

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	TGACAAGCTTAACAATGATCATCATCATCAAA
JAZ7- <i>EcoRI</i> -R	ATAGGAATTCTATCGGTACCGTGGTA
JAZ7-EAR- <i>HIII</i> - <i>Sma</i> -F	CAAAA <u>AGCTTGAGCCGGG</u> ACAAAATGCGACTTGAACCTGCC
JAZ7_EAR_STOP- <i>EcoRI</i> -R	CAGAGAATTCTCAAGAACGTAAGAACGGCGAAGTTCAAGTCGCAT
CUC1- <i>HIII</i> -F	TTCTAAGCTTAACAATGGATGTTGATGTTAACGGTTG
CUC1-STOPdel- <i>Sma</i> -R	CATGGCCC GGGG GAGAGTAAACGCCACACACTCACGGCGG
TPL-F	AAAAAGCAGGCTTCACCATGTCTCTTAGTAGAGAGCTCG
TPL-R	CAAGAAAGCTGGGTTCATCTGAGGCTGATCAGATGC
JAM1-F	AAAAAGCAGGCTTCACCATGAATATGAGTGATTAGGTTGG
JAM1-R	CAAGAAAGCTGGGTTATATATCACCAAGAGACCTGTG
MYC2-F	AAAAAGCAGGCTTCACCATGACTGATTACCGGCTACAAC
MYC2-R	CAAGAAAGCTGGGTACCGATTTGAAATCAAACATTGC
MYC3-F	AAAAAGCAGGCTTCACCATGAACGGCACAACATCATCAATC
MYC3-R	CAAGAAAGCTGGGTATAGTTTCTCGACTTCGTC
MYC4-F	AAAAAGCAGGCTTCACCATGTCTCCGACGAATGTTCAAG
MYC4-R	CAAGAAAGCTGGGTTGGACATTCTCAACTTCTCC
JAZ7-F	AAAAAGCAGGCTTCACCATGATCATCATCATCAAAAATG
JAZ7-R	CAAGAAAGCTGGGTCTCGTAACGGTGGTA
JAZ7-R2	CAAGAAAGCTGGGTCTCGTAACGGTGGTAAGG
JAZ8-F	AAAAAGCAGGCTTCACCATGAAGCTACAGCAAAATTGTG
JAZ8-R	CAAGAAAGCTGGGTTATCGTCGTGAATGGTAC
JAZ8-R2	CAAGAAAGCTGGGTCTCGTCGTGAATGGTACGG
JAZ5-F	AAAAAGCAGGCTTCACCATGTCGTCGAGCAATGAAATGC
JAZ5-R	CAAGAAAGCTGGGTCTAGCCTAGATCGAGATCT
JAZ5-R2	CAAGAAAGCTGGGTCTAGCCTAGATCGAGATCT
pAttB1	GGGGACAAGTTGTACAAAAAAGCAGGCT
pAttB2	GGGGACCACTTGTACAAGAAAGCTGGGT

Supplementary Table S3. Primers used for qRT-PCR.

Primer ID	Gene Locus (AGI)	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
ACT-8	At1g49240		GAGGATAGCATGTGGAAGTGAGAA
ACT-2	At3g18780		GATGGCATGGAGGAAGAGAGAAC
ACT-7	At5g09810		GAGGAAGAGCATTCCCTCGTA
ACTuni		AGTGGTCGTACAACCGGTATTGT	
JAZ1	At1g19180	CGGTAGTTGGAGATCTGAG	TCACAAGGAAATAAACTCATGG
JAZ2	At1g74950	CCTCTGGGACCAAAGAAGAT	CCATAACTCGACCACCGTAG
JAZ3	At3g17860	TTTATGATTCAACCCGAAA	CGACATGGAAACTGCGTTAG
JAZ4	At1g48500	CAATCTTTATGCCGGTTCA	CGGTTAGCATGAGGTCCAT
JAZ5	At1g17380	CACGTAGAGCTTCCCTCCAT	TGGGAGGATAACGATGATGA
JAZ6	At1g72450	GGAACGCATTGCAAGAAGA	GGAAGATGACTACCGTGTGG
JAZ7	At2g34600	GACTTGGAACTTCGCCCTCTT	TCTGAGATTCTGCTTGGTTG
JAZ7 exon1 specific	At2g34600	CATCATAAAAACTGCGACAA	GAAGTAAGAAGGCGAAGTCCA
JAZ7 exon2 specific	At2g34600	CAACAATCCCAAACAATTG	GAAGTTGCTTGAATCCGAAGA
JAZ8	At1g30135	CAGCAAAATTGTGACTTGGAA	TGGATTTCCAGAACTGGTTG
JAZ9	At1g70700	CACAATCTTTATGGCGGAAC	TCCAGTTCACCTTCAAACC
JAZ10	At5g13220	ATCTCGTTCGGTTCCGTCA	ACAGTTCCGAAACGAGTTC
JAZ11	At3g43440	TTTGGTGGGAGTTTAGCGTA	TTGTCTAGTGGCTTAGCTG
JAZ12	At5g20900	GCTGCACAGCCATTCTA	CTCGAGGAATCGTTGAAGC
MYC2	At1g32640	TCATACGACGGTTGCCAGAA	AGCAACGTTACAAGCTTGATTG
ERF1	At3g23240	TCAGAAGACCCAAAAGCTCTCA	TTGATCACCGCTCCGTGAAGTTAG
LOX3	At1G17420	TAACGATGCTGGTGTCCATC	AATTGCCTGTGTGCAGCTAA
PDF1.2	At5g44420	TTTGCTGCTTCGACGCAC	CGCAAACCCCTGACCATG
Thi2.1	At1g72260	CTCAGCTGATGCTACCAATGAGC	GCTCCATTACAATTCACTTGC
PR3-F	At3g12500	ATCAGCGCTGCAAAGTCCTC	GTGCTGTAGCCCACCCACCTG
VSP2	At5g24770	CCTAAAGAACGACACCGTCA	TCGGTCTCTGTGCTTCCGTA
SAG12	At5g45890	AAAGGCGAAGACGCTACTTG	TCATCAGTGCTGCTCATCA
GSTF6	At1g02930	GTCGACTTGAATTGTTCATG	CCTTGCCAGTTGAGAGAAGG
DHAR1	At1g19570	CTCTGACAAACCCAGTGGTT	CAACGATGACGTGGAAATCA
PR1	AT2G14610	AAGAGGCAACTGCAGACTCA	TCTCGCTAACCCACATGTTC
PR2	At3g57260	AGCTTAGCCTCACCAACCAAT	CCCGTAGCATACTCCGATT
NATA1	AT2G39030	TTCTTCCGAACTACCCAAG	GCGGTAGTAGCAGTTTCC

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the first time, the author has been able to identify the species of all the individuals. The results are presented in Table 1. The mean age at maturity was 3 years for males and 4 years for females. The mean age at first capture was 1 year for both sexes. The mean age at last capture was 10 years for males and 8 years for females. The mean age at death was 12 years for males and 10 years for females. The mean age at death was significantly higher than the mean age at last capture for both males and females ($P < 0.05$).

The mean length at maturity was 100 cm for males and 90 cm for females. The mean length at first capture was 70 cm for both sexes. The mean length at last capture was 120 cm for males and 110 cm for females. The mean length at death was 140 cm for males and 130 cm for females. The mean length at death was significantly higher than the mean length at last capture for both males and females ($P < 0.05$).

the first two years of the study, the mean age of the children was 1.6 years (SD = 0.2). The mean age of the mothers was 31.1 years (SD = 3.7). The mean age of the fathers was 33.3 years (SD = 4.1). The mean family size was 3.6 (SD = 0.5). The mean income was \$34,000 (SD = \$11,000). The mean education level was 13.1 years (SD = 2.1). The mean marital status was 1.4 (SD = 0.7), where 0 = married, 1 = separated, 2 = divorced, and 3 = widowed. The mean ethnicity was 0.2 (SD = 0.3), where 0 = non-Hispanic white, 1 = African American, and 2 = Hispanic. The mean race was 0.2 (SD = 0.3), where 0 = white, 1 = black, and 2 = Hispanic. The mean gender was 0.5 (SD = 0.2), where 0 = male and 1 = female. The mean marital status was 0.2 (SD = 0.3), where 0 = married, 1 = separated, 2 = divorced, and 3 = widowed. The mean ethnicity was 0.2 (SD = 0.3), where 0 = non-Hispanic white, 1 = African American, and 2 = Hispanic. The mean race was 0.2 (SD = 0.3), where 0 = white, 1 = black, and 2 = Hispanic. The mean gender was 0.5 (SD = 0.2), where 0 = male and 1 = female.

The mean age of the children was 1.6 years (SD = 0.2). The mean age of the mothers was 31.1 years (SD = 3.7). The mean age of the fathers was 33.3 years (SD = 4.1). The mean family size was 3.6 (SD = 0.5). The mean income was \$34,000 (SD = \$11,000). The mean education level was 13.1 years (SD = 2.1). The mean marital status was 1.4 (SD = 0.7), where 0 = married, 1 = separated, 2 = divorced, and 3 = widowed. The mean ethnicity was 0.2 (SD = 0.3), where 0 = non-Hispanic white, 1 = African American, and 2 = Hispanic. The mean race was 0.2 (SD = 0.3), where 0 = white, 1 = black, and 2 = Hispanic. The mean gender was 0.5 (SD = 0.2), where 0 = male and 1 = female. The mean marital status was 0.2 (SD = 0.3), where 0 = married, 1 = separated, 2 = divorced, and 3 = widowed. The mean ethnicity was 0.2 (SD = 0.3), where 0 = non-Hispanic white, 1 = African American, and 2 = Hispanic. The mean race was 0.2 (SD = 0.3), where 0 = white, 1 = black, and 2 = Hispanic. The mean gender was 0.5 (SD = 0.2), where 0 = male and 1 = female.

Mr. Smith, a man with a past, and a past that he is trying to leave behind him. He has been a member of the Communist Party for many years, and during his time in the party, he has been involved in various illegal activities. He has been arrested several times, and has served time in prison. He has also been involved in some financial scandals, and has lost a significant amount of money. Despite all of this, he still continues to work for the party, and to support its goals. He is a dedicated member, and is willing to do whatever it takes to further the cause of communism.

On the other hand, Mr. Johnson, a man who is trying to move forward and leave his past behind him. He has been involved in some illegal activities in the past, but has since turned his life around. He is now a successful businessman, and is involved in a variety of legitimate industries. He is a family man, and is trying to provide for his wife and children. He is a hard worker, and is always looking for ways to improve himself and his business. He is a man who has learned from his mistakes, and is now trying to make a better life for himself and his family.

the United States. The first major breakthrough came in 1955 with the development of the polio vaccine by Dr. Jonas Salk. This was followed by the introduction of the rubella vaccine in 1962 and the varicella vaccine in 1971. In 1976, the National Vaccine Injury Compensation Program was established to provide a no-fault alternative for those who suffered from a preventable disease or injury. The program has since compensated thousands of victims and helped to ensure the safety and effectiveness of vaccines.

The second major breakthrough came in 1977 with the development of the first successful AIDS vaccine. This vaccine, known as the AIDSVax, was developed by Dr. Robert Gallo and Dr. Luc Montagnier. It was the first vaccine to show promise in preventing the spread of AIDS. However, despite years of research and development, there is still no effective vaccine for AIDS. The third major breakthrough came in 1985 with the development of the first hepatitis C vaccine. This vaccine, known as the Hepatitis C Vaccine, was developed by Dr. Charles Rice and Dr. Thomas Frieden. It is the first vaccine to show promise in preventing the spread of hepatitis C. The fourth major breakthrough came in 1996 with the development of the first hepatitis B vaccine. This vaccine, known as the Hepatitis B Vaccine, was developed by Dr. Robert Gallo and Dr. Luc Montagnier. It is the first vaccine to show promise in preventing the spread of hepatitis B.

1. The first step is to identify the specific type of error or issue you are experiencing. This could be anything from a simple syntax error to a more complex logic error or performance issue.

2. Once you have identified the issue, it's important to gather as much information as possible about it. This includes:

- The exact error message or exception that is being thrown.
- The code snippet where the error occurred.
- The environment in which the error is occurring (e.g., development, test, production).
- Any relevant logs or system metrics that may be available.

3. Based on the information gathered, you can start to narrow down the cause of the error. This may involve:

- Reviewing the code for any obvious mistakes or violations of best practices.
- Checking for any dependencies or external factors that may be contributing to the issue.
- Testing the code in different environments to see if the problem is consistent across all of them.

4. Once you have a good understanding of the problem, you can begin to work on a solution. This may involve:

- Modifying the code to fix the error.
- Adding additional logging or monitoring to help track down the issue.
- Consulting documentation or seeking help from other developers if you're stuck.

5. Finally, it's important to thoroughly test the code after making changes to ensure that the error has been resolved and that no new issues have been introduced. This may involve:

- Running unit tests to verify that individual components are working correctly.
- Performing integration tests to ensure that different parts of the system work together as expected.
- Testing the code in a real-world scenario to make sure it behaves as intended.

6. Once you are confident that the error has been resolved, you can move on to the next step in your development process.

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	proteasel (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	caffeyl-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	pectinacetyl esterase	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-glucoronosyl/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-glucoronosyl/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

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the first time in the history of the world, the people of the United States have had a Government which has been created by themselves, and which rests entirely on their own consent and authority. They have now, for the first time, a Government which is responsible to them, and which they can, if they so desire, disestablish whenever they please. They have now, for the first time, a Government which is entirely their own, and which they can, if they so desire, alter or abolish whenever they please. They have now, for the first time, a Government which is entirely their own, and which they can, if they so desire, alter or abolish whenever they please.

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Humanity is in danger of becoming extinct. We must find a way to live in harmony with nature, or we will face a future of environmental degradation and social collapse. We must work together to protect our planet and its resources, and to ensure that all people have access to the necessities of life. This requires a fundamental shift in our thinking and behavior, and a commitment to sustainable development and environmental stewardship.

The world is facing a range of challenges, from climate change and pollution to poverty and inequality. These challenges require urgent action and cooperation at all levels of society. We must work together to address these issues, and to build a better future for all. This requires a fundamental shift in our thinking and behavior, and a commitment to sustainable development and environmental stewardship.

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He had a very good chance to do well in the competition, but he did not have enough time to prepare. He was very nervous and did not perform well. He did not win the competition, but he still did well and showed his potential.

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the first time, the author has been able to identify the species of all the individuals. The results are presented in Table 1. The mean age at maturity was 3 years for males and 4 years for females. The mean age at first capture was 1 year for both sexes. The mean age at last capture was 10 years for males and 11 years for females. The mean age at death was 12 years for males and 13 years for females. The mean age at death was significantly higher than the mean age at last capture for both males and females ($P < 0.05$).

The mean length at maturity was 100 cm for males and 110 cm for females. The mean length at first capture was 50 cm for both sexes. The mean length at last capture was 120 cm for males and 130 cm for females. The mean length at death was 140 cm for males and 150 cm for females. The mean length at death was significantly higher than the mean length at last capture for both males and females ($P < 0.05$). The mean weight at maturity was 10 kg for males and 12 kg for females. The mean weight at first capture was 2 kg for both sexes. The mean weight at last capture was 25 kg for males and 30 kg for females. The mean weight at death was 40 kg for males and 50 kg for females. The mean weight at death was significantly higher than the mean weight at last capture for both males and females ($P < 0.05$).

The mean total length was 100 cm for males and 110 cm for females. The mean total length at first capture was 50 cm for both sexes. The mean total length at last capture was 120 cm for males and 130 cm for females. The mean total length at death was 140 cm for males and 150 cm for females. The mean total length at death was significantly higher than the mean total length at last capture for both males and females ($P < 0.05$). The mean total weight was 10 kg for males and 12 kg for females. The mean total weight at first capture was 2 kg for both sexes. The mean total weight at last capture was 25 kg for males and 30 kg for females. The mean total weight at death was 40 kg for males and 50 kg for females. The mean total weight at death was significantly higher than the mean total weight at last capture for both males and females ($P < 0.05$).

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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	TAIR description	
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	pectinacetyl esterase	
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	protease (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:jasmone 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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