

Supplemental Data

Chemical Inhibition of a Subset
of *Arabidopsis Thaliana* GSK3-like Kinases

Activates Brassinosteroid Signaling

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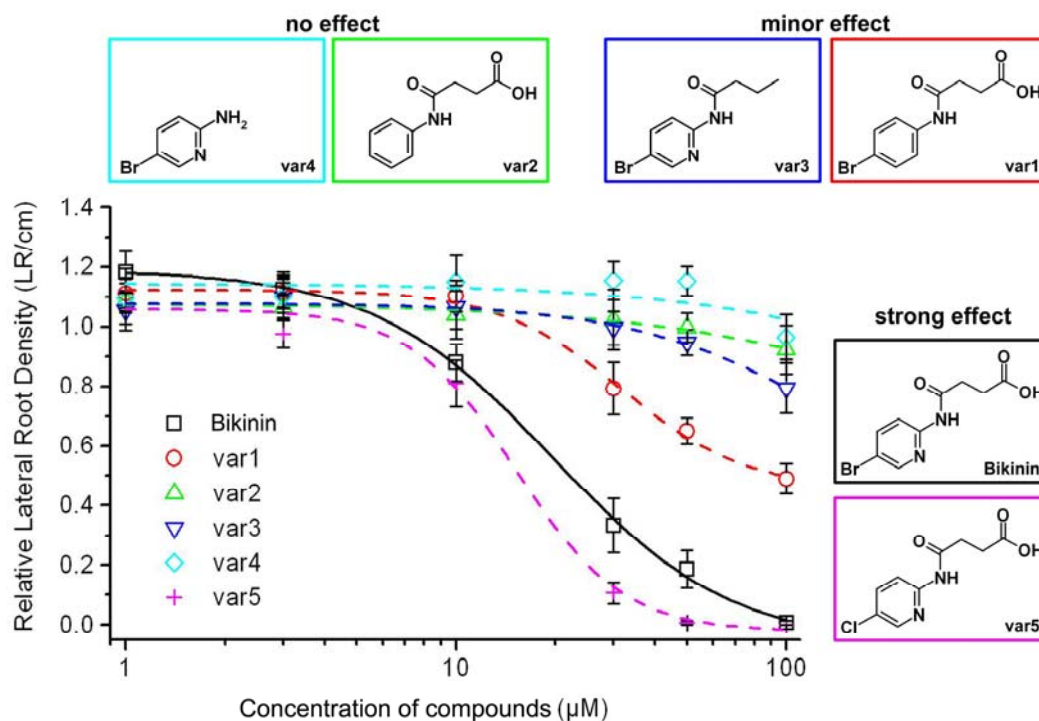


Figure S1. Decrease of Lateral Root Density by Bikinin and Its Variants

Dose-response analysis of bikinin and its derivate structures. Three days after germination, seedlings were transferred to medium containing bikinin or DMSO and grown for an additional seven days. Lateral root density (number of lateral roots/cm) of compound-treated plants was compared to DMSO-treated plants (relative lateral root density). All results are means \pm s.e. ($n \geq 10$ for each data point) and experiments were repeated at least twice.

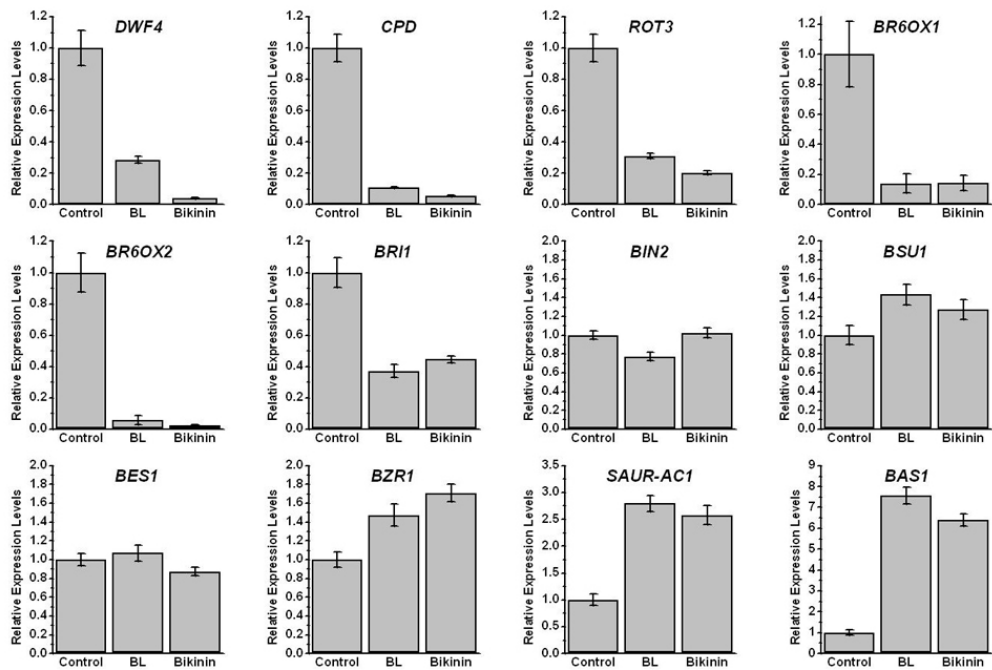


Figure S2. Transcriptional Regulation of the BR Pathway by Bikinin and BL
 Quantitative RT-PCR experiment measuring the relative expression levels of five BR-biosynthetic genes (*DWF4*, *CPD*, *ROT3*, *BR6OX1*, and *BR6OX2*), five BR-regulated genes (*BRI1*, *BIN2*, *BSU1*, *BES1*, and *BZR1*), and two BR-upregulated genes (*SAUR-AC1* and *BAS1*) on 3-day-old seedlings after treatment with BL (1 μM) or bikinin (30 μM) for 6 h compared to DMSO-treated controls. All results are means ± s.d. Individual reactions were done in triplicate and experiments were repeated at least twice.

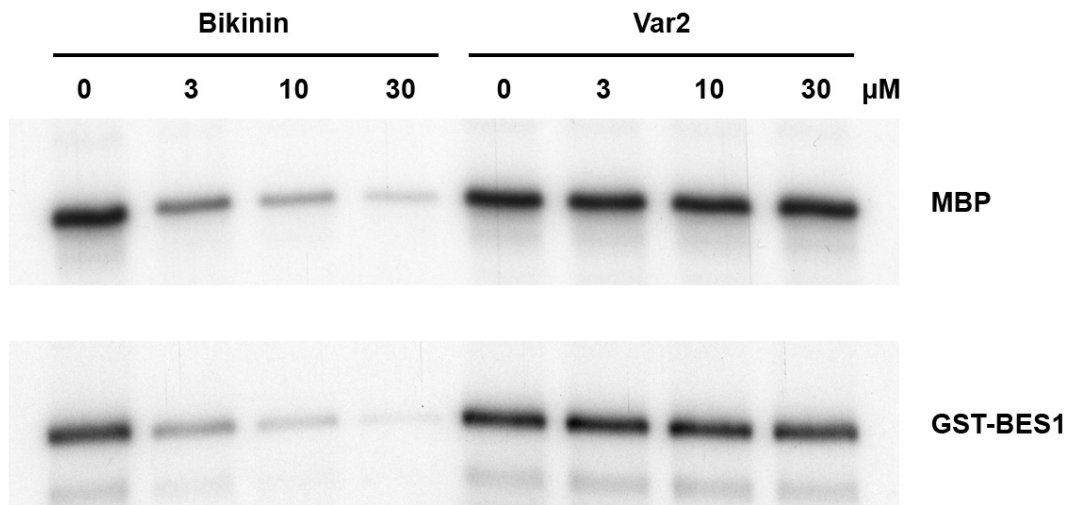
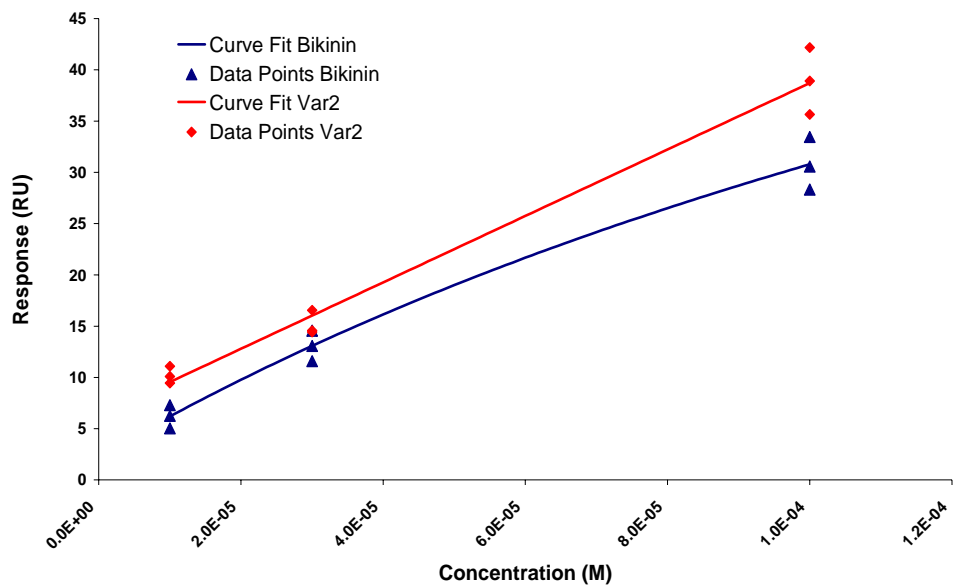


Figure S3. Autoradiography of a Kinase Assay with GST-BIN2
 A concentration gradient of Bikinin or the inactive variant 2 were assayed and either MBP or GST-BES1 was used as a substrate.



	KD (M)	Rmax (RU)	offset (RU)	Chi ² (RU ²)
Bikinin	2.41E-04	97.1	2.3	3.37
Var2	4.899	1587401.3	6.3	4.83

Figure S4. Affinity Curves for Bikinin and var2 (Top) and Calculated Affinity Parameters for Both Compounds (Bottom)

Reference and blank data are subtracted. The experiment was done in triplicate for each concentration.

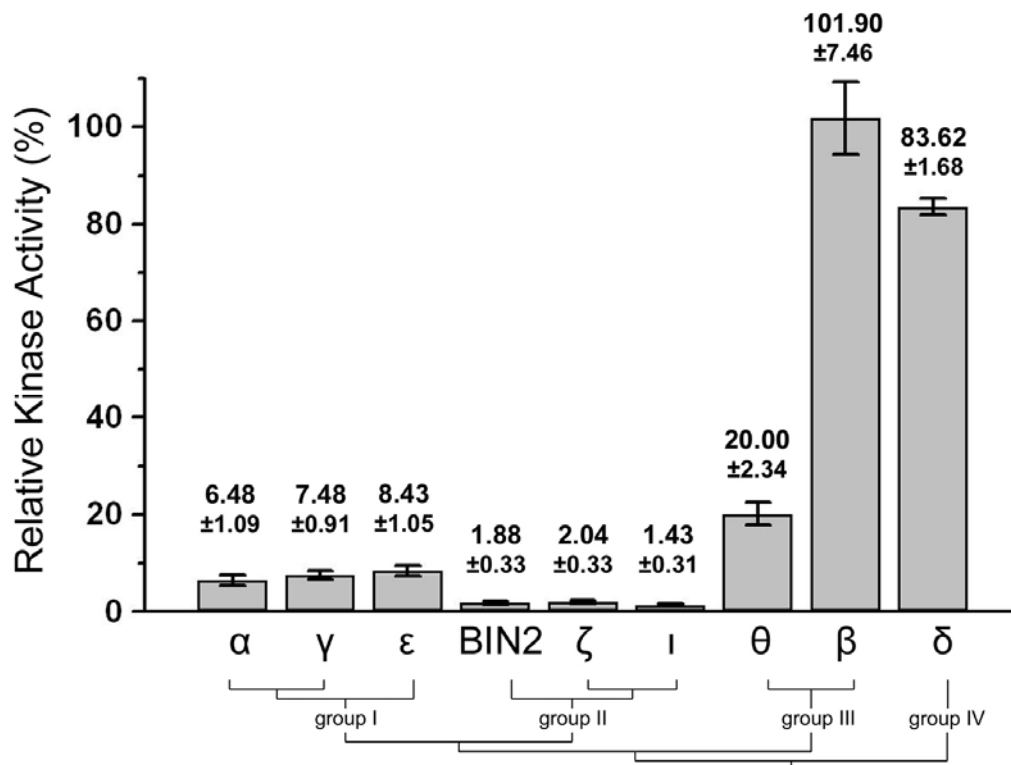


Figure S5. Quantification of the Inhibitory Effect of 10 μ M Bikinin on ASK Activity

The activity without bikinin was set to 100% for each kinase. All results are represented as means \pm s.d. Experiments were repeated four times.

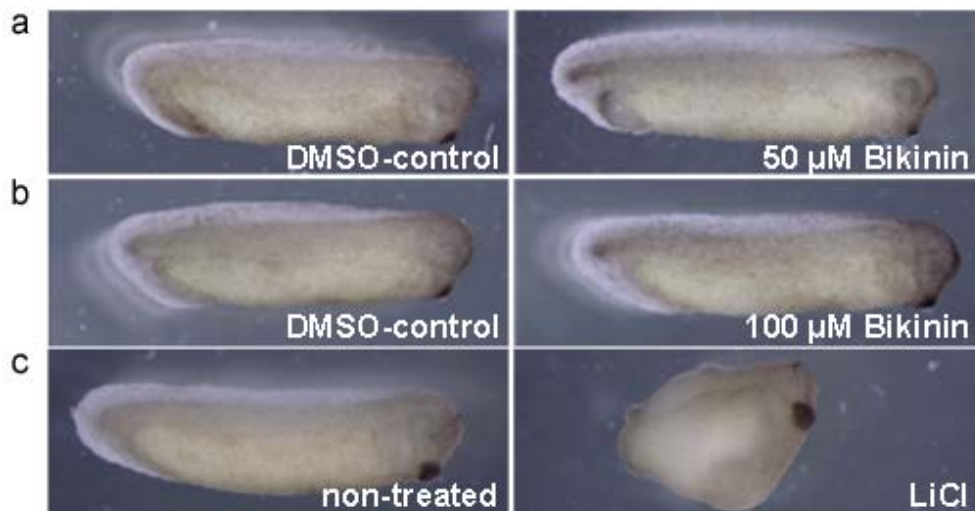


Figure S6. In Vivo Effect of Bikinin on *Xenopus laevis* Embryos

Early blastula embryos (\pm 32-cell stage) of *Xenopus* were treated for 24 h with 50 μ M or 100 μ M bikinin (A and B) in 0.1x Marc's modified Ringer's (MMR) solution (0.01 M NaCl; 0.18 mM KCl; 0.2 mM CaCl₂; 0.1 mM MgCl₂; 0.5 mM HEPES, pH 7.6) and those treated with DMSO were used as negative controls (A and B). As a standard test to induce dorsalization, early blastula embryos were treated with 0.3 M LiCl for 10 min (C). Embryos were washed several times with 0.1x MMR and photographed 48 hr later.

SI - Table 1. In vitro effect of 1 μ M bikinin and 10 μ M bikinin on the remaining activity of 77 human kinases (means \pm s.d.; experiments were performed in triplicate)

Tested Kinase name	residual activity when treated with 1 μ M bikinin		residual activity when treated with 10 μ M bikinin	
	mean	s.d.	mean	s.d.
MKK1	89.5	4.65	98.4	5.56
ERK1	78.0	7.61	78.7	6.79
ERK2	84.6	9.86	83.0	9.68
JNK1	111.3	3.01	112.0	2.18
JNK2	118.9	4.00	93.0	0.73
JNK3	89.0	6.45	85.8	12.39
p38a MAPK	88.9	8.56	100.6	3.39
P38b MAPK	86.6	8.48	95.1	10.79
p38g MAPK	99.6	6.43	101.3	9.15
p38s MAPK	109.2	4.00	85.0	1.91
ERK8	94.9	12.44	70.4	5.42
RSK1	95.0	8.89	79.6	1.34
RSK2	107.7	13.69	117.6	0.13
PDK1	88.0	3.50	87.9	0.13
PKBa	111.0	13.04	116.2	7.00
PKBb	95.7	14.94	91.9	11.17
SGK1	106.9	5.00	107.4	6.00
S6K1	97.0	4.08	90.0	4.32
PKA	88.6	2.45	92.9	4.70
ROCK 2	92.6	0.15	102.5	14.08
PRK2	88.0	14.76	72.6	4.45
PKCa	87.6	2.77	80.2	7.33
PKC zeta	107.4	9.82	99.1	14.50
PKD1	97.4	4.44	96.4	12.79
MSK1	104.7	2.18	113.6	9.45
MNK1	80.5	1.59	84.5	1.18
MNK2	109.3	4.09	92.3	4.00
MAPKAP-K2	93.0	6.61	105.3	11.04
MAPKAP-K3	110.9	7.50	118.2	6.95
PRAK	84.7	2.82	88.2	4.20
CAMKKb	97.0	7.37	83.5	3.00
CAMK1	86.3	4.07	91.4	12.83
SmMLCK	96.2	2.04	122.4	12.50
PHK	92.5	6.04	94.9	13.30
CHK1	99.7	2.40	103.9	0.26
CHK2	92.7	0.00	101.1	-
GSK3b	80.5	4.67	54.4	0.21
CDK2-Cyclin A	88.8	3.01	82.5	3.90
PLK1	92.1	2.40	85.2	9.60

PLK1 (Okadaic Acid)	74.3	11.42	78.2	3.32
AURORA B	72.7	2.40	30.6	0.82
AURORA C	67.8	7.68	57.2	7.94
AMPK	107.4	2.11	112.0	1.26
MARK3	78.2	4.90	67.5	2.66
BRSK2	108.7	5.28	109.1	12.93
MELK	101.4	10.37	102.0	5.52
CK1	93.6	4.93	66.5	0.36
CK2	86.7	5.15	95.1	3.86
DYRK1A	101.5	5.79	100.8	2.92
DYRK2	80.1	6.43	61.2	2.60
DYRK3	84.4	6.78	70.5	13.62
NEK2a	100.1	7.00	100.2	12.50
NEK6	105.8	12.53	106.1	0.18
NEK7	101.1	9.83	93.9	3.23
IKKb	69.7	3.77	61.2	3.35
PIM1	105.6	0.31	111.1	8.34
PIM2	113.2	6.19	113.0	1.97
PIM3	83.5	2.06	93.4	3.50
SRPK1	94.8	2.90	106.1	5.01
MST2	86.5	3.25	89.3	3.82
EF2K	103.8	10.20	94.8	0.53
HIPK2	78.4	1.83	86.8	8.42
HIPK3	114.5	9.34	118.3	9.24
PAK4	99.0	8.00	93.2	2.18
PAK5	99.6	1.70	105.8	9.00
PAK6	97.6	3.86	107.2	10.40
Src	117.9	3.53	97.7	2.34
Lck	101.6	5.21	100.5	3.05
CSK	93.8	14.49	108.8	3.92
FGF-R1	98.0	7.56	96.3	1.59
IRR	91.6	7.00	78.9	7.08
EPH A2	83.1	13.12	120.5	15.35
MST4	85.3	5.92	81.0	5.04
SYK	57.0	7.68	85.4	8.99
YES1	113.9	0.59	98.3	13.31
IKKe	107.8	5.65	100.2	6.00
TBK1	113.2	7.73	109.8	3.88

SI - Table 2. List of the 272 significant genes.

The p-values give the level of significance of the three effects that regulate gene expression, namely: time (duration of hormone treatment), type of hormone treatment (treatment) and treatment and time (interaction between time and hormone treatment).

Affymetrix no.	Accession no.	Annotation	30 BIK	30 BL	30 DMSO	120 BIK	120 BL	120 DMSO	Fold	Orig. p-values (Treatment)	Orig. p-values (Time)	Orig. p-values (interaction)	Pbenj&hoch(Treatment)	Pbenj&hoch(Time)	Pbenj&hoch(interact)
255177_at	AT4G08040	1-aminocyclopropane-1-carboxylate synth	5.5	9.1	70.7	4.7	4.7	261.5	56.1	3.1E-11	1.9E-01	4.3E-05	7.2E-07	4.1E-01	3.4E-02
245362_at	AT4G17460	homeobox-leucine zipper protein 1 (HAT1)	205.4	386.5	717.1	30.6	53.1	280.2	9.1	2.1E-10	1.3E-11	4.2E-05	2.4E-06	1.7E-08	3.4E-02
246284_at	AT4G36780	brassinosteroid signalling positive regulatc	157.6	230.2	324.1	9.8	25.4	284.9	29.1	3.2E-10	7.2E-11	3.3E-08	2.4E-06	5.5E-08	7.6E-04
257858_at	AT3G12920	expressed protein	450.2	819.9	1006.9	241.7	324.9	787.5	3.3	2.4E-09	1.8E-08	2.1E-04	1.1E-05	2.5E-06	8.6E-02
261772_at	AT1G76240	expressed protein, contains Pfam profile F	126.5	181.0	318.6	22.7	49.1	303.7	13.4	2.2E-09	3.0E-08	6.7E-06	1.2E-05	3.5E-06	1.5E-02
256598_at	AT3G30180	Encodes a cytochrome p450 enzyme that	32.9	114.2	362.6	5.0	5.3	80.2	15.9	1.5E-08	4.5E-09	2.3E-03	5.9E-05	9.2E-07	2.9E-01
267305_at	AT2G30070	potassium transporter (KUP1), identical to	260.9	345.7	427.1	88.2	155.0	405.6	4.6	3.5E-08	1.3E-07	3.4E-05	8.9E-05	9.5E-06	3.2E-02
258196_at	AT3G13980	expressed protein	64.4	181.1	256.8	10.3	56.0	125.9	12.2	3.0E-08	1.5E-07	6.0E-03	9.7E-05	1.0E-05	4.3E-01
265158_at	AT1G31040	zinc-binding protein-related, simialr to zinc	13.9	9.0	10.3	41.9	10.7	9.6	4.4	3.4E-08	2.2E-05	8.6E-06	9.8E-05	3.6E-04	1.6E-02
261443_at	AT1G28480	glutaredoxin family protein, contains INTE	6.7	6.5	6.6	26.4	9.2	6.7	4.0	5.2E-08	1.8E-08	7.7E-08	1.2E-04	2.4E-06	8.8E-04
251039_at	AT5G02020	expressed protein	4.7	4.6	4.7	11.2	4.7	4.9	2.4	7.4E-08	3.5E-07	1.3E-07	1.4E-04	1.9E-05	9.6E-04
261456_at	AT1G21050	expressed protein, contains Pfam profile F	258.2	592.9	819.5	77.3	124.1	558.8	7.2	6.9E-08	1.5E-07	9.9E-04	1.4E-04	1.0E-05	1.9E-01
247191_at	AT5G65310	homeobox-leucine zipper protein 5 (HB-5)	622.8	625.6	690.7	83.4	113.3	420.7	5.0	1.1E-07	1.8E-11	4.8E-07	1.8E-04	1.8E-08	2.2E-03
245784_at	AT1G32190	expressed protein	134.9	186.0	185.3	12.1	18.8	169.8	14.1	1.0E-07	1.5E-09	5.9E-07	1.8E-04	4.8E-07	2.3E-03
261892_at	AT1G80840	WRKY family transcription factor, similar t	106.8	66.2	248.1	190.9	51.7	949.4	18.3	1.6E-07	1.9E-03	2.3E-03	2.5E-04	1.1E-02	2.9E-01
257642_at	AT3G25710	basic helix-loop-helix (bHLH) family proteir	79.3	177.3	166.5	12.0	61.7	117.2	9.8	1.7E-07	2.8E-07	3.0E-04	2.5E-04	1.6E-05	1.0E-01
250327_at	AT5G12050	expressed protein	2775.0	3909.6	5320.3	773.6	967.0	2870.0	3.7	2.0E-07	1.9E-09	1.2E-03	2.7E-04	5.3E-07	2.0E-01
253828_at	AT4G27970	C4-dicarboxylate transporter/malic acid tra	160.8	79.2	66.1	308.2	129.8	101.5	3.0	2.5E-07	1.1E-05	4.7E-01	3.1E-04	2.2E-04	7.2E-01
259848_at	AT1G72180	leucine-rich repeat transmembrane proteir	512.4	834.0	953.5	82.4	161.1	725.3	8.8	2.9E-07	2.6E-08	5.5E-05	3.4E-04	3.1E-06	3.8E-02
266265_at	AT2G29340	short-chain dehydrogenase/reductase (SD	394.0	216.8	253.7	1367.4	473.2	366.2	3.7	3.3E-07	8.8E-08	9.8E-04	3.8E-04	7.3E-06	1.9E-01
252184_at	AT3G50660	steroid 22-alpha-hydroxylase (CYP90B1) (186.8	185.3	394.8	11.6	12.4	540.6	46.6	4.0E-07	1.0E-06	2.7E-05	4.1E-04	4.0E-05	2.9E-02
257374_at	AT2G43280	far-red impaired responsive family protein	85.3	91.7	108.9	48.5	51.1	101.2	2.1	3.9E-07	1.9E-07	2.0E-04	4.2E-04	1.2E-05	8.4E-02
261400_at	AT1G79630	protein phosphatase 2C family protein / Pf	77.6	97.6	124.6	26.6	28.8	76.9	2.9	5.9E-07	3.3E-09	7.9E-04	5.6E-04	7.8E-07	1.6E-01

265245_at	AT2G43060	expressed protein, similar to cDNA bHLH f	62.9	93.4	89.3	25.1	23.5	82.2	3.5	6.8E-07	2.1E-08	6.3E-06	6.2E-04	2.7E-06	1.6E-02
247177_at	AT5G65300	expressed protein	31.7	25.4	100.7	27.7	40.6	111.4	4.0	7.2E-07	2.1E-01	1.1E-01	6.3E-04	4.3E-01	3.9E-01
262040_at	AT1G80080	leucine-rich repeat family protein, contains	77.4	158.3	121.1	40.4	216.1	83.7	5.3	7.5E-07	2.4E-02	3.1E-03	6.3E-04	8.2E-02	3.2E-01
267393_at	AT2G44500	expressed protein, contains Pfam PF0313	593.7	548.9	472.4	1465.4	1373.4	667.7	2.2	8.3E-07	9.0E-10	1.6E-04	6.8E-04	3.2E-07	7.4E-02
245987_at	AT5G13180	no apical meristem (NAM) family protein, c	1333.7	1844.5	1727.6	564.1	715.3	1436.1	2.5	1.5E-06	1.2E-08	5.9E-05	1.2E-03	1.8E-06	4.0E-02
263002_at	AT1G54200	expressed protein	36.9	65.7	75.4	11.6	29.4	47.8	4.1	1.8E-06	1.3E-06	2.7E-02	1.3E-03	4.6E-05	3.8E-01
261382_at	AT1G05470	endonuclease/exonuclease/phosphatase f	36.0	26.3	25.3	69.2	28.0	26.7	2.6	2.0E-06	1.2E-03	2.3E-03	1.4E-03	7.5E-03	2.8E-01
258100_at	AT3G23550	MATE efflux family protein, similar to riper	1866.1	2339.0	2787.2	242.8	198.9	644.3	3.2	2.0E-06	1.1E-12	1.8E-04	1.4E-03	3.7E-09	8.0E-02
251321_at	AT3G61460	zinc finger (C3HC4-type RING finger) fami	420.7	758.0	977.7	145.2	193.4	449.0	3.1	2.2E-06	2.4E-08	4.3E-02	1.5E-03	2.9E-06	3.2E-01
252586_at	AT3G45610	Dof-type zinc finger domain-containing prc	5.8	5.6	6.2	14.4	5.9	5.6	2.6	2.6E-06	3.1E-05	1.8E-06	1.7E-03	4.8E-04	5.9E-03
258091_at	AT3G14560	expressed protein	329.7	458.1	562.7	188.1	267.1	536.8	2.9	2.9E-06	1.3E-04	1.6E-02	1.8E-03	1.4E-03	4.5E-01
250907_at	AT5G03670	expressed protein	8.1	8.0	13.3	7.2	8.4	22.8	3.2	3.3E-06	7.9E-02	1.5E-02	2.1E-03	2.1E-01	4.6E-01
251072_at	AT5G01740	expressed protein, wound-inducible protei	817.4	1320.6	2478.2	1414.5	1937.4	4128.8	3.0	3.5E-06	3.5E-04	7.7E-01	2.1E-03	3.0E-03	9.0E-01
246495_at	AT5G16200	50S ribosomal protein-related, contains w	23.9	45.4	65.0	7.3	15.1	75.6	10.4	3.9E-06	4.7E-04	5.4E-03	2.3E-03	3.8E-03	4.1E-01
262124_at	AT1G59660	nucleoporin family protein, contains Pfam	45.9	53.0	31.7	210.3	225.2	71.5	3.1	4.3E-06	2.7E-09	7.4E-03	2.4E-03	7.0E-07	4.5E-01
252230_at	AT3G49810	U-box domain-containing protein, contains	166.4	114.1	128.7	180.6	89.9	161.7	2.0	4.3E-06	6.3E-01	6.7E-03	2.4E-03	8.5E-01	4.5E-01
267171_at	AT2G37590	Dof-type zinc finger domain-containing prc	28.0	16.5	18.4	97.7	20.1	16.8	5.8	4.6E-06	1.7E-03	9.3E-04	2.4E-03	9.9E-03	1.8E-01
262543_at	AT1G34245	expressed protein	121.2	179.4	204.6	22.4	172.7	116.0	7.7	4.8E-06	4.0E-05	4.1E-04	2.5E-03	5.8E-04	1.1E-01
262550_at	AT1G31310	hydroxyproline-rich glycoprotein family pro	10.5	7.7	9.0	26.2	7.9	10.7	3.3	5.2E-06	2.0E-04	5.9E-04	2.6E-03	1.9E-03	1.3E-01
253103_at	AT4G36110	auxin-responsive protein, putative, similar	193.3	391.3	166.6	736.7	1253.8	159.4	7.9	5.1E-06	5.3E-05	2.3E-03	2.6E-03	7.1E-04	2.9E-01
255942_at	AT1G22360	UDP-glucuronosyl/UDP-glucosyl transfera	873.1	1001.5	1066.0	166.3	151.2	517.1	3.4	5.5E-06	1.1E-10	4.4E-05	2.6E-03	7.5E-08	3.3E-02
245136_at	AT2G45210	auxin-responsive protein-related, weakly s	122.4	275.5	359.6	90.8	80.1	372.5	4.7	5.5E-06	1.2E-03	2.5E-03	2.7E-03	7.6E-03	3.0E-01
245325_at	AT4G14130	xyloglucan:xyloglucosyl transferase, putati	63.3	146.7	172.3	6.9	26.3	346.3	50.3	6.2E-06	5.2E-04	5.0E-04	2.9E-03	4.1E-03	1.2E-01
259985_at	AT1G76620	expressed protein, contains Pfam profile F	12.4	12.9	13.7	13.2	17.4	47.4	3.6	7.6E-06	5.1E-06	3.3E-05	3.3E-03	1.3E-04	3.3E-02
252972_at	AT4G38840	auxin-responsive protein, putative, auxin-ir	1536.2	1913.6	1520.9	1790.6	2321.5	916.0	2.5	7.3E-06	3.5E-01	3.2E-04	3.3E-03	6.1E-01	1.0E-01
253255_at	AT4G34760	auxin-responsive family protein, auxin-ind	286.8	641.4	516.7	279.0	727.3	449.2	2.6	8.2E-06	8.7E-01	4.6E-01	3.4E-03	9.5E-01	7.2E-01
246063_at	AT5G19340	expressed protein	43.0	35.5	52.1	14.1	23.7	60.9	4.3	9.0E-06	1.7E-04	2.0E-04	3.7E-03	1.7E-03	8.3E-02
267628_at	AT2G42280	basic helix-loop-helix (bHLH) family protei	327.0	479.0	489.0	119.6	173.9	428.2	3.6	1.0E-05	1.6E-06	1.1E-03	3.9E-03	5.4E-05	2.0E-01
253423_at	AT4G32280	auxin-responsive AUX/IAA family protein, i	41.6	86.3	130.5	9.3	15.5	71.9	7.7	1.0E-05	3.4E-06	3.0E-02	3.9E-03	9.4E-05	3.5E-01
263652_at	AT1G04330	expressed protein, EST gb:H76414 comes	12.5	11.2	10.7	56.4	16.6	12.8	4.4	1.0E-05	3.3E-06	7.5E-05	4.0E-03	9.2E-05	4.4E-02
254024_at	AT4G25780	pathogenesis-related protein, putative, sirr	9.7	62.2	84.0	4.9	7.2	27.4	8.6	1.0E-05	1.5E-05	2.3E-02	4.0E-03	2.8E-04	4.1E-01
262635_at	AT1G06570	4-hydroxyphenylpyruvate dioxygenase (HF	314.7	302.7	346.7	91.2	85.0	320.1	3.8	1.1E-05	1.7E-07	7.0E-05	4.2E-03	1.1E-05	4.2E-02
251342_at	AT3G60690	auxin-responsive family protein, similar to	178.9	136.8	220.1	161.9	102.8	273.8	2.7	1.2E-05	4.6E-01	4.3E-02	4.4E-03	7.2E-01	3.2E-01
260727_at	AT1G48100	glycoside hydrolase family 28 protein / pol	8.1	9.3	8.7	10.7	32.4	28.0	3.0	1.2E-05	1.3E-08	1.1E-04	4.4E-03	2.0E-06	5.9E-02
246321_at	AT1G16640	transcriptional factor B3 family protein, low	7.7	6.9	6.8	15.5	6.7	7.0	2.3	1.3E-05	1.0E-03	2.1E-04	4.4E-03	6.8E-03	8.7E-02
260287_at	AT1G80440	kelch repeat-containing F-box family prote	631.6	796.6	465.2	915.3	926.9	316.2	2.9	1.3E-05	6.1E-01	1.1E-02	4.4E-03	8.3E-01	4.6E-01

247351_at	AT5G63790	no apical meristem (NAM) family protein, c	1430.3	791.5	1629.2	2361.2	921.6	3426.8	3.7	1.4E-05	9.4E-04	1.2E-01	4.5E-03	6.3E-03	3.9E-01
259596_at	AT1G28130	encodes an IAA-amido synthase that conj	63.9	85.8	100.4	27.5	19.5	68.4	3.5	1.4E-05	1.1E-07	4.7E-04	4.5E-03	8.3E-06	1.2E-01
253812_at	AT4G28240	wound-responsive protein-related, wound-	722.2	1148.3	1483.1	242.7	304.7	739.8	3.0	1.5E-05	1.2E-07	5.1E-02	4.6E-03	9.0E-06	3.2E-01
260243_at	AT1G63720	expressed protein, similar to putative prote	10.3	8.2	11.1	7.9	8.3	48.8	6.1	1.6E-05	4.1E-03	1.2E-04	4.7E-03	2.0E-02	6.0E-02
245229_at	AT4G25620	hydroxyproline-rich glycoprotein family pro	357.0	616.4	705.5	280.8	487.0	568.9	2.0	1.5E-05	9.4E-03	9.9E-01	4.7E-03	3.9E-02	1.0E+00
247880_at	AT5G57780	expressed protein, similar to unknown prot	64.8	75.8	182.8	13.3	11.8	100.0	8.5	1.6E-05	7.1E-06	3.4E-02	4.7E-03	1.6E-04	3.3E-01
246464_at	AT5G16980	NADP-dependent oxidoreductase, putative	89.4	92.8	80.6	255.6	105.0	83.4	3.1	1.7E-05	4.3E-05	4.8E-05	4.7E-03	6.1E-04	3.4E-02
250248_at	AT5G13740	sugar transporter family protein, contains I	55.5	52.4	68.2	10.6	16.5	46.0	4.4	1.6E-05	5.4E-08	3.4E-04	4.7E-03	5.3E-06	1.1E-01
264083_at	AT2G31230	encodes a member of the ERF (ethylene r	34.3	26.7	16.1	120.5	104.2	38.0	3.2	1.5E-05	9.8E-08	1.5E-01	4.8E-03	7.7E-06	4.3E-01
253573_at	AT4G31020	expressed protein	36.8	21.1	13.8	174.6	20.1	30.1	8.7	1.7E-05	5.3E-04	5.9E-03	4.9E-03	4.1E-03	4.3E-01
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein, c	870.6	693.1	614.1	3839.9	1910.7	1673.7	2.3	1.8E-05	4.4E-10	1.5E-02	5.0E-03	2.0E-07	4.6E-01
245885_at	AT5G09440	phosphate-responsive protein, putative, sim	426.1	652.8	1123.5	516.1	509.6	3838.3	7.5	1.9E-05	3.8E-02	1.1E-02	5.2E-03	1.2E-01	4.5E-01
253281_at	AT4G34138	UDP-gluconosyl/UDP-glucosyl transfera	296.5	228.1	194.8	484.7	267.0	153.4	3.2	2.1E-05	1.2E-01	1.2E-02	5.4E-03	2.9E-01	4.6E-01
257506_at	AT1G29440	auxin-responsive family protein, similar to	702.5	983.2	673.5	567.0	788.7	269.1	2.9	2.1E-05	7.4E-05	3.7E-03	5.5E-03	9.2E-04	3.4E-01
266799_at	AT2G22860	phytosulfokines 2 (PSK2), identical to phyt	86.6	108.8	126.6	26.9	61.1	137.9	5.1	2.3E-05	2.3E-04	1.6E-03	5.8E-03	2.2E-03	2.3E-01
251910_at	AT3G53810	lectin protein kinase, putative, similar to re	92.9	32.7	40.7	265.0	141.6	118.8	2.8	2.3E-05	5.7E-08	2.1E-01	5.8E-03	5.5E-06	5.0E-01
246516_at	AT5G15740	expressed protein, contains Pfam PF0313	225.5	275.4	289.8	175.5	247.5	357.5	2.0	2.3E-05	3.5E-01	9.4E-03	5.9E-03	6.2E-01	4.5E-01
248646_at	AT5G49100	expressed protein	160.4	156.9	224.1	176.2	107.9	282.6	2.6	2.4E-05	8.2E-01	1.1E-02	5.9E-03	9.3E-01	4.6E-01
259875_s_at	AT1G76690;AT	[AT1G76690, 12-oxophytodienoate reduct	7692.3	7248.5	5643.9	15527.4	7340.2	5350.0	2.9	2.4E-05	1.1E-02	2.1E-03	5.9E-03	4.5E-02	2.7E-01
255538_at	AT4G01680	myb family transcription factor (MYB55)	3.9	9.5	18.8	3.5	3.6	25.6	7.3	2.4E-05	2.2E-01	5.5E-02	6.0E-03	4.4E-01	3.2E-01
245761_at	AT1G66890	expressed protein	62.0	68.9	95.5	6.7	16.2	47.3	7.0	2.5E-05	8.7E-08	1.5E-03	6.1E-03	7.3E-06	2.3E-01
267028_at	AT2G38470	WRKY family transcription factor, contains	813.7	152.6	402.9	2218.6	951.7	1661.1	5.3	2.6E-05	2.4E-07	8.4E-02	6.1E-03	1.4E-05	3.5E-01
252387_at	AT3G47800	aldose 1-epimerase family protein, similar	311.6	361.4	341.5	92.2	42.7	163.1	3.8	2.7E-05	1.6E-10	9.7E-06	6.2E-03	9.6E-08	1.7E-02
245662_at	AT1G28190	expressed protein	85.7	20.1	30.7	147.6	52.3	89.7	4.3	2.7E-05	3.7E-05	2.8E-01	6.2E-03	5.5E-04	5.8E-01
266447_at	AT2G43290	calmodulin-like protein (MSS3), identical to	573.3	875.5	707.7	1178.0	2430.4	814.1	3.0	2.8E-05	3.2E-06	1.8E-03	6.2E-03	9.0E-05	2.5E-01
260602_at	AT1G55920	serine O-acetyltransferase, putative, identi	4391.7	2083.1	2004.0	7783.5	3621.3	3600.1	2.2	2.9E-05	6.8E-05	9.9E-01	6.4E-03	8.6E-04	1.0E+00
266124_at	AT2G45080	cyclin family protein, similar to cyclin 2 (Tr	5.3	5.8	6.9	8.0	20.9	77.8	9.7	3.4E-05	4.3E-07	3.0E-04	7.2E-03	2.2E-05	1.0E-01
259783_at	AT1G29510	auxin-responsive protein, putative, similar	730.1	966.4	742.3	639.6	885.4	319.6	2.8	3.4E-05	3.1E-04	1.4E-03	7.2E-03	2.7E-03	2.1E-01
259982_at	AT1G76410	zinc finger (C3HC4-type RING finger) fami	12.5	36.9	23.0	7.0	18.4	42.9	6.2	3.5E-05	1.6E-01	4.9E-03	7.2E-03	3.5E-01	4.0E-01
264900_at	AT1G23080	auxin efflux carrier protein, putative, simila	1161.1	1277.6	1438.8	299.6	440.2	919.5	3.1	3.7E-05	2.6E-08	1.1E-03	7.5E-03	3.1E-06	2.0E-01
249752_at	AT5G24660	expressed protein	16.3	8.9	6.7	35.3	22.1	9.8	3.6	3.7E-05	1.0E-04	2.2E-01	7.6E-03	1.2E-03	5.1E-01
263126_at	AT1G78460	SOUL heme-binding family protein, weak s	1524.3	1322.1	1502.6	2609.5	1559.8	1045.7	2.5	3.8E-05	5.5E-02	6.4E-05	7.6E-03	1.5E-01	4.2E-02
247601_at	AT5G60850	Dof-type zinc finger domain-containing pro	261.0	558.6	512.7	251.9	428.8	391.3	2.1	3.9E-05	3.2E-02	4.1E-01	7.6E-03	1.0E-01	6.8E-01
249435_at	AT5G39970	expressed protein, low similarity to up-regu	11.7	8.9	8.2	23.4	8.7	8.8	2.7	3.9E-05	1.2E-02	8.7E-03	7.6E-03	4.6E-02	4.4E-01
261203_at	AT1G12845	expressed protein	80.1	136.0	133.2	27.8	161.6	75.5	5.8	4.1E-05	3.0E-03	7.8E-03	7.6E-03	1.6E-02	4.4E-01
252501_at	AT3G46880	expressed protein, ; expression supportec	39.2	22.0	26.2	88.4	35.0	58.7	2.5	4.0E-05	2.9E-06	2.0E-01	7.7E-03	8.4E-05	4.9E-01

253737_at	AT4G28703	expressed protein	53.4	23.2	27.3	290.0	42.0	47.2	6.9	4.0E-05	1.3E-04	2.9E-02	7.7E-03	1.4E-03	3.6E-01
262050_at	AT1G80130	expressed protein	117.8	136.9	131.2	109.7	223.8	626.8	5.7	4.1E-05	3.7E-05	1.2E-04	7.7E-03	5.5E-04	5.9E-02
247444_at	AT5G62630	expressed protein	158.4	123.6	97.9	216.4	119.7	94.9	2.3	4.4E-05	2.9E-01	1.4E-01	8.1E-03	5.4E-01	4.2E-01
257066_at	AT3G18280	protease inhibitor/seed storage/lipid transf	689.7	714.5	672.2	294.7	704.0	761.7	2.6	4.7E-05	1.5E-03	4.8E-05	8.6E-03	9.0E-03	3.5E-02
263325_at	AT2G04240	zinc finger (C3HC4-type RING finger) fami	256.4	482.6	331.7	413.8	675.6	240.8	2.8	4.9E-05	7.7E-02	5.4E-03	8.9E-03	2.0E-01	4.1E-01
258432_at	AT3G16570	rapid alkalization factor (RALF) family pr	500.0	813.7	926.1	273.7	650.4	749.9	2.7	4.9E-05	4.7E-03	2.3E-01	8.9E-03	2.2E-02	5.3E-01
249947_at	AT5G19200	short-chain dehydrogenase/reductase (SD	24.3	29.5	24.2	29.1	64.7	26.2	2.5	5.1E-05	3.2E-04	2.8E-03	9.1E-03	2.8E-03	3.1E-01
255502_at	AT4G02410	lectin protein kinase family protein, contair	359.4	91.3	138.5	819.3	311.8	528.1	3.9	5.2E-05	2.4E-06	3.0E-01	9.2E-03	7.5E-05	5.9E-01
255037_at	AT4G09460	myb family transcription factor	255.5	221.4	170.0	555.2	468.6	169.7	3.3	5.3E-05	2.2E-04	1.0E-02	9.4E-03	2.1E-03	4.5E-01
246926_at	AT5G25240	expressed protein	87.2	142.1	117.5	136.1	232.1	63.0	3.7	5.5E-05	2.6E-01	3.2E-04	9.6E-03	5.1E-01	1.0E-01
264279_s_at	AT1G78820;AT	[AT1G78820, curculin-like (mannose-bindi	9365.4	6448.4	7347.6	8832.3	4145.8	4795.5	2.1	5.6E-05	7.1E-04	7.0E-02	9.8E-03	5.1E-03	3.3E-01
259364_at	AT1G13260	DNA-binding protein RAV1 (RAV1), identic	321.1	600.7	988.7	667.1	979.5	1454.9	3.1	5.9E-05	4.3E-04	4.5E-01	1.0E-02	3.5E-03	7.1E-01
245041_at	AT2G26530	expressed protein	204.1	66.9	164.1	783.0	340.7	394.1	3.0	5.8E-05	9.6E-08	5.5E-02	1.0E-02	7.7E-06	3.2E-01
245176_at	AT2G47440	DNAJ heat shock N-terminal domain-cont	1629.1	2004.7	1527.0	2296.5	3108.0	1396.6	2.2	6.2E-05	3.2E-03	1.1E-02	1.0E-02	1.7E-02	4.6E-01
254292_at	AT4G23030	MATE efflux protein-related, contains Pfan	22.4	19.1	14.0	106.3	44.6	20.3	5.2	6.1E-05	8.2E-06	7.3E-03	1.0E-02	1.8E-04	4.5E-01
258537_at	AT3G04210	disease resistance protein (TIR-NBS class	118.3	48.1	54.3	231.5	73.5	73.1	3.2	6.4E-05	5.0E-03	5.4E-01	1.0E-02	2.3E-02	7.7E-01
251832_at	AT3G55150	exocyst subunit EXO70 family protein, cor	20.8	4.6	6.1	23.8	6.3	50.0	7.9	6.9E-05	4.7E-04	1.3E-03	1.1E-02	3.8E-03	2.1E-01
245369_at	AT4G15975	zinc finger (C3HC4-type RING finger) fami	65.3	30.9	28.0	210.3	67.3	64.1	3.3	6.8E-05	1.7E-05	4.6E-01	1.1E-02	3.1E-04	7.1E-01
267238_at	AT2G44130	kelch repeat-containing F-box family prote	14.9	21.4	13.2	181.2	147.8	23.5	7.7	6.7E-05	1.5E-07	8.1E-04	1.1E-02	1.0E-05	1.7E-01
251827_at	AT3G55120	chalcone-flavanone isomerase / chalcone	455.2	476.9	485.4	238.2	411.9	603.0	2.5	7.2E-05	7.2E-03	2.6E-04	1.1E-02	3.1E-02	9.3E-02
253351_at	AT4G33700	CBS domain-containing protein, contains I	107.8	119.6	148.0	44.7	59.7	117.4	2.6	7.3E-05	5.8E-06	1.5E-02	1.1E-02	1.4E-04	4.6E-01
249494_at	AT5G39050	transferase family protein, similar to antho	494.5	450.3	332.6	1795.4	605.7	982.7	3.0	7.5E-05	6.5E-08	4.4E-04	1.1E-02	5.9E-06	1.2E-01
252890_at	AT4G39400	brassinosteroid insensitive 1 (BRI1), identi	1443.1	1962.7	2045.6	841.2	1030.7	1817.5	2.2	7.7E-05	3.2E-05	1.8E-02	1.2E-02	4.9E-04	4.5E-01
257766_at	AT3G23030	auxin-responsive protein / indoleacetic aci	2550.6	3020.2	4608.2	866.9	1379.2	3499.4	4.0	8.1E-05	8.3E-05	5.7E-02	1.2E-02	9.9E-04	3.2E-01
256762_at	AT3G25655	expressed protein	5.1	5.0	5.1	10.8	8.1	69.9	8.6	8.3E-05	1.1E-06	9.4E-05	1.2E-02	4.3E-05	5.4E-02
248191_at	AT5G54130	calcium-binding EF hand family protein, cc	112.4	137.4	133.4	60.2	172.9	196.4	3.3	8.4E-05	9.8E-01	1.5E-03	1.2E-02	9.9E-01	2.2E-01
248801_at	AT5G47370	homeobox-leucine zipper protein 2 (HAT2)	917.4	1693.4	1803.3	339.2	688.6	790.0	2.3	8.9E-05	1.1E-06	7.9E-01	1.3E-02	4.3E-05	9.1E-01
258651_at	AT3G09920	phosphatidylinositol-4-phosphate 5-kinase	88.1	53.0	56.5	73.1	29.1	68.4	2.5	8.9E-05	4.4E-02	1.1E-02	1.3E-02	1.3E-01	4.6E-01
248164_at	AT5G54490	calcium-binding EF-hand protein, putative,	23.1	11.6	31.8	721.8	413.1	235.8	3.1	1.1E-04	6.8E-14	4.5E-06	1.4E-02	7.8E-10	1.3E-02
246781_at	AT5G27350	sugar-porter family protein 1 (SFP1), ident	598.0	619.4	557.5	693.5	907.6	444.9	2.0	9.3E-05	6.8E-02	1.3E-03	1.3E-02	1.8E-01	2.1E-01
253617_at	AT4G30410	expressed protein, similar to cDNA bHLH f	28.1	29.3	30.1	25.1	25.0	55.9	2.2	9.4E-05	7.7E-02	2.7E-04	1.3E-02	2.0E-01	9.3E-02
257855_at	AT3G13040	myb family transcription factor, contains P	392.1	355.4	421.6	196.7	221.9	412.2	2.1	9.4E-05	1.5E-05	1.4E-03	1.3E-02	2.9E-04	2.1E-01
255403_at	AT4G03400	auxin-responsive GH3 family protein, simil	322.4	446.6	261.4	207.6	338.1	160.7	2.1	1.0E-04	3.1E-04	5.6E-01	1.4E-02	2.7E-03	7.8E-01
249467_at	AT5G39610	no apical meristem (NAM) family protein, c	24.3	21.9	33.6	12.6	8.1	36.4	4.5	1.1E-04	1.2E-03	1.2E-02	1.4E-02	7.6E-03	4.6E-01
262531_at	AT1G17230	leucine-rich repeat family protein / protein	297.6	293.1	272.4	81.4	138.5	367.0	4.5	1.1E-04	2.9E-05	3.4E-05	1.4E-02	4.6E-04	3.0E-02
253247_at	AT4G34610	homeodomain-containing protein, similarit	265.8	223.3	260.0	115.8	104.0	279.8	2.7	1.1E-04	1.9E-05	5.0E-04	1.5E-02	3.3E-04	1.2E-01

257746_at	AT3G29200	chorismate mutase, chloroplast (CM1), ide	302.0	321.1	362.1	230.4	309.9	470.6	2.0	1.1E-04	8.0E-01	7.9E-03	1.5E-02	9.2E-01	4.4E-01
249558_at	AT5G38310	expressed protein	4.4	4.3	4.4	9.3	4.6	4.9	2.0	1.2E-04	5.3E-05	1.7E-04	1.5E-02	7.1E-04	7.8E-02
255895_at	AT1G18020;AT	[AT1G18020, 12-oxophytodienoate reduct	306.2	186.6	234.5	336.8	95.0	189.5	3.5	1.2E-04	3.5E-02	4.5E-02	1.5E-02	1.1E-01	3.2E-01
252965_at	AT4G38860	auxin-responsive protein, putative, auxin-ir	366.0	641.5	465.7	882.8	1320.3	388.1	3.4	1.3E-04	4.6E-04	1.9E-03	1.6E-02	3.7E-03	2.5E-01
260034_at	AT1G68810	basic helix-loop-helix (bHLH) family proteir	170.3	234.7	212.2	58.0	117.3	140.8	2.4	1.4E-04	8.7E-07	1.6E-02	1.7E-02	3.6E-05	4.6E-01
255933_at	AT1G12750	rhomboid family protein, contains PFAM d	430.2	339.4	294.8	500.9	246.1	313.7	2.0	1.4E-04	6.0E-01	3.0E-02	1.7E-02	8.3E-01	3.5E-01
247077_at	AT5G66420	expressed protein	184.7	208.9	200.9	75.8	76.9	179.4	2.4	1.4E-04	2.9E-07	2.4E-04	1.7E-02	1.7E-05	9.0E-02
264056_at	AT2G28510	Dof-type zinc finger domain-containing prc	340.4	249.9	266.6	305.0	132.1	257.0	2.3	1.4E-04	4.3E-03	1.3E-02	1.7E-02	2.1E-02	4.6E-01
259864_at	AT1G72800	nuM1-related, contains similarity with nuM	243.7	230.0	212.3	487.0	645.9	226.9	2.8	1.5E-04	5.1E-06	8.3E-04	1.8E-02	1.2E-04	1.7E-01
247774_at	AT5G58660	oxidoreductase, 2OG-Fe(II) oxygenase far	25.2	28.2	30.1	10.3	28.7	106.4	10.3	1.5E-04	4.4E-01	5.6E-04	1.8E-02	7.1E-01	1.3E-01
262500_at	AT1G21760	F-box family protein, Contains PF:00646 F	317.0	426.3	419.5	152.6	201.0	333.4	2.2	1.5E-04	2.5E-06	1.4E-02	1.8E-02	7.7E-05	4.7E-01
259373_at	AT1G69160	expressed protein	184.2	288.4	273.1	34.9	62.2	105.0	3.0	1.5E-04	8.7E-09	2.9E-02	1.8E-02	1.5E-06	3.7E-01
258282_at	AT3G26910	hydroxyproline-rich glycoprotein family pro	299.4	129.9	120.2	711.0	230.7	385.1	3.1	1.6E-04	2.9E-05	2.4E-01	1.8E-02	4.6E-04	5.3E-01
252296_at	AT3G48970	copper-binding family protein, similar to cc	53.8	131.3	135.9	77.7	121.9	206.0	2.7	1.7E-04	8.8E-02	2.6E-01	1.9E-02	2.2E-01	5.6E-01
261265_at	AT1G26800	zinc finger (C3HC4-type RING finger) fami	15.2	21.4	14.2	54.4	75.5	12.4	6.1	1.7E-04	1.6E-04	2.9E-03	1.9E-02	1.7E-03	3.2E-01
261700_at	AT1G32690	expressed protein, similar to hypothetical p	28.6	68.8	74.8	15.9	29.8	61.8	3.9	1.6E-04	4.4E-03	2.6E-01	1.9E-02	2.1E-02	5.6E-01
248686_at	AT5G48540	33 kDa secretory protein-related, contains	1071.5	442.5	438.0	1775.8	484.1	875.7	3.7	1.6E-04	1.3E-02	2.7E-01	1.9E-02	5.0E-02	5.6E-01
264091_at	AT1G79110	expressed protein	98.2	162.7	149.3	44.7	76.7	99.8	2.2	1.7E-04	7.4E-06	1.8E-01	1.9E-02	1.6E-04	4.6E-01
250004_at	AT5G18750	DNAJ heat shock N-terminal domain-conta	125.0	67.6	65.6	113.3	50.6	90.1	2.2	1.8E-04	8.1E-01	5.8E-02	2.0E-02	9.3E-01	3.2E-01
247543_at	AT5G61600	encodes a member of the ERF (ethylene r	289.5	254.7	549.9	1458.0	1471.8	715.7	2.2	8.5E-01	6.3E-09	1.6E-05	9.1E-01	1.2E-06	2.0E-02
261648_at	AT1G27730	zinc finger (C2H2 type) family protein (ZA	352.5	113.3	634.3	2304.8	1544.1	2179.9	5.6	1.8E-04	1.3E-08	6.5E-03	2.0E-02	2.0E-06	4.5E-01
253414_at	AT4G33050	calmodulin-binding family protein, contain	3322.6	1389.1	1397.5	5818.0	2105.1	3693.3	2.8	1.9E-04	2.7E-04	2.2E-01	2.0E-02	2.5E-03	5.2E-01
260655_at	AT1G19320	pathogenesis-related thaumatin family pro	70.8	109.9	136.1	17.5	13.5	35.0	2.6	1.9E-04	1.1E-09	1.4E-02	2.0E-02	3.7E-07	4.7E-01
256453_at	AT1G75270	dehydroascorbate reductase, putative, sirr	805.4	882.3	693.4	2327.6	1473.7	888.3	2.6	1.8E-04	3.2E-06	2.5E-03	2.0E-02	9.1E-05	3.0E-01
250752_at	AT5G05690	cytochrome P450 90A1 (CYP90A1) (CYP	1587.8	2328.1	2502.8	278.1	386.3	953.2	3.4	1.9E-04	1.4E-08	1.8E-02	2.1E-02	2.1E-06	4.5E-01
257805_at	AT3G18830	This gene encodes a plasma membrane-l	2097.8	1424.2	1279.0	3108.0	1358.3	1195.1	2.6	2.0E-04	3.9E-01	1.6E-01	2.1E-02	6.5E-01	4.5E-01
255941_at	AT1G20350	mitochondrial import inner membrane tran	3.8	3.8	3.8	10.9	4.4	4.1	2.7	2.0E-04	7.9E-05	2.4E-04	2.1E-02	9.6E-04	8.9E-02
256337_at	AT1G72060	expressed protein	96.8	42.5	44.2	453.5	69.5	76.0	6.5	2.1E-04	1.2E-03	9.9E-02	2.2E-02	7.6E-03	3.7E-01
248732_at	AT5G48070	putative xyloglucan endotransglycosylase/	28.5	21.5	19.3	163.5	55.7	45.0	3.6	2.1E-04	4.0E-07	1.9E-02	2.2E-02	2.1E-05	4.4E-01
256960_at	AT3G13510	expressed protein, Pfam profile PF03080:	202.2	252.2	237.3	80.6	159.2	192.6	2.4	2.1E-04	1.3E-05	7.1E-03	2.2E-02	2.5E-04	4.4E-01
252047_at	AT3G52490	heat shock protein-related, contains simila	16.2	12.9	13.9	33.3	15.0	13.8	2.4	2.1E-04	3.5E-03	7.4E-03	2.2E-02	1.8E-02	4.5E-01
246584_at	AT5G14730	expressed protein	175.3	141.3	120.0	2339.5	1472.9	597.6	3.9	2.1E-04	3.3E-10	1.3E-02	2.2E-02	1.7E-07	4.6E-01
248190_at	AT5G54120	expressed protein	65.1	82.4	79.2	42.7	104.5	111.7	2.6	2.2E-04	5.6E-01	8.5E-03	2.2E-02	8.0E-01	4.4E-01
245543_at	AT4G15260	UDP-glucuronosyl/UDP-glucosyl transfera	290.2	207.2	205.8	229.6	100.7	150.6	2.3	2.2E-04	1.8E-04	6.0E-02	2.2E-02	1.8E-03	3.2E-01
265511_at	AT2G05540	glycine-rich protein	1428.3	1849.2	2008.9	928.5	799.6	1722.2	2.2	2.2E-04	2.2E-05	6.5E-03	2.2E-02	3.7E-04	4.5E-01
265806_at	AT2G18010	auxin-responsive family protein, similar to	81.4	96.6	60.5	93.2	216.3	23.7	9.1	2.2E-04	9.9E-01	6.9E-03	2.2E-02	1.0E+00	4.4E-01

255926_at	AT1G22190	AP2 domain-containing transcription facto	97.7	181.5	218.5	163.9	291.3	327.2	2.2	2.3E-04	9.6E-04	9.1E-01	2.3E-02	6.5E-03	9.6E-01
262653_at	AT1G14130	2-oxoglutarate-dependent dioxygenase, pt	72.7	82.9	65.8	177.0	93.7	71.6	2.5	2.4E-04	1.7E-04	5.7E-04	2.3E-02	1.7E-03	1.3E-01
247074_at	AT5G66590	allergen V5/Tpx-1-related family protein, c	88.1	200.1	165.5	53.0	100.0	171.4	3.2	2.8E-04	1.2E-02	1.0E-01	2.6E-02	4.7E-02	3.7E-01
252646_at	AT3G44610	protein kinase family protein, similar to vir	25.0	31.5	30.1	12.3	33.2	32.2	2.7	2.9E-04	6.1E-02	8.4E-03	2.7E-02	1.7E-01	4.5E-01
245479_at	AT4G16140	proline-rich family protein, contains proline	478.5	667.7	556.9	266.0	537.0	400.4	2.0	2.9E-04	2.0E-04	1.4E-01	2.7E-02	1.9E-03	4.2E-01
261597_at	AT1G49780	U-box domain-containing protein, similar to	27.2	20.4	38.6	16.7	8.2	29.7	3.6	3.0E-04	1.4E-03	1.7E-01	2.7E-02	8.5E-03	4.6E-01
245051_at	AT2G23320	WRKY family transcription factor, identical	935.6	569.3	665.5	1470.4	624.5	1239.5	2.4	2.9E-04	1.5E-03	1.1E-01	2.7E-02	8.9E-03	3.8E-01
247933_at	AT5G56980	expressed protein, non-consensus CG do	18.6	32.7	43.6	9.9	9.1	44.8	4.9	3.0E-04	3.6E-03	3.1E-02	2.7E-02	1.8E-02	3.5E-01
260434_at	AT1G68330	expressed protein	46.0	23.5	26.1	81.2	50.9	29.2	2.8	3.0E-04	1.1E-03	9.1E-02	2.7E-02	7.2E-03	3.6E-01
247478_at	AT5G62360	invertase/pectin methylesterase inhibitor f	1696.3	2986.0	3236.8	139.4	252.7	558.5	4.0	3.0E-04	2.2E-09	9.3E-02	2.7E-02	6.0E-07	3.6E-01
253044_at	AT4G37290	expressed protein	5.0	4.7	5.2	69.0	11.4	28.2	6.1	3.0E-04	1.4E-08	5.0E-04	2.7E-02	2.1E-06	1.2E-01
267614_at	AT2G26710	Encodes a member of the cytochrome p4f	41.1	88.4	56.8	102.8	246.4	45.4	5.4	3.0E-04	3.1E-03	1.2E-02	2.7E-02	1.6E-02	4.6E-01
261023_at	AT1G12200	flavin-containing monooxygenase family p	570.3	441.0	395.7	764.4	485.7	346.8	2.2	3.2E-04	3.1E-01	1.5E-01	2.8E-02	5.7E-01	4.3E-01
253062_at	AT4G37590	phototropic-responsive NPH3 family protei	352.7	305.6	339.6	112.2	136.8	258.6	2.3	3.3E-04	5.8E-08	3.7E-04	2.9E-02	5.4E-06	1.1E-01
252173_at	AT3G50650	scarecrow-like transcription factor 7 (SCL7	288.7	223.0	191.3	481.0	353.1	193.8	2.5	3.3E-04	4.3E-03	9.6E-02	2.9E-02	2.1E-02	3.6E-01
259773_at	AT1G29500	auxin-responsive protein, putative, similar	675.3	863.6	682.8	498.8	783.1	306.3	2.6	3.4E-04	4.3E-04	1.4E-02	2.9E-02	3.5E-03	4.7E-01
254809_at	AT4G12410	auxin-responsive family protein, similar to	15.2	23.7	23.1	13.5	19.0	43.0	3.2	3.4E-04	4.1E-01	1.9E-02	3.0E-02	6.8E-01	4.4E-01
246993_at	AT5G67450	zinc finger (C2H2 type) protein 1 (AZF1), i	516.7	149.7	83.7	557.1	271.0	305.4	6.2	3.6E-04	3.7E-03	5.4E-02	3.0E-02	1.9E-02	3.2E-01
259784_at	AT1G29450	auxin-responsive protein, putative, similar	280.5	370.0	278.8	224.9	365.9	136.5	2.7	3.6E-04	4.6E-03	2.3E-02	3.0E-02	2.2E-02	4.0E-01
253629_at	AT4G30450	glycine-rich protein	22.3	23.3	26.4	16.6	25.1	42.9	2.6	3.6E-04	2.8E-01	6.4E-03	3.0E-02	5.3E-01	4.4E-01
245276_at	AT4G16780	homeobox-leucine zipper protein 4 (HAT4)	26.4	30.5	49.2	20.6	25.1	49.3	2.4	3.6E-04	2.1E-01	6.4E-01	3.0E-02	4.3E-01	8.2E-01
258021_at	AT3G19380	U-box domain-containing protein, contains	18.3	18.9	27.1	12.3	7.0	25.6	3.7	3.7E-04	1.7E-03	2.4E-02	3.0E-02	1.0E-02	4.0E-01
250493_at	AT5G09800	U-box domain-containing protein, low simil	49.4	37.8	47.5	131.1	48.4	163.0	3.4	3.7E-04	9.7E-06	1.0E-02	3.0E-02	2.0E-04	4.5E-01
259751_at	AT1G71030	Encodes a putative myb family transcrip	242.6	219.1	262.4	29.9	8.2	65.1	8.0	3.7E-04	9.2E-09	1.6E-03	3.0E-02	1.6E-06	2.3E-01
267515_at	AT2G45680	TCP family transcription factor, putative, s	158.6	287.3	316.2	99.7	176.8	215.3	2.2	3.8E-04	1.7E-03	9.3E-01	3.1E-02	9.9E-03	9.7E-01
259683_at	AT1G63050	membrane bound O-acyl transferase (MB	141.1	185.9	189.1	33.4	48.5	121.8	3.6	3.8E-04	6.9E-07	6.8E-03	3.1E-02	3.0E-05	4.4E-01
266908_at	AT2G34650	protein kinase PINOID (PID), identical to p	32.8	48.6	31.5	114.0	147.6	45.2	3.3	4.0E-04	5.3E-06	2.0E-02	3.1E-02	1.3E-04	4.3E-01
253999_at	AT4G26200	1-aminocyclopropane-1-carboxylate synth	220.0	57.8	198.3	394.2	184.8	1652.1	8.9	4.0E-04	2.3E-04	7.4E-02	3.1E-02	2.1E-03	3.4E-01
261768_at	AT1G15550	gibberellin 3-beta-dioxygenase / gibberellir	142.4	207.2	159.6	84.5	188.2	98.5	2.2	4.1E-04	1.4E-03	1.4E-01	3.1E-02	8.6E-03	4.2E-01
256818_at	AT3G21420	oxidoreductase, 2OG-Fe(II) oxygenase far	10.8	10.7	9.6	20.7	11.2	8.7	2.4	4.1E-04	1.9E-02	2.9E-03	3.1E-02	6.7E-02	3.2E-01
256528_at	AT1G66140	zinc finger (C2H2 type) family protein, con	217.9	264.1	189.0	154.2	206.3	94.2	2.2	4.0E-04	1.8E-04	9.7E-02	3.1E-02	1.8E-03	3.7E-01
247610_at	AT5G60630	expressed protein, predicted protein, Arab	13.4	12.7	13.5	29.5	15.3	13.4	2.2	3.9E-04	2.0E-04	5.5E-04	3.1E-02	1.9E-03	1.3E-01
254231_at	AT4G23810	WRKY family transcription factor, AR411 -	875.7	107.7	152.0	620.2	340.7	620.1	8.1	4.1E-04	2.8E-03	7.2E-03	3.1E-02	1.5E-02	4.5E-01
250569_at	AT5G08130	basic helix-loop-helix (bHLH) family proteir	264.3	275.2	348.3	90.5	104.3	246.9	2.7	4.0E-04	3.8E-06	2.3E-02	3.1E-02	1.0E-04	4.0E-01
252970_at	AT4G38850	auxin-responsive protein / small auxin up f	608.3	867.1	605.3	974.9	1333.6	439.5	3.0	4.0E-04	9.2E-02	1.6E-02	3.2E-02	2.3E-01	4.5E-01
262315_at	AT1G70990	proline-rich family protein	104.1	97.6	61.4	408.7	259.1	116.8	3.5	4.2E-04	7.1E-06	1.2E-01	3.2E-02	1.6E-04	4.0E-01

262630_at	AT1G06520	Encodes a membrane associated mitoch	43.7	54.7	34.8	87.0	118.6	38.2	3.1	4.2E-04	8.0E-04	7.0E-02	3.2E-02	5.6E-03	3.3E-01
253779_at	AT4G28490	leucine-rich repeat transmembrane proteir	281.8	233.8	234.3	445.9	151.7	194.1	2.9	4.3E-04	5.9E-01	7.8E-03	3.2E-02	8.2E-01	4.5E-01
251839_at	AT3G54950	patatin-related, low similarity to patatin (Gl	21.8	32.3	37.7	21.5	19.7	50.2	2.6	4.3E-04	5.0E-01	3.4E-02	3.2E-02	7.5E-01	3.4E-01
258189_at	AT3G17860	expressed protein	147.1	203.7	188.5	124.5	203.1	276.0	2.2	4.5E-04	4.0E-01	4.3E-02	3.3E-02	6.6E-01	3.2E-01
253736_at	AT4G28780	GDSL-motif lipase/hydrolase family proteir	134.4	166.9	133.7	158.9	289.4	126.4	2.3	4.6E-04	1.8E-02	2.9E-02	3.4E-02	6.5E-02	3.7E-01
250537_at	AT5G08565	expressed protein	47.1	57.2	54.0	46.9	90.5	115.5	2.5	4.8E-04	3.1E-04	7.7E-03	3.4E-02	2.7E-03	4.5E-01
263150_at	AT1G54050	17.4 kDa class III heat shock protein (HSF	50.6	47.8	43.8	163.3	204.2	57.1	3.6	4.8E-04	1.3E-06	2.1E-03	3.4E-02	4.9E-05	2.7E-01
266693_at	AT2G19800	expressed protein, similar to myo-inositol c	1217.3	636.1	530.8	4161.9	3334.9	1871.8	2.3	4.9E-04	7.7E-08	3.0E-01	3.5E-02	6.7E-06	5.9E-01
262259_s_at	AT1G53870;AT	[AT1G53870, expressed protein, contains	22.1	45.1	50.9	10.1	15.2	19.8	2.3	4.9E-04	3.2E-06	5.6E-01	3.5E-02	9.0E-05	7.8E-01
247625_at	AT5G60200	Dof-type zinc finger domain-containing prc	99.3	59.8	73.2	273.3	118.5	71.0	3.9	5.0E-04	1.1E-03	1.9E-02	3.5E-02	7.0E-03	4.4E-01
249765_at	AT5G24030	C4-dicarboxylate transporter/malic acid tra	1169.1	711.5	497.6	1740.5	1987.6	1046.3	2.3	5.0E-04	1.6E-05	8.5E-02	3.5E-02	2.9E-04	3.5E-01
257398_at	AT2G01990	expressed protein, similar to hypothetical p	37.1	17.8	19.6	56.6	23.4	22.0	2.6	5.1E-04	7.0E-02	6.7E-01	3.5E-02	1.9E-01	8.4E-01
251176_at	AT3G63380	calcium-transporting ATPase, plasma mer	124.0	127.2	146.2	106.7	95.2	1000.2	10.5	5.1E-04	3.6E-02	1.5E-03	3.6E-02	1.1E-01	2.2E-01
247754_at	AT5G59080	expressed protein	25.5	34.5	55.8	17.5	23.6	44.2	2.5	5.2E-04	2.5E-02	8.7E-01	3.6E-02	8.3E-02	9.4E-01
259787_at	AT1G29460	auxin-responsive protein, putative, similar	143.4	235.1	176.1	156.4	250.7	69.6	3.6	5.2E-04	4.8E-02	5.9E-03	3.6E-02	1.4E-01	4.3E-01
258075_at	AT3G25900	homocysteine S-methyltransferase 1 (HM	166.8	147.7	126.4	1062.0	883.2	397.3	2.7	5.3E-04	1.5E-09	2.2E-02	3.6E-02	4.8E-07	4.1E-01
247940_at	AT5G57190	phosphatidylserine decarboxylase, putativ	16.0	12.6	12.1	32.6	12.3	20.6	2.6	5.6E-04	7.3E-04	1.6E-02	3.8E-02	5.2E-03	4.6E-01
249480_s_at	AT5G38990;AT	[AT5G38990, protein kinase family protein	183.4	123.0	130.9	323.4	114.8	155.5	2.8	5.7E-04	6.9E-02	1.0E-01	3.8E-02	1.8E-01	3.7E-01
246858_at	AT5G25930	leucine-rich repeat family protein / protein	520.3	192.0	196.3	733.3	335.8	530.2	2.7	5.7E-04	6.3E-04	1.9E-01	3.8E-02	4.7E-03	4.8E-01
246735_at	AT5G27670	histone H2A, putative, similar to histone H	849.8	923.8	1079.8	298.0	362.2	725.4	2.4	5.8E-04	1.1E-06	2.4E-02	3.9E-02	4.3E-05	3.9E-01
252178_at	AT3G50750	brassinosteroid signalling positive regulatc	44.4	69.7	70.3	14.2	15.9	45.9	3.2	6.0E-04	3.2E-06	1.4E-02	3.9E-02	9.1E-05	4.7E-01
249188_at	AT5G42830	transferase family protein, similar to anthr	7.8	6.6	7.6	123.6	28.0	45.2	4.4	6.0E-04	2.0E-09	3.0E-03	3.9E-02	5.6E-07	3.1E-01
256522_at	AT1G66160	U-box domain-containing protein, similar to	1158.7	627.6	570.6	1823.4	1169.4	956.4	2.0	6.0E-04	3.4E-04	8.1E-01	4.0E-02	2.9E-03	9.2E-01
251774_at	AT3G55840	expressed protein	16.5	16.8	15.8	147.5	157.1	21.2	7.4	6.1E-04	1.2E-06	9.8E-04	4.0E-02	4.6E-05	1.9E-01
261292_at	AT1G36940	expressed protein	24.2	47.8	53.4	9.1	10.8	28.7	3.1	6.2E-04	1.4E-05	9.0E-02	4.0E-02	2.7E-04	3.6E-01
262951_at	AT1G75500	nodulin MtN21 family protein, similar to Mt	2383.3	3220.5	3545.8	891.5	1363.5	2427.1	2.7	6.4E-04	1.5E-05	8.7E-02	4.1E-02	2.8E-04	3.5E-01
262072_at	AT1G59590	expressed protein	29.0	13.9	14.6	578.9	286.9	278.6	2.1	6.3E-04	1.7E-11	9.7E-01	4.1E-02	1.9E-08	9.9E-01
248419_at	AT5G51550	phosphate-responsive 1 family protein, sin	1353.0	1649.3	1435.7	1906.5	2425.3	933.8	2.6	6.4E-04	2.6E-01	2.7E-03	4.1E-02	5.0E-01	3.1E-01
245262_at	AT4G16563	aspartyl protease family protein, contains l	275.0	340.1	236.9	1345.1	2352.3	813.8	2.9	6.5E-04	5.2E-09	6.5E-02	4.1E-02	1.0E-06	3.3E-01
246389_at	AT1G77380	amino acid carrier, putative / amino acid p	24.0	17.1	18.2	18.9	7.6	19.0	2.5	6.5E-04	5.9E-03	1.4E-02	4.1E-02	2.7E-02	4.7E-01
264746_at	AT1G62300	WRKY family transcription factor, similar to	192.3	77.1	121.9	578.1	174.2	817.0	4.7	6.6E-04	1.4E-05	7.6E-02	4.1E-02	2.7E-04	3.4E-01
251162_at	AT3G63300	expressed protein	47.7	38.6	37.8	83.2	45.4	40.2	2.1	6.7E-04	6.3E-03	5.8E-02	4.1E-02	2.8E-02	3.2E-01
253662_at	AT4G30080	transcriptional factor B3 family protein, cor	41.1	43.5	46.2	16.8	20.2	41.3	2.5	6.7E-04	9.6E-06	4.2E-03	4.1E-02	2.0E-04	3.7E-01
253483_at	AT4G31910	transferase family protein, low similarity to	57.7	101.0	100.4	46.1	126.6	115.2	2.7	6.9E-04	7.4E-01	3.8E-01	4.2E-02	9.0E-01	6.6E-01
262505_at	AT1G21680	expressed protein, similar to ToIB protein j	651.0	891.9	795.9	711.7	454.7	353.5	2.0	1.1E-02	3.4E-06	6.9E-05	1.9E-01	9.4E-05	4.3E-02
250598_at	AT5G07690	myb family transcription factor (MYB29), s	12.6	17.8	21.7	9.4	13.9	34.9	3.7	7.1E-04	8.8E-01	8.9E-02	4.3E-02	9.6E-01	3.6E-01

266363_at	AT2G41250	haloacid dehalogenase-like hydrolase fam	130.0	144.1	158.5	45.5	60.3	136.4	3.0	7.1E-04	2.1E-05	8.8E-03	4.4E-02	3.5E-04	4.4E-01
248282_at	AT5G52900	expressed protein	171.2	394.0	291.6	120.1	228.4	114.9	2.3	7.3E-04	2.0E-04	1.6E-01	4.4E-02	2.0E-03	4.4E-01
246200_at	AT4G37240	expressed protein	273.5	425.7	347.2	1111.4	1782.7	766.1	2.3	7.4E-04	1.1E-08	1.9E-02	4.4E-02	1.8E-06	4.4E-01
247205_at	AT5G64890	expressed protein	5.1	4.9	5.0	12.8	5.0	5.9	2.5	7.4E-04	5.0E-04	1.2E-03	4.4E-02	4.0E-03	2.0E-01
254424_at	AT4G21510	F-box family protein, contains Pfam PF006	83.5	118.9	80.9	185.0	152.1	72.7	2.5	7.5E-04	6.2E-03	6.8E-03	4.4E-02	2.8E-02	4.4E-01
253751_at	AT4G29070	expressed protein	155.0	179.8	199.3	79.4	118.7	160.0	2.0	7.6E-04	7.6E-05	8.3E-02	4.5E-02	9.4E-04	3.5E-01
262830_at	AT1G14700	purple acid phosphatase, putative, contain	111.1	153.9	211.3	44.1	55.6	94.1	2.1	7.6E-04	2.3E-06	7.4E-01	4.5E-02	7.3E-05	8.8E-01
266591_at	AT2G46225	Encodes a subunit of the WAVE complex.	598.5	506.7	520.8	246.7	197.5	422.8	2.1	7.7E-04	1.2E-07	5.7E-04	4.5E-02	8.7E-06	1.3E-01
258367_at	AT3G14370	protein kinase family protein, contains prot	65.3	126.5	59.4	303.2	491.6	140.7	3.5	7.8E-04	3.8E-06	2.3E-01	4.5E-02	1.0E-04	5.3E-01
245119_at	AT2G41640	expressed protein, contains Pfam domain,	150.5	64.3	76.7	967.0	548.2	382.7	2.5	7.8E-04	1.1E-08	3.1E-01	4.5E-02	1.7E-06	6.0E-01
248134_at	AT5G54860	integral membrane transporter family prot	216.1	117.0	127.5	599.6	246.1	298.8	2.4	7.9E-04	1.4E-05	6.7E-01	4.5E-02	2.7E-04	8.4E-01
254810_at	AT4G12390	invertase/pectin methylesterase inhibitor fr	420.0	536.2	561.4	163.0	247.9	374.4	2.3	7.8E-04	3.4E-06	7.2E-02	4.5E-02	9.4E-05	3.3E-01
245272_at	AT4G17250	expressed protein	9.1	6.5	7.6	42.6	23.4	12.8	3.3	8.0E-04	3.1E-07	6.9E-03	4.6E-02	1.7E-05	4.4E-01
267592_at	AT2G39710	aspartyl protease family protein, contains	132.0	68.2	54.6	825.3	329.0	327.6	2.5	8.1E-04	9.7E-08	7.6E-01	4.6E-02	7.7E-06	8.9E-01
246401_at	AT1G57560	myb family transcription factor (MYB50), s	5.7	5.0	4.8	18.9	17.5	7.1	2.7	8.2E-04	4.1E-07	5.1E-03	4.6E-02	2.1E-05	4.1E-01
255443_at	AT4G02700	sulfate transporter, identical to sulfate tran	33.9	32.5	19.3	43.1	23.9	19.9	2.2	8.3E-04	9.1E-01	1.4E-01	4.6E-02	9.7E-01	4.2E-01
254294_at	AT4G23070	rhomboid family protein, contains PFAM d	12.7	6.4	6.3	38.1	20.4	10.0	3.8	8.2E-04	1.1E-04	1.9E-01	4.6E-02	1.3E-03	4.8E-01
248040_at	AT5G55970	zinc finger (C3HC4-type RING finger) fami	5.0	5.4	5.2	12.9	9.1	5.0	2.6	8.3E-04	2.4E-05	5.0E-04	4.6E-02	3.9E-04	1.2E-01
245075_at	AT2G23180	cytochrome P450, putative	84.1	138.7	125.9	47.9	56.6	134.5	2.8	8.3E-04	1.4E-03	1.4E-02	4.6E-02	8.7E-03	4.6E-01
266835_at	AT2G29990	pyridine nucleotide-disulphide oxidoreduct	35.5	23.2	24.7	68.0	23.5	49.2	2.9	8.4E-04	2.3E-03	6.3E-02	4.6E-02	1.3E-02	3.2E-01
246580_at	AT1G31770	ABC transporter family protein, contains P	101.0	110.0	110.8	37.3	48.1	75.3	2.0	8.5E-04	6.2E-08	5.2E-03	4.6E-02	5.7E-06	4.1E-01
263207_at	AT1G10550	xyloglucan:xyloglucosyl transferase, putati	274.1	291.6	218.1	514.1	678.9	309.4	2.2	8.5E-04	1.4E-05	1.0E-01	4.6E-02	2.6E-04	3.7E-01
263931_at	AT2G36220	expressed protein	597.5	639.4	543.9	1994.5	1893.5	723.7	2.8	8.5E-04	2.1E-06	5.9E-03	4.6E-02	6.7E-05	4.2E-01
266150_s_at	AT2G12290;AT	[AT2G12290, expressed protein];[AT4G19	13.1	27.6	34.7	15.2	15.9	28.8	2.6	8.6E-04	1.5E-01	1.2E-01	4.7E-02	3.3E-01	4.0E-01
250012_x_at	AT5G18060	auxin-responsive protein, putative, similar	510.6	676.1	512.3	448.4	724.8	204.8	3.5	8.6E-04	2.0E-02	1.4E-02	4.7E-02	7.0E-02	4.6E-01
245439_at	AT4G16670	expressed protein	14.0	13.9	17.7	8.9	9.0	26.0	2.9	8.7E-04	1.9E-01	2.1E-02	4.7E-02	4.0E-01	4.2E-01
255931_at	AT1G12710	F-box family protein / SKP1 interacting pai	37.3	53.3	42.1	53.9	80.2	38.1	2.1	8.9E-04	1.7E-02	4.5E-02	4.8E-02	6.1E-02	3.2E-01
263823_s_at	AT2G40340;AT	[AT2G40340, encodes a member of the D	19.0	15.7	13.5	115.3	60.6	36.1	3.2	8.9E-04	7.1E-08	4.7E-02	4.8E-02	6.2E-06	3.2E-01
247617_at	AT5G60270	lectin protein kinase family protein, contain	216.1	126.4	79.1	305.9	185.3	192.8	2.7	8.9E-04	6.8E-04	1.6E-01	4.8E-02	5.0E-03	4.4E-01
265877_at	AT2G42380	bZIP transcription factor family protein	21.6	43.9	35.7	25.9	53.0	20.8	2.6	9.0E-04	6.4E-01	4.4E-02	4.8E-02	8.5E-01	3.2E-01
245319_at	AT4G16146	expressed protein	366.8	330.0	401.8	168.8	189.8	346.8	2.1	9.2E-04	2.3E-05	1.4E-02	4.9E-02	3.8E-04	4.7E-01
247704_at	AT5G59510	expressed protein	4.2	4.1	4.2	20.0	4.2	33.4	8.0	9.4E-04	1.4E-05	1.2E-03	4.9E-02	2.7E-04	2.0E-01
265732_at	AT2G01300	expressed protein	84.3	134.0	115.4	294.5	455.6	94.3	4.8	9.6E-04	1.3E-04	1.3E-03	5.0E-02	1.4E-03	2.1E-01

SI - Table 3A Overrepresented Gene Ontology functional categories - 272 genes

Overrepresentation

Selected statistical test : Hypergeometric test

Selected correction : Benjamini & Hochberg False Discovery Rate (FDR) correction

Selected significance level : 0.05

Testing option : Test cluster versus whole annotation

Number of annotated genes in selection : 234

Number of annotated genes in network/whole annotation : 25168

GO-ID	p-value	corr p-val	# selected	# total	Description	Genes in test set
9725	2.88E-17	1.55E-14	33	413	response to hormone stimulus	AT4G34760 AT3G50660 AT2G34650 AT3G60690 AT5G08130 AT1G29460 AT5G65310 AT4G32280 AT2G45210 AT4G38860 AT1G71030 AT5G18060 AT2G26710 AT2G18010 AT2G31230 AT3G23030 AT3G61460 AT1G57560 AT1G29510 AT4G36110 AT1G15550 AT4G38840 AT4G12410 AT5G47370 AT4G30080 AT1G29450 AT1G13260 AT1G29440 AT4G03400 AT5G54490 AT1G29500 AT4G39400 AT4G38850
9733	1.44E-14	3.86E-12	23	201	response to auxin stimulus	AT4G36110 AT4G34760 AT4G38840 AT2G34650 AT3G60690 AT4G12410 AT5G47370 AT4G30080 AT1G29460 AT1G29450 AT1G29440 AT4G32280 AT2G45210 AT4G03400 AT4G38860 AT5G54490 AT5G18060 AT2G18010 AT3G23030 AT1G29500 AT1G57560 AT4G38850 AT1G29510
9719	1.35E-13	2.42E-11	34	584	response to endogenous stimulus	AT4G34760 AT3G50660 AT2G34650 AT3G60690 AT5G08130 AT1G29460 AT5G65310 AT4G32280 AT2G45210 AT4G38860 AT1G71030 AT5G18060 AT2G26710 AT2G18010 AT2G31230 AT3G23030 AT3G61460 AT1G57560 AT1G29510 AT4G36110 AT1G15550 AT1G8840 AT4G38840 AT4G12410 AT5G47370 AT4G30080 AT1G29450 AT1G29440 AT1G13260 AT4G03400 AT5G54490 AT1G29500 AT4G39400 AT4G38850

42221	2.73E-12	3.65E-10	37	775	response to chemical stimulus	AT5G16980 AT4G34760 AT3G50660 AT2G34650 AT3G60690 AT5G08130 AT1G29460 AT5G65310 AT4G32280 AT2G45210 AT4G38860 AT1G71030 AT5G18060 AT2G26710 AT2G18010 AT2G31230 AT3G23030 AT3G61460 AT1G57560 AT1G29510 AT4G36110 AT1G15550 AT1G80840 AT4G38840 AT4G12410 AT5G47370 AT4G30080 AT3G23550 AT1G29450 AT1G29440 AT1G13260 AT4G03400 AT5G54490 AT4G23030 AT1G29500 AT4G39400 AT4G38850
50896	1.08E-07	1.16E-05	48	1755	response to stimulus	AT5G16980 AT4G34760 AT3G50660 AT2G34650 AT3G60690 AT1G55920 AT5G08130 AT2G43280 AT1G29460 AT5G05690 AT5G65310 AT4G32280 AT2G45210 AT4G38860 AT1G71030 AT5G18060 AT2G26710 AT2G18010 AT2G31230 AT3G23030 AT3G61460 AT1G57560 AT1G29510 AT2G04240 AT3G04210 AT4G36110 AT1G15550 AT1G54050 AT1G80840 AT4G38840 AT4G12410 AT5G47370 AT4G30080 AT4G37590 AT3G23550 AT1G29450 AT1G29440 AT1G13260 AT4G03400 AT4G17250 AT5G54490 AT3G55120 AT4G23030 AT1G29500 AT1G19320 AT4G39400 AT4G38850 AT5G67450
9741	1.71E-05	1.53E-03	6	14	response to brassinosteroid stimulus	AT1G13260 AT3G50660 AT2G26710 AT5G08130 AT3G61460 AT4G39400
30528	5.56E-04	4.25E-02	35	1370	transcription regulator activity	AT1G16640 AT3G25710 AT2G42280 AT2G42380 AT5G13180 AT5G08130 AT5G63790 AT4G23810 AT5G65310 AT3G13040 AT5G61600 AT1G31310 AT2G37590 AT1G71030 AT2G38470 AT2G31230 AT2G45680 AT1G57560 AT2G23320 AT2G28510 AT1G80840 AT1G68810 AT3G50650 AT5G39610 AT5G47370 AT4G30080 AT5G60200 AT1G22190 AT4G30410 AT3G50750 AT3G45610 AT1G62300 AT5G67450 AT4G36780 AT2G43060

3700	1.83E-03	1.23E-01	31	1178	transcription factor activity	AT3G25710 AT1G16640 AT2G42280 AT2G42380 AT5G08130 AT5G13180 AT5G63790 AT4G23810 AT5G65310 AT3G13040 AT5G61600 AT1G31310 AT1G71030 AT2G37590 AT2G38470 AT2G31230 AT2G45680 AT2G23320 AT1G57560 AT2G28510 AT1G80840 AT1G68810 AT3G50650 AT5G39610 AT4G30080 AT5G60200 AT1G22190 AT4G30410 AT3G45610 AT1G62300 AT2G43060
10268	7.83E-02	4.66E+00	3	5	brassinosteroid homeostasis	AT2G26710 AT4G39400 AT5G05690
3677	1.45E-01	7.76E+00	33	1600	DNA binding	AT3G25710 AT1G16640 AT2G42280 AT2G42380 AT5G13180 AT5G08130 AT5G63790 AT4G23810 AT5G65310 AT3G13040 AT5G61600 AT1G31310 AT1G71030 AT2G37590 AT2G38470 AT5G27670 AT2G31230 AT2G45680 AT1G57560 AT2G23320 AT2G28510 AT1G80840 AT1G68810 AT3G50650 AT5G39610 AT4G30080 AT5G60200 AT1G22190 AT4G30410 AT1G13260 AT3G45610 AT1G62300 AT2G43060
16128	6.40E-01	2.86E+01	3	9	phytosteroid metabolism	AT3G50660 AT2G26710 AT5G05690
16131	6.40E-01	2.86E+01	3	9	brassinosteroid metabolism	AT3G50660 AT2G26710 AT5G05690
8395	8.61E-01	3.55E+01	2	2	steroid hydroxylase activity	AT3G50660 AT2G26710
16567	7.19E+00	2.73E+02	5	76	protein ubiquitination	AT3G19380 AT1G49780 AT1G66160 AT5G09800 AT3G49810
10224	8.05E+00	2.73E+02	3	20	response to UV-B	AT3G55120 AT4G39400 AT5G05690
9755	8.58E+00	2.73E+02	5	79	hormone-mediated signaling	AT5G65310 AT2G34650 AT5G47370 AT2G31230 AT5G08130
9653	8.65E+00	2.73E+02	7	212	morphogenesis	AT3G50660 AT2G34650 AT5G47370 AT2G46225 AT4G39400 AT2G22860 AT5G05690
9628	1.10E+01	3.19E+02	13	513	response to abiotic stimulus	AT2G04240 AT1G54050 AT4G38840 AT2G43280 AT4G37590 AT5G05690 AT4G03400 AT1G71030 AT4G17250 AT2G26710 AT3G55120 AT4G39400 AT5G67450
32446	1.13E+01	3.19E+02	5	84	protein modification by small protein conjugation	AT3G19380 AT1G49780 AT1G66160 AT5G09800 AT3G49810
16132	1.26E+01	3.22E+02	2	6	brassinosteroid biosynthesis	AT3G50660 AT5G05690
16129	1.26E+01	3.22E+02	2	6	phytosteroid biosynthesis	AT3G50660 AT5G05690
9826	1.49E+01	3.64E+02	4	53	unidimensional cell growth	AT3G50660 AT5G47370 AT4G39400 AT5G05690

7148	1.78E+01	4.02E+02	5	93	cell morphogenesis	AT3G50660 AT5G47370 AT2G46225 AT4G39400 AT5G05690
5634	1.80E+01	4.02E+02	25	1427	nucleus	AT3G25710 AT2G42280 AT2G42380 AT3G13040 AT1G31310 AT5G61600 AT1G71030 AT1G59660 AT2G37590 AT5G27670 AT3G23030 AT2G31230 AT2G45680 AT2G23320 AT1G57560 AT1G80840 AT1G68810 AT5G39610 AT4G30080 AT5G60200 AT1G22190 AT3G55120 AT1G29500 AT5G67450 AT2G43060
9416	2.07E+01	4.44E+02	7	190	response to light stimulus	AT4G03400 AT2G26710 AT3G55120 AT2G43280 AT4G37590 AT4G39400 AT5G05690
151	2.24E+01	4.49E+02	5	98	ubiquitin ligase complex	AT3G19380 AT1G49780 AT1G66160 AT5G09800 AT3G49810
9314	2.26E+01	4.49E+02	7	193	response to radiation	AT4G03400 AT2G26710 AT3G55120 AT2G43280 AT4G37590 AT4G39400 AT5G05690

SI - Table 3B Overrepresented Gene Ontology functional categories - 31 BIK specific genes

Overrepresentation

Selected statistical test : Hypergeometric test

Selected correction : Benjamini & Hochberg False Discovery Rate (FDR) correction

Selected significance level : 0.05

Testing option : Test cluster versus whole annotation

Number of annotated genes in selection : 26

Number of annotated genes in network/whole annotation : 25168

GO-ID	p-value	corr p-val	# selected	# total	Description	Genes in test set
15591	1.03E+01	3.00E+02	1	1	D-ribose transporter activity	AT3G18830
15575	1.03E+01	3.00E+02	1	1	mannitol transporter activity	AT3G18830
15576	1.03E+01	3.00E+02	1	1	sorbitol transporter activity	AT3G18830
5365	1.03E+01	3.00E+02	1	1	myo-inositol transporter activity	AT3G18830
15148	1.03E+01	3.00E+02	1	1	D-xylose transporter activity	AT3G18830
15146	1.03E+01	3.00E+02	1	1	pentose transporter activity	AT3G18830
15168	2.07E+01	3.59E+02	1	2	glycerol transporter activity	AT3G18830
5354	2.07E+01	3.59E+02	1	2	galactose transporter activity	AT3G18830
9970	2.07E+01	3.59E+02	1	2	cellular response to sulfate starvation	AT1G55920
15166	2.07E+01	3.59E+02	1	2	polyol transporter activity	AT3G18830
9001	3.10E+01	3.99E+02	1	3	serine O-acetyltransferase activity	AT1G55920
16412	3.10E+01	3.99E+02	1	3	serine O-acyltransferase activity	AT1G55920
15665	3.10E+01	3.99E+02	1	3	alcohol transporter activity	AT3G18830
5402	4.13E+01	3.99E+02	1	4	cation:sugar symporter activity	AT3G18830
5403	4.13E+01	3.99E+02	1	4	hydrogen:sugar symporter activity	AT3G18830
15295	4.13E+01	3.99E+02	1	4	solute:hydrogen symporter activity	AT3G18830
5355	4.13E+01	3.99E+02	1	4	glucose transporter activity	AT3G18830
16413	4.13E+01	3.99E+02	1	4	O-acetyltransferase activity	AT1G55920
15149	5.16E+01	4.72E+02	1	5	hexose transporter activity	AT3G18830

SI - Table 4A Fold-change of BIK and BL regulated genes.

The comparisons from left-to-right are: BIK- vs. mock-treated 0.5h; BL- vs. mock-treated 0.5h; BIK- vs. mock-treated 2h; BL- vs. mock-treated 2h

**COMMON DOWNREGULATED GENES
EARLY**

Affymetrix nc	Accession no.	Annotation	treatment/mock			
			0.5h		2h	
			BIK	BL	BIK	BL
250248_at	AT5G13740	sugar transporter family protein	0.8	0.8	0.2	0.4
245439_at	AT4G16670	expressed protein	0.8	0.8	0.3	0.3
257374_at	AT2G43280	far-red impaired responsive family protein / FAR1 far	0.8	0.8	0.5	0.5
266124_at	AT2G45080	cyclin family protein, similar to cyclin 2	0.8	0.8	0.1	0.3
250569_at	AT5G08130	basic helix-loop-helix (bHLH) protein (BIM1)	0.8	0.8	0.4	0.4
253351_at	AT4G33700	CBS domain-containing protein	0.7	0.8	0.4	0.5
258100_at	AT3G23550	MATE efflux family protein	0.7	0.8	0.4	0.3
261400_at	AT1G79630	protein phosphatase 2C family protein / PP2C family	0.6	0.8	0.3	0.4
267305_at	AT2G30070	potassium transporter (KUP1)	0.6	0.8	0.2	0.4
258091_at	AT3G14560	expressed protein	0.6	0.8	0.4	0.5
250598_at	AT5G07690	myb family transcription factor (MYB29)	0.6	0.8	0.3	0.4
260655_at	AT1G19320	pathogenesis-related thaumatin family protein	0.5	0.8	0.5	0.4
253812_at	AT4G28240	wound-responsive protein-related	0.5	0.8	0.3	0.4
257858_at	AT3G12920	expressed protein	0.4	0.8	0.3	0.4
251321_at	AT3G61460	zinc finger (C3HC4-type RING finger) (BRH1)	0.4	0.8	0.3	0.4
247933_at	AT5G56980	expressed protein	0.4	0.8	0.2	0.2
266150_s_at	AT2G12290;AT4G19700	[AT2G12290, expressed protein];[AT4G19700, expr	0.4	0.8	0.5	0.6
246584_at	AT5G14730	expressed protein	0.4	0.8	0.5	0.6
245136_at	AT2G45210	auxin-responsive protein-related	0.3	0.8	0.2	0.2
246063_at	AT5G19340	expressed protein	0.8	0.7	0.2	0.4
249467_at	AT5G39610	no apical meristem (NAM) family protein	0.7	0.7	0.3	0.2
248646_at	AT5G49100	expressed protein	0.7	0.7	0.6	0.4
258021_at	AT3G19380	U-box domain-containing protein	0.7	0.7	0.5	0.3
245761_at	AT1G66890	expressed protein	0.6	0.7	0.1	0.3
257766_at	AT3G23030	auxin-responsive protein (IAA2)	0.6	0.7	0.2	0.4
262830_at	AT1G14700	purple acid phosphatase	0.5	0.7	0.5	0.6
250327_at	AT5G12050	expressed protein	0.5	0.7	0.3	0.3
246284_at	AT4G36780	similar to BZR1 protein (BEH2)	0.5	0.7	0.0	0.1
246495_at	AT5G16200	50S ribosomal protein-related	0.4	0.7	0.1	0.2
253423_at	AT4G32280	auxin-responsive AUX/IAA family protein (IAA29)	0.3	0.7	0.1	0.2
261456_at	AT1G21050	expressed protein	0.3	0.7	0.1	0.2
258196_at	AT3G13980	expressed protein	0.3	0.7	0.1	0.4
254024_at	AT4G25780	pathogenesis-related protein	0.1	0.7	0.2	0.3
250907_at	AT5G03670	expressed protein	0.6	0.6	0.3	0.4
245276_at	AT4G16780	homeobox-leucine zipper protein 4 (HAT4)	0.5	0.6	0.4	0.5
247754_at	AT5G59080	expressed protein	0.5	0.6	0.4	0.5
261772_at	AT1G76240	expressed protein	0.4	0.6	0.1	0.2
245885_at	AT5G09440	phosphate-responsive protein	0.4	0.6	0.1	0.1
259364_at	AT1G13260	DNA-binding protein RAV1 (RAV1)	0.3	0.6	0.5	0.7
261597_at	AT1G49780	U-box domain-containing protein, similar to immediat	0.7	0.5	0.6	0.3
252184_at	AT3G50660	steroid 22-alpha-hydroxylase (CYP90B1) (DWF4)	0.5	0.5	0.0	0.0
251072_at	AT5G01740	expressed protein, wound-inducible protein wun1 pro	0.3	0.5	0.3	0.5
245362_at	AT4G17460	homeobox-leucine zipper protein 1 (HAT1)	0.3	0.5	0.1	0.2
255538_at	AT4G01680	myb family transcription factor (MYB55)	0.2	0.5	0.1	0.1
247880_at	AT5G57780	expressed protein	0.4	0.4	0.1	0.1
261892_at	AT1G80840	WRKY family transcription factor	0.4	0.3	0.2	0.1
265245_at	AT2G43060	similar to cDNA bHLH transcription factor (bHLH zeta	0.3	0.3	0.2	0.4
247177_at	AT5G65300	expressed protein	0.3	0.3	0.2	0.4

256598_at	AT3G30180	cytochrome p450 enzyme (BR6OX2)	0.1	0.3	0.1	0.1
255177_at	AT4G08040	1-aminocyclopropane-1-carboxylate synthase, putativ	0.1	0.1	0.0	0.0
262259_s_at	AT1G53870;AT1G53870	[AT1G53870, expressed protein, contains Pfam profil	0.4	1.0	0.5	0.8
267515_at	AT2G45680	TCP family transcription factor, putative, similar to PC	0.5	1.0	0.5	0.8
264091_at	AT1G79110	expressed protein	0.7	1.0	0.4	0.8
260034_at	AT1G68810	basic helix-loop-helix (bHLH) family protein, contains	0.8	1.0	0.4	0.8
253751_at	AT4G29070	expressed protein	0.8	1.0	0.5	0.7
246516_at	AT5G15740	expressed protein, contains Pfam PF03138: Plant pro	0.8	1.0	0.5	0.7
257746_at	AT3G29200	chorismate mutase, chloroplast (CM1), identical to ch	0.8	1.0	0.5	0.7
258189_at	AT3G17860	expressed protein	0.8	1.0	0.5	0.7
254810_at	AT4G12390	invertase/pectin methylesterase inhibitor family protei	0.7	1.0	0.4	0.7
252890_at	AT4G39400	brassinosteroid insensitive 1 (BR1)	0.7	1.0	0.5	0.6
262500_at	AT1G21760	F-box family protein, Contains PF:00646 F-box doma	0.8	1.0	0.5	0.6
253629_at	AT4G30450	glycine-rich protein	0.8	1.0	0.4	0.6
252296_at	AT3G48970	copper-binding family protein, similar to copper home	0.4	1.0	0.4	0.6
262951_at	AT1G75500	nodulin MtN21 family protein, similar to MtN21 GB:C/	0.7	1.0	0.4	0.6
259373_at	AT1G69160	expressed protein	0.7	1.0	0.3	0.6
265511_at	AT2G05540	glycine-rich protein	0.7	1.0	0.5	0.5
246735_at	AT5G27670	histone H2A, putative, similar to histone H2A Lycoper	0.8	1.0	0.4	0.5
245987_at	AT5G13180	no apical meristem (NAM) family protein, contains Pf	0.8	1.0	0.4	0.5
264900_at	AT1G23080	auxin efflux carrier protein, putative, similar to efflux c	0.8	1.0	0.3	0.5
261700_at	AT1G32690	expressed protein, similar to hypothetical protein GB:	0.4	1.0	0.3	0.5
247478_at	AT5G62360	invertase/pectin methylesterase inhibitor family protei	0.5	1.0	0.2	0.5
257642_at	AT3G25710	basic helix-loop-helix (bHLH) family protein, contains	0.5	1.0	0.1	0.5
251839_at	AT3G54950	patatin-related, low similarity to patatin (GI:169500)(S	0.6	1.0	0.4	0.4
245075_at	AT2G23180	cytochrome P450, putative	0.7	1.0	0.4	0.4
266363_at	AT2G41250	haloacid dehalogenase-like hydrolase family protein,	0.8	1.0	0.3	0.4
261292_at	AT1G36940	expressed protein	0.5	1.0	0.3	0.4
254809_at	AT4G12410	auxin-responsive family protein, similar to GP:546362	0.7	1.0	0.3	0.4
250752_at	AT5G05690	cytochrome P450 90A1 (CYP90A1) (CYP90) (CPD)	0.6	1.0	0.3	0.4
267628_at	AT2G42280	basic helix-loop-helix (bHLH) family protein	0.7	1.0	0.3	0.4
259683_at	AT1G63050	membrane bound O-acyl transferase (MBOAT) family	0.7	1.0	0.3	0.4
266799_at	AT2G22860	phytosulfokines 2 (PSK2), identical to phytosulfokines	0.7	1.0	0.2	0.4
259596_at	AT1G28130	encodes an IAA-amido synthase that conjugates Asp	0.6	1.0	0.4	0.3
255942_at	AT1G22360	UDP-glucuronosyl/UDP-glucosyl transferase family p	0.8	1.0	0.3	0.3
252178_at	AT3G50750	brassinosteroid signalling positive regulator (BE	0.6	1.0	0.3	0.3
259848_at	AT1G72180	leucine-rich repeat transmembrane protein kinase, pu	0.5	1.0	0.1	0.2
245784_at	AT1G32190	expressed protein	0.7	1.0	0.1	0.1
251176_at	AT3G63380	calcium-transporting ATPase, plasma membrane-typ	0.8	1.0	0.1	0.1
245325_at	AT4G14130	xyloglucan:xyloglucosyl transferase, putative / xyloglu	0.4	1.0	0.0	0.1
257855_at	AT3G13040	myb family transcription factor, contains Pfam profile:	1.0	0.8	0.5	0.5
245319_at	AT4G16146	expressed protein	1.0	0.8	0.5	0.5
250493_at	AT5G09800	U-box domain-containing protein, low similarity to imr	1.0	0.8	0.8	0.3
247351_at	AT5G63790	no apical meristem (NAM) family protein, contains Pf	1.0	0.5	0.7	0.3
260243_at	AT1G63720	expressed protein, similar to putative protein GB:CA	1.0	0.7	0.2	0.2
259751_at	AT1G71030	Encodes a putative myb family transcription factor. Ir	1.0	0.8	0.5	0.1
253999_at	AT4G26200	1-aminocyclopropane-1-carboxylate synthase, putativ	1.0	0.3	0.2	0.1
LATE						
250537_at	AT5G08565	expressed protein	1.0	1.0	0.4	0.8
256960_at	AT3G13510	expressed protein	1.0	1.0	0.4	0.8
251827_at	AT3G55120	chalcone-flavanone isomerase	1.0	1.0	0.4	0.7
246580_at	AT1G31770	ABC transporter family protein	1.0	1.0	0.5	0.6
253062_at	AT4G37590	phototropic-responsive NPH3 family protein	1.0	1.0	0.4	0.5
253662_at	AT4G30080	transcriptional factor B3 family protein	1.0	1.0	0.4	0.5
266591_at	AT2G46225	Encodes a subunit of the WAVE complex	1.0	1.0	0.6	0.5
253617_at	AT4G30410	expressed protein, similar to cDNA bHLH transcriptio	1.0	1.0	0.4	0.4

247077_at	AT5G66420	expressed protein	1.0	1.0	0.4	0.4
253247_at	AT4G34610	homeodomain-containing protein, similarity to homeo	1.0	1.0	0.4	0.4
248419_at	AT5G51550	phosphate-responsive 1 family protein	1.0	1.0	0.4	0.4
259985_at	AT1G76620	expressed protein	1.0	1.0	0.3	0.4
262531_at	AT1G17230	leucine-rich repeat family protein / protein kinase fam	1.0	1.0	0.2	0.4
262050_at	AT1G80130	expressed protein	1.0	1.0	0.2	0.4
252387_at	AT3G47800	aldose 1-epimerase family protein	1.0	1.0	0.6	0.3
262635_at	AT1G06570	4-hydroxyphenylpyruvate dioxygenase (HPD)	1.0	1.0	0.3	0.3
251342_at	AT3G60690	auxin-responsive family protein, similar to auxin-induc	1.0	1.0	0.3	0.3
247191_at	AT5G65310	homeobox-leucine zipper protein 5 (HB-5) / HD-ZIP tr	1.0	1.0	0.2	0.3
247704_at	AT5G59510	expressed protein	1.0	1.0	0.6	0.1
256762_at	AT3G25655	expressed protein	1.0	1.0	0.2	0.1

COMMON UPREGULATED GENES

EARLY

253103_at	AT4G36110	auxin-responsive protein, putative	1.2	2.3	4.6	7.9
264083_at	AT2G31230	encodes a member of the ERF (ethylene response fa	2.1	1.7	3.2	2.7
255443_at	AT4G02700	sulfate transporter	1.8	1.7	2.2	1.2
262124_at	AT1G59660	nucleoporin family protein	1.4	1.7	2.9	3.1
260287_at	AT1G80440	kelch repeat-containing F-box family protein	1.4	1.7	2.9	2.9
255403_at	AT4G03400	auxin-responsive GH3 family protein	1.2	1.7	1.3	2.1
262315_at	AT1G70990	proline-rich family protein	1.7	1.6	3.5	2.2
265806_at	AT2G18010	auxin-responsive family protein (SAUR10)	1.3	1.6	3.9	9.1
262630_at	AT1G06520	membrane associated mitochondrial localized protein	1.3	1.6	2.3	3.1
249765_at	AT5G24030	C4-dicarboxylate transporter/malic acid transport fam	2.3	1.4	1.7	1.9
254292_at	AT4G23030	MATE efflux protein-related	1.6	1.4	5.2	2.2
245262_at	AT4G16563	aspartyl protease family protein	1.2	1.4	1.7	2.9
256528_at	AT1G66140	zinc finger (C2H2 type) family protein	1.2	1.4	1.6	2.2
249752_at	AT5G24660	expressed protein	2.4	1.3	3.6	2.3
247444_at	AT5G62630	expressed protein	1.6	1.3	2.3	1.3
255037_at	AT4G09460	myb family transcription factor	1.5	1.3	3.3	2.8
263207_at	AT1G10550	xyloglucan:xyloglucosyl transferase	1.3	1.3	1.7	2.2
256453_at	AT1G75270	dehydroascorbate reductase	1.2	1.3	2.6	1.7
253828_at	AT4G27970	C4-dicarboxylate transporter/malic acid transport fam	2.4	1.2	3.0	1.3
266693_at	AT2G19800	expressed protein	2.3	1.2	2.2	1.8
253281_at	AT4G34138	UDP-glucuronosyl/UDP-glucosyl transferase family p	1.5	1.2	3.2	1.7
252173_at	AT3G50650	scarecrow-like transcription factor 7 (SCL7)	1.5	1.2	2.5	1.8
263823_s_at	AT2G40340;AT2	[AT2G40340, encodes a member of the DREB subfa	1.4	1.2	3.2	1.7
258075_at	AT3G25900	homocysteine S-methyltransferase 1 (HMT-1)	1.3	1.2	2.7	2.2
263002_at	AT1G54200	expressed protein	1.3	1.2	2.2	2.1
267393_at	AT2G44500	expressed protein	1.3	1.2	2.2	2.1
263150_at	AT1G54050	17.4 kDa class III heat shock protein (HSP17.4-CIII),	1.2	1.0	2.9	3.6
246401_at	AT1G57560	myb family transcription factor (MYB50), similar to DM	1.2	1.0	2.7	2.5
254294_at	AT4G23070	rhomboid family protein, contains PFAM domain PF0	2.0	1.0	3.8	2.0
245272_at	AT4G17250	expressed protein	1.2	1.0	3.3	1.8
260434_at	AT1G68330	expressed protein	1.8	1.0	2.8	1.7
261023_at	AT1G12200	flavin-containing monooxygenase family protein / FM	1.4	1.0	2.2	1.4
263652_at	AT1G04330	expressed protein, EST gb:H76414 comes from this g	1.2	1.0	4.4	1.3
266265_at	AT2G29340	short-chain dehydrogenase/reductase (SDR) family p	1.6	1.0	3.7	1.3
267171_at	AT2G37590	Dof-type zinc finger domain-containing protein	1.5	1.0	5.8	1.2
248732_at	AT5G48070	putative xyloglucan endotransglycosylase/hydrolase,	1.5	1.0	3.6	1.2
256522_at	AT1G66160	U-box domain-containing protein, similar to immediat	2.0	1.0	1.9	1.2
267238_at	AT2G44130	kelch repeat-containing F-box family protein, very low	1.0	1.6	7.7	6.3
261265_at	AT1G26800	zinc finger (C3HC4-type RING finger) family protein, c	1.0	1.5	4.4	6.1
250012_x_at	AT5G18060	auxin-responsive protein, putative, similar to auxin-inc	1.0	1.3	2.2	3.5
258367_at	AT3G14370	protein kinase family protein, contains protein kinase	1.0	2.1	2.2	3.5
266908_at	AT2G34650	protein kinase PINOID (PID), identical to protein kina	1.0	1.5	2.5	3.3

252970_at	AT4G38850	auxin-responsive protein / small auxin up RNA (SAUR)	1.0	1.4	2.2	3.0
257506_at	AT1G29440	auxin-responsive family protein, similar to auxin-induc	1.0	1.5	2.1	2.9
259783_at	AT1G29510	auxin-responsive protein, putative, similar to auxin-inc	1.0	1.3	2.0	2.8
259784_at	AT1G29450	auxin-responsive protein, putative, similar to auxin-inc	1.0	1.3	1.6	2.7
263931_at	AT2G36220	expressed protein	1.0	1.2	2.8	2.6
259773_at	AT1G29500	auxin-responsive protein, putative, similar to auxin-inc	1.0	1.3	1.6	2.6
252972_at	AT4G38840	auxin-responsive protein, putative, auxin-inducible SAUR	1.0	1.3	2.0	2.5
253736_at	AT4G28780	GDSL-motif lipase/hydrolase family protein	1.0	1.2	1.3	2.3
245176_at	AT2G47440	DNAJ heat shock N-terminal domain-containing prote	1.0	1.3	1.6	2.2
254424_at	AT4G21510	F-box family protein	1.0	1.5	2.5	2.1
255931_at	AT1G12710	F-box family protein / SKP1 interacting partner 3-relat	1.0	1.3	1.4	2.1
262653_at	AT1G14130	2-oxoglutarate-dependent dioxygenase, putative, sim	1.0	1.3	2.5	1.3
246464_at	AT5G16980	NADP-dependent oxidoreductase	1.0	1.2	3.1	1.3

LATE

251774_at	AT3G55840	expressed protein	1.0	1.0	7.0	7.4
259864_at	AT1G72800	nuM1-related	1.0	1.0	2.1	2.8
247774_at	AT5G58660	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.0	1.0	2.1	2.8
246781_at	AT5G27350	sugar-porter family protein 1 (SFP1)	1.0	1.0	1.6	2.0
247617_at	AT5G60270	lectin protein kinase family protein	1.0	1.0	2.6	1.8
248040_at	AT5G55970	zinc finger (C3HC4-type RING finger) family protein	1.0	1.0	2.6	1.8
263126_at	AT1G78460	SOUL heme-binding family protein	1.0	1.0	2.5	1.5
261443_at	AT1G28480	glutaredoxin family protein	1.0	1.0	4.0	1.4
256818_at	AT3G21420	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.0	1.0	2.4	1.3

GENES WITH OPPOSITE EXPRESSION PATTERN

EARLY

247940_at	AT5G57190	phosphatidylserine decarboxylase, putative	1.3	1.0	1.6	0.6
250004_at	AT5G18750	DNAJ heat shock N-terminal domain-containing prote	1.9	1.0	1.3	0.6
248686_at	AT5G48540	33 kDa secretory protein-related	2.4	1.0	2.0	0.6
245543_at	AT4G15260	UDP-glucuronosyl/UDP-glucosyl transferase family p	1.4	1.0	1.5	0.7
258282_at	AT3G26910	hydroxyproline-rich glycoprotein family protein	2.5	1.0	1.8	0.6
248134_at	AT5G54860	integral membrane transporter family protein)	1.7	1.0	2.0	0.8
258651_at	AT3G09920	phosphatidylinositol-4-phosphate 5-kinase family prot	1.6	1.0	1.1	0.4
266835_at	AT2G29990	pyridine nucleotide-disulphide oxidoreductase family	1.4	1.0	1.4	0.5
245051_at	AT2G23320	WRKY family transcription factor	1.4	1.0	1.2	0.5
249480_s_at	AT5G38990;AT5G38990	[AT5G38990, protein kinase family protein, contains p	1.4	1.0	2.1	0.7
252230_at	AT3G49810	U-box domain-containing protein	1.3	1.0	1.1	0.6
264056_at	AT2G28510	Dof-type zinc finger domain-containing protein	1.3	1.0	1.2	0.5
262550_at	AT1G31310	hydroxyproline-rich glycoprotein family protein	1.2	1.0	2.4	0.7
253779_at	AT4G28490	leucine-rich repeat transmembrane protein kinase	1.2	1.0	2.3	0.8
253414_at	AT4G33050	calmodulin-binding family protein	2.4	1.0	1.6	0.6
246858_at	AT5G25930	leucine-rich repeat family protein / protein kinase fam	2.7	1.0	1.4	0.6
252501_at	AT3G46880	expressed protein	1.5	0.8	1.5	0.6
255895_at	AT1G18020;AT1G18020	[AT1G18020, 12-oxophytodienoate reductase, putativ	1.3	0.8	1.8	0.5
255502_at	AT4G02410	lectin protein kinase family protein	2.6	0.7	1.6	0.6
245662_at	AT1G28190	expressed protein	2.8	0.7	1.6	0.6
267028_at	AT2G38470	WRKY family transcription factor	2.0	0.4	1.3	0.6
262040_at	AT1G80080	protein kinase family protein	0.6	1.3	0.5	2.6
253255_at	AT4G34760	auxin-responsive family protein, auxin-induced protei	0.6	1.2	0.6	1.6
245479_at	AT4G16140	proline-rich family protein	1.0	1.2	0.7	1.3
261203_at	AT1G12845	expressed protein	0.6	1.0	0.4	2.1
262543_at	AT1G34245	expressed protein	0.6	1.0	0.2	1.5

LATE

249188_at	AT5G42830	transferase family protein	1.0	1.0	2.7	0.6
253044_at	AT4G37290	expressed protein	1.0	1.0	2.4	0.4
260727_at	AT1G48100	glycoside hydrolase family 28 protein	1.0	1.0	0.4	1.2

COMPLEX

EARLY

262505_at	AT1G21680	expressed protein	0.8	1.0	2.0	1.3
248164_at	AT5G54490	calcium-binding EF-hand protein, putative, similar to l	0.7	0.4	3.1	1.8
247543_at	AT5G61600	encodes a member of the ERF (ethylene response fa	0.5	0.5	2.0	2.1
255926_at	AT1G22190	AP2 domain-containing transcription factor, putative,	0.4	0.8	0.5	1.0
261648_at	AT1G27730	zinc finger (C2H2 type) family protein (ZAT10) / salt-t	0.6	0.2	1.0	0.7
259982_at	AT1G76410	zinc finger (C3HC4-type RING finger) family protein, c	0.5	1.6	0.2	0.4
247074_at	AT5G66590	allergen V5/Tpx-1-related family protein	0.5	1.2	0.3	0.6
267614_at	AT2G26710	cytochrome p450 family (BAS1)	0.7	1.6	2.3	5.4
263325_at	AT2G04240	zinc finger (C3HC4-type RING finger) family protein	0.8	1.5	1.7	2.8
252965_at	AT4G38860	auxin-responsive protein (SAUR16)	0.8	1.4	2.3	3.4
259787_at	AT1G29460	auxin-responsive protein (SAUR65)	0.8	1.3	2.2	3.6
266447_at	AT2G43290	calmodulin-like protein (MSS3)	0.8	1.2	1.4	3.0
265877_at	AT2G42380	bZIP transcription factor family protein	0.6	1.2	1.3	2.6
246200_at	AT4G37240	expressed protein	0.8	1.2	1.5	2.3
246926_at	AT5G25240	expressed protein	0.7	1.2	2.2	3.7
265732_at	AT2G01300	expressed protein	0.7	1.2	3.1	4.8
248282_at	AT5G52900	expressed protein	0.6	1.4	1.0	2.0
249494_at	AT5G39050	transferase family protein	1.5	1.4	1.8	0.6
255933_at	AT1G12750	rhomboid family protein	1.5	1.2	1.6	0.8
253573_at	AT4G31020	expressed protein	2.7	1.5	5.8	0.7
253483_at	AT4G31910	transferase family protein	1.5	1.2	1.6	0.8
267592_at	AT2G39710	aspartyl protease family protein	2.4	1.3	2.5	1.0
246993_at	AT5G67450	zinc finger (C2H2 type) protein 1 (AZF1)	6.2	1.8	1.8	1.0
246389_at	AT1G77380	amino acid carrier, putative	1.3	1.0	1.0	0.4
245119_at	AT2G41640	expressed protein	2.0	0.8	2.5	1.4
247625_at	AT5G60200	Dof-type zinc finger domain-containing protein	1.4	0.8	3.9	1.7
251910_at	AT3G53810	lectin protein kinase	2.3	0.8	2.2	1.2
245041_at	AT2G26530	expressed protein	1.2	0.4	2.0	1.0
254231_at	AT4G23810	WRKY family transcription factor	5.8	0.7	1.0	0.5
251832_at	AT3G55150	exocyst subunit EXO70 family protein	3.4	0.8	0.5	0.1
264746_at	AT1G62300	WRKY family transcription factor	1.6	0.6	0.7	0.2

SI - Table 4B Fold-change of BIK regulated genes.

The comparisons from left-to-right are: BIK- vs. mock-treated 0.5h; BL- vs. mock-treated 0.5h; BIK- vs. BIK specific

Affymetrix nc	Accession no.	Annotation	treatment/mock			
			BIK 0.5h	BL 0.5h	BIK 2h	BL 2h
DOWNREGULATED						
EARLY						
252646_at	AT3G44610	protein kinase family protein	0.8	1.0	0.4	1.0
248190_at	AT5G54120	expressed protein	0.8	1.0	0.4	1.0
248191_at	AT5G54130	calcium-binding EF hand family protein	0.8	1.0	0.3	1.0
258432_at	AT3G16570	rapid alkalization factor (RALF) family protein	0.5	1.0	0.4	1.0
247601_at	AT5G60850	Dof-type zinc finger domain-containing protein	0.5	1.0	0.6	1.0
248801_at	AT5G47370	homeobox-leucine zipper protein 2 (HAT2)	0.5	1.0	0.4	1.0
245229_at	AT4G25620	hydroxyproline-rich glycoprotein family protein	0.5	1.0	0.5	1.0
LATE						
257066_at	AT3G18280	protease inhibitor/seed storage/lipid transfer protein (1.0	1.0	0.4	1.0
UPREGULATED						
EARLY						
245369_at	AT4G15975	zinc finger (C3HC4-type RING finger) family protein	2.3	1.0	3.3	1.0
256337_at	AT1G72060	expressed protein	2.2	1.0	6.0	1.0
258537_at	AT3G04210	disease resistance protein (TIR-NBS class)	2.2	1.0	3.2	1.0
260602_at	AT1G55920	serine O-acetyltransferase	2.2	1.0	2.2	1.0
253737_at	AT4G28703	expressed protein	2.0	1.0	6.1	1.0
259875_s_at	AT1G76690;AT1G76690	[AT1G76690, 12-oxophytodienoate reductase (OPR2	2.0	1.0	6.1	1.0
262072_at	AT1G59590	expressed protein	2.0	1.0	2.1	1.0
257398_at	AT2G01990	expressed protein	1.9	1.0	2.6	1.0
257805_at	AT3G18830	monosaccharide-H ⁺ -symporter	1.6	1.0	2.6	1.0
265158_at	AT1G31040	zinc-binding protein-related	1.4	1.0	4.4	1.0
249435_at	AT5G39970	expressed protein	1.4	1.0	2.7	1.0
261382_at	AT1G05470	endonuclease/exonuclease/phosphatase family prote	1.4	1.0	2.6	1.0
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein	1.4	1.0	2.3	1.0
264279_s_at	AT1G78820;AT1G78820	[AT1G78820, curculin-like (mannose-binding) lectin f	1.3	1.0	1.8	1.0
251162_at	AT3G63300	expressed protein	1.3	1.0	2.1	1.0
252047_at	AT3G52490	heat shock protein-related	1.2	1.0	2.4	1.0
LATE						
255941_at	AT1G20350	mitochondrial import inner membrane translocase sul	1.0	1.0	2.7	1.0
252586_at	AT3G45610	Dof-type zinc finger domain-containing protein	1.0	1.0	2.6	1.0
251039_at	AT5G02020	expressed protein	1.0	1.0	2.3	1.0
247610_at	AT5G60630	expressed protein	1.0	1.0	2.2	1.0
246321_at	AT1G16640	transcriptional factor B3 family protein	1.0	1.0	2.2	1.0
247205_at	AT5G64890	expressed protein	1.0	1.0	2.2	1.0
249558_at	AT5G38310	expressed protein	1.0	1.0	1.9	1.0

SI - Table 4C Fold-change of BL regulated genes.

The comparisons from left-to-right are: BIK- vs. mock-treated 0.5h; BL- vs. mock-treated 0.5h; BIK- vs. BL specific

Affymetrix nc	Accession no.	Annotation	treatment/mock			
			0.5h		2h	
			BIK	BL	BIK	BL
UPREGULATED						
EARLY						
261768_at	AT1G15550	gibberellin 3-beta-dioxygenase / gibberellin 3 beta-hy	1.0	1.3	1.0	1.9
249947_at	AT5G19200	short-chain dehydrogenase/reductase (SDR) family p	1.0	1.2	1.0	2.5

SI - Table 5. Primers used in quantitative RT-PCR

Gene (At-code)	Forward Primer	Reverse Primer
<i>DWF4</i> (At3g50660)	GTGATCTCAGCCGTACATTTGGA	CACGTGCAAAAACTACCACTTCCT
<i>CPD</i> (At5g05690)	CCCAAACCACTTCAAAGATGCT	GGGCCTGTCGTTACCGAGTT
<i>BAS1</i> (At2g26710)	TTGGCTTCATACCGTTTGGC	TTACAGCGAGTGTCAATTTGGC
<i>ROT3</i> (At4g36380)	ATTGGCGCGTTCCTCAGAT	CAAGACGCCAAAGTGAGAACA
<i>BR6OX1</i> (At5g38970)	TGGCCAATCTTTGGCGAA	TCCCGTATCGGAGTCTTTGGT
<i>BR6OX2</i> (At3g30180)	CAATAGTCTCAATGGACGCAGAGT	AACCGCAGCTATGTTGCATG
<i>BR11</i> (At4g39400)	GGTGAAACAGCACGCAAACT	CACGCAACCGCAACTTTTAA
<i>BIN2</i> (At4g18710)	GTGACTTTGGCAGTGCGAAAC	CAGCATTTTCTCCGGGAAATAATGG
<i>BSU1</i> (At1g03445)	GGCGGTTTTTCGTCAACAATTCC	CCATCTAAACTGATCTCGGGTAAGG
<i>BES1</i> (At1g19350)	CAACCTCGCCTACCTTCAATCTC	TTGGCTGTTCTCAAACCTTAACTCG
<i>BZR1</i> (At1g75080)	CCTCTACATTCTTCCCTTTCCTCAG	GCTTAGCGATAGATTCCCAGTTAGG
<i>Saur-AC1</i> (At4g38850)	TTGGGTGCTAAGCAAATTATTTCG	TCTCCTACATAGACCGCCATGA
<i>CDKA1;1</i> (At3g48750)	ATTGCGTATTGCCACTCTCATAGG	TCCTGACAGGGATAACCGAATGC
<i>EEF1α4</i> (At5g60390)	CTGGAGGTTTTGAGGCTGGTAT	CCAAGGGTGAAAGCAAG AAGA

Table S6. Primers used for *in vitro* mutagenesis of BIN2

Mutation	Forward primer	Reverse primer
M115L	5'-GAGCTTTTCTTGAAGTTGGTTCTGGAGTATGTCCTGAGAGCTTG-3'	5'-CAAGCTCTCAGGGACATACTCCAGAACCAAGTTCAAGAAAAGCTC-3'
T65/K	5'-GGAGACTGGAGAAAAGGTGGCGATAAAGAAGGTTTGGCAAGATAG-3'	5'-CTATCTTGCAAAACCTTCTTTATCGCCACCTTTTCTCCAGTCTCC-3'
Y117/F	5'-GAGCTTTTCTTGAAGTTGGTTATGGAGTTTGTCCCTGAGAGCTTG-3'	5'-CAAGCTCTCAGGGACAAACTCCATAACCAAGTTCAAGAAAAGCTC-3'