	1.32	1.49	ABC1 family protein	

Supplementary Table S9. Genes differentially expressed ≤ 2 -fold in the *jaz7-1D* line relative to wild-type under MeJA treatment.

AGI	P-value	MeJA	MeJA inducibility		TAIR description
		<i>jaz7-1D</i> / WT	WT MeJA / control	<i>jaz7-1D</i> MeJA / control	
AT5G63450	7.19E-03	0.34	3.26	1.47	cytochrome P450
AT1G43160	1.56E-02	0.35	4.1	2.61	AP2 domain-containing protein (RAP2.6)
AT5G65080	4.03E-02	0.36	1.48	1.46	MADS-box family protein
AT1G05560	9.32E-03	0.37	0.45	0.43	UDP-glucose transferase (UGT75B2)
AT5G37770	4.01E-02	0.4	0.81	0.33	touch-responsive protein
AT3G28310	1.48E-02	0.41	0.57	0.49	expressed protein
AT4G38860	9.09E-03	0.43	0.42	0.32	auxin-responsive protein
AT2G21650	2.78E-03	0.44	0.67	0.39	myb family transcription factor
AT1G51090	3.61E-03	0.44	0.66	0.41	heavy-metal-associated domain-containing protein
AT3G45730	6.90E-03	0.45	0.66	0.45	expressed protein
AT3G48100	1.77E-02	0.45	0.47	0.32	response regulator 5 (ARR5)
AT4G34135	1.11E-02	0.46	0.33	0.63	UDP-glucuronosyl/UDP-glucosyl transferase
AT5G16970	1.83E-02	0.46	0.63	0.54	NADP-dependent oxidoreductase
AT3G06070	4.17E-02	0.46	0.78	0.43	expressed protein
AT5G62360	4.89E-05	0.47	2.67	2.92	invertase/pectin methylesterase inhibitor family protein
AT1G34760	1.82E-02	0.48	1.43	1.38	14-3-3 protein GF14 omicron (GRF11)
AT1G48330	1.46E-02	0.49	0.53	0.37	expressed protein
AT2G29490	3.19E-02	0.49	0.37	0.66	glutathione S-transferase
AT1G29510	1.73E-02	0.5	0.62	0.34	auxin-responsive protein
AT5G16990	1.91E-02	0.5	0.5	0.61	NADP-dependent oxidoreductase
AT5G24580	1.10E-03	0.5	0.57	0.48	copper-binding family protein

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