

Supplemental Table S1 Up-regulated genes in irJAZh plants compared to WT plants by microarray.

Classification	Fold Change	Bincode (TAIR)	Annotation	Probe number	ACC number
Cell wall. Degradation	3.29	10.6.2	Glycosyl hydrolase family 3 protein	CUST_146896_PI422650789	NP_196618
Lipid metabolism	4.80	11.8.7	Putative trans-2-enoyl-CoA reductase	CUST_75436_PI422650789	NP_566881
	4.42	11.8.7	Putative trans-2-enoyl-CoA reductase	CUST_33708_PI422650789	NP_566881
	4.32	11.9.2.1	Lipase class 3 family protein	CUST_160928_PI422650789	NP_565701
	4.13	11.8.8	Squalene synthase	CUST_163980_PI422650789	AAM27472
	3.81	11.3.7	Gamma-tocopherol methyltransferase	CUST_112272_PI422650789	ABE41795
	3.75	11.1.15	Acyl-[acyl-carrier-protein] desaturase	CUST_41928_PI422650789	P46253
	3.57	11.9.2.1	Glycerolipase A1	CUST_160212_PI422650789	ACZ57767
	3.33	11.8.1	Sphingolipid delta-8 desaturase	CUST_80400_PI422650789	ABO31111
Amino acid metabolism	3.36	13.1.7.4	Cyclase	CUST_99572_PI422650789	AAS46038
Secondary metabolism	5.22	16.1.5	5-epi-aristolochene synthase	CUST_46640_PI422650789	AAO85555
	4.01	16.1.5	5-epi-aristolochene synthase (EAS)	CUST_34180_PI422650789	Q40577
	3.86	16.1.5	Plastid 1,8-cineol synthase precursor	CUST_12108_PI422650789	ABP88782
	3.54	16.1.5	5-epi-aristolochene synthase 34	CUST_173668_PI422650789	AAP05761

Hormone metabolism	7.68	17.8.1	SAMT(salicylic acid methyltransferase)	CUST_33280_PI422650789	AAW66850
	3.35	17.1.1.1.11	Short chain alcohol dehydrogenase	CUST_42160_PI422650789	CAA11153
	3.34	17.5.2	Ethylene responsive element binding factor 1	CUST_115772_PI422650789	BAA32418
Tetrapyrrole synthesis	3.25	19.99	ATCLH2; chlorophyllase	CUST_94136_PI422650789	NP_199199
Stress	30.80	20.1	Gamma-thionin (Plant defensins)	CUST_57516_PI422650789	AAS13436
	15.27	20.1	Gamma-thionin (Plant defensins)	CUST_8140_PI422650789	AAS13436
	4.58	20.1.7.6.1	Kunitz trypsin inhibitor	CUST_14168_PI422650789	ACL12055
	3.88	20.1.7.6.1	6-domain trypsin inhibitor precursor	CUST_9024_PI422650789	AAQ56588
	3.78	20.1	Proteinase inhibitor I-B (PI-IB)	CUST_11524_PI422650789	Q03199
	3.47	20.1.7.6.1	Kunitz trypsin inhibitor	CUST_79416_PI422650789	ACL12055
	3.35	20.1.7.6.1	Miraculin-like protein	CUST_8752_PI422650789	ADK62529
Miscellaneous enzyme families	8.13	26.10	CYP71D5v3	CUST_103900_PI422650789	ABC69398
	4.59	26.10	CYP71D47v1	CUST_102916_PI422650789	ABC69394
	4.02	26.10	Cytochrome P-450-like protein	CUST_143016_PI422650789	BAB10537
	3.70	26.8	FAD-binding domain-containing protein	CUST_127228_PI422650789	NP_193818
	3.42	26.2	UDP-glucuronosyl/UDP-glucosyl transferase family protein	CUST_43496_PI422650789	NP_180576
	3.21	26.28	GDSL-motif lipase/hydrolase family protein	CUST_64232_PI422650789	NP_563774

RNA. Regulation of transcription	5.13	27.3.27	ATNAC2 (Arabidopsis NAC domain containing protein 2)	CUST_14684_PI422650789	NP_188170
	4.55	27.3.6	Basic helix-loop-helix (bHLH) family protein	CUST_157324_PI422650789	NP_567195
	3.25	27.3.5	ARR4 (Arabidopsis regulation regulator 4)	CUST_56432_PI422650789	NP_172517
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DNA.synthesis	3.75	28.1.3	Histone H1	CUST_32040_PI422650789	AAC41651
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Protein. Degradation	6.07	29.5.9	AAA-type ATPase family protein	CUST_76132_PI422650789	NP_200556
	5.53	29.5	Putative metalloprotease inhibitor precursor	CUST_139476_PI422650789	BAJ25782
	5.03	29.5	Putative metalloprotease inhibitor precursor	CUST_31104_PI422650789	BAJ25782
	4.50	29.5.11.4.3.2	F-box family protein	CUST_86652_PI422650789	NP_566277
	3.69	29.5.11.4.2	RING/U-box domain-containing protein	CUST_21448_PI422650789	AAG43550
	3.41	29.5	Putative metalloprotease inhibitor precursor	CUST_40216_PI422650789	BAJ25781
	3.19	29.5.9	AAA-type ATPase family protein	CUST_78344_PI422650789	NP_849972
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Cell.organisation	4.22	31.1	AtPP2-A11 (Phloem protein 2-A11)	CUST_73344_PI422650789	NP_176497
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Development	9.16	33.99	Tumor-related protein	CUST_16488_PI422650789	BAA05479
	6.07	33.1	Patatin homolog	CUST_168304_PI422650789	AAB08428
	4.01	33.1	Patatin	CUST_1460_PI422650789	AAB08428
	3.63	33.1	Patatin homolog	CUST_81764_PI422650789	AAB08428
	3.50	33.1	Patatin homolog	CUST_142932_PI422650789	AAB08427
	3.27	33.99	Transducin family protein / WD-40 repeat family protein	CUST_170740_PI422650789	NP_190535

Transport	6.61	34.9	Mitochondrial carrier protein	CUST_124384_PI422650789	ABO36621
	5.69	34.16	ATP-binding cassette transporter, putative	CUST_87856_PI422650789	XP_002525837
	5.24	34.4	Nitrate transporter	CUST_171856_PI422650789	BAC56915
	4.83	34.16	WBC11 (White-Brown Complex homolog protein 11)	CUST_163156_PI422650789	NP_173226
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Not assigned	5.84	35.1	Phosphorylase family protein	CUST_71848_PI422650789	NP_567699
	4.77	35.1	FAD-binding domain-containing protein	CUST_37768_PI422650789	NP_196715
	4.59	35.2	JAZ8 (Jasmonate ZIM domain protein 8)	CUST_80752_PI422650789	NP_564349
	3.59	35.2	JAZ3 (Jasmonate ZIM-domain protein 3)	CUST_52900_PI422650789	BAG68657
	3.39	35.1.40	Glycine-rich protein	CUST_69052_PI422650789	BAA95941

* Microarray data is processed by SAM after 75% percentile normalization (FDR=4.82).

* Up-regulated genes were determined by a greater than 3-fold induction of normalized signals in their expression ratio (irJAZh / WT) of 2h-WOS treated leaves. The values are the average ratio of 3 biological replicates of the microarrays.

* All changes in gene expression were statistically significant by t-test ($P < 0.05$)

* Gene annotation is processed by Blast X (E-value $< 1e-5$)

* Classification of genes is based on GO classification from TAIR (<http://www.arabidopsis.org>).

Supplemental Table S2 Down-regulated genes in irJAZh plants compared to WT plants by microarray.

Classification	Fold Change	Bincode (TAIR)	Annotation	Probe number	ACC number
Photosynthesis	3.03	1.1.2.2	Photosystem I P700 apoprotein A2	CUST_32628_PI422650789	ABB90040
	3.33	1.2.2	Glycolate oxidase	CUST_6068_PI422650789	ADM26718
Major Carbohydrates	3.03	2.2.2.1	Alpha-amylase	CUST_12856_PI422650789	ACZ26470
Lipid metabolism	10.00	11.3.1	Acyltransferase-like protein	CUST_12976_PI422650789	BAD93693
	6.25	11.3.1	Acyltransferase-like protein	CUST_134584_PI422650789	BAD93693
Metal handling	4.00	15.3	Vacuolar iron transporter-like protein	CUST_26436_PI422650789	NP_173538
	3.03	15.1	Ferric-chelate reductase	CUST_64152_PI422650789	AAP46144
	4.17	15.2	Metallothionein-like protein type 2	CUST_144048_PI422650789	CAC12823
Secondary metabolism	3.45	16.1.5	Sesquiterpene synthase	CUST_166968_PI422650789	NP_001239041
	12.50	16.1.5	Plastid 1,8-cineol synthase precursor	CUST_44188_PI422650789	ABP88782
	12.50	16.1.5	Plastid 1,8-cineol synthase precursor	CUST_20468_PI422650789	ABP88782
	9.09	16.1.5	Plastid 1,8-cineol synthase precursor	CUST_14120_PI422650789	ABP88782
	8.33	16.1.5	Monoterpene synthase 2	CUST_165928_PI422650789	AAX69064

	7.14	16.8.3	Terpene cyclase/mutase-related	CUST_11104_PI422650789	NP_195062
Hormone metabolism	3.33	17.2.3	SAUR-like auxin-responsive protein	CUST_59948_PI422650789	NP_187035
	3.23	17.4.1	Cytokinin-O-glucosyltransferase 2	CUST_173124_PI422650789	NP_173656
	4.17	17.5.2	ERF transcription factor 5	CUST_116820_PI422650789	AAU81956
Stress	3.57	20.2.3	Early dehydration inducible protein	CUST_55152_PI422650789	AAR26237
	3.57	20.2.3	Salt responsive protein 1	CUST_45184_PI422650789	ACG50003
	3.23	20.1.7	CC-NBS-LRR putative disease resistance protein	CUST_167984_PI422650789	ACB70404
	3.13	20.2	Pathogenesis-related protein	CUST_15548_PI422650789	BAD15090
Miscellaneous enzyme families	3.85	26.10	Elicitor-inducible cytochrome P450	CUST_25520_PI422650789	AAK62342
	2.94	26.10	Elicitor-inducible cytochrome P450	CUST_96052_PI422650789	AAK62343
	3.85	26.22	Short-chain dehydrogenase/reductase family protein	CUST_122964_PI422650789	XP_002869743
	4.55	26.3.2	Beta-galactosidase STBG5	CUST_18760_PI422650789	ADO34790
	3.57	26.3.2	Beta-galactosidase STBG5	CUST_888_PI422650789	ADO34790
	3.85	26.10	CYP71D49v2	CUST_119780_PI422650789	ABC69401
RNA. regulation of transcription	2.94	27.3.11	Zinc finger protein 4	CUST_73116_PI422650789	NP_176788
	4.76	27.3.22	Class 2 knotted1-like protein	CUST_139276_PI422650789	BAF95776
	3.33	27.3.35	bZIP transcription factor BZI-2	CUST_107720_PI422650789	AAK92213
	4.17	27.3.6	Basic helix-loop-helix (bHLH) family protein	CUST_56184_PI422650789	NP_181549

	3.33	27.3.6	Transcription factor style2.1	CUST_33216_PI422650789	ABX82930
	3.33	27.1.19	Ribonuclease H-like protein	CUST_79632_PI422650789	NP_172471
	4.55	27.1.19	RNase H family protein	CUST_121612_PI422650789	ABI34372
	3.23	27.3	Transcription factor style2.1	CUST_163752_PI422650789	ABX82930
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Protein. degradation	3.85	29.5	Class S F-box protein	CUST_152204_PI422650789	ABR18786
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Signaling	3.03	30.5	Transducin/WD40 domain-containing protein	CUST_21460_PI422650789	NP_199823
	3.03	30.3	Calcineurin B-like protein	CUST_107040_PI422650789	ABQ23353
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Development	3.23	33.3	Squamosa promoter-binding-like protein 12	CUST_109112_PI422650789	NP_191562
	4.00	33.99	Nodulin MtN21 family protein	CUST_29984_PI422650789	NP_181622
	4.00	33.99	Senescence-associated protein-related	CUST_6080_PI422650789	NP_564160
	3.03	33.99	Fruitfull-like MADS-box protein	CUST_42876_PI422650789	ABF82231
	2.94	33.99	NAC domain protein	CUST_81900_PI422650789	AAU43923
	4.00	33.99	Putative gag polyprotein, identical	CUST_81856_PI422650789	AAT39964
	4.55	33.99	Ripening regulated protein DDTFR18	CUST_97944_PI422650789	AAG49032
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Transport	3.13	34.4	Nitrate transporter (NTL1)	CUST_131240_PI422650789	AAG52554
	3.45	34.12	Metal transporter	CUST_159740_PI422650789	AAP21819
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Not assigned	3.13	35.1	Oxidoreductase family protei	CUST_25856_PI422650789	NP_193468
	4.00	35.2	Transducin family protein / WD-40 repeat family protein	CUST_54908_PI422650789	NP_196176
	3.33	35.2	Jasmonate ZIM-domain protein 1	CUST_40368_PI422650789	BAG68655
	3.03	35.2	GC-rich sequence DNA-binding factor	CUST_122872_PI422650789	NP_196472
	3.85	35.2	Serine-threonine protein kinase, plant-type, putative	CUST_171656_PI422650789	XP_002532616

* Microarray data is processed by SAM after 75% percentile normalization (FDR=4.82).

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* All changes in gene expression were statistically significant by t-test ($P < 0.05$)

* Gene annotation is processed by Blast X (E-value $< 1e-5$)

* Classification of genes is based on GO classification from TAIR (<http://www.arabidopsis.org>).

Supplemental Table S3. Primer sequences used for cloning of *JAZ* genes from *N. attenuata*

Gene name	Primer sequences
NtJAZa-FP	GACAGAAAAAGCAAAATATTTACAA
NtJAZa-RP	ACAATAGGAAGTAAAACTTAAGCC
NtJAZb-FP	GTAATCCTAAATCTTTGAGAAAGTG
NtJAZb-RP	AATTCAAAAATCCATTTGCCTTGAA
NtJAZc-FP	TTTCTGGGGTTTGGTGTTTTGAGC
NtJAZc-RP	GATGAAAGAGAATTAAGTACAGC
NaJAZc.1-FP ^{&}	CATTCAAAGCTCAATCCGC
NaJAZc.2-RP ^{&}	CGATGGAAGTATTGAGTGAGG
NtJAZd-FP-1*	TATCTTTCTCAAGCTTATTACAGATTCTTG
NtJAZd-FP-2*	ATTTAGTTTTTTGCCACCGGAAAACAAA
NtJAZe-FP	TAAGTGAAAATAATGGAGAGAGATT
NtJAZe-RP	TACAAAAGGCTCGTAGTGTTTTCAGATG
NtJAZf-FP	TTGGCTGAAGTTGAATAAAG
NtJAZf-RP	CTAGCATCATTATCCATTATATTTCC
NtJAZp-FP	ATTCTGTCAGATATATTTCAAGTTTCTG
NtJAZp-RP	TCAATAGTTCACTCTCTTTGACACTA
NtJAZh-FP	CAACTTGTTCAAGTTGTAAAATTGTAG
NtJAZh-RP	CATGGAATTGCAACTGGGGGACTCTTTA
NtJAZj-FP	TTGTGGCTGAAGTTAAACGAAG
NtJAZj-RP	CAAAATATATGTACAAATGGAACTA
NtJAZk-FP	TTAAACGCCGGAAGTTGACAGC
NtJAZk-RP	GCAATATGGACAATGATACTGCC
NaJAZc.1-FP ^{&}	CAGAAACTCCATTGAATGCTAC
NaJAZc.2-RP ^{&}	ACCTGTCTTTTCGCTTCTCA
NtJAZl-FP-1*	GCACAGACTGAGAAAATGTATTGC
NtJAZl-FP-2*	ATGTATTGCAGCTCCAAAGTGCC
NtJAZm-FP-1*	AAGGAAGAAAACAATAGGCATAAAG
NtJAZm-FP-2*	ATAAGCTAAGCAATTCCCCCACATTG

* cloned as 3'RACE product

& Primers used to confirm alternative splicing form of NaJAZc and JAZk transcripts.

Supplemental Table S4. Primer sequences used in quantitative real time PCR of *NaJAZ* genes

Gene name	Primer sequences
NaJAZa FP	CAGTGAAAGCTGAGCAATTCTAGTACTC
NaJAZa RP	AGCCTTAGACGAATTGAATACCTACAC
NaJAZb FP	GGGAAAGCTAATTCAAGACAAATGG
NaJAZb RP	TGTATTCTTTAGCCACCAATCTAGC
NaJAZc FP	GGAAAGGGTGATGAACGCTGCA
NaJAZc RP	TATGGCAATAGGCTGCCTTCAGAC
NaJAZd FP	GCCTTGCGTAACTGATGAAGTTG
NaJAZd RP	GGCAGCCCAGTGC ACTAAGC
NaJAZe FP	CAATTTGGTCAAGGAGACGTGA
NaJAZe RP	GGCTCTGATCACAATTACAAGG
NaJAZf FP	CAAGTAGAGAAATGGAGGAG
NaJAZf RP	GCTAGTGATGATATGGAGAAG
NaJAZg FP	CAAAGCATCCTTGGCTCGGTTC
NaJAZg RP	CGCATCTACATTGACTTGCCATC
NaJAZh FP	TTCTGCTACGCCGCAAGTACTG
NaJAZh RP	GGTATGGCGCTCTAGCCGTTG
NaJAZj FP	CATCATCACCAATTTTCAGAGCCTTC
NaJAZj RP	TCCAATTTTCCAATTTCTCCCAGCA
NaJAZk FP	TCTATGGTGATGTGCCTGCTGAC
NaJAZk RP	AACGGATATCCAAGCTAGCTGTTG
NaJAZl FP	TTGCCAGAAGGAAATCCCTGAAGAG
NaJAZl RP	TCCATCAAAAGCTAGCCCTACTTAGC
NaJAZm FP	AGTGCGTCAAATTTGAGAGCACCA
NaJAZm RP	GCTGCTTGAATCCTCCTTTCTCTTC

Supplemental Table S5. Primer sequences used in quantitative real time PCR experiments

Gene name	Primer sequences
Hsr203 FP	CAC TGT CTA CAC GCG CCT A
Hsr203 RP	GAG GAG GGC GGC GAA ACC
Hin1 FP	GCGTCCAGTATTCAAAGGTCA
Hin1 RP	CGCATGTAAAGCTTCACTTCC
NaVPE361 FP	GCTGAAGCGTGTTCAACCTGTA
NaVPE361 RP	GTGAGACTGCAAATTCCATGGCGT