SUPPLEMENTAL MATERIALS

Supplemental Table S1. The list of selected genes differentially regulated by MeJA

Supplemental Table S2. The list of selected genes differentially regulated by JA-Ile

Supplemental Table S3. The list of selected genes differentially regulated by JA-Leu

Supplemental Table S4. The list of selected genes differentially regulated by JA-Val

Supplemental Figure S1. Phytohormone screening of *irjar4/6* plants. Mean (± SE) JA-Ile/Leu, JA-Val and JA concentrations of four replicate WT and 8 lines of *irjar4/6* plants 1h after OS-treatment. *Irjar4/6 plants* are F1 heterozygous plants generated by crossing JAR4 and JAR6 independently silenced T2 homozygous plants (*irjar4-1, irjar4-2, irjar6-1, and irjar6-2).* Each line was used as both female and male parent and a total of 8 lines were constructed. Two lines (*irjar4-2/6-2* and *irjar6-1/4-1*) were selected for further experiments owing to their lower JA-Ile/Leu levels. N.d., not detected.

Supplemental Figure S2. JA-Ile elicits transcriptional responses of WT plants that are different from those elicited by MeJA, JA-Leu, and JA-Val as determined by microarray analyses. A, Venn diagrams of the number of overlapping or non-overlapping genes up- or down-regulated in response to MeJA (left) and JA-Ile, JA-Leu, or JA-Val (right) treatment. Expression data for all of the differentially regulated genes are listed in Supplemental Tables 1 to 4. Rosette-stage +1 leaves were wounded and treated with 0.25 μmol MeJA, JA-Ile, JA-Val, JA-Leu or water. 3 h after treatment, leaves were harvested for RNA isolation. Microarrays were hybridized with cDNA reverse-transcribed from mRNA pooled from 3 independently

treated plants and labeled with Cy3 (for jasmonate treatments) or Cy5 (for water treatment). B, A PCA of the logarithmic expression ratios from four cDNA microarrays. PCA 1, 2, and 3 accounts for 68.21, 12.68, and 19.11% of variance, respectively.

Table S1. The list of selected genes differentially regulated by MeJA

Accession No.	Gene name	Plant	Gene description / putative annotation	Ratio	*P*-value
AF272244	TEAS	*N.t.*	5-epi-aristolochene synthase	4.31	0.00072
AF212316	CMT	*C.a.*	Caffeic acid O-methyltransferase	4.04	0.00014
BQ519121	SAGT	*S.t.*	UDP-glucose:salicylic acid glucosyltransferase	3.07	0.00006
BQ516602	JA2	*S.t.*	Jasmonic acid 2	3.02	0.00538
BQ115240	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	2.84	0.00038
BQ112770	PIN	*S.t.*	Cysteine protease	2.82	0.00002
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	2.80	0.00059
BQ113865	LADOX	*S.t.*	Leucoanthocyanidin dioxygenase-like protein	2.72	0.00001
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	2.65	0.00118
BQ113381	LSP	*S.t.*	Lanthionine synthetase C-like protein	2.59	0.00000
AJ007630	αDOX	*N.t.*	Pathogen induced oxygenase	2.55	0.00001
CF920207	GPO	*N.a.*	Glutathione peroxidase	2.41	0.00003
AF229926	αDOX	*N.a.*	Pathogen inducible alpha-dioxygenase	2.39	0.00134
BQ514441	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 1	2.31	0.00612
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	2.26	0.00010
BQ113456	4CL	*S.t.*	4-coumarate--CoA ligase	2.25	0.00016
BQ114198	C4H	*S.t.*	Cinnamic acid 4-hydroxylase	2.21	0.00002
AY254347	LOX1	*N.a.*	Lipoxygenase 1	2.19	0.02810
DQ768747	PAL	*N.a.*	NaPAL2	2.19	0.00023
AF212318	C4H	*C.a.*	Cinnamic acid 4-hydroxylase C4H	2.16	0.00000
BQ113872	LIS	*S.t.*	Linalool synthase-like protein	2.10	0.00044
BU494500	αDOX	*N.a.*	Pathogen-inducible a-dioxygenase	2.09	0.00238
BQ120675	PhD	*S.t.*	Prephenate dehydratase,	2.08	0.01172
X63560	SHK	*S.l.*	Shikimate kinase precursor	2.06	0.00169
BQ516725	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	2.05	0.00667
AJ007630	αDOX	*N.t.*	Pathogen induced oxygenase	2.04	0.00000
AJ242551	OPR	*S.l.*	12-oxophytodienoate reductase	2.02	0.00002
AF272244	TEAS	*N.t.*	N. tabacum 5-epi-aristolochene synthase	1.96	0.00018
BQ511035	PP2C	*S.t.*	Protein phosphatase 2C	1.95	0.00006
BQ121693	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	1.93	0.00004
BQ514499	4CL	*S.t.*	4-coumarate:coenzyme A ligase	1.93	0.00009
AW191813	GERMIN	*N.a.*	Germin-like protein	1.90	0.00414
AW191821	αDOX	*N.a.*	Pathogen-inducible alpha-dioxygenase	1.88	0.00036
AJ344155	CDPK3	*N.t.*	Calcium-dependent protein kinase 3	1.88	0.00053
AW191813	GERMIN	*N.a.*	Germin-like protein	1.85	0.00001
M62755	4CL	*S.n.*	4-courmarate--CoA ligase	1.85	0.00002
BQ513122	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 2	1.85	0.00006
AF229926	αDOX	*N.a.*	Pathogen inducible alpha-dioxygenase(PIOX)	1.83	0.00124
BQ511530	PP2C	*S.t.*	Protein phosphatase 2C	1.82	0.00002
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	1.81	0.00019
AJ242551	OPR	*S.l.*	12-oxophytodienoate reductase	1.80	0.00030
BQ115114	DOXPS	*S.t.*	1-deoxyxylulose 5-phosphate synthase	1.77	0.00001

BQ518541	PES	*S.t.*	Pectinesterase 3 precursor	1.74	0.02124
CA591862	PAL1	*N.a.*	Phenylalanine ammonialyase 1	1.72	0.00080
Z12753	PIN2	*S.t.*	Proteinase inhibitor II.	1.71	0.00005
BQ510318	GLUS	*S.t.*	NADH-dependent glutamate synthase	1.71	0.00886
BQ511968	SAP	*S.t.*	Senescence-associated protein-like	1.69	0.00094
L46847	DHYS	*S.l.*	Dehydroquinate synthase	1.68	0.00015
A27686	PPO	*S.t.*	Polyphenol oxidase	1.67	0.00070
BQ112708	APH	*S.t.*	Putative acid phosphatase	1.66	0.00002
CF920211	JMT	*N.a.*	Jasmonic acid carboxyl methyltransferase- like	1.66	0.00002
CA591716	AOS	*N.a.*	Allene oxide synthase	1.65	0.00152
CA591872	αDOX	*N.a.*	Pathogen-inducible alpha-dioxygenase	1.63	0.00018
AF230371	AOS	*S.l.*	Allene oxide cyclase	1.61	0.00860
BQ508766	CDPK	*S.t.*	Calcium-dependent protein kinase	1.61	0.00094
BQ507870	PAL	*S.t.*	Phenylalanine ammonia-lyase	1.61	0.00032
AY426751	PIN	*N.a.*	Proteinase inhibitor repeat region	1.59	0.00007
BQ113079	LOX	*S.t.*	13-lipoxygenase	1.57	0.00009
BQ511245	DEHYDRIN	*S.t.*	Abscisic acid and environmental stress inducible protein	1.55	0.02250
BQ118479	PPO	*S.t.*	Polyphenol oxidase A chloroplast precursor	1.54	0.00217
M90692	PAL	*S.l.*	Phenylalanine ammonia-lyase	1.52	0.00409
AJ278332	OPR3	*S.l.*	12-oxophytodienoate reductase 3	1.51	0.00059
AB125232	GA2ox1	*N.t.*	Gibberellin-2-Oxidase 1	1.50	0.00001
BQ111457	WINP	*S.t.*	Wound inductive gene	-1.50	0.03296
AY460335	NIR	*N.a.*	Nitrate reductase	-1.50	0.00032
CF920198	PR-10	*N.a.*	Pathogen related protein 10	-1.51	0.00009
X66145	NIR1	*N.t.*	Nitrite reductase	-1.53	0.00291
AY456266	Defensin	*N.a.*	Defensin	-1.54	0.00003
BQ121879	ABP19a	*S.t.*	Auxin-binding protein ABP19a precursor	-1.55	0.00005
CA591795	RUBISCO	*N.a.*	Ribulose-1,5-bisphosphate carboxylase small subunit pseudogene	-1.55	0.00233
AW191829	RUBISCO	*N.a.*	Small subunit of ribulose bisphosphate carboxylase	-1.58	0.00603
CA591850	ATPS	*N.a.*	ATP synthase beta chain, mitochondrial precursor	-1.59	0.00003
CA591841	RUBISCO	*N.a.*	N. tabacum ribulose-1,5-bisphosphate carboxylase small subunit psuedogene	-1.63	0.00307
BQ118187	MDH	*S.t.*	Malate dehydrogenase-like protein	-1.63	0.00023
CF920204	PR-10	*N.a.*	Pathogen related protein 10	-1.67	0.00000
CA591837	MTH	*N.a.*	Metallothionein-like protein	-1.68	0.00006
X56266	AUX	*N.t.*	Auxin-induced mRNA	-1.72	0.00128
CA591773	PSI-II	*N.a.*	6.1 kDa polypeptide of photosystem II	-1.74	0.00013
CA591793	PSI-II	*N.a.*	Photosystem II	-1.80	0.00003
X14058	NIA1	*N.t.*	Nitrate reductase	-1.81	0.00021
BU494544	RUBISCO	*N.a.*	Small subunit of rubisco	-1.82	0.00014
CA591784	RUBISCO	*N.a.*	Ribulose-1,5-bisphosphate carboxylase small subunit pseudogene	-1.83	0.00087

BQ120559	t-KETO	*S.t.*	Transketolase chloroplast precursor	-1.85	0.00000
BU494505	WRKY	*N.a.*	WRKY family transcription factor	-1.86	0.00130
AW191829	RUBISCO	*N.a.*	Small subunit RUBISCO	-2.00	0.00059
BQ115513	RUBISCO	*S.t.*	Ribulose bisphosphate carboxylase small chain 2A	-2.06	0.00005
AF393847	AMY	*S.t.*	Beta-amylase	-2.08	0.00030
BQ516640	CYP76A2	*S.t.*	Cytochrome P450 76A2	-2.46	0.00600
BQ114644	bMSD	*S.t.*	Beta-mannosidase enzyme	-2.62	0.00011

Ratio refers to the absolute expression of the MeJA treatment divided by the absolute expression in the control. The *P*-value denotes the significance of the ratio after a *t*-test on the intensity values of the four replicate spots. *N. a.*, *Nicotiana attenuata*; *S.t.*, *Solanum tuberosum*; *N.t.*, *Nicotiana tabacum*; *S.l.*, *Solanum lycopersicum*; *C.a.*, *Capsicum anum*; *S.a.*, *Solanum americanum*; *S.n.*, *Solanum nigrum*; *A.t.*, *Arabidopsis thaliana*.

Table S2. The list of selected genes differentially regulated by JA-Ile

Accession No.	Gene name	Plant	Gene description / putative annotation	Ratio	*P*-Value
BQ516725	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	2.96	0.00000
BQ512427	NEC4	*S.t.*	Putative xyloglucanase inhibitor	2.47	0.02709
BQ121693	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	2.09	0.00001
BQ113794	APH	*S.t.*	Putative acid phosphatase	1.85	0.00001
BQ115240	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	1.83	0.00105
AI484262	GERMIN	*S.l.*	Germin	1.83	0.00016
AJ414400	HPL	*N.a.*	Hydroperoxide lyase	1.81	0.00005
BQ115689	VP4B	*S.t.*	Vacuolar protein sorting factor 4B-like	1.80	0.00055
BQ111809	HPL	*S.t.*	Fatty acid hydroperoxide lyase	1.78	0.00004
BQ117543	DSI	*S.t.*	Protein disulfide isomerase-like	1.78	0.02999
BQ505800	Ghfe1	*S.t.*	Cell elongation protein DIMINUTO	1.76	0.00227
DQ359730	JAR6	*N.a.*	JAR 6	1.73	0.00011
AJ414400	HPL	*N.a.*	Hydroperoxide lyase(HPL)	1.73	0.00000
BQ117632	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	1.71	0.01223
AY426751	PIN	*N.a.*	Proteinase inhibitor repeat region	1.67	0.00190
BQ118639	GPPH	*S.t.*	Alpha-glucan phosphorylase H isozyme	1.67	0.00056
BQ113651	BiP	*S.t.*	Luminal binding protein precursor (BiP)	1.66	0.00024
BQ113295	TBC	*S.t.*	Plastocyanin chloroplast precursor	1.62	0.00349
BQ111457	WINP	*S.t.*	Wound inductive gene	1.62	0.00009
X56266	AUX	*N.t.*	Auxin-induced mRNA	1.61	0.00133
AF193439	GST	*S.l.*	Glutathione S-transferase	1.59	0.00000
BQ121887	CPK1	*S.t.*	Protein kinase CPK1	1.59	0.00095
BQ118187	MDH	*S.t.*	Malate dehydrogenase-like protein	1.57	0.00000
CA591813	HMGR2	*N.a.*	3-hydroxy-3-methylglutaryl-coenzyme A reductase	1.54	0.01955
AJ007630	αDOX	*N.t.*	Pathogen induced oxygenase	1.54	0.00359
AB055499	Hxk	*N.t.*	Hexokinase	1.54	0.00055
BQ513582	APH	*S.t.*	Putative acid phosphatase	1.52	0.00012
A27686	PPO	*S.t.*	Polyphenol oxidase	1.51	0.00000
BQ507669	TRX-H1	*S.t.*	Thioredoxin H-type 1	1.50	0.00010
BQ514441	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 1	-1.50	0.00018
BQ120646	AAT	*S.t.*	Alcohol acyl transferase	-1.53	0.00029
BU494545	RUBISCOa	*N.a.*	Rubisco activase	-1.55	0.00484
BU494544	RUBISCO	*N.a.*	Small subunit of rubisco	-1.63	0.00035
Z21793	DAHPS2	*S.l.*	DAHP synthase 2 precursor	-1.67	0.00006
BQ515363	AdoMetDC	*S.t.*	S-adenosyl-L-methionine decarboxylase proenzyme	-1.87	0.00004
AF272244	TEAS	*N.t.*	5-epi-aristolochene synthase	-1.88	0.01484
AB038494	QPT	*N.t.*	Quinolinatephosphoribosyltransferase	-1.98	0.00005
CA591725	EIN3b1	*N.a.*	EIN3-binding F-box protein 1	-2.69	0.00360
AY426756	ACO	*N.a.*	ACC oxidase 1	-3.54	0.00001

Ratio refers to the absolute expression of the JA-Ile treatment divided by the absolute expression in the control. The *P*-value denotes the significance of the ratio after a *t*-test on the intensity values of the four replicate spots. *N. a.*, *Nicotiana attenuata*; *S.t.*, *Solanum tuberosum*; *N.t.*, *Nicotiana tabacum*; *S.l.*, *Solanum lycopersicum*.

Table S3. The list of selected genes differentially regulated by JA-Leu

Accession No.	Gene name	Plant	Gene description / putative annotation	Ratio	*P*-Value
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	2.99	0.00331
AF272244	TEAS	*N.t.*	5-epi-aristolochene synthase	2.64	0.00506
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	2.62	0.00002
Z12753	PIN2	*S.t.*	Proteinase inhibitor II.	2.41	0.00020
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	2.24	0.00025
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	2.22	0.00005
CF920209	FBH	*N.a.*	Putative flavonol synthase	2.16	0.00184
BQ115114	DOXPS	*S.t.*	1-deoxyxylulose 5-phosphate synthase	2.08	0.00321
A27686	PPO	*S.t.*	Polyphenol oxidase	2.06	0.00024
AJ007630	αDOX	*N.t.*	Pathogen induced oxygenase	2.06	0.00016
BQ516725	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	1.98	0.00397
BQ113872	LIS	*S.t.*	Linalool synthase-like protein	1.96	0.00043
BU494535	GLT	*N.a.*	Beta 1,3-glycosyltransferase-like protein I	1.92	0.00001
BQ516602	JA2	*S.t.*	Jasmonic acid 2	1.92	0.03484
AY426751	PIN	*N.a.*	Proteinase inhibitor repeat region	1.91	0.00000
X63560	SHK	*S.l.*	Shikimate kinase precursor	1.89	0.04689
DQ768747	PAL	*N.a.*	NaPAL2	1.88	0.00005
BQ514441	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 1	1.86	0.00065
M62755	4CL	*N.s.*	4-courmarate--CoA ligase	1.86	0.00234
BQ115240	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	1.86	0.00015
AF229926	αDOX	*N.a.*	Pathogen inducible alpha-dioxygenase	1.75	0.00500
AF229926	αDOX	*N.a.*	Pathogen inducible alpha-dioxygenase	1.73	0.02010
BQ513122	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 2	1.72	0.00003
BQ113812	SPDSY1	*S.t.*	Spermidine synthase 1	1.71	0.00001
BQ514499	4CL	*S.t.*	4-coumarate:coenzyme A ligase	1.66	0.00005
A27686	PPO	*S.t.*	Polyphenol oxidase	1.66	0.01264
BQ112770	PIN	*S.t.*	Cysteine protease	1.62	0.00054
AJ344155	CDPK3	*N.t.*	Calcium-dependent protein kinase 3	1.61	0.00055
BQ121693	αDOX	*S.t.*	Pathogen-inducible alpha-dioxygenase	1.60	0.00088
BQ114198	C4H	*S.t.*	Cinnamic acid 4-hydroxylase	1.60	0.00006
AF212318	C4H	*C.a.*	Cinnamic acid 4-hydroxylase	1.59	0.00111
AB006692	SPDSY	*N.s.*	Spermidine synthase	1.58	0.00022
M90692	PAL	*S.l.*	Phenylalanine ammonia-lyase	1.57	0.00226
L46847	DHYS	*S.l.*	Dehydroquinate synthase	1.57	0.03263
AW191821	αDOX	*N.a.*	Pathogen-inducible alpha-dioxygenase	1.55	0.00040
AJ007630	αDOX	*N.t.*	Pathogen induced oxygenase	1.55	0.00019
CA591716	AOS	*N.a.*	Allene oxide synthase	1.54	0.00545
BQ511530	PP2C	*S.t.*	Protein phosphatase 2C	1.54	0.00360
AF280402	PMT1	*N.a.*	Putrescine N-methyltransferase 1	1.53	0.02130

AF542547	PIN	*N.a.*	Proteinase inhibitor full length	1.52	0.00014
AF071786	SPS	*S.l.*	Sucrose-phosphate synthase	1.51	0.00106
AF000375	SYS	*N.s.*	Prosystemin	1.51	0.00019
M61905	EPSPS	*N.t.*	5-enolpyruvylshikimate-3-phosphate synthase	1.51	0.00284
AY460335	NIR	*N.a.*	Nitrate reductase	-1.51	0.01316
X73477	SPS	*S.t.*	Sucrose-phosphate-synthase	-1.51	0.00062
BQ515829	PME	*S.t.*	Pectin methyl esterase	-1.52	0.00013
BQ115513	RUBISCO	*S.t.*	Ribulose bisphosphate carboxylase small chain 2A	-1.53	0.02644
CA591818	MTH	*N.a.*	Metallothionein-like protein	-1.56	0.00013
AJ344156	CDPK2	*N.b.*	Calcium-dependent protein kinase 2	-1.58	0.00524
CA591730	CCR4	*N.a.*	Putative CCR4-associated factor 1	-1.58	0.01395
CA591773	PSI-II	*N.a.*	6.1 kDa polypeptide of photosystem II	-1.58	0.00025
CA591843	GST	*N.a.*	Glutathione S-transferase	-1.61	0.00023
CA591837	MTH	*N.a.*	Metallothionein-like protein type 2	-1.62	0.00227
AW191829	RUBISCO	*N.a.*	N. silvestris small subunit RUBISCO	-1.64	0.00595
BQ516569	AdoMetDC	*S.t.*	Adenosylmethionine decarboxylase	-1.68	0.00263
BQ111888	AMNT2	*S.t.*	Aminotransferase 2	-1.69	0.01491
X66145	NIR1	*N.t.*	Nitrite reductase	-1.69	0.00029
BQ121879	ABP19a	*S.t.*	Auxin-binding protein ABP19a precursor	-1.71	0.00004
BQ121735	FBPA	*S.t.*	Fructose-bisphosphate aldolase cytoplasmic isozyme 1	-1.74	0.00007
BQ112525	FBPA	*S.t.*	Fructose-bisphosphate aldolase cytoplasmic isozyme 1	-1.85	0.00009
AF186777	XET4	*S.l.*	Xyloglucan endotransglycosylase	-1.89	0.00042
BU494544	RUBISCO	*N.a.*	Small subunit of rubisco	-1.92	0.00197
BQ114644	bMSD	*S.t.*	Beta-mannosidase enzyme	-2.16	0.02570
X14058	NIA1	*N.t.*	Nitrate reductase	-2.94	0.00001

Ratio refers to the absolute expression of the JA-Leu treatment divided by the absolute expression in the control. The *P*-value denotes the significance of the ratio after a *t*-test on the intensity values of the four replicate spots. *N. a.*, *Nicotiana attenuata*; *S.t.*, *Solanum tuberosum*; *N.t.*, *Nicotiana tabacum*; *S.l.*, *Solanum lycopersicum*; *C.a.*, *Capsicum anum*; *S.a.*, *Solanum americanum*; *S.n.*, *Solanum nigrum*; *N.b.*, *Nicotiana benthamiana*.

Table S4. The list of selected genes differentially regulated by JA-Val

Accession No.	Gene name	Plant	Gene description / putative annotation	Ratio	*P*-Value
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	5.51	0.00001
AF209709	SaPIN2a	*S.a.*	Proteinase inhibitor IIb	5.26	0.00007
Z12753	PIN2	*S.t.*	Proteinase inhibitor II.	4.53	0.00000
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	4.50	0.00001
BQ113381	LSP	*S.t.*	Putative 7-transmembrane G-protein-coupled receptor	3.72	0.00008
K03291	PIN2	*S.l.*	Inhibitor 2 of Ser proteases	3.66	0.00001
AY426751	PIN	*N.a.*	Proteinase inhibitor repeat region	3.20	0.00007
AF272244	TEAS	*N.t.*	5-epi-aristolochene synthase	3.15	0.00256
A27686	PPO	*S.t.*	Polyphenol oxidase	3.04	0.00016
BQ119647	HPL	*S.t.*	Fatty acid hydroperoxide lyase	2.88	0.00007
BU494535	GLT	*N.a.*	Beta 1,3-glycosyltransferase-like protein	2.84	0.00628
BQ113872	LIS	*S.t.*	Linalool synthase-like protein	2.41	0.00006
A27686	PPO	*S.t.*	Polyphenol oxidase	2.31	0.00007
BQ516725	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	2.22	0.00575
BQ113812	SPDSY1	*S.t.*	Spermidine synthase 1	2.19	0.00000
AY426751	PIN	*N.a.*	Proteinase inhibitor signal peptide and first repeat	2.18	0.00001
AF542547	PIN	*N.a.*	Proteinase inhibitor full length	2.04	0.00333
M93719	CAT	*S.l.*	Catalase1	2.02	0.00641
CF920209	FBH	*N.a.*	Putative flavonol synthase	2.00	0.00001
AB006692	SPDSY	*N.s.*	Spermidine synthase	1.97	0.00028
AF272244	TEAS	*N.t.*	5-epi-aristolochene synthase	1.91	0.00004
BQ516602	JA2	*S.t.*	Jasmonic acid 2	1.90	0.01190
BQ115114	DOXPS	*S.t.*	1-deoxyxylulose 5-phosphate synthase	1.88	0.00445
BQ113079	LOX	*S.t.*	13-lipoxygenase	1.88	0.00001
M62755	4CL	*S.n.*	4-courmarate--CoA ligase	1.85	0.00020
M93719	CAT	*S.l.*	Catalase1	1.80	0.00091
BQ112096	ADC1	*S.t.*	Arginine decarboxylase 1	1.78	0.00033
AY456268	THIONIN	*N.a.*	Gamma-thionin	1.78	0.00008
BU494528	THIONIN	*N.a.*	Flower-specific thionin	1.76	0.00028
X63560	SHK	*S.l.*	Shikimate kinase precursor	1.76	0.00004
DQ768747	PAL	*N.a.*	NaPAL2	1.74	0.00556
BQ515053	SESQ2	*S.t.*	Sesquiterpene synthase 2	1.73	0.00031
AF174381	SaPIN2b	*S.a.*	Proteinase inhibitor IIb	1.71	0.00041
BQ117632	IPPI	*S.t.*	Isopentenyl diphosphate isomerase 1	1.71	0.00755
BQ121269	CAT2	*S.t.*	Catalase isozyme 1	1.70	0.00123
BQ509014	AdoMetS	*S.t.*	S-adenosylmethionine synthetase 1	1.70	0.00112
BQ112708	APH	*S.t.*	Putative acid phosphatase	1.69	0.00002
AF542547	TPS	*N.a.*	Trypsin proteinase inhibitor	1.68	0.00001
BQ113865	LADOX	*S.t.*	Leucoanthocyanidin dioxygenase-like protein	1.66	0.00865
AF174381	SaPIN2b	*S.a.*	Proteinase inhibitor IIb	1.64	0.00004

M61905	EPSPS	*N.t.*	5-enolpyruvylshikimate-3-phosphate synthase	1.64	0.00002
BQ114604	SPDSY	*S.t.*	Spermidine synthase	1.63	0.00000
BQ514441	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 1	1.62	0.00180
BQ117729	PPO	*S.t.*	Polyphenol oxidase	1.62	0.00034
AB012873	ADC	*N.s.*	Arginine decarboxylase	1.61	0.00024
AF280402	PMT1	*N.a.*	Putrescine N-methyltransferase 1	1.60	0.01487
L46847	DHYS	*S.l.*	Dehydroquinate synthase	1.59	0.00001
BQ514499	4CL	*S.t.*	4-coumarate:coenzyme A ligase	1.57	0.00001
AY254349	LOX3	*N.a.*	Lipoxygenase	1.55	0.00438
BQ513122	CSH	*S.t.*	P-coumaroyl shikimate 3'-hydroxylase isoform 2	1.53	0.00023
CF920211	JMT	*N.a.*	Jasmonic acid carboxyl methyltransferase- like	1.52	0.00201
BQ111809	HPL	*S.t.*	Fatty acid hydroperoxide lyase	1.52	0.00008
AF229926	αDOX	*N.a.*	Pathogen inducible alpha-dioxygenase	1.51	0.03185
BQ513669	CPR	*S.t.*	Cysteine protease	1.51	0.00132
BQ114448	SODM	*S.t.*	Superoxide dismutase	1.51	0.00113
AY426757	GLS	*N.a.*	Glutamine synthetase	-1.52	0.00021
AW191824	GLS	*N.a.*	Glutamate synthase precursor	-1.52	0.01377
AF280402	PMT2	*N.a.*	Putrescine N-methyltransferase 1	-1.53	0.00015
AF186777	XET4	*S.l.*	Xyloglucan endotransglycosylase	-1.57	0.00262
BU494505	WRKY	*N.a.*	WRKY family transcription factor	-1.59	0.00001
BU494559	PSI-I	*N.a.*	Photosystem I reaction center subunit XI	-1.62	0.00000
CA591793	PSI-II	*N.a.*	Photosystem II	-1.62	0.00003
BQ120559	t-KETO	*S.t.*	Transketolase chloroplast precursor	-1.64	0.00019
BQ115513	RUBISCO	*S.t.*	Ribulose bisphosphate carboxylase small chain 2A	-1.65	0.00001
CF920205	WIBP	*N.a.*	Wound induced basic protein	-1.67	0.00473
BQ121940	ABP19a	*S.t.*	Auxin-binding protein ABP19a precursor	-1.71	0.00022
BQ510851	FBP	*S.t.*	Fructose-1 6-bisphosphatase cytosolic	-1.75	0.00020
BQ515388	CYP72B	*S.t.*	Cytochrome P450 monooxygenase CYP72B	-1.77	0.00011
X66145	NIR1	*N.t.*	Nitrite reductase	-1.77	0.00027
CA591837	MTH	*N.a.*	Metallothionein-like protein	-1.82	0.00006
AF510035	ANK1	*N.t.*	Ankyrin domain protein	-1.84	0.00043
AW191829	RUBISCO	*N.a.*	Small subunit of ribulose bisphosphate carboxylase	-1.86	0.00735
BQ113804	AMNT2	*S.t.*	Aminotransferase 2	-1.86	0.00062
CA591841	RUBISCO	*N.a.*	Ribulose-1,5-bisphosphate carboxylase small subunit psuedogene	-1.89	0.00023
X76946	FBP	*S.t.*	Fructose-1,6-bisphosphatase	-1.90	0.00020
CA591818	MTH	*N.a.*	Metallothionein-like protein	-1.97	0.00002
BQ121735	FBPA	*S.t.*	Fructose-bisphosphate aldolase	-1.97	0.00067
BQ511858	FBP	*S.t.*	Fructose-1 6-bisphosphatase	-1.98	0.00001
AF186777	XET4	*S.l.*	Xyloglucan endotransglycosylase	-1.99	0.00000

BQ111888	AMNT2	*S.t.*	Aminotransferase 2	-2.10	0.00041
BQ121879	ABP19a	*S.t.*	Auxin-binding protein ABP19a precursor	-2.11	0.00007
CA591784	RUBISCO	*N.a.*	Ribulose-1,5-bisphosphate carboxylase small subunit pseudogene	-2.12	0.00024
BU494545	RUBISCOa	*N.a.*	Rubisco activase	-2.13	0.00060
AW191829	RUBISCO	*N.a.*	Small subunit RUBISCO	-2.24	0.00383
X14058	NIA1	*N.t.*	Nitrate reductase (nia-1)	-2.35	0.00006
BQ112525	FBPA	*S.t.*	Fructose-bisphosphate aldolase cytoplasmic isozyme 1	-2.49	0.00000
BQ114644	bMSD	*S.t.*	Beta-mannosidase enzyme	-2.60	0.00009
CA591725	EIN3b1	*N.a.*	EIN3-binding F-box protein 1	-2.66	0.00012
BU494544	RUBISCO	*N.a.*	Small subunit of rubisco	-3.40	0.00000

Ratio refers to the absolute expression of the JA-Val treatment divided by the absolute expression in the control. The *P*-value denotes the significance of the ratio after a *t*-test on the intensity values of the four replicate spots. *N. a.*, *Nicotiana attenuata*; *S.t.*, *Solanum tuberosum*; *N.t.*, *Nicotiana tabacum*; *S.l.*, *Solanum lycopersicum*; *S.a.*, *Solanum americanum*; *A.t.*, *Arabidopsis thaliana*; *N.s.*, *Nicotiana sylvestris*.

Figure S1

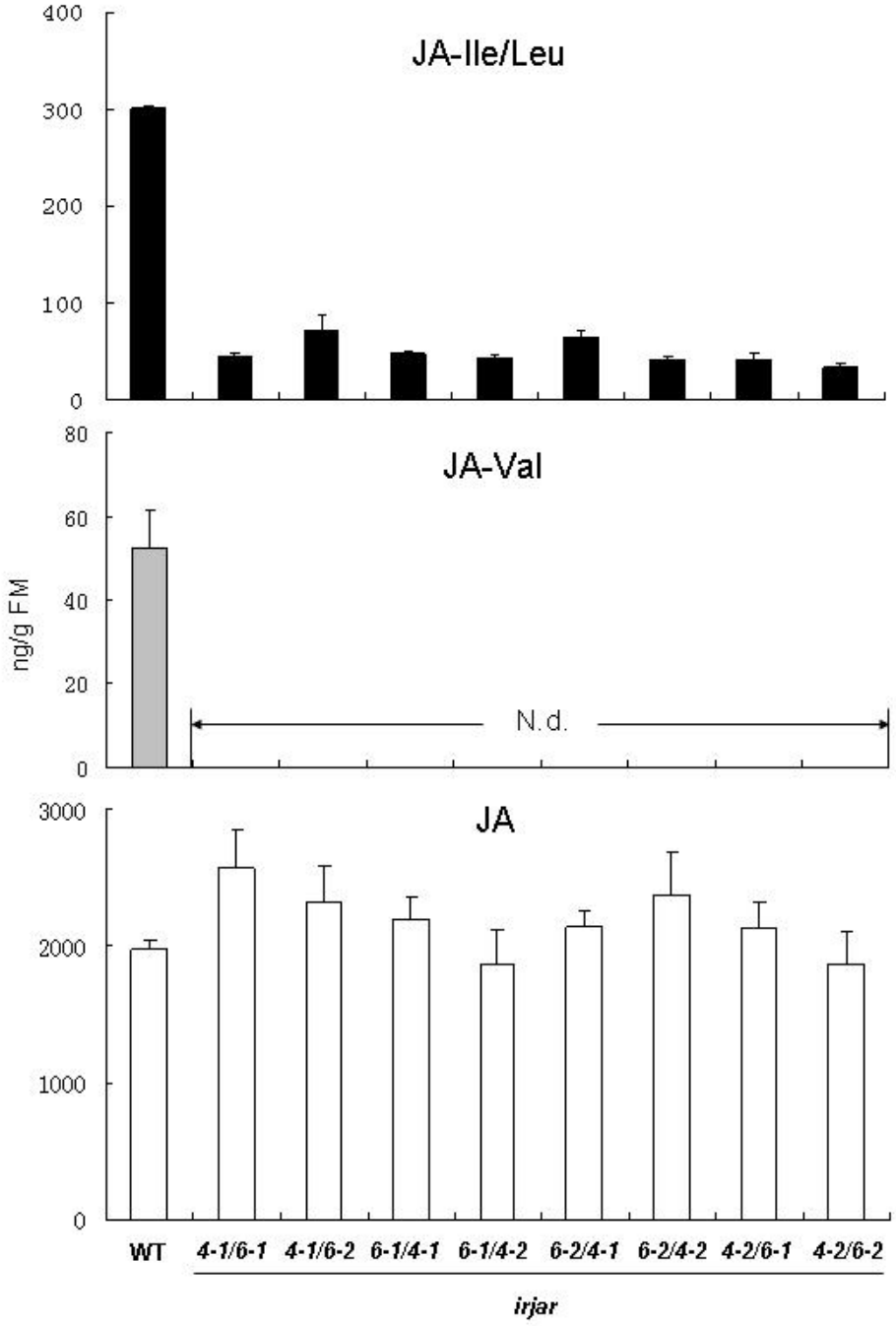
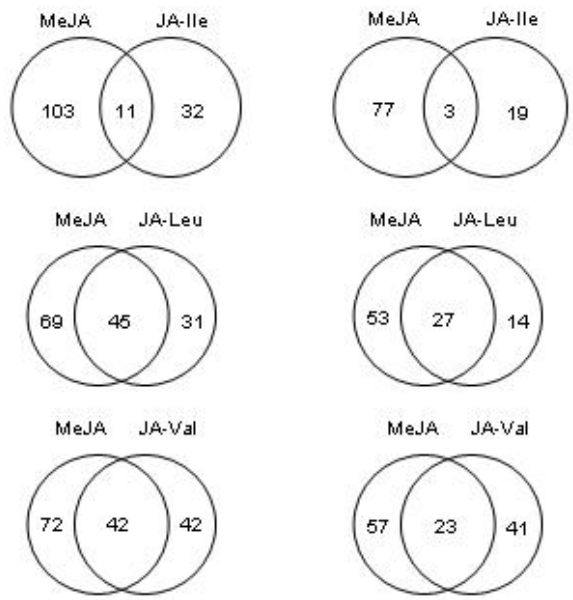
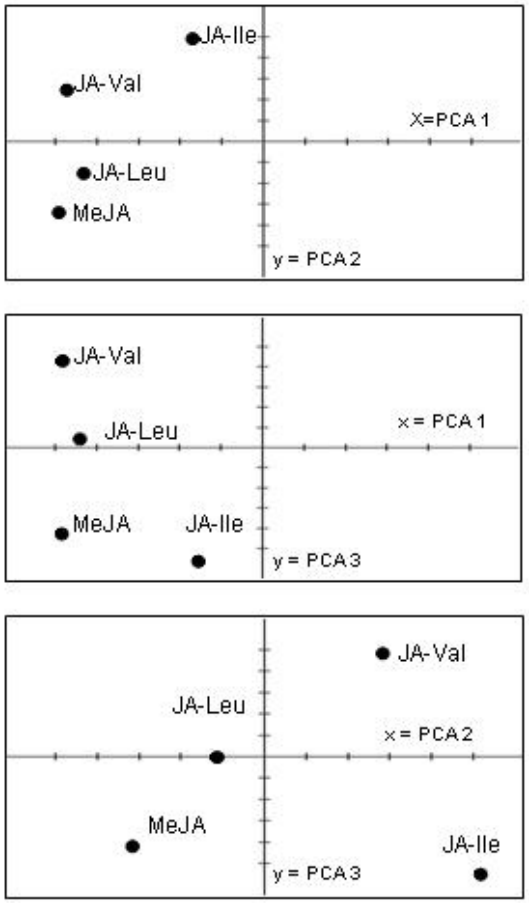

JA-Ile/Leu
400
300
200
100
0
JA-Val
80
60
40
20
0
ng/g FM
N.d.
JA
3000
2000
1000
0
WT
4-1/6-1
4-1/6-2
6-1/4-1
6-1/4-2
6-2/4-1
6-2/4-2
4-2/6-1
4-2/6-2
irjar

Figure S2

A


MeJA
JA-Ile
103
11
32
MeJA
JA-Ile
77
3
19
MeJA
JA-Leu
69
45
31
MeJA
JA-Leu
53
27
14
MeJA
JA-Val
72
42
42
MeJA
JA-Val
57
23
41
Up-regulated genes
Down- regulated genes

B


JA-Ile
JA-Val
X=PCA 1
JA-Leu
MeJA
y = PCA 2
JA-Val
JA-Leu
x = PCA 1
MeJA
JA-Ile
y = PCA 3
JA-Val
JA-Leu
x = PCA 2
MeJA
JA-Ile
y = PCA 3