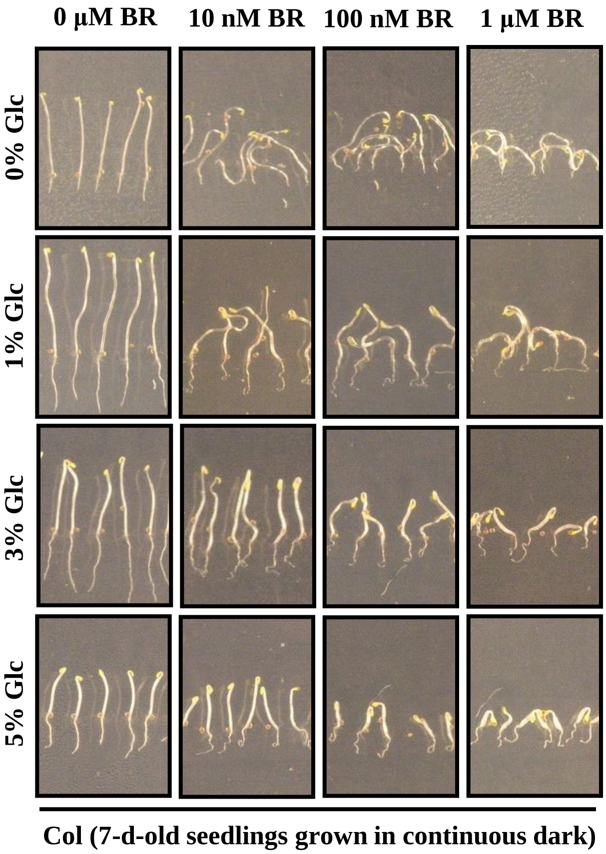
		Whole Genome	BR regulated	BR upregulated	BR downregulated	BR-Glc coregulated	Synergistically regulated by BR and Glc	Antagonistically regulated by BR and Glc	Extent of BR regulation affected by Glc	Synergistic affect of Glc on extent of BR regulation	Antagonistic affect of Glc on extent of BR regulation
A			**303**	**190**	**113**	**217**	**125**	**92**	**256**	**110**	**146**
	Nucleus	37.73	31.14	32.04	29.63	31.40	31.93	30.68	28.83	26.67	30.77
	Chloroplast	15.83	11.77	9.39	15.74	14.49	11.77	18.18	12.61	10.48	14.53
	Plasma membrane	13.48	15.23	16.58	12.96	14.98	15.97	13.64	15.32	17.14	13.68
	Mitochondria	12.47	9.00	6.63	12.96	10.15	10.92	9.09	9.01	11.43	6.84
	Extracellular	10.68	**22.15**	**24.86**	**17.59**	**20.77**	**21.01**	**20.46**	**22.07**	**22.86**	**21.37**
	Cytosol	7.39	6.92	7.18	6.48	7.25	10.08	3.41	7.66	11.43	14.27
	Plastid	5.97	2.77	1.66	4.63	3.87	4.20	3.41	2.70	3.81	1.71
	Golgi apparatus	4.14	5.54	7.74	1.85	6.76	5.04	9.09	5.86	5.71	5.98
	ER	3.11	3.11	3.32	2.78	2.90	3.36	2.27	15.30	4.76	1.71
	Cell wall	2.72	**9.00**	**11.05**	**5.56**	**8.70**	**7.56**	**10.23**	**9.01**	**10.48**	**7.69**
	Ribosome	2.01	0.35	0.00	0.93	0.48	0.84	0.00	0.45	0.95	0.00
B	**DNA or RNA binding**	16.20	9.89	9.47	10.58	9.69	7.83	12.35	9.57	8.08	10.91
	Transferase activity	14.46	16.48	20.12	10.58	17.86	20.00	14.82	17.23	20.20	14.55
	Hydrolase activity	13.84	15.39	14.20	17.31	13.27	13.04	13.58	17.70	18.18	17.27
	Nucleotide binding	13.76	11.36	13.61	7.69	12.76	17.39	6.17	11.98	17.17	6.36
	Protein binding	12.19	10.26	10.65	9.62	10.20	9.57	11.11	9.57	10.10	9.09
	Transcription factor activity	6.92	**11.35**	**11.83**	**10.58**	**10.71**	**12.17**	**8.64**	**10.05**	**11.11**	**9.09**
	Kinase activity	5.98	4.40	6.51	0.96	5.10	6.96	2.47	3.35	6.06	0.91
	Nucleic acid binding	5.79	3.30	2.96	3.85	4.08	5.22	2.47	3.83	5.05	2.73
	Transporter activity	5.62	3.30	1.18	6.73	3.06	3.48	2.47	3.35	4.04	2.73
	Structural molecule activity	2.20	0.37	0.59	0.00	0.51	0.00	1.24	0.48	0.00	0.91
	Receptor binding or activity	0.86	1.83	1.78	1.92	1.53	1.74	1.24	1.44	2.02	0.91
C	**Protein metabolism**	22.38	16.14	17.78	13.33	17.24	18.97	14.94	16.90	18.63	15.39
	Response to stress	18.36	**29.83**	**36.11**	**19.05**	**31.53**	**36.21**	**25.29**	**20.22**	**32.35**	**26.50**
	Response to abiotic /biotic stimulus	16.86	**27.72**	**33.89**	**17.14**	**28.08**	**31.03**	**24.14**	**26.48**	**28.43**	**24.79**
	Cell organization and biogenesis	16.41	17.90	20.56	13.33	17.73	13.38	19.54	19.64	18.63	20.51
	Transport	15.25	14.74	15.56	13.33	14.29	13.79	14.94	15.53	12.75	17.95
	Developmental processes	15.25	14.39	12.22	18.10	13.30	12.07	14.94	14.61	14.71	14.53
	Transcription, DNA-dependent	12.31	12.98	13.33	12.38	12.81	14.66	10.35	11.42	12.75	10.26
	Signal transduction	9.38	**18.25**	**21.67**	**12.38**	**17.24**	**18.10**	**16.09**	**17.35**	**20.59**	**14.53**
	DNA or RNA metabolism	3.99	1.05	0.56	1.91	1.48	0.86	2.30	1.37	0.98	1.71
	Energy pathways	2.84	1.40	1.67	0.95	0.49	0.00	1.15	1.83	0.00	3.42

Supplemental figure S1. Functional categorization of BR- and Glc- regulated genes on the basis of **A,** gene ontology (GO) cellular component; **B,** gene ontology (GO) molecular function; and **C,** gene ontology (GO) biological process. (The numbers highlighted in red show % values of most enriched GO category as compared to whole genome categorization).

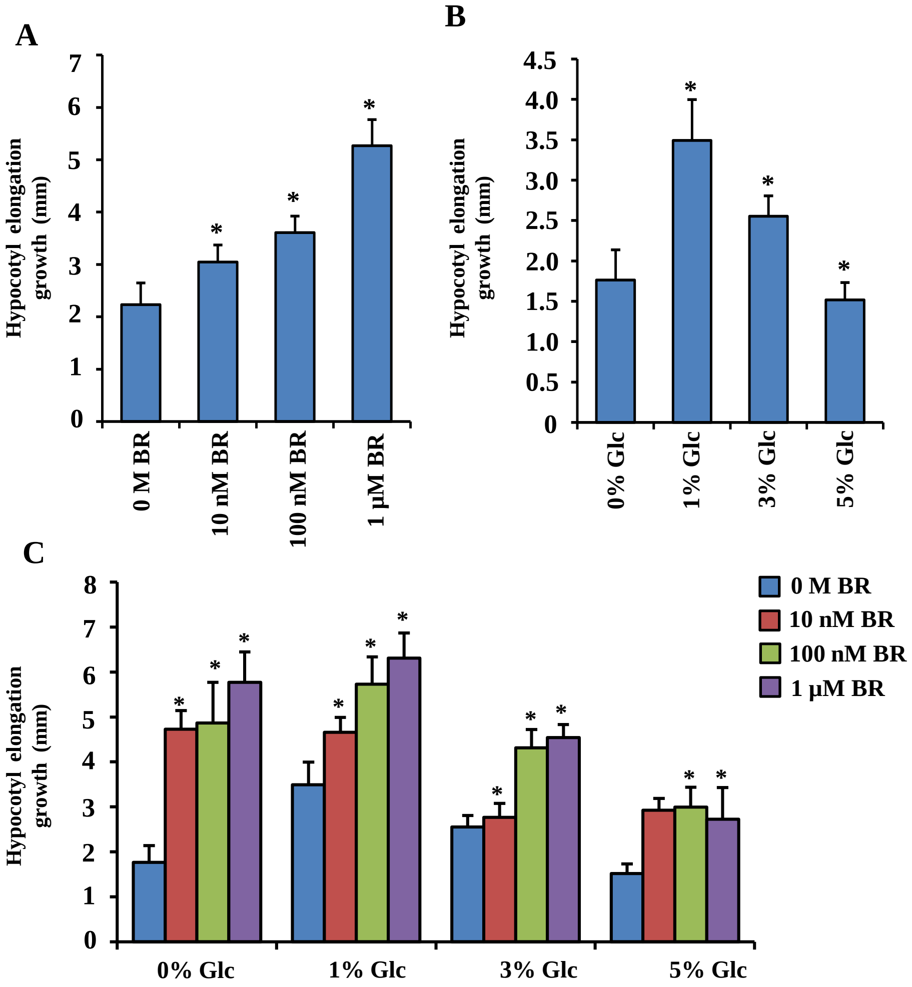
	BR regulated	BR up-regulated	BR down-regulated	BR-Glc co regulated	Synergistically regulated by BR and Glc	Antagonistically regulated by BR and Glc	Extent of BR regulation affected by Glc	Synergistic affect of Glc on extent of BR regulation	Antagonistic affect of Glc on extent of BR regulation
Total no of genes	811	527	284	673	371	302	712	336	376
No. of TF	75	46	29	60	30	30	66	28	38
%	**9.2**	**8.7**	**10.2**	**8.9**	**8.1**	**9.9**	**9.3**	**8.3**	**10.1**

1	**ABI3VP1**	1	1	0	0	0	0	1	1	0
2	**AP2-EREBP**	15	9	6	13	5	8	15	4	11
3	**bHLH**	10	5	5	5	2	3	10	3	7
4	**bZIP**	2	0	2	2	1	1	1	0	1
5	**BZR**	1	0	1	0	0	0	1	1	0
6	**C2C2-CO-like**	2	1	1	2	1	1	1	0	1
7	**C2C2-GATA**	1	1	0	1	1	0	1	1	0
8	**C2H2**	6	5	1	6	5	1	6	5	1
9	**C3H**	5	4	1	5	1	4	5	1	4
10	**GRAS**	2	1	1	2	1	1	1	0	1
11	**GRF**	1	1	0	0	0	0	0	0	0
12	**Homeobox**	5	1	4	3	2	1	4	3	1
13	**HSF**	4	4	0	4	3	1	3	2	1
14	**MYB**	10	6	4	8	4	4	9	4	5
15	**NAC**	6	4	2	5	3	2	5	3	2
16	**Trihelix**	1	0	1	1	0	1	1	0	1
17	**WRKY**	3	3	0	3	1	2	2	0	2

Supplemental figure S2. Transcription factor family enrichment analysis of BR- and Glc-regulated genes (1.5 fold +/-) in etiolated seedlings.



Supplemental figure S3. Regulation of hypocotyl growth by Glc and BR in etiolated seedlings.



Supplemental figure S4. Glc and BR regulation of hypocotyl elongation growth in light grown seedlings.

A, Quantification of hypocotyl length in 7-d-old light grown WT (Col-0) seedlings treated without or with increasing concentrations of BR. **B,** Quantification of hypocotyl length in 7-d-old light grown WT (Col-0) seedlings treated without or with increasing concentrations of Glc. **C,** Quantification of hypocotyl length in 7-d-old light grown WT (Col-0) seedlings growing on Glc free or increased Glc concentration containing ½ MS medium supplemented without or with increasing concentrations of BR. Glc and BR work antagonistically at lower Glc concentration but act synergistically at higher Glc concentrations for hypocotyl elongation regulation. Values represent the average from a representative biological replicate having 15 seedlings and error bars represent SD. (Student's T-test, $P<0.001$; * control vs. treatment).

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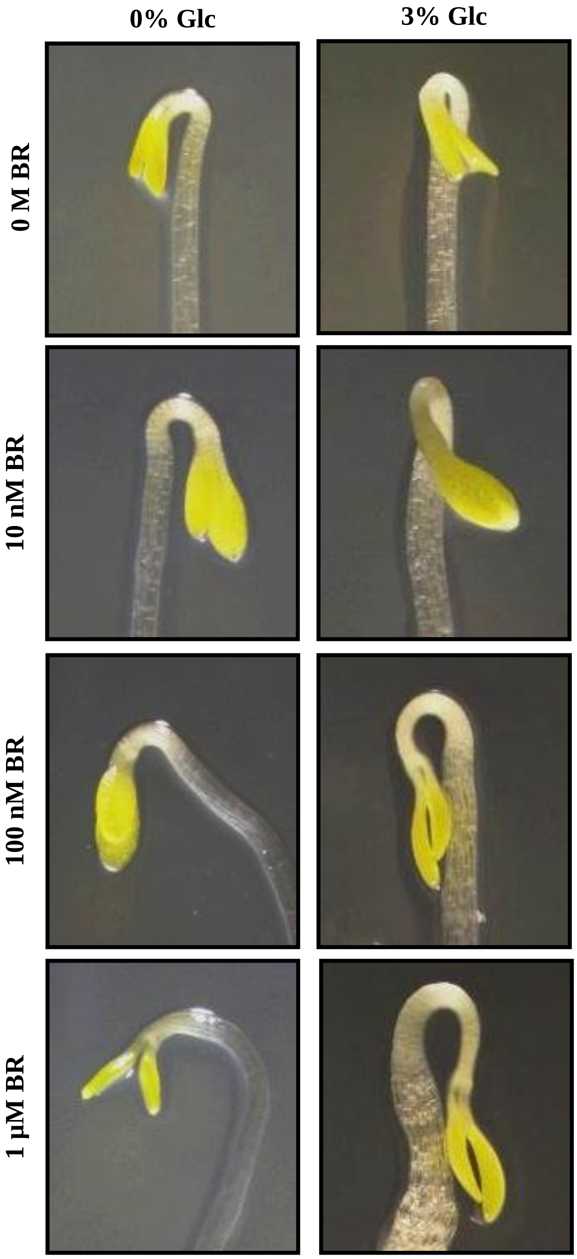
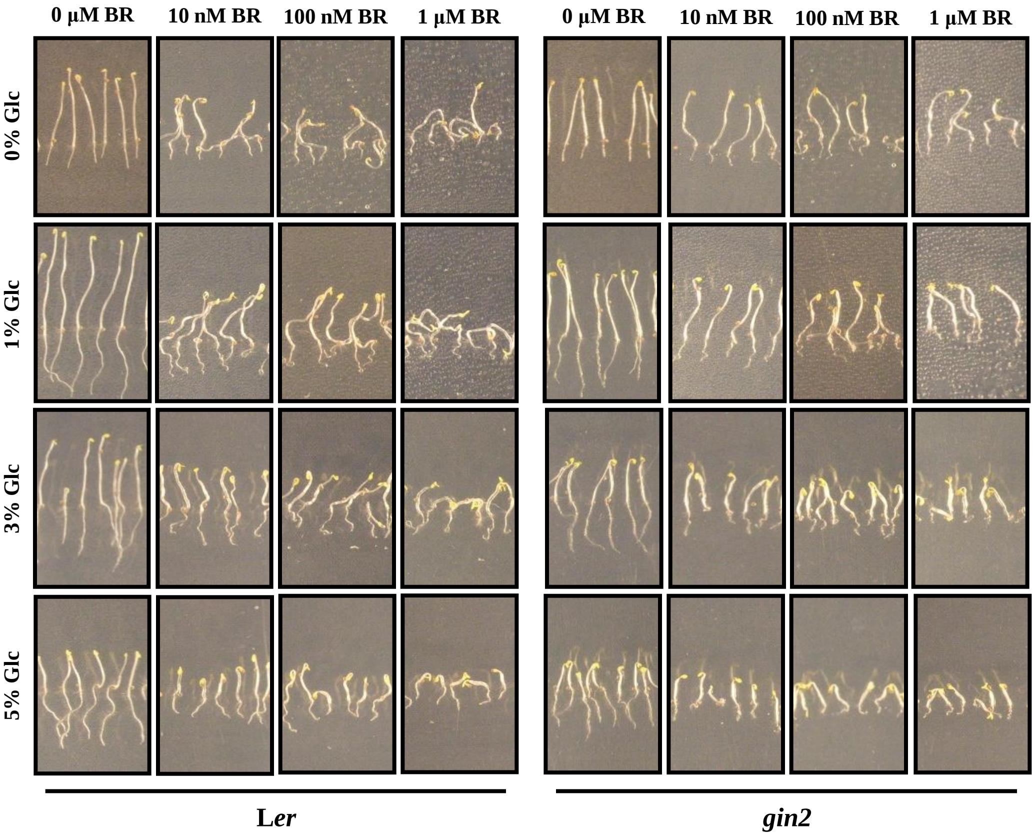
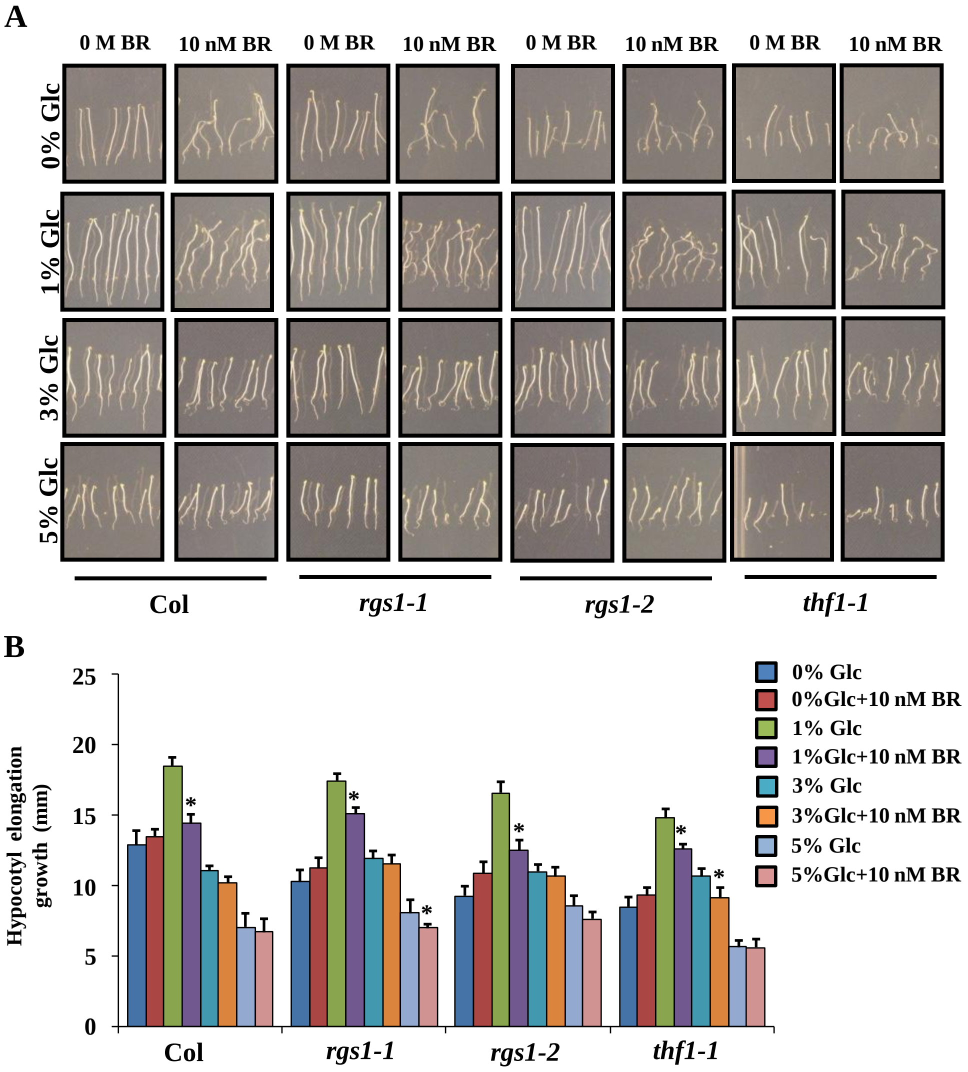


Supplemental figure S5. Regulation of apical hook development by Glc and BR in etiolated seedlings.

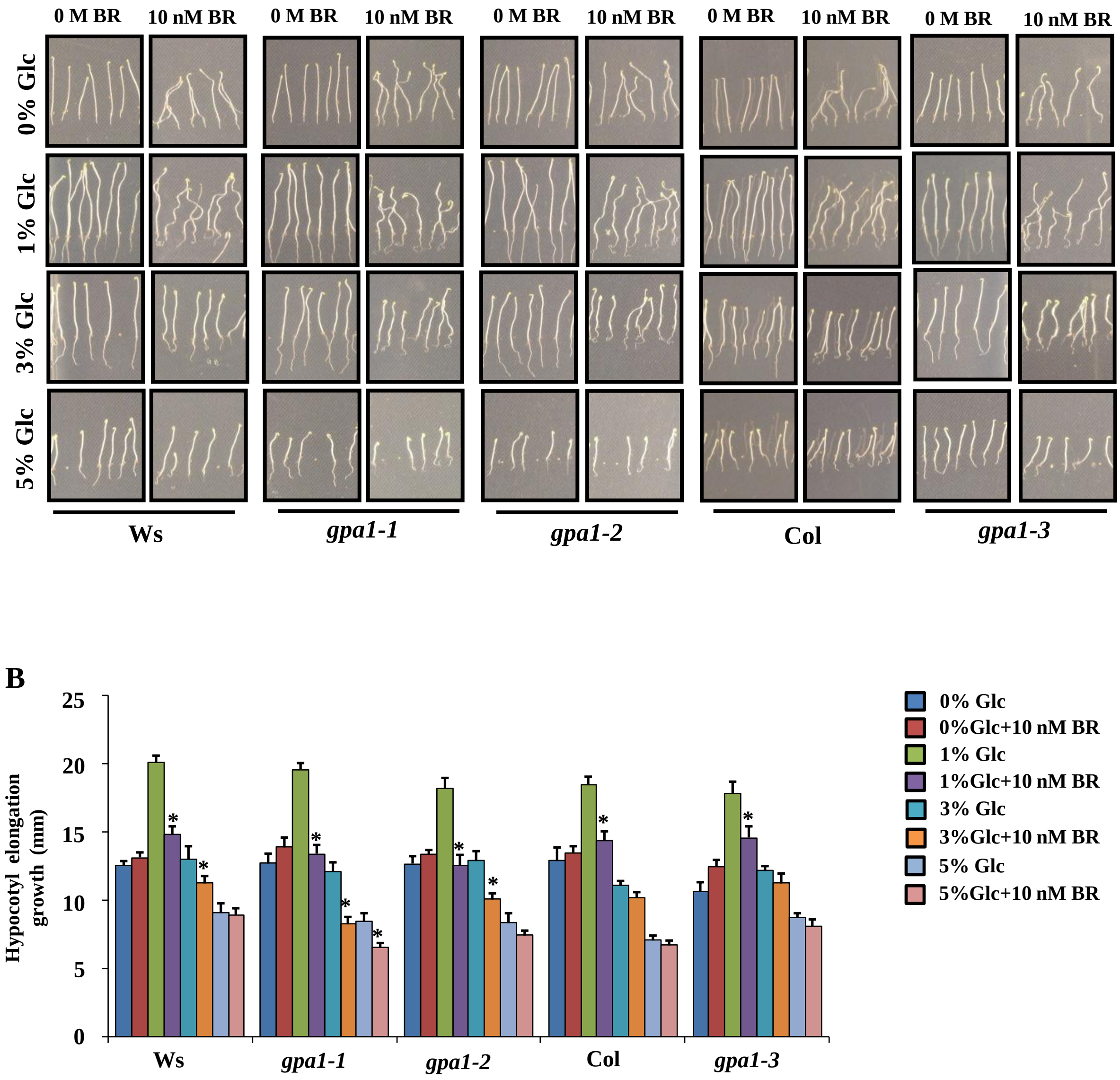


Supplemental figure S6. Glc-BR regulation of hypocotyl growth in HXK1-dependennt Glc signaling mutant *gin2-1*.



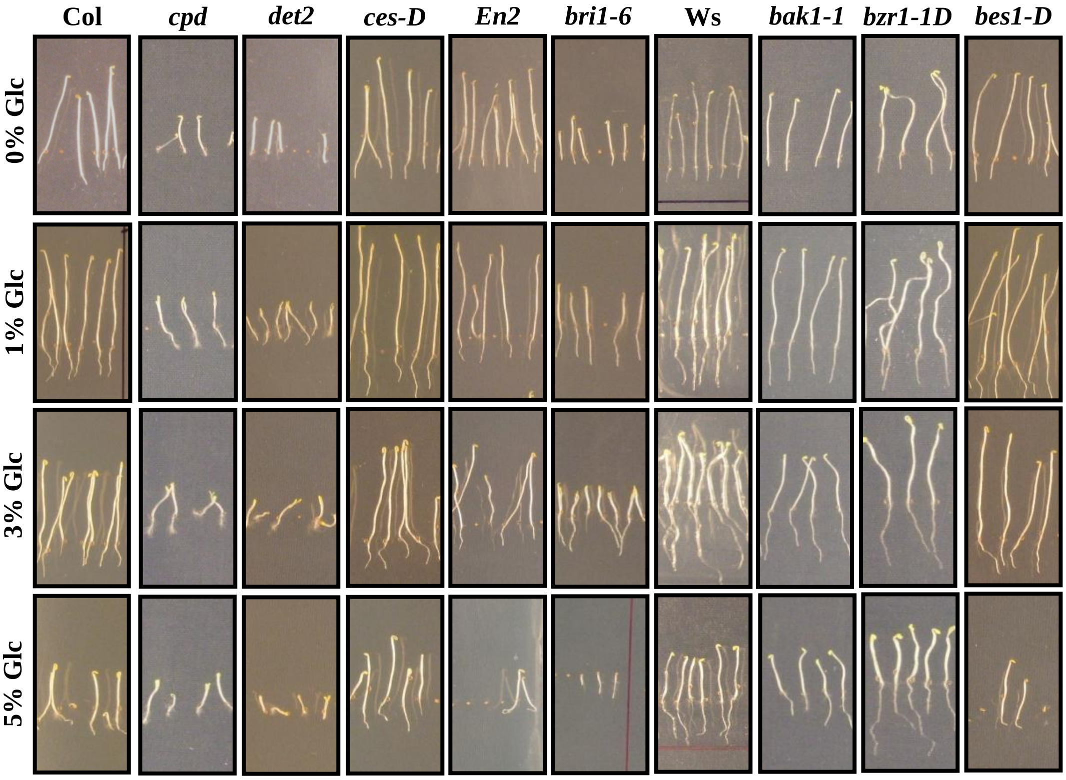
Supplemental figure S7. Glc-BR control of hypocotyl length in HXK1-independent pathway mutants *rgs1* and *thf1*

A, Pictures and **B,** Quantification of etiolated hypocotyl growth in 7-d-old seedlings of WT (Col-0) and HXK1-independent pathway mutants *rgs1-1*, *rgs1-2* and *thf1-1* growing on Glc free (0%) or increasing Glc concentration (1%, 3%, 5%) containing ½ MS media supplemented without or with 10 nM BR. The *rgs1-1*, *rgs1-2* and *thf1-1* mutants were found to have similar sensitivity towards BR application at different Glc concentrations as compared to WT. Values represent the average from two biological replicates each having 30 seedlings and error bars represent SE. Student's T-test, $P<0.05$.

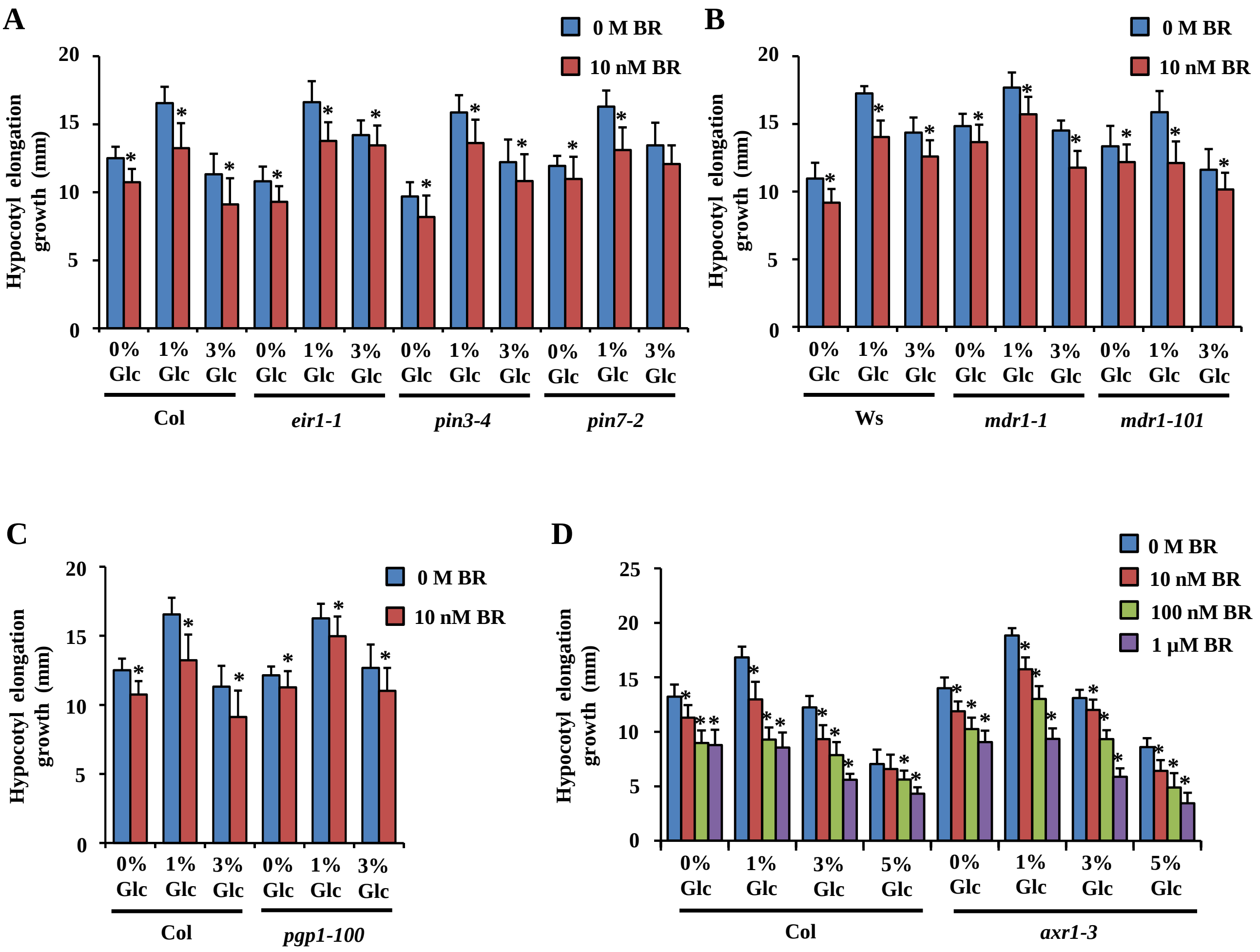


Supplemental figure S8. Glc-BR control of hypocotyl length in HXK1-independent pathway mutants *gpa1*

A, Pictures and **B,** Quantification of etiolated hypocotyl growth in 7-d-old seedlings of WT (Col-0, Ws) and HXK1-independent pathway mutants *gpa1-1*, *gpa1-2* and *gpa1-3* growing on Glc free (0%) or increasing Glc concentration (1%, 3%, 5%) containing ½ MS media supplemented without or with 10 nM BR. The mutants *gpa1-1*, *gpa1-2* and *gpa1-3* were found to have similar sensitivity towards BR application at different Glc concentrations as compared to their respective WTs. Values represent the average from two biological replicates each having 30 seedlings and error bars represent SE. Student's T-test, P<0.05.



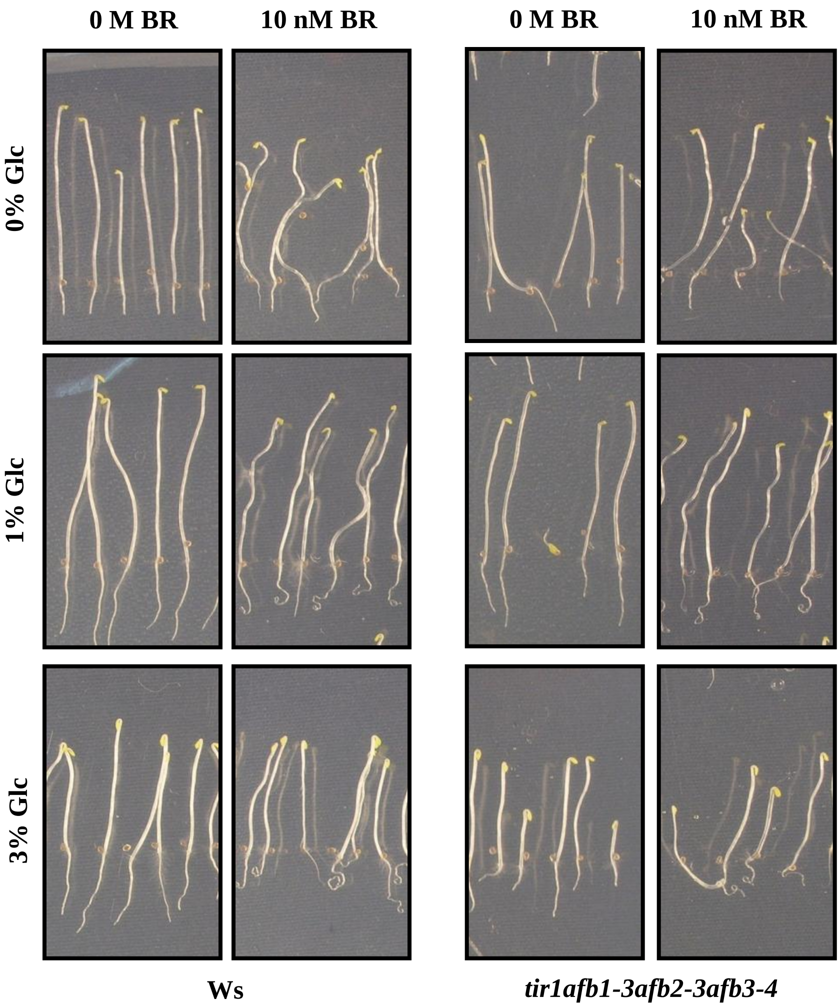
Supplemental figure S9. Glc regulation of hypocotyl growth in BR signaling mutants.



Supplemental figure S10. Glc-BR control of hypocotyl elongation growth in auxin transport/signaling defective mutants.

A-D, Quantification of hypocotyl length in 7-d-old etiolated WT (Col-0, Ws); auxin transport defective mutants: *eir1-1*, *pin3-4*, *pin7-2*, *mdr1-1*, *mdr1-101*, *pgp1-100;* and auxin-signaling mutant *axr1-3* seedlings growing in independent or combined Glc/BR treatment media.

Values represent the average from two independent biological replicates each having 20 seedlings and error bars represent SE. (Student’s T-test, $P<0.05$; * control vs. treatment).



Supplemental figure S11. Glc-BR regulation of etiolated hypocotyl elongation growth in auxin perception mutant.

S.no.	**Gene name**	**Representative Public ID**	**Forward (5ʹ ---- 3ʹ)**	**Reverse (5ʹ ---- 3ʹ)**
1.	***DWF4***	***AT3G50660***	GCATCATACTCTCTTACCTCTTCTT	CCAAATTTTTATATATCATTGGGCA
2.	***BR6OX1***	***AT5G38970***	TCCTCTGCGTGCATAAAATCTATATT	GCACCAAAAGGCTTCCATCTT
3.	***BR6OX2***	***AT3G30180***	TCTCTCTTTCTCTCTGTACATTATCCATCT	AGGGTCATTTTGTAGGGCTAATTAAC
4.	***IAA19***	***AT3G15540***	CGGATGCTACCGGGTTTG	TGCTTCTTGTTCAAGTCATCATCA
5.	***ARF6***	***AT1G30330***	GGTCTGACCGGTTCCCAAA	TCGATAAGCTCCCGAGCAA
6.	***GH3.1***	***AT2G14960***	CCCACAGTGAAAAAAAACGAGTAA	CTTGCTGGTGCTTTAGTTTTTCTTC
7.	***EXLA2***	***AT4G38400***	ATCACCGTGGTTCCTTTGCT	GCTTCCAGGTCAGATGCAAGA
8.	***XTH6***	***AT5G65730***	CGGTCACCGCTTTCTACATGA	CAAGAACTCAAAATCTAGCTCGTCTCT
9.	***XTH18***	***AT4G30280***	TCAAATGAAACTTGTCCCTGGTAA	AGTTCCCGGAGACTTAAGATAGAATG
10.	***TCH4***	***AT5g57560***	TGCGAAGAGGTTCCCTCAAG	TTCCTCTCTCAACTCTTTACTCTCTCTATG
11.	***LAX3***	***AT1G77690***	CGGGTTTGTTTAATTTGTTATGTTGA	TTGGCCTAAGATAGCCATCACA
12.	***EXP17***	***AT4G01630***	GAAGAAGCGGAGGGATGAGA	CCCTCCTGCTACGTTTGAGATG

Supplemental figure S12. List of primers used in this study.

BR regulated genes (303 genes)

Probe set_ID	Representative Public ID	0% Glc + 100 nM BR vs 0% Glc	3% Glc vs 0% Glc	3% Glc + 100 nM BR vs 0% Glc
A_84_P12287|8	AT1G01480	-2.83	1.67	-1.04
A_84_P10559|8	AT1G01560	4.05	8.02	5.59
A_84_P21249|8	AT1G02650	2.19	-7.91	-1.46
A_84_P801239,A	AT1G02920	2.53	4.53	5.73
A_84_P812454,A	AT1G02930	2.80	4.12	4.90
A_84_P18950,A_	AT1G04660	3.51	-1.52	1.47
A_84_P799181,A	AT1G05660	2.69	3.75	12.70
A_84_P14703|5	T1G05835///TC2666	-2.99	-1.55	-4.56
A_84_P17191|8	AT1G07160	2.66	10.68	17.93
A_84_P522242|	AT1G07985	-3.13	-1.62	-5.80
A_84_P233559|	AT1G10340	2.17	-9.80	-6.34
A_84_P20977|8	AT1G14480	2.04	2.00	3.91
A_84_P16226|8	AT1G14540	2.14	3.86	5.06
A_84_P22847|8	AT1G14550	2.24	12.93	6.45
A_84_P14310|8	AT1G14720	-2.07	1.11	1.30
A_84_P12389|8	AT1G14860	-3.64	-3.65	-10.03
A_84_P826352,A	AT1G16750	-2.14	3.14	1.32
A_84_P516067|	AT1G17345	-2.31	-15.23	-8.79
A_84_P23422|8	AT1G18280	2.04	-12.08	-5.01
A_84_P11448|8	AT1G18870	-3.01	7.17	-2.07
A_84_P14313,A_	AT1G19970	2.08	45.37	40.93
A_84_P16097|8	AT1G24140	10.84	13.42	24.87
A_84_P13252|8	AT1G24470	2.85	1.57	5.07
A_84_P541789,A	AT1G26250	2.21	-3.37	-1.95
A_84_P19294,A_	AT1G26380	3.10	41.95	40.12
A_84_P20237|8	AT1G26420	2.74	10.06	10.35
A_84_P12872|8	AT1G29270	2.17	-9.86	-3.80
A_84_P537376|	AT1G29420	2.13	-2.32	1.30
A_84_P21517|8	AT1G31310	-2.11	-1.38	1.80
A_84_P210918|	AT1G32190	-2.31	1.48	-1.71
A_84_P10364|8	AT1G34050	3.61	1.83	4.86
A_84_P20998,A_	AT1G35140	2.92	-20.48	-6.43
A_84_P16055	T1G35612///TC2596	-2.04	-5.04	-20.42
A_84_P13577|8	AT1G36940	-2.77	-2.21	-1.33
A_84_P816739,A	AT1G44970	-2.67	-1.28	1.29
A_84_P268780,A	AT1G45010	2.47	11.44	9.87
A_84_P18845|8	AT1G48000	-2.37	1.88	1.37
A_84_P13870|8	AT1G50600	-15.89	-17.12	-14.48
A_84_P824506,A	AT1G51680	-2.05	1.88	2.80
A_84_P276600|	AT1G52910	2.00	-1.27	1.59
A_84_P10747|8	AT1G53700	2.39	3.58	14.54
A_84_P12484|8	AT1G58170	-2.22	10.87	1.37
A_84_P138279|	AT1G58420	2.75	3.13	11.45
A_84_P17985|8	AT1G61170	2.36	-1.15	2.19

A_84_P799584,A	AT1G62975	-2.44	2.01	2.68
A_84_P251265,A	AT1G63720	-4.14	1.26	-1.79
A_84_P18119|8	AT1G64400	2.23	1.00	1.80
A_84_P14255|8	AT1G64970	2.59	7.08	6.47
A_84_P297064|	AT1G65310	4.03	-1.17	8.39
A_84_P11417|8	AT1G65730	-2.05	-3.33	-7.36
A_84_P13393|8	AT1G66090	3.16	9.50	10.06
A_84_P842079	AT1G67195	2.55	10.13	20.48
A_84_P184384|	AT1G68440	2.00	-2.54	-1.88
A_84_P560506|	AT1G69430	2.55	4.44	14.03
A_84_P20854|8	AT1G70300	-2.11	-1.01	-1.11
A_84_P11184|8	AT1G72240	2.45	1.50	-2.01
A_84_P157715|	AT1G72930	2.74	20.54	26.13
A_84_P16209|8	AT1G74110	4.31	-1.00	2.41
A_84_P14468|8	AT1G75450	-2.79	-3.05	-3.22
A_84_P805374,A	AT1G76160	2.62	-4.95	-1.33
A_84_P260340|	AT1G76240	-4.42	-10.27	-4.71
A_84_P21869|8	AT1G77690	-3.17	1.63	1.63
A_84_P268090,A	AT2G01300	2.33	-1.50	1.01
A_84_P258420|	AT2G04500	3.63	-5.10	-2.12
A_84_P20150|8	AT2G04550	-7.04	-18.33	-9.28
A_84_P601261|	AT2G07140	2.15	-7.42	-3.08
A_84_P13475|8	AT2G11810	3.74	2.05	2.00
A_84_P15343|8	AT2G14960	8.03	-1.06	1.70
A_84_P61660|8	AT2G15220	2.85	6.20	6.94
A_84_P22914,A_	AT2G15490	-2.09	23.93	10.61
A_84_P16321|8	AT2G20420	-2.17	1.49	1.95
A_84_P10627|8	AT2G20880	5.02	-3.87	-2.10
A_84_P221516,A	AT2G21900	2.17	-4.13	-1.71
A_84_P51530|8	AT2G22470	2.91	6.51	4.77
A_84_P16316|8	AT2G23180	-2.21	2.47	2.98
A_84_P16369|8	AT2G23380	3.14	4.26	8.05
A_84_P15423|8	AT2G23620	-2.05	-9.34	-24.54
A_84_P22001|8	AT2G24710	-2.15	-13.67	-5.67
A_84_P558814|	AT2G25780	-2.78	-10.71	-4.45
A_84_P19231|8	AT2G26150	3.66	75.17	91.66
A_84_P10647|8	AT2G26480	6.77	6.60	5.05
A_84_P14435|8	AT2G26710	2.22	-3.39	-3.67
A_84_P546443|	AT2G28085	3.22	-1.75	1.37
A_84_P12547|8	AT2G30750	2.19	32.94	11.97
A_84_P207798|	AT2G31540	2.42	1.03	4.67
A_84_P14433|8	AT2G32990	-2.59	7.39	4.70
A_84_P180484|	AT2G33570	2.06	1.52	3.59
A_84_P14490|8	AT2G34180	8.77	-7.00	-2.00
A_84_P11613|8	AT2G34930	3.37	1.85	10.71
A_84_P23919|8	AT2G35980	2.40	17.21	10.99
A_84_P74914|8	AT2G36840	2.26	2.23	3.36
A_84_P13527|8	AT2G37030	-4.60	-5.16	5.32

A_84_P13482|8	AT2G38760	2.08	3.63	-4.93
A_84_P14494|8	AT2G39430	-2.23	-2.19	-14.69
A_84_P14479|8	AT2G40250	7.20	-1.16	2.52
A_84_P22053,A_	AT2G41100	2.68	-4.04	-6.85
A_84_P53570|8	AT2G41810	-2.10	1.30	3.77
A_84_P248025|	AT2G42800	-3.15	5.44	7.69
A_84_P81529,A_	AT2G43060	-2.38	1.20	-1.49
A_84_P21007|8	AT2G43570	2.99	7.91	5.29
A_84_P16277,A_	AT2G43610	2.40	1.14	-1.68
A_84_P757973|	AT2G44578	2.59	12.05	15.42
A_84_P17343|8	AT2G44840	7.30	1.99	3.98
A_84_P786490,A	AT2G46400	4.23	2.63	5.39
A_84_P186814|	AT2G46495	2.17	8.66	6.12
A_84_P579358|	AT3G01516	-9.47	-6.32	-6.85
A_84_P11694,A_	AT3G01830	3.38	6.39	9.64
A_84_P15464|8	AT3G03670	2.32	-27.10	-7.54
A_84_P21159|8	AT3G04010	-3.75	1.90	1.07
A_84_P90109|8	AT3G05800	2.53	1.49	4.42
A_84_P280900,A	AT3G07350	-2.10	-32.87	-22.74
A_84_P19256|8	AT3G09220	-2.29	-9.86	-20.91
A_84_P762751|	AT3G10986	2.02	2.10	5.23
A_84_P536803|	AT3G11550	-2.16	-1.14	-1.18
A_84_P10829|8	AT3G13730	-6.01	2.47	1.15
A_84_P842922,A	AT3G13980	-3.46	-2.46	-7.29
A_84_P15501|8	AT3G15370	4.19	-8.23	-1.26
A_84_P805073	AT3G15450	2.34	-38.08	-47.79
A_84_P14556|8	AT3G15540	2.75	-1.22	2.26
A_84_P11727|8	AT3G15670	2.67	10.47	26.81
A_84_P178324|	AT3G18710	-7.04	1.69	1.42
A_84_P81479|8	AT3G19380	-3.83	1.20	-1.29
A_84_P841540,A	AT3G20830	-2.36	-2.90	-4.69
A_84_P591926|	AT3G21680	3.16	6.13	13.44
A_84_P23101|8	AT3G21890	2.70	4.67	2.50
A_84_P23070|8	AT3G22740	-2.13	-23.15	-18.79
A_84_P15503,A_	AT3G22830	2.35	24.77	2.76
A_84_P860303,A	AT3G23170	-2.56	3.70	2.18
A_84_P10788|8	AT3G25900	2.48	-1.91	1.15
A_84_P247395|	AT3G26470	2.05	4.10	4.50
A_84_P12704,A_	AT3G27200	-2.16	2.50	3.00
A_84_P759661|	AT3G27500	2.24	-4.89	1.45
A_84_P22181|8	AT3G28210	2.21	23.22	25.81
A_84_P100746|	AT3G28220	-2.37	-5.70	-5.18
A_84_P12725|8	AT3G28510	2.04	19.37	21.18
A_84_P826388,A	AT3G30180	-4.26	-2.54	-1.95
A_84_P19357|8	AT3G44990	2.10	1.80	-4.27
A_84_P18416|8	AT3G46080	3.36	12.33	18.44
A_84_P19362|8	AT3G46090	3.94	2.55	7.08
A_84_P12747|8	AT3G46700	-2.37	-12.45	-16.41

A_84_P22215|8	AT3G49630	-3.12	-1.35	-1.54
A_84_P192624|	AT3G49840	2.49	2.33	4.26
A_84_P13706|8	AT3G50140	2.16	-3.67	-1.66
A_84_P24110|8	AT3G50270	2.12	-2.49	-2.52
A_84_P12763|8	AT3G50560	2.21	-19.43	-5.61
A_84_P869611,	AT3G50660	-8.48	-1.18	-7.55
A_84_P157735|	AT3G51400	-11.97	-5.48	-18.10
A_84_P13719|8	AT3G53150	2.13	1.82	-1.20
A_84_P807670	AT3G53990	2.07	1.28	-10.47
A_84_P813219,	AT3G54810	2.04	2.64	4.90
A_84_P522715|	AT3G54830	2.48	-1.60	1.90
A_84_P821534	AT3G55010	3.02	5.94	9.34
A_84_P14678|8	AT3G56000	2.17	-10.06	-4.44
A_84_P849984,	AT3G56080	2.08	9.90	10.44
A_84_P16571|8	AT3G56400	2.48	-3.09	-1.95
A_84_P861025,	AT3G56910	-2.14	-2.93	-6.59
A_84_P14682|8	AT3G57010	-3.87	38.95	22.51
A_84_P20359|8	AT3G57540	-2.11	4.48	3.88
A_84_P15632|8	AT3G58390	2.21	1.17	2.88
A_84_P18473|8	AT3G59140	2.36	11.40	11.98
A_84_P22262|8	AT3G60390	-2.30	-1.19	-3.14
A_84_P556409|	AT3G60650	3.84	-3.04	-1.26
A_84_P173361|	AT3G62570	2.29	-3.84	-1.97
A_84_P20381|8	AT3G63110	-2.27	5.70	4.69
A_84_P14717|8	AT4G01630	10.87	32.65	99.38
A_84_P93489,A_	AT4G01670	-2.03	-1.17	-1.53
A_84_P16609,A_	AT4G01870	-5.15	2.09	-5.65
A_84_P10949|8	AT4G05100	-2.06	2.07	-2.37
A_84_P22299|8	AT4G07960	3.12	-2.60	1.01
A_84_P10014|8	AT4G10160	2.25	-9.61	-6.59
A_84_P20416|8	AT4G10350	2.33	1.53	32.51
A_84_P13799|8	AT4G11230	2.34	-1.67	1.92
A_84_P827321,	AT4G11890	2.23	-1.07	2.47
A_84_P14749|8	AT4G12430	2.45	1.99	-2.23
A_84_P763492,	AT4G12510	-2.43	-1.24	1.96
A_84_P813874,	AT4G12720	2.87	1.33	-2.17
A_84_P855052,	AT4G14130	-4.04	-3.29	-49.79
A_84_P596516|	AT4G14450	-2.46	3.57	2.27
A_84_P10124|8	AT4G14560	-2.67	-3.41	-16.52
A_84_P12960|8	AT4G14630	2.20	-3.61	-1.86
A_84_P576905,	AT4G16515	2.12	-3.09	1.56
A_84_P10131|8	AT4G16690	-2.26	-22.66	-17.10
A_84_P17597|8	AT4G18880	2.62	7.74	11.60
A_84_P11926|8	AT4G19380	-4.19	-18.03	-3.78
A_84_P765234|	AT4G21745	2.16	-13.72	-2.46
A_84_P812152,	AT4G21850	2.46	-2.08	-1.11
A_84_P534335|	AT4G21970	2.74	-7.44	-3.83
A_84_P17611|8	AT4G22460	-3.71	-3.42	-1.59

A_84_P18557|8	AT4G22470	-2.70	2.14	1.09
A_84_P14776|8	AT4G23180	2.07	2.21	4.29
A_84_P528136,	AT4G23190	2.09	3.83	3.61
A_84_P11953|8	AT4G25780	-3.14	-1.88	-2.84
A_84_P15734|8	AT4G25810	2.80	-3.57	-1.32
A_84_P20466|8	AT4G26260	2.77	-33.86	-10.48
A_84_P785948,	AT4G26320	2.22	-6.09	-2.31
A_84_P823127,	AT4G27050	-2.08	-2.20	-11.95
A_84_P15741|8	AT4G27280	2.49	-1.31	2.07
A_84_P564464,	AT4G27460	2.10	-4.13	-1.80
A_84_P606349|	AT4G28460	2.74	6.26	4.69
A_84_P825877,	AT4G28650	2.91	3.03	9.11
A_84_P824302,	AT4G29310	2.52	-1.95	2.00
A_84_P19534|8	AT4G29340	2.22	4.04	3.89
A_84_P79989|8	AT4G29520	3.43	7.41	15.46
A_84_P212828|	AT4G30280	2.39	-3.32	1.02
A_84_P10083|8	AT4G30290	3.19	2.50	35.89
A_84_P14814|8	AT4G31470	4.39	4.82	29.48
A_84_P18604|8	AT4G33020	-2.16	2.34	1.99
A_84_P22388|8	AT4G33070	-2.16	17.22	15.20
A_84_P853187,	AT4G34150	2.03	1.93	4.42
A_84_P10101,A_	AT4G34610	-2.07	3.65	4.41
A_84_P537048,	AT4G36105	8.73	-1.28	1.94
A_84_P12944,A_	AT4G36110	3.89	-3.21	2.18
A_84_P162603|	AT4G36780	-2.38	-1.30	-18.27
A_84_P159605,	AT4G37070	-2.68	-3.81	-2.57
A_84_P765161|	AT4G37608	-2.09	2.24	3.35
A_84_P16729|8	AT4G37770	3.46	-1.06	4.19
A_84_P10114|8	AT4G38400	2.58	-10.13	-3.35
A_84_P12005|8	AT4G38410	2.77	1.69	9.57
A_84_P12950,A_	AT4G38420	2.59	1.48	2.09
A_84_P810008	AT4G39330	2.12	10.37	17.00
A_84_P12011|8	AT4G39800	-4.38	7.27	4.67
A_84_P12956|8	AT4G39830	2.66	-1.29	3.15
A_84_P765351|	AT4G40011	2.05	1.66	22.08
A_84_P586802|	AT5G01015	5.09	-1.19	2.27
A_84_P23380|8	AT5G01540	3.30	5.35	13.06
A_84_P10141|8	AT5G01550	3.22	6.50	20.39
A_84_P22435|8	AT5G01740	-66.18	-2.81	-17.23
A_84_P506004|	AT5G01790	2.21	13.35	16.49
A_84_P70894|8	AT5G01840	-2.78	2.75	1.59
A_84_P556555|	AT5G02490	3.10	5.86	9.32
A_84_P103716|	AT5G03350	2.79	-3.53	1.02
A_84_P19609|8	AT5G05390	2.52	3.96	6.49
A_84_P575222|	AT5G09800	-2.82	7.17	7.52
A_84_P18678|8	AT5G09870	2.11	2.92	5.72
A_84_P18683|8	AT5G10970	2.53	7.76	9.74
A_84_P524680,	AT5G13220	2.07	-2.59	-1.16

A_84_P829727,A	AT5G13320	6.22	-1.18	1.79
A_84_P14907|8	AT5G13700	-2.16	2.09	-1.35
A_84_P18691,A_	AT5G13740	-2.20	-4.96	-50.86
A_84_P19794|8	AT5G14750	2.93	3.09	9.02
A_84_P226699|	AT5G15050	2.16	5.72	11.93
A_84_P17749|8	AT5G15120	2.15	1.01	-10.63
A_84_P22481|8	AT5G16590	2.27	-1.95	1.58
A_84_P20748|8	AT5G17520	-2.03	3.27	2.99
A_84_P16807|8	AT5G17760	-2.01	4.79	1.80
A_84_P20594|8	AT5G18560	-9.13	1.07	-3.07
A_84_P13031|8	AT5G19110	4.51	-2.77	-1.80
A_84_P92929,A_	AT5G19240	2.70	4.18	10.61
A_84_P223799|	AT5G22100	-3.16	3.01	4.22
A_84_P243945|	AT5G22580	-14.18	1.38	-1.89
A_84_P174931|	AT5G22940	2.14	-2.77	-1.20
A_84_P13987|8	AT5G25190	2.87	3.07	19.10
A_84_P825802,A	AT5G25250	2.93	2.20	3.20
A_84_P826308	AT5G25820	3.18	7.69	8.44
A_84_P258360|	AT5G26290	-2.97	8.19	5.75
A_84_P515865|	AT5G26690	2.47	-6.63	-1.38
A_84_P16971,A_	AT5G28840	-2.10	-4.30	-14.55
A_84_P848499	AT5G35935	-2.32	1.21	-5.06
A_84_P20622|8	AT5G36260	3.31	1.65	5.91
A_84_P18737|8	AT5G38710	5.65	-10.48	-14.44
A_84_P20630|8	AT5G38970	-14.60	-1.44	-4.69
A_84_P16848,A_	AT5G39580	2.05	-2.19	-1.39
A_84_P612712|	AT5G41300	2.12	-9.08	-3.77
A_84_P23478,A_	AT5G41750	5.86	7.00	9.52
A_84_P769417|	AT5G41761	-2.19	-10.28	-3.07
A_84_P13077,A_	AT5G42380	3.98	10.22	15.09
A_84_P14969|8	AT5G43030	2.19	-3.86	-1.45
A_84_P511454|	AT5G43570	-2.67	-15.35	-24.80
A_84_P19706|8	AT5G45000	2.32	1.55	2.39
A_84_P17815|8	AT5G45200	3.38	2.48	6.84
A_84_P22546,A_	AT5G45670	2.86	1.42	5.09
A_84_P20664|8	AT5G48010	-2.10	42.14	34.73
A_84_P139909|	AT5G49100	-2.48	2.01	1.98
A_84_P199394,A	AT5G49900	-2.30	-1.39	-1.87
A_84_P220678|	AT5G50590	2.09	-13.22	-5.48
A_84_P296724,A	AT5G51190	2.21	-1.54	1.03
A_84_P15946|8	AT5G51440	2.64	37.76	3.92
A_84_P21622|8	AT5G51480	6.00	-1.61	1.50
A_84_P302000|	AT5G53250	2.01	-14.19	-15.03
A_84_P262520|	AT5G55620	-2.31	10.48	24.24
A_84_P12181,A_	AT5G56000	2.44	11.34	12.58
A_84_P13130|8	AT5G57220	2.25	12.62	5.10
A_84_P17859|8	AT5G57560	3.36	-12.77	-15.49
A_84_P828057,A	AT5G57780	-5.80	-3.43	-3.84

A_84_P559359|	AT5G57785	-10.18	-5.77	-53.15
A_84_P604788|	AT5G59510	-2.25	1.91	2.37
A_84_P17872|8	AT5G60520	2.20	6.83	17.10
A_84_P530135,A	AT5G60880	2.21	4.02	9.49
A_84_P15043|8	AT5G62340	2.62	-2.29	-1.00
A_84_P20724,A_	AT5G63790	-2.31	4.19	1.48
A_84_P161403|	AT5G63820	2.88	-7.16	-1.22
A_84_P800757,A	AT5G64260	-2.76	-2.57	-7.66
A_84_P173491|	AT5G64770	3.85	-1.19	5.25
A_84_P12218|8	AT5G64870	2.42	-1.02	2.04
A_84_P160863|	AT5G64980	2.16	8.40	9.25
A_84_P555846|	AT5G65030	-2.77	8.50	5.12
A_84_P60290|8	AT5G65300	-6.54	2.62	-1.17
A_84_P16948|8	AT5G65730	-2.02	-110.66	-36.27
A_84_P23570|8	AT5G65800	4.67	1.29	7.77
A_84_P23571|8	AT5G66080	-7.36	1.30	-2.06
A_84_P10332|8	AT5G66110	-2.06	-12.06	-9.16
A_84_P16006|8	AT5G66590	-2.57	-1.05	-17.07
A_84_P546117|	AT5G66985	-2.06	7.44	3.50

Gene Description	Gene Symbol
1-aminocyclopropane-1-carboxylate	ACS2
mitogen-activated protein kinase,	MPK11
DNAJ heat shock N-terminal domain-	
GLUTATHIONE S-TRANSFERASE 7;	GSTF7
ARABIDOPSIS THALIANA GLUATIONE S-	GSTF6
Arabidopsis thaliana glycine-rich protein	
Arabidopsis thaliana Pectin lyase-like	
similar to unknown protein [Arabidopsis	
protein phosphatase 2C, putative / PP2C,	
Expressed protein [At1g07985.1]	
ankyrin repeat family protein contains	
ankyrin repeat family protein contains	
anionic peroxidase, putative similar to	PER4
anionic peroxidase, putative similar to	
xyloglucan:xyloglucosyl transferase /	XTR2
MutT/nudix family protein low similarity	NUDT18
Arabidopsis thaliana uncharacterized	
auxin-responsive protein-related similar	
protease inhibitor/seed storage/lipid	
isochorismate synthase, putative /	ATICS2
Arabidopsis thaliana ER lumen protein	
matrixin family protein similar to matrix	
short-chain dehydrogenase/reductase	ATKCR2;BETA-
Arabidopsis thaliana Proline-rich	
Arabidopsis thaliana FAD-binding and	
FAD-binding domain-containing protein	
expressed protein [At1g29270.1]	
auxin-responsive family protein Similar	
hydroxyproline-rich glycoprotein family	
expressed protein [At1g32190.1]	
ankyrin repeat family protein contains	
PHI-1 (PHOSPHATE-INDUCED 1)	PHI-1
Q9LQF9 (Q9LQF9) F15O4.26, complete	
hypothetical protein [At1g36940.1]	
Arabidopsis thaliana peroxidase 9	
Arabidopsis thaliana TRAM, LAG1 and	
myb family transcription factor similar to	MYB112
scarecrow-like transcription factor 5	SCL5
4CL1 (4-COUMARATE:COA LIGASE 1); 4-	4CL1
expressed protein [At1g52910.1]	
protein kinase, putative similar to	WAG1
disease resistance-responsive protein-	
expressed protein [At1g58420.1]	
expressed protein [At1g61170.1]	

upregulated

Arabidopsis thaliana transcription factor	
Arabidopsis thaliana uncharacterized	
long-chain-fatty-acid--CoA ligase,	LACS3
expressed protein [At1g64970.1];	G-TMT
xyloglucan:xyloglucosyl transferase,	XTH17
oligopeptide transporter OPT family	YSL7
disease resistance protein (TIR-NBS	
MIR414	MIR414
expressed protein [At1g68440.1]	
hypothetical protein [At1g69430.1]	
potassium transporter, putative similar	KUP6
expressed protein [At1g72240.1]	
Toll-Interleukin-Resistance (TIR) domain-	TIR
cytochrome P450 family protein similar	CYP78A10
FAD-binding domain-containing protein /	CKX5
SKS5 (SKU5 Similar 5); copper ion binding	sks5
expressed protein contains Pfam profile	
amino acid permease, putative similar to	LAX3
Arabidopsis thaliana uncharacterized	
DC1 domain-containing protein contains	
dual specificity protein phosphatase 1E;	DSPTP1E; IBR5
F-box family protein contains	
1,2-diacylglycerol 3-beta-	MONOGALACT
auxin-responsive GH3 family protein	GH3.1
secretory protein, putative similar to	
UGT73B4; UDP-glycosyltransferase/	UGT73B4
succinyl-CoA ligase [GDP-forming] beta-	
AP2 domain-containing transcription	ATERF53;ERF
WRKY59 (WRKY DNA-binding protein 59);	WRKY59
arabinogalactan-protein (AGP2) identical	AGP2
cytochrome P450, putative	CYP96A1
curly leaf protein (CURLY LEAF) /	CLF
esterase, putative similar to ethylene-	MES1
glutamate receptor family protein	GLR2.3
hypothetical protein [At2g25780.1]	
HEAT SHOCK TRANSCRIPTION FACTOR	ATHSFA2
UDP-glucoronosyl/UDP-glucosyl	UDP-GLUCOSYL
cytochrome P450, putative	PHYB
auxin-responsive family protein similar	
cytochrome P450 71A12, putative	CYP71A12
GDSL-motif lipase/hydrolase family	
glycosyl hydrolase family 9 protein	GH9B8
expressed protein [At2g33570.1]	
CBL-interacting protein kinase 13	CIPK13;
disease resistance family protein	
harpin-induced family protein (YLS9) /	YLS9
ACT domain-containing protein contains	ACR10
auxin-responsive family protein similar	

annexin 3 (ANN3) nearly identical to	ANN3
disease resistance-responsive protein-	
GDSL-motif lipase/hydrolase family	
TCH3 (TOUCH 3)	TCH3
expressed protein contains Pfam profile	
leucine-rich repeat family protein	RLP29
transcription factor	IBH1
chitinase, putative similar to chitinase	
Arabidopsis thaliana putative chitinase	
Arabidopsis thaliana RING/U-box domain-	
ethylene-responsive element-binding	EREBP; ERF13
WRKY46 (WRKY DNA-binding protein	WRKY46
zinc finger (C3HC4-type RING finger)	
expressed protein [At3g01516.1]	
Arabidopsis thaliana putative calcium-	
peroxidase, putative similar to	
glycosyl hydrolase family 17 protein	
ACTIVATION-TAGGED BRI1 SUPPRESSOR	ATBS1; AIF1
Arabidopsis thaliana uncharacterized	
laccase family protein / diphenol oxidase	LAC7
Arabidopsis thaliana LURP-one-like	
CASPARIAN STRIP MEMBRANE DOMAIN	CASP2
cytochrome P450, putative similar to	CYP90D1
Arabidopsis thaliana uncharacterized	
expansin, putative (EXP12) similar to	ATEXPA12;
similar to unknown protein [Arabidopsis	
auxin-responsive protein / indoleacetic	MSG2; IAA19
late embryogenesis abundant protein,	
U-box domain-containing protein similar	PUB29
U-box domain-containing protein	PUB25
Arabidopsis thaliana AGC (cAMP-	
expressed protein [At3g21680.1]	
zinc finger (B-box type) family protein	
homocysteine S-methyltransferase 3	HMT3
AT-HSFA6B (Arabidopsis thaliana heat	HSFA6B
Arabidopsis thaliana uncharacterized	
homocysteine S-methyltransferase 1	HMT-1
expressed protein [At3g26470.1]	
Arabidopsis thaliana plastocyanin-like	
Arabidopsis thaliana cysteine/histidine-	
zinc finger (AN1-like) family protein	SAP12; PMZ
meprin and TRAF homology domain-	
AAA-type ATPase family protein contains	
BR6OX2/CYP85A2 (BRASSINOSTEROID-6-	BR6OX2
xyloglucan:xyloglucosyl transferase,	XTR8
zinc finger (C2H2 type) family protein	
zinc finger (C2H2 type) family protein	ZAT7
UDP-glucoronosyl/UDP-glucosyl	

2-oxoacid-dependent oxidase, putative	
proline-rich family protein contains	
expressed protein contains Pfam profile	
transferase family protein similar to	
short-chain dehydrogenase/reductase	
CYTOCHROME P450 90B1; DWARF	DWF4;
expressed protein contains Pfam profile	
UDP-glucoronosyl/UDP-glucosyl	UDP-GLUCOSYL
universal stress protein (USP) family	
BME3/BME3-ZF (BLUE MICROPYLAR	BME3
amino acid transporter family protein	
ATPURM/PUR5;	EMBRYO
glycosyl transferase family 2 protein	CSLA14
Arabidopsis thaliana At3g56080 mRNA	
WRKY family transcription factor DNA-	WRKY70
PSRP5 (PLASTID-SPECIFIC 50S	PSRP5
strictosidine synthase family protein	
remorin family protein contains Pfam	
eukaryotic release factor 1 family protein	
ABC transporter family protein putative	MRP14
homeobox-leucine zipper protein 3	HAT3
expressed protein [At3g60650.1]	
DNAJ heat shock N-terminal domain-	
adenylate isopentenyltransferase 3 /	IPT3
expansin, putative (EXP17) similar to	ATEXP17;
Arabidopsis thaliana uncharacterized	
Arabidopsis thaliana tolB-related protein	
myb family transcription factor (MYB74)	MYB74
glycosyl transferase family 2 protein	CSLC12
zinc finger (C3HC4-type RING finger)	
no apical meristem (NAM) family protein	ANAC070
respiratory burst oxidase, putative /	
ABA- AND OSMOTIC-STRESS-INDUCIBLE	ARCK1
trehalose-6-phosphate phosphatase,	TPPF
Arabidopsis thaliana bifunctional	
AtNUDT7 (ARABIDOPSIS THALIANA	NUDT7
XTR7 (XYLOGLUCAN	XTH15
expressed protein [At4g14450.1]	
auxin-responsive protein / indoleacetic	IAA1; AXR5
germin-like protein (GLP9) identical to	GLP9
unknown protein;GOLVEN 1; CLE-LIKE 6;	RGF6
esterase/lipase/thioesterase family	MES16
heat shock transcription factor 21	HSF A4A
alcohol oxidase-related similar to long	
Arabidopsis thaliana PAK-box/P21-Rho-	
methionine sulfoxide reductase domain-	MSRB9
expressed protein contains Pfam profile	
protease inhibitor/seed storage/lipid	

protease inhibitor/seed storage/lipid	
receptor-like protein kinase 4, putative	RLK4;CYSTEINE-
CRK11 (CYSTEINE-RICH RLK11); kinase	CRK11
pathogenesis-related protein, putative	
xyloglucan:xyloglucosyl transferase,	
expressed protein similar to myo-inositol	CIL
AGP13 (ARABINOGALACTAN PROTEIN	AGP13
Arabidopsis thaliana F-box protein	
calcium-binding EF hand family protein	WES1; GH3.5
Arabidopsis thaliana cystathionine beta-	
hypothetical protein [At4g28460.1]	
Arabidopsis thaliana putative leucine-	
Arabidopsis thaliana uncharacterized	
profilin 3 (PRO3) (PFN3) identical to	
expressed protein [At4g29520.1]	PROFILIN 4
xyloglucan:xyloglucosyl transferase,	
xyloglucan:xyloglucosyl transferase,	XTH18
pathogenesis-related protein, putative;	FLA5
metal transporter, putative (ZIP9)	
pyruvate decarboxylase, putative strong	ATZIP9; ZIP9
Arabidopsis thaliana calcium-dependent	
BLH6 (BELL1-LIKE HOMEODOMAIN 5);	BLH6
Arabidopsis thaliana uncharacterized	
Arabidopsis thaliana SAUR-like auxin-	
brassinosteroid signalling positive	AtPMT6
PLA IVA/PLP1; nutrient reservoir;	PLP1; BEH2
Arabidopsis thaliana uncharacterized	
1-aminocyclopropane-1-carboxylate	
expansin family protein (EXPL2) contains	1-AMINO-
dehydrin, putative similar to dehydrin	ATEXLA2;
SKS9 (SKU5 Similar 9); copper ion binding	sks9
mannitol dehydrogenase, putative;	CAD9
inositol-3-phosphate synthase isozyme 1	MIPS1
L-ascorbate oxidase, putative similar to	
Arabidopsis thaliana uncharacterized	
expressed protein [At5g01015.1]	
lectin protein kinase, putative similar to	LECRKA4.1
lectin protein kinase, putative similar to	LECRKA4.2
expressed protein wound-inducible	
expressed protein [At5g01790.1]	
ovate family protein 59% similar to ovate	OFP1
heat shock cognate 70 kDa protein 2	AtHsp70-2;
legume lectin family protein contains	
laccase, putative / diphenol oxidase,	LAC12
U-box domain-containing protein low	
cellulose synthase, catalytic subunit,	CESA5
zinc finger (C2H2 type) family protein	
JAS1/JAZ10/TIFY9 (JASMONATE-ZIM-	JAZ10

PBS3 (AVRPPHB SUSCEPTIBLE 3);	PBS3
polyamine oxidase, putative similar to	ATPAO1
ZIF1 (ZINC INDUCED FACILITATOR 1);	ZIF1
myb family transcription factor (MYB66)	ATMYB66
glycosyltransferase family 14 protein /	
expressed protein [At5g15120.1]	
leucine-rich repeat transmembrane	LRR1
root cap 1 (RCP1) identical to GI:6137138	RCP1
AAA-type ATPase family protein contains	
AP2 domain-containing transcription	PUCHI
extracellular dermal glycoprotein-related	
Arabidopsis thaliana GPI-anchored	
RNA cyclase family protein contains	
expressed protein [At5g22580.1]	
exostosin family protein contains Pfam	F8H
ethylene-responsive element-binding	ESE3
Arabidopsis thaliana Flotillin-like protein	FLOT1
exostosin family protein	
meprin and TRAF homology domain-	
heavy-metal-associated domain-	
GDP-D-MANNOSE 3',5'-EPIMERASE; GDP-	GME
transposable element gene	
aspartyl protease family protein contains	
proline oxidase, putative / osmotic stress-	
cytochrome P450, putative similar to	BR6OX1
Arabidopsis thaliana peroxidase 62	
receptor-like protein kinase-related	
Arabidopsis thaliana TIR-NBS-LRR class	
Arabidopsis thaliana uncharacterized	
CML37/CML39; calcium ion binding	CML37
DC1 domain-containing protein contains	
serine protease inhibitor, potato	
Toll-Interleukin-Resistance (TIR) domain-	
disease resistance protein (TIR-NBS-LRR	
Arabidopsis thaliana GDSL	
pentacyclic triterpene synthase, putative	THAS1
expressed protein [At5g49100.1]	
Arabidopsis thaliana Beta-glucosidase,	
short-chain dehydrogenase/reductase	AtHSD4
Arabidopsis thaliana ethylene-responsive	
23.5 kDa mitochondrial small heat shock	
multi-copper oxidase type I family	sks2
arabinogalactan-protein, putative	AGP22
expressed protein similar to unknown	
heat shock protein 81-4 (HSP81-4)	Hsp81.4
cytochrome P450, putative similar to	CYP81F2
xyloglucan:xyloglucosyl transferase /	XTH22; TCH4
Arabidopsis thaliana uncharacterized	P1R1

expressed protein [At5g57785.1]	
expressed protein [At5g59510.1]; DEVIL	DVL18; RTFL5
late embryogenesis abundant protein-	
unknown protein; BREAKING OF	BASL
invertase/pectin methylesterase	
ANAC102 (Arabidopsis NAC domain	NAC102
expressed protein contains Pfam profile	
phosphate-responsive protein, putative;	EXL2
expressed protein [At5g64770.1];	GLV2; CLEL 9;
expressed protein [At5g64870.1]	
expressed protein [At5g64980.1]	
expressed protein ; expression	
expressed protein [At5g65300.1]	
xyloglucan:xyloglucosyl transferase,	XTH6
1-aminocyclopropane-1-carboxylate	ACS5; ETO2;
protein phosphatase 2C family protein /	
HEAVY METAL ASSOCIATED	HIPP27
allergen V5/Tpx-1-related family protein	
expressed protein [At5g66985.1]	

color key	
downregulated	unchanged

BR regulated genes up- and down-regulated by Glc alone (217 genes)

Probe set_ID	Representative Public ID	0% Glc + 100 nM BR vs 0% Glc	3% Glc vs 0% Glc	3% Glc + 100 nM BR vs 0% Glc	Gene Description
A_84_P10559	AT1G01560	4.05	8.02	5.59	mitogen-
A_84_P21249	AT1G02650	2.19	-7.91	-1.46	DNAJ heat
A_84_P801239	AT1G02920	2.53	4.53	5.73	GLUTATHIONE
A_84_P812454	AT1G02930	2.80	4.12	4.90	ARABIDOPSIS
A_84_P799181	AT1G05660	2.69	3.75	12.70	Arabidopsis
A_84_P17191	AT1G07160	2.66	10.68	17.93	protein
A_84_P233559	AT1G10340	2.17	-9.80	-6.34	ankyrin repeat
A_84_P20977	AT1G14480	2.04	2.00	3.91	ankyrin repeat
A_84_P16226	AT1G14540	2.14	3.86	5.06	anionic
A_84_P22847	AT1G14550	2.24	12.93	6.45	anionic
A_84_P12389	AT1G14860	-3.64	-3.65	-10.03	MutT/nudix
A_84_P826352	AT1G16750	-2.14	3.14	1.32	Arabidopsis
A_84_P516067	AT1G17345	-2.31	-15.23	-8.79	auxin-
A_84_P23422	AT1G18280	2.04	-12.08	-5.01	protease
A_84_P11448	AT1G18870	-3.01	7.17	-2.07	isochorismate
A_84_P14313,	AT1G19970	2.08	45.37	40.93	Arabidopsis
A_84_P16097	AT1G24140	10.84	13.42	24.87	matrixin family
A_84_P541789	AT1G26250	2.21	-3.37	-1.95	Arabidopsis
A_84_P19294,	AT1G26380	3.10	41.95	40.12	Arabidopsis
A_84_P20237	AT1G26420	2.74	10.06	10.35	FAD-binding
A_84_P12872	AT1G29270	2.17	-9.86	-3.80	expressed
A_84_P537376	AT1G29420	2.13	-2.32	1.30	auxin-
A_84_P20998,	AT1G35140	2.92	-20.48	-6.43	PHI-1
A_84_P16055	T1G35612///TC2596	-2.04	-5.04	-20.42	Q9LQF9
A_84_P13577	AT1G36940	-2.77	-2.21	-1.33	hypothetical
A_84_P268780	AT1G45010	2.47	11.44	9.87	Arabidopsis
A_84_P13870	AT1G50600	-15.89	-17.12	-14.48	scarecrow-like
A_84_P10747	AT1G53700	2.39	3.58	14.54	protein kinase,
A_84_P12484	AT1G58170	-2.22	10.87	1.37	disease
A_84_P138279	AT1G58420	2.75	3.13	11.45	expressed
A_84_P799584	AT1G62975	-2.44	2.01	2.68	Arabidopsis
A_84_P14255	AT1G64970	2.59	7.08	6.47	expressed
A_84_P11417	AT1G65730	-2.05	-3.33	-7.36	oligopeptide
A_84_P13393	AT1G66090	3.16	9.50	10.06	disease
A_84_P842079	AT1G67195	2.55	10.13	20.48	MIR414
A_84_P184384	AT1G68440	2.00	-2.54	-1.88	expressed
A_84_P560506	AT1G69430	2.55	4.44	14.03	hypothetical
A_84_P157715	AT1G72930	2.74	20.54	26.13	Toll-Interleukin-
A_84_P14468	AT1G75450	-2.79	-3.05	-3.22	FAD-binding
A_84_P805374	AT1G76160	2.62	-4.95	-1.33	SKS5 (SKU5
A_84_P260340	AT1G76240	-4.42	-10.27	-4.71	expressed
A_84_P258420	AT2G04500	3.63	-5.10	-2.12	DC1 domain-

A_84_P20150	AT2G04550	-7.04	-18.33	-9.28	dual specificity
A_84_P601261	AT2G07140	2.15	-7.42	-3.08	F-box family
A_84_P13475	AT2G11810	3.74	2.05	2.00	1,2-
A_84_P61660	AT2G15220	2.85	6.20	6.94	secretory
A_84_P22914,	AT2G15490	-2.09	23.93	10.61	UGT73B4; UDP-
A_84_P10627	AT2G20880	5.02	-3.87	-2.10	AP2 domain-
A_84_P22151	AT2G21900	2.17	-4.13	-1.71	WRKY59 (WRKY
A_84_P51530	AT2G22470	2.91	6.51	4.77	arabinogalacta
A_84_P16316	AT2G23180	-2.21	2.47	2.98	cytochrome
A_84_P16369	AT2G23380	3.14	4.26	8.05	curly leaf
A_84_P15423	AT2G23620	-2.05	-9.34	-24.54	esterase,
A_84_P22001	AT2G24710	-2.15	-13.67	-5.67	glutamate
A_84_P558814	AT2G25780	-2.78	-10.71	-4.45	hypothetical
A_84_P19231	AT2G26150	3.66	75.17	91.66	HEAT SHOCK
A_84_P10647	AT2G26480	6.77	6.60	5.05	UDP-
A_84_P14435	AT2G26710	2.22	-3.39	-3.67	cytochrome
A_84_P12547	AT2G30750	2.19	32.94	11.97	cytochrome
A_84_P14433	AT2G32990	-2.59	7.39	4.70	glycosyl
A_84_P14490	AT2G34180	8.77	-7.00	-2.00	CBL-interacting
A_84_P23919	AT2G35980	2.40	17.21	10.99	harpin-induced
A_84_P74914	AT2G36840	2.26	2.23	3.36	ACT domain-
A_84_P13527	AT2G37030	-4.60	-5.16	5.32	auxin-
A_84_P13482	AT2G38760	2.08	3.63	-4.93	annexin 3
A_84_P14494	AT2G39430	-2.23	-2.19	-14.69	disease
A_84_P22053,	AT2G41100	2.68	-4.04	-6.85	TCH3 (TOUCH
A_84_P24802	AT2G42800	-3.15	5.44	7.69	leucine-rich
A_84_P21007	AT2G43570	2.99	7.91	5.29	chitinase,
A_84_P75797	AT2G44578	2.59	12.05	15.42	Arabidopsis
A_84_P78649	AT2G46400	4.23	2.63	5.39	WRKY46 (WRKY
A_84_P186814	AT2G46495	2.17	8.66	6.12	zinc finger
A_84_P57935	AT3G01516	-9.47	-6.32	-6.85	expressed
A_84_P11694,	AT3G01830	3.38	6.39	9.64	Arabidopsis
A_84_P15464	AT3G03670	2.32	-27.10	-7.54	peroxidase,
A_84_P28090	AT3G07350	-2.10	-32.87	-22.74	Arabidopsis
A_84_P19256	AT3G09220	-2.29	-9.86	-20.91	laccase family
A_84_P762751	AT3G10986	2.02	2.10	5.23	Arabidopsis
A_84_P10829	AT3G13730	-6.01	2.47	1.15	cytochrome
A_84_P84292	AT3G13980	-3.46	-2.46	-7.29	Arabidopsis
A_84_P15501	AT3G15370	4.19	-8.23	-1.26	expansin,
A_84_P80507	AT3G15450	2.34	-38.08	-47.79	similar to
A_84_P11727	AT3G15670	2.67	10.47	26.81	late
A_84_P84154	AT3G20830	-2.36	-2.90	-4.69	Arabidopsis
A_84_P59192	AT3G21680	3.16	6.13	13.44	expressed
A_84_P23101	AT3G21890	2.70	4.67	2.50	zinc finger (B-
A_84_P23070	AT3G22740	-2.13	-23.15	-18.79	homocysteine S-

A_84_P15503,	AT3G22830	2.35	24.77	2.76	AT-HSFA6B
A_84_P860303	AT3G23170	-2.56	3.70	2.18	Arabidopsis
A_84_P247395	AT3G26470	2.05	4.10	4.50	expressed
A_84_P12704,	AT3G27200	-2.16	2.50	3.00	Arabidopsis
A_84_P759661	AT3G27500	2.24	-4.89	1.45	Arabidopsis
A_84_P22181|	AT3G28210	2.21	23.22	25.81	zinc finger (AN1-
A_84_P100746	AT3G28220	-2.37	-5.70	-5.18	meprin and
A_84_P12725|	AT3G28510	2.04	19.37	21.18	AAA-type
A_84_P826388	AT3G30180	-4.26	-2.54	-1.95	BR6OX2/CYP85
A_84_P18416|	AT3G46080	3.36	12.33	18.44	zinc finger
A_84_P19362|	AT3G46090	3.94	2.55	7.08	zinc finger
A_84_P12747|	AT3G46700	-2.37	-12.45	-16.41	UDP-
A_84_P192624	AT3G49840	2.49	2.33	4.26	proline-rich
A_84_P13706|	AT3G50140	2.16	-3.67	-1.66	expressed
A_84_P24110|	AT3G50270	2.12	-2.49	-2.52	transferase
A_84_P12763|	AT3G50560	2.21	-19.43	-5.61	short-chain
A_84_P157735	AT3G51400	-11.97	-5.48	-18.10	expressed
A_84_P813219	AT3G54810	2.04	2.64	4.90	BME3/BME3-ZF
A_84_P821534	AT3G55010	3.02	5.94	9.34	ATPURM/PUR5;
A_84_P14678|	AT3G56000	2.17	-10.06	-4.44	glycosyl
A_84_P849984	AT3G56080	2.08	9.90	10.44	Arabidopsis
A_84_P16571|	AT3G56400	2.48	-3.09	-1.95	WRKY family
A_84_P861025	AT3G56910	-2.14	-2.93	-6.59	PSRP5 (PLASTID-
A_84_P14682|	AT3G57010	-3.87	38.95	22.51	strictosidine
A_84_P20359|	AT3G57540	-2.11	4.48	3.88	remorin family
A_84_P18473|	AT3G59140	2.36	11.40	11.98	ABC
A_84_P556409	AT3G60650	3.84	-3.04	-1.26	expressed
A_84_P173361	AT3G62570	2.29	-3.84	-1.97	DNAJ heat
A_84_P20381|	AT3G63110	-2.27	5.70	4.69	adenylate
A_84_P14717|	AT4G01630	10.87	32.65	99.38	expansin,
A_84_P16609,	AT4G01870	-5.15	2.09	-5.65	Arabidopsis
A_84_P10949|	AT4G05100	-2.06	2.07	-2.37	myb family
A_84_P22299|	AT4G07960	3.12	-2.60	1.01	glycosyl
A_84_P10014|	AT4G10160	2.25	-9.61	-6.59	zinc finger
A_84_P855052	AT4G14130	-4.04	-3.29	-49.79	XTR7
A_84_P596516	AT4G14450	-2.46	3.57	2.27	expressed
A_84_P10124|	AT4G14560	-2.67	-3.41	-16.52	auxin-
A_84_P12960|	AT4G14630	2.20	-3.61	-1.86	germin-like
A_84_P576905	AT4G16515	2.12	-3.09	1.56	unknown
A_84_P10131|	AT4G16690	-2.26	-22.66	-17.10	esterase/lipase
A_84_P17597|	AT4G18880	2.62	7.74	11.60	heat shock
A_84_P11926|	AT4G19380	-4.19	-18.03	-3.78	alcohol oxidase-
A_84_P765234	AT4G21745	2.16	-13.72	-2.46	Arabidopsis
A_84_P812152	AT4G21850	2.46	-2.08	-1.11	methionine
A_84_P534335	AT4G21970	2.74	-7.44	-3.83	expressed

A_84_P17611	AT4G22460	-3.71	-3.42	-1.59	protease
A_84_P18557	AT4G22470	-2.70	2.14	1.09	protease
A_84_P14776	AT4G23180	2.07	2.21	4.29	receptor-like
A_84_P52813	AT4G23190	2.09	3.83	3.61	CRK11
A_84_P15734	AT4G25810	2.80	-3.57	-1.32	xyloglucan:xylo
A_84_P20466	AT4G26260	2.77	-33.86	-10.48	expressed
A_84_P78594	AT4G26320	2.22	-6.09	-2.31	AGP13
A_84_P82312	AT4G27050	-2.08	-2.20	-11.95	Arabidopsis
A_84_P56446	AT4G27460	2.10	-4.13	-1.80	Arabidopsis
A_84_P60634	AT4G28460	2.74	6.26	4.69	hypothetical
A_84_P82587	AT4G28650	2.91	3.03	9.11	Arabidopsis
A_84_P19534	AT4G29340	2.22	4.04	3.89	profilin 3
A_84_P79989	AT4G29520	3.43	7.41	15.46	expressed
A_84_P21282	AT4G30280	2.39	-3.32	1.02	xyloglucan:xylo
A_84_P10083	AT4G30290	3.19	2.50	35.89	xyloglucan:xylo
A_84_P14814	AT4G31470	4.39	4.82	29.48	pathogenesis-
A_84_P18604	AT4G33020	-2.16	2.34	1.99	metal
A_84_P22388	AT4G33070	-2.16	17.22	15.20	pyruvate
A_84_P10101,	AT4G34610	-2.07	3.65	4.41	BLH6 (BELL1-
A_84_P12944,	AT4G36110	3.89	-3.21	2.18	Arabidopsis
A_84_P15960	AT4G37070	-2.68	-3.81	-2.57	PLA IVA/PLP1;
A_84_P76516	AT4G37608	-2.09	2.24	3.35	Arabidopsis
A_84_P10114	AT4G38400	2.58	-10.13	-3.35	expansin family
A_84_P81000	AT4G39330	2.12	10.37	17.00	mannitol
A_84_P12011	AT4G39800	-4.38	7.27	4.67	inositol-3-
A_84_P23380	AT5G01540	3.30	5.35	13.06	lectin protein
A_84_P10141	AT5G01550	3.22	6.50	20.39	lectin protein
A_84_P22435	AT5G01740	-66.18	-2.81	-17.23	expressed
A_84_P50600	AT5G01790	2.21	13.35	16.49	expressed
A_84_P70894	AT5G01840	-2.78	2.75	1.59	ovate family
A_84_P55655	AT5G02490	3.10	5.86	9.32	heat shock
A_84_P10371	AT5G03350	2.79	-3.53	1.02	legume lectin
A_84_P19609	AT5G05390	2.52	3.96	6.49	laccase,
A_84_P57522	AT5G09800	-2.82	7.17	7.52	U-box domain-
A_84_P18678	AT5G09870	2.11	2.92	5.72	cellulose
A_84_P18683	AT5G10970	2.53	7.76	9.74	zinc finger
A_84_P52468	AT5G13220	2.07	-2.59	-1.16	JAS1/JAZ10/TIF
A_84_P14907	AT5G13700	-2.16	2.09	-1.35	polyamine
A_84_P18691,	AT5G13740	-2.20	-4.96	-50.86	ZIF1 (ZINC
A_84_P19794	AT5G14750	2.93	3.09	9.02	myb family
A_84_P22669	AT5G15050	2.16	5.72	11.93	glycosyltransfer
A_84_P20748	AT5G17520	-2.03	3.27	2.99	root cap 1
A_84_P16807	AT5G17760	-2.01	4.79	1.80	AAA-type
A_84_P13031	AT5G19110	4.51	-2.77	-1.80	extracellular
A_84_P92929,	AT5G19240	2.70	4.18	10.61	Arabidopsis

A_84_P223799	AT5G22100	-3.16	3.01	4.22	RNA cyclase
A_84_P174931	AT5G22940	2.14	-2.77	-1.20	exostosin
A_84_P13987|	AT5G25190	2.87	3.07	19.10	ethylene-
A_84_P825802	AT5G25250	2.93	2.20	3.20	Arabidopsis
A_84_P826308	AT5G25820	3.18	7.69	8.44	exostosin
A_84_P258360	AT5G26290	-2.97	8.19	5.75	meprin and
A_84_P515865	AT5G26690	2.47	-6.63	-1.38	heavy-metal-
A_84_P16971,	AT5G28840	-2.10	-4.30	-14.55	GDP-D-
A_84_P18737|	AT5G38710	5.65	-10.48	-14.44	proline oxidase,
A_84_P16848,	AT5G39580	2.05	-2.19	-1.39	Arabidopsis
A_84_P612712	AT5G41300	2.12	-9.08	-3.77	receptor-like
A_84_P23478,	AT5G41750	5.86	7.00	9.52	Arabidopsis
A_84_P769417	AT5G41761	-2.19	-10.28	-3.07	Arabidopsis
A_84_P13077,	AT5G42380	3.98	10.22	15.09	CML37/CML39;
A_84_P14969|	AT5G43030	2.19	-3.86	-1.45	DC1 domain-
A_84_P511454	AT5G43570	-2.67	-15.35	-24.80	serine protease
A_84_P17815|	AT5G45200	3.38	2.48	6.84	disease
A_84_P20664|	AT5G48010	-2.10	42.14	34.73	pentacyclic
A_84_P139909	AT5G49100	-2.48	2.01	1.98	expressed
A_84_P220678	AT5G50590	2.09	-13.22	-5.48	short-chain
A_84_P15946|	AT5G51440	2.64	37.76	3.92	23.5 kDa
A_84_P302000	AT5G53250	2.01	-14.19	-15.03	arabinogalacta
A_84_P262520	AT5G55620	-2.31	10.48	24.24	expressed
A_84_P12181,	AT5G56000	2.44	11.34	12.58	heat shock
A_84_P13130|	AT5G57220	2.25	12.62	5.10	cytochrome
A_84_P17859|	AT5G57560	3.36	-12.77	-15.49	xyloglucan:xylo
A_84_P828057	AT5G57780	-5.80	-3.43	-3.84	Arabidopsis
A_84_P559359	AT5G57785	-10.18	-5.77	-53.15	expressed
A_84_P17872|	AT5G60520	2.20	6.83	17.10	late
A_84_P530135	AT5G60880	2.21	4.02	9.49	unknown
A_84_P15043|	AT5G62340	2.62	-2.29	-1.00	invertase/pecti
A_84_P20724,	AT5G63790	-2.31	4.19	1.48	ANAC102
A_84_P161403	AT5G63820	2.88	-7.16	-1.22	expressed
A_84_P800757	AT5G64260	-2.76	-2.57	-7.66	phosphate-
A_84_P160863	AT5G64980	2.16	8.40	9.25	expressed
A_84_P555846	AT5G65030	-2.77	8.50	5.12	expressed
A_84_P60290|	AT5G65300	-6.54	2.62	-1.17	expressed
A_84_P16948|	AT5G65730	-2.02	-110.66	-36.27	xyloglucan:xylo
A_84_P10332|	AT5G66110	-2.06	-12.06	-9.16	HEAVY METAL
A_84_P546117	AT5G66985	-2.06	7.44	3.50	expressed

All Gene Symbols	Gene Symbol
MAP KINASE 11	
GSTF7; GST11	GSTF7
GSTF6	
PEROXIDASE 4	
NUDIX	
ATICS2	
PHOSPHATE-	PHI-1
SCARECROW-	
PROTEIN	
G-TMT	
YELLOW STRIPE	
MICRORNA414	
TOLL/INTERLEU	
CKX5; ATCKX6	
SKU5 SIMILAR 5	sks5

color key		
upregulated	**downregulated**	**unchanged**

DSPTP1E; IBR5	
MONOGALACT	
UDP-	UGT73B4
ATERF53;ERF	
WRKY DNA-	WRKY59
AGP2	
CYP96A1	
CLF	
METHYL	
GLR2.3	
ATHSFA2	
UDP-GLUCOSYL	
PHYB	
CYP71A12	
GH9B8	
CIPK13; ATWL2;	
YELLOW-LEAF-	
ACR10	
ANN3	
TOUCH 3	TCH3
RECEPTOR LIKE	
CHITINASE,	
WRKY DNA-	WRKY46
LACCASE 7	
CYP90D1	
ATEXPA12;	
HOMOCYSTEIN	

HSFA6B	
STRESS-	
BR6OX2	
ZAT7	
BME3-	BME3
EMBRYO	
CSLA14	
WRKY DNA-	
PLASTID-	PSRP5
MULTIDRUG	
ISOPENTENYLT	
ATEXP17;	
MYB DOMAIN	
CSLC12	
XYLOGLUCAN	XTH15
IAA1; AXR5	
GLP9	
GLV1; CLEL 6;	RGF6
ARABIDOPSIS	
ARABIDOPSIS	
METHIONINE	MSRB9

RLK4;CYSTEINE-	
RECEPTOR LIKE	CRK11
CIL	
MYO-INOSITOL	AGP13
PROFILIN 4	
XYLOGLUCAN	
FLA5	
ATZIP9; ZIP9	
BLH6	
PLP1; BEH2	
1-AMINO-	
CAD9	
MYO-INOSITOL-	
LECTIN	
LECTIN	
OVATE FAMILY	
AtHsp70-2;	
LACCASE 12	
CESA5	
JASMONATE-	JAZ10
POLYAMINE	
ZINC INDUCED	ZIF1
WEREWOLF	
MALTOSE	

F8H	
ESE3	
FLOT1	
GME	GME
CML37	
THALIANOL	
HYDROXYSTER	
AGP22	
Hsp81.4	Hsp81.4
CYP81F2	
XYLOGLUCAN	
P1R1 P1R1	
BASL	BASL
NAC DOMAIN	NAC102
EXL2	EXL2
XYLOGLUCAN	
HIPP27	

Genes in which BR regulation is affected (2 fold more/less or lost) significantly in prese

Probe set_ID	Representative Public ID	0% Glc + 100 nM BR vs 0% Glc	3% Glc vs 0% Glc	3% Glc + 100 nM BR vs 0% Glc
A_84_P14717|8	AT4G01630	10.87	32.65	99.38
A_84_P19231|8	AT2G26150	3.66	75.17	91.66
A_84_P18691,A_	AT5G13740	-2.20	-4.96	-50.86
A_84_P855052,	AT4G14130	-4.04	-3.29	-49.79
A_84_P559359|	AT5G57785	-10.18	-5.77	-53.15
A_84_P14313,A_	AT1G19970	2.08	45.37	40.93
A_84_P19294,A_	AT1G26380	3.10	41.95	40.12
A_84_P16948|8	AT5G65730	-2.02	-110.66	-36.27
A_84_P10083|8	AT4G30290	3.19	2.50	35.89
A_84_P20416|8	AT4G10350	2.33	1.53	32.51
A_84_P14814|8	AT4G31470	4.39	4.82	29.48
A_84_P11727|8	AT3G15670	2.67	10.47	26.81
A_84_P22181|8	AT3G28210	2.21	23.22	25.81
A_84_P157715|	AT1G72930	2.74	20.54	26.13
A_84_P15423|8	AT2G23620	-2.05	-9.34	-24.54
A_84_P511454|	AT5G43570	-2.67	-15.35	-24.80
A_84_P280900,	AT3G07350	-2.10	-32.87	-22.74
A_84_P765351|	AT4G40011	2.05	1.66	22.08
A_84_P12725|8	AT3G28510	2.04	19.37	21.18
A_84_P19256|8	AT3G09220	-2.29	-9.86	-20.91
A_84_P16055	1G35612///TC2596	-2.04	-5.04	-20.42
A_84_P842079	AT1G67195	2.55	10.13	20.48
A_84_P10141|8	AT5G01550	3.22	6.50	20.39
A_84_P23070|8	AT3G22740	-2.13	-23.15	-18.79
A_84_P13987|8	AT5G25190	2.87	3.07	19.10
A_84_P162603|	AT4G36780	-2.38	-1.30	-18.27
A_84_P17191|8	AT1G07160	2.66	10.68	17.93
A_84_P18416|8	AT3G46080	3.36	12.33	18.44
A_84_P17872|8	AT5G60520	2.20	6.83	17.10
A_84_P810008	AT4G39330	2.12	10.37	17.00
A_84_P10131|8	AT4G16690	-2.26	-22.66	-17.10
A_84_P16006|8	AT5G66590	-2.57	-1.05	-17.07
A_84_P506004|	AT5G01790	2.21	13.35	16.49
A_84_P12747|8	AT3G46700	-2.37	-12.45	-16.41
A_84_P16097|8	AT1G24140	10.84	13.42	24.87
A_84_P10124|8	AT4G14560	-2.67	-3.41	-16.52
A_84_P757973|	AT2G44578	2.59	12.05	15.42
A_84_P14494|8	AT2G39430	-2.23	-2.19	-14.69
A_84_P16971,A_	AT5G28840	-2.10	-4.30	-14.55
A_84_P10747|8	AT1G53700	2.39	3.58	14.54

A_84_P79989|8	AT4G29520	3.43	7.41	15.46
A_84_P560506|	AT1G69430	2.55	4.44	14.03
A_84_P13077,A	AT5G42380	3.98	10.22	15.09
A_84_P591926|	AT3G21680	3.16	6.13	13.44
A_84_P12181,A	AT5G56000	2.44	11.34	12.58
A_84_P799181,A	AT1G05660	2.69	3.75	12.70
A_84_P823127,A	AT4G27050	-2.08	-2.20	-11.95
A_84_P12547|8	AT2G30750	2.19	32.94	11.97
A_84_P226699|	AT5G15050	2.16	5.72	11.93
A_84_P23380|8	AT5G01540	3.30	5.35	13.06
A_84_P18473|8	AT3G59140	2.36	11.40	11.98
A_84_P17597|8	AT4G18880	2.62	7.74	11.60
A_84_P138279|	AT1G58420	2.75	3.13	11.45
A_84_P23919|8	AT2G35980	2.40	17.21	10.99
A_84_P849984,A	AT3G56080	2.08	9.90	10.44
A_84_P92929,A	AT5G19240	2.70	4.18	10.61
A_84_P20237|8	AT1G26420	2.74	10.06	10.35
A_84_P268780,A	AT1G45010	2.47	11.44	9.87
A_84_P11613|8	AT2G34930	3.37	1.85	10.71
A_84_P530135,A	AT5G60880	2.21	4.02	9.49
A_84_P18683|8	AT5G10970	2.53	7.76	9.74
A_84_P10332|8	AT5G66110	-2.06	-12.06	-9.16
A_84_P160863|	AT5G64980	2.16	8.40	9.25
A_84_P13393|8	AT1G66090	3.16	9.50	10.06
A_84_P12005|8	AT4G38410	2.77	1.69	9.57
A_84_P516067|	AT1G17345	-2.31	-15.23	-8.79
A_84_P12389|8	AT1G14860	-3.64	-3.65	-10.03
A_84_P821534	AT3G55010	3.02	5.94	9.34
A_84_P11694,A	AT3G01830	3.38	6.39	9.64
A_84_P556555|	AT5G02490	3.10	5.86	9.32
A_84_P825877,A	AT4G28650	2.91	3.03	9.11
A_84_P157735|	AT3G51400	-11.97	-5.48	-18.10
A_84_P19794|8	AT5G14750	2.93	3.09	9.02
A_84_P11417|8	AT1G65730	-2.05	-3.33	-7.36
A_84_P826308	AT5G25820	3.18	7.69	8.44
A_84_P16369|8	AT2G23380	3.14	4.26	8.05
A_84_P800757,A	AT5G64260	-2.76	-2.57	-7.66
A_84_P861025,A	AT3G56910	-2.14	-2.93	-6.59
A_84_P297064|	AT1G65310	4.03	-1.17	8.39
A_84_P22847|8	AT1G14550	2.24	12.93	6.45
A_84_P61660|8	AT2G15220	2.85	6.20	6.94
A_84_P19609|8	AT5G05390	2.52	3.96	6.49
A_84_P186814|	AT2G46495	2.17	8.66	6.12
A_84_P14255|8	AT1G64970	2.59	7.08	6.47
A_84_P842922,A	AT3G13980	-3.46	-2.46	-7.29

A_84_P23478,A_	AT5G41750	5.86	7.00	9.52
A_84_P18678|8	AT5G09870	2.11	2.92	5.72
A_84_P22001|8	AT2G24710	-2.15	-13.67	-5.67
A_84_P17815|8	AT5G45200	3.38	2.48	6.84
A_84_P801239,A	AT1G02920	2.53	4.53	5.73
A_84_P762751|	AT3G10986	2.02	2.10	5.23
A_84_P19362|8	AT3G46090	3.94	2.55	7.08
A_84_P23570|8	AT5G65800	4.67	1.29	7.77
A_84_P16226|8	AT1G14540	2.14	3.86	5.06
A_84_P813219,A	AT3G54810	2.04	2.64	4.90
A_84_P13130|8	AT5G57220	2.25	12.62	5.10
A_84_P100746|	AT3G28220	-2.37	-5.70	-5.18
A_84_P848499	AT5G35935	-2.32	1.21	-5.06
A_84_P522242|	AT1G07985	-3.13	-1.62	-5.80
A_84_P20622|8	AT5G36260	3.31	1.65	5.91
A_84_P247395|	AT3G26470	2.05	4.10	4.50
A_84_P853187,A	AT4G34150	2.03	1.93	4.42
A_84_P841540,A	AT3G20830	-2.36	-2.90	-4.69
A_84_P21007|8	AT2G43570	2.99	7.91	5.29
A_84_P207798|	AT2G31540	2.42	1.03	4.67
A_84_P20150|8	AT2G04550	-7.04	-18.33	-9.28
A_84_P22546,A_	AT5G45670	2.86	1.42	5.09
A_84_P14776|8	AT4G23180	2.07	2.21	4.29
A_84_P13252|8	AT1G24470	2.85	1.57	5.07
A_84_P812454,A	AT1G02930	2.80	4.12	4.90
A_84_P576905,A	AT4G16515	2.12	6.60	1.92
A_84_P22481|8	AT5G16590	2.27	3.63	1.80
A_84_P10949|8	AT4G05100	-2.06	2.07	-1.53
A_84_P537376|	AT1G29420	2.13	2.05	1.58
A_84_P522715|	AT3G54830	2.48	1.99	1.90
A_84_P296724,A	AT5G51190	2.21	1.99	1.56
A_84_P759661|	AT3G27500	2.24	1.82	1.59
A_84_P268090,A	AT2G01300	2.33	1.80	1.45
A_84_P22262|8	AT3G60390	-2.30	-1.19	-1.33
A_84_P159605,A	AT4G37070	-2.68	-3.81	-1.71
A_84_P769417|	AT5G41761	-2.19	-10.28	-1.18
A_84_P212828|	AT4G30280	2.39	1.50	1.30
A_84_P10788|8	AT3G25900	2.48	1.33	1.37
A_84_P11953|8	AT4G25780	-3.14	-1.88	-1.87
A_84_P14468|8	AT1G75450	-2.79	-3.05	-1.49
A_84_P558814|	AT2G25780	-2.78	-10.71	-1.04
A_84_P103716|	AT5G03350	2.79	1.28	1.02
A_84_P14703|5	T1G05835///TC2666	-2.99	-1.55	-1.11
A_84_P18950,A_	AT1G04660	3.51	1.14	1.47
A_84_P22299|8	AT4G07960	3.12	1.01	1.01

A_84_P17611|8	AT4G22460	-3.71	-3.42	-1.59
A_84_P546443|	AT2G28085	3.22	-1.06	1.01
A_84_P826388,A	AT3G30180	-4.26	-2.54	-1.95
A_84_P251265,A	AT1G63720	-4.14	1.26	-1.79
A_84_P81479|8	AT3G19380	-3.83	1.20	-1.29
A_84_P579358|	AT3G01516	-9.47	-6.32	-6.85
A_84_P13475|8	AT2G11810	3.74	-1.16	1.02
A_84_P12944,A_	AT4G36110	3.89	-1.18	1.15
A_84_P586802|	AT5G01015	5.09	-1.19	2.27
A_84_P260340|	AT1G76240	-4.42	-10.27	-1.54
A_84_P524680,A	AT5G13220	2.07	-1.28	-1.16
A_84_P17343|8	AT2G44840	7.30	-1.50	3.98
A_84_P13719|8	AT3G53150	2.13	-1.52	-1.20
A_84_P174931|	AT5G22940	2.14	-1.54	-1.20
A_84_P14310|8	AT1G14720	-2.07	1.11	1.30
A_84_P16848,A_	AT5G39580	2.05	-1.60	-1.39
A_84_P826352,A	AT1G16750	-2.14	3.14	1.32
A_84_P812152,A	AT4G21850	2.46	-1.61	-1.11
A_84_P12484|8	AT1G58170	-2.22	10.87	1.37
A_84_P15043|8	AT5G62340	2.62	-1.75	-1.00
A_84_P14969|8	AT5G43030	2.19	-1.91	-1.45
A_84_P21249|8	AT1G02650	2.19	-1.95	-1.46
A_84_P18845|8	AT1G48000	-2.37	1.88	1.37
A_84_P18557|8	AT4G22470	-2.70	2.14	1.09
A_84_P20724,A_	AT5G63790	-2.31	4.19	1.48
A_84_P16609,A_	AT4G01870	-5.15	2.09	-1.35
A_84_P16807|8	AT5G17760	-2.01	4.79	1.80
A_84_P13706|8	AT3G50140	2.16	-2.08	-1.66
A_84_P515865|	AT5G26690	2.47	-2.19	-1.38
A_84_P221516,A	AT2G21900	2.17	-2.29	-1.71
A_84_P184384|	AT1G68440	2.00	-38.08	-1.88
A_84_P564464,A	AT4G27460	2.10	-2.32	-1.80
A_84_P21517|8	AT1G31310	-2.11	-1.38	1.80
A_84_P805374,A	AT1G76160	2.62	-2.49	-1.33
A_84_P816739,A	AT1G44970	-2.67	-1.28	1.29
A_84_P12960|8	AT4G14630	2.20	-2.54	-1.86
A_84_P16277,A_	AT2G43610	2.40	-2.59	-1.68
A_84_P161403|	AT5G63820	2.88	-2.60	-1.22
A_84_P16321|8	AT2G20420	-2.17	1.49	1.95
A_84_P15734|8	AT4G25810	2.80	-2.77	-1.32
A_84_P18604|8	AT4G33020	-2.16	2.34	1.99
A_84_P541789,A	AT1G26250	2.21	-2.77	-1.95
A_84_P173361|	AT3G62570	2.29	-3.04	-1.97
A_84_P70894|8	AT5G01840	-2.78	2.75	1.59
A_84_P763492,A	AT4G12510	-2.43	-1.24	1.96

A_84_P16571|8	AT3G56400	2.48	-3.09	-1.95
A_84_P829727,A	AT5G13320	6.22	-3.09	1.79
A_84_P139909|	AT5G49100	-2.48	2.01	1.98
A_84_P11184|8	AT1G72240	2.45	-3.21	-2.01
A_84_P21622|8	AT5G51480	6.00	-3.32	1.50
A_84_P785948,A	AT4G26320	2.22	-3.37	-2.31
A_84_P765234|	AT4G21745	2.16	-3.39	-2.46
A_84_P604788|	AT5G59510	-2.25	1.91	2.37
A_84_P24110|8	AT3G50270	2.12	-3.53	-2.52
A_84_P14479|8	AT2G40250	7.20	-3.57	2.52
A_84_P14749|8	AT4G12430	2.45	-3.61	-2.23
A_84_P596516|	AT4G14450	-2.46	3.57	2.27
A_84_P860303,A	AT3G23170	-2.56	3.70	2.18
A_84_P21869|8	AT1G77690	-3.17	1.63	1.63
A_84_P21159|8	AT3G04010	-3.75	1.90	1.07
A_84_P824506,A	AT1G51680	-2.05	1.88	2.80
A_84_P20748|8	AT5G17520	-2.03	3.27	2.99
A_84_P813874,A	AT4G12720	2.87	-3.67	-2.17
A_84_P556409|	AT3G60650	3.84	-3.84	-1.26
A_84_P799584,A	AT1G62975	-2.44	2.01	2.68
A_84_P12704,A_	AT3G27200	-2.16	2.50	3.00
A_84_P16316|8	AT2G23180	-2.21	2.47	2.98
A_84_P601261|	AT2G07140	2.15	-3.86	-3.08
A_84_P23571|8	AT5G66080	-7.36	1.30	-2.06
A_84_P60290|8	AT5G65300	-6.54	2.62	-1.17
A_84_P765161|	AT4G37608	-2.09	2.24	3.35
A_84_P15501|8	AT3G15370	4.19	-3.87	-1.26
A_84_P546117|	AT5G66985	-2.06	7.44	3.50
A_84_P10647|8	AT2G26480	6.77	-4.04	1.03
A_84_P258420|	AT2G04500	3.63	-4.13	-2.12
A_84_P53570|8	AT2G41810	-2.10	1.30	3.77
A_84_P14435|8	AT2G26710	2.22	-4.13	-3.67
A_84_P612712|	AT5G41300	2.12	-4.89	-3.77
A_84_P10114|8	AT4G38400	2.58	-4.95	-3.35
A_84_P12872|8	AT1G29270	2.17	-5.10	-3.80
A_84_P20359|8	AT3G57540	-2.11	4.48	3.88
A_84_P20594|8	AT5G18560	-9.13	1.07	-3.07
A_84_P13031|8	AT5G19110	4.51	-6.09	-1.80
A_84_P15343|8	AT2G14960	8.03	-6.63	1.70
A_84_P19357|8	AT3G44990	2.10	-7.00	-4.27
A_84_P10101,A_	AT4G34610	-2.07	3.65	4.41
A_84_P534335|	AT4G21970	2.74	-7.16	-3.83
A_84_P14678|8	AT3G56000	2.17	-7.42	-4.44
A_84_P537048,A	AT4G36105	8.73	-7.44	1.94
A_84_P20381|8	AT3G63110	-2.27	5.70	4.69

A_84_P13482|8	AT2G38760	2.08	-7.91	-4.93
A_84_P23422|8	AT1G18280	2.04	-8.23	-5.01
A_84_P10627|8	AT2G20880	5.02	-9.08	-2.10
A_84_P10829|8	AT3G13730	-6.01	2.47	1.15
A_84_P14433|8	AT2G32990	-2.59	7.39	4.70
A_84_P223799|	AT5G22100	-3.16	3.01	4.22
A_84_P220678|	AT5G50590	2.09	-9.61	-5.48
A_84_P12763|8	AT3G50560	2.21	-9.80	-5.61
A_84_P555846|	AT5G65030	-2.77	8.50	5.12
A_84_P178324|	AT3G18710	-7.04	1.69	1.42
A_84_P233559|	AT1G10340	2.17	-9.86	-6.34
A_84_P258360|	AT5G26290	-2.97	8.19	5.75
A_84_P10014|8	AT4G10160	2.25	-10.06	-6.59
A_84_P12011|8	AT4G39800	-4.38	7.27	4.67
A_84_P20998,A_	AT1G35140	2.92	-10.13	-6.43
A_84_P22053,A_	AT2G41100	2.68	-10.48	-6.85
A_84_P15464|8	AT3G03670	2.32	-12.08	-7.54
A_84_P20630|8	AT5G38970	-14.60	-1.44	-4.69
A_84_P13527|8	AT2G37030	-4.60	-5.16	5.32
A_84_P575222|	AT5G09800	-2.82	7.17	7.52
A_84_P14490|8	AT2G34180	8.77	-12.77	-2.00
A_84_P248025|	AT2G42800	-3.15	5.44	7.69
A_84_P243945|	AT5G22580	-14.18	1.38	-1.89
A_84_P807670	AT3G53990	2.07	-13.22	-10.47
A_84_P22914,A_	AT2G15490	-2.09	23.93	10.61
A_84_P17749|8	AT5G15120	2.15	-13.72	-10.63
A_84_P20466|8	AT4G26260	2.77	-14.19	-10.48
A_84_P302000|	AT5G53250	2.01	-33.86	-15.03
A_84_P22388|8	AT4G33070	-2.16	17.22	15.20
A_84_P17859|8	AT5G57560	3.36	-19.43	-15.49
A_84_P18737|8	AT5G38710	5.65	-20.48	-14.44
A_84_P14682|8	AT3G57010	-3.87	38.95	22.51
A_84_P262520|	AT5G55620	-2.31	10.48	24.24
A_84_P20664|8	AT5G48010	-2.10	42.14	34.73
A_84_P22435|8	AT5G01740	-66.18	-2.81	-17.23
A_84_P805073	AT3G15450	2.34	-27.10	-47.79

nce of Glc (256 genes)

Gene Description	Gene Symbol	Change in extent of regulation
expansin, putative (EXP17) similar to	ATEXP17;	88.51
HEAT SHOCK TRANSCRIPTION FACTOR	ATHSFA2	88.00
ZIF1 (ZINC INDUCED FACILITATOR 1);	ZIF1	48.66
XTR7 (XYLOGLUCAN	XTH15	45.75
expressed protein [At5g57785.1]		42.96
Arabidopsis thaliana ER lumen protein		38.85
Arabidopsis thaliana FAD-binding and		37.02
xyloglucan:xyloglucosyl transferase,	XTH6	34.24
xyloglucan:xyloglucosyl transferase,	XTH18	32.70
no apical meristem (NAM) family protein	ANAC070	30.18
pathogenesis-related protein, putative;	FLA5	25.09
late embryogenesis abundant protein,		24.14
zinc finger (AN1-like) family protein	SAP12; PMZ	23.61
Toll-Interleukin-Resistance (TIR) domain-	TIR	23.39
esterase, putative similar to ethylene-	MES1	22.49
serine protease inhibitor, potato		22.13
Arabidopsis thaliana uncharacterized		20.64
Arabidopsis thaliana uncharacterized		20.04
AAA-type ATPase family protein contains		19.14
laccase family protein / diphenol oxidase	LAC7	18.62
Q9LQF9 (Q9LQF9) F15O4.26, complete		18.37
MIR414	MIR414	17.92
lectin protein kinase, putative similar to	LECRKA4.2	17.17
homocysteine S-methyltransferase 3	HMT3	16.66
ethylene-responsive element-binding	ESE3	16.24
brassinosteroid signalling positive	AtPMT6	15.89
protein phosphatase 2C, putative / PP2C,		15.27
zinc finger (C2H2 type) family protein		15.08
late embryogenesis abundant protein-		14.90
mannitol dehydrogenase, putative;	CAD9	14.88
esterase/lipase/thioesterase family	MES16	14.85
allergen V5/Tpx-1-related family protein		14.50
expressed protein [At5g01790.1]		14.28
UDP-glucoronosyl/UDP-glucosyl		14.04
matrixin family protein similar to matrix		14.03
auxin-responsive protein / indoleacetic	IAA1; AXR5	13.85
Arabidopsis thaliana RING/U-box domain-		12.83
disease resistance-responsive protein-		12.46
GDP-D-MANNOSE 3',5'-EPIMERASE; GDP-	GME	12.45
protein kinase, putative similar to	WAG1	12.14

upregulated
BR-up/d
BR-up/d
BR-u

expressed protein [At4g29520.1]	PROFILIN 4	**12.02**
hypothetical protein [At1g69430.1]		**11.48**
CML37/CML39; calcium ion binding	CML37	**11.11**
expressed protein [At3g21680.1]		**10.29**
heat shock protein 81-4 (HSP81-4)	Hsp81.4	**10.13**
Arabidopsis thaliana Pectin lyase-like		**10.00**
Arabidopsis thaliana F-box protein		**9.86**
cytochrome P450 71A12, putative	CYP71A12	**9.78**
glycosyltransferase family 14 protein /		**9.78**
lectin protein kinase, putative similar to	LECRKA4.1	**9.75**
ABC transporter family protein putative	MRP14	**9.63**
heat shock transcription factor 21	HSF A4A	**8.99**
expressed protein [At1g58420.1]		**8.69**
harpin-induced family protein (YLS9) /	YLS9	**8.59**
Arabidopsis thaliana At3g56080 mRNA		**8.36**
Arabidopsis thaliana GPI-anchored		**7.92**
FAD-binding domain-containing protein		**7.61**
Arabidopsis thaliana TRAM, LAG1 and		**7.40**
disease resistance family protein		**7.35**
unknown protein; BREAKING OF	BASL	**7.28**
zinc finger (C2H2 type) family protein		**7.21**
HEAVY METAL ASSOCIATED	HIPP27	**7.10**
expressed protein [At5g64980.1]		**7.09**
disease resistance protein (TIR-NBS		**6.91**
dehydrin, putative similar to dehydrin	ATEXLA2;	**6.80**
auxin-responsive protein-related similar		**6.48**
MutT/nudix family protein low similarity	NUDT18	**6.39**
ATPURM/PUR5;	EMBRYO	**6.32**
Arabidopsis thaliana putative calcium-		**6.26**
heat shock cognate 70 kDa protein 2	AtHsp70-2;	**6.22**
Arabidopsis thaliana putative leucine-		**6.20**
expressed protein contains Pfam profile		**6.13**
myb family transcription factor (MYB66)	ATMYB66	**6.09**
oligopeptide transporter OPT family	YSL7	**5.31**
exostosin family protein		**5.27**
curly leaf protein (CURLY LEAF) /	CLF	**4.91**
phosphate-responsive protein, putative;	EXL2	**4.90**
PSRP5 (PLASTID-SPECIFIC 50S	PSRP5	**4.46**
xyloglucan:xyloglucosyl transferase,	XTH17	**4.37**
anionic peroxidase, putative similar to		**4.21**
secretory protein, putative similar to		**4.09**
laccase, putative / diphenol oxidase,	LAC12	**3.97**
zinc finger (C3HC4-type RING finger)		**3.95**
expressed protein [At1g64970.1];	G-TMT	**3.87**
Arabidopsis thaliana uncharacterized		**3.82**

Arabidopsis thaliana TIR-NBS-LRR class		3.66
cellulose synthase, catalytic subunit,	CESA5	3.61
glutamate receptor family protein	GLR2.3	3.52
disease resistance protein (TIR-NBS-LRR		3.46
GLUTATHIONE S-TRANSFERASE 7;	GSTF7	3.21
Arabidopsis thaliana LURP-one-like		3.20
zinc finger (C2H2 type) family protein	ZAT7	3.14
1-aminocyclopropane-1-carboxylate	ACS5; ETO2;	3.10
anionic peroxidase, putative similar to	PER4	2.92
BME3/BME3-ZF (BLUE MICROPYLAR	BME3	2.86
cytochrome P450, putative similar to	CYP81F2	2.85
meprin and TRAF homology domain-		2.80
transposable element gene		2.74
Expressed protein [At1g07985.1]		2.66
aspartyl protease family protein contains		2.60
expressed protein [At3g26470.1]		2.45
Arabidopsis thaliana calcium-dependent		2.39
Arabidopsis thaliana AGC (cAMP-		2.33
chitinase, putative similar to chitinase		2.30
GDSL-motif lipase/hydrolase family		2.25
dual specificity protein phosphatase 1E;	DSPTP1E; IBR5	2.24
Arabidopsis thaliana GDSL		2.23
receptor-like protein kinase 4, putative	RLK4;CYSTEINE-	2.22
short-chain dehydrogenase/reductase	ATKCR2;BETA-	2.21
ARABIDOPSIS THALIANA GLUATIONE S-	GSTF6	2.09
unknown protein;GOLVEN 1; CLE-LIKE 6;	RGF6	-0.20
leucine-rich repeat transmembrane	LRR1	-0.47
myb family transcription factor (MYB74)	MYB74	-0.53
auxin-responsive family protein Similar		-0.55
amino acid transporter family protein		-0.58
Arabidopsis thaliana ethylene-responsive		-0.65
Arabidopsis thaliana cysteine/histidine-		-0.66
Arabidopsis thaliana uncharacterized		-0.88
homeobox-leucine zipper protein 3	HAT3	-0.97
PLA IVA/PLP1; nutrient reservoir;	PLP1; BEH2	-0.97
Arabidopsis thaliana uncharacterized		-1.01
xyloglucan:xyloglucosyl transferase,		-1.09
homocysteine S-methyltransferase 1	HMT-1	-1.11
pathogenesis-related protein, putative		-1.27
FAD-binding domain-containing protein /	CKX5	-1.31
hypothetical protein [At2g25780.1]		-1.74
legume lectin family protein contains		-1.78
similar to unknown protein [Arabidopsis		-1.88
Arabidopsis thaliana glycine-rich protein		-2.04
glycosyl transferase family 2 protein	CSLC12	-2.10

protease inhibitor/seed storage/lipid		-2.12
auxin-responsive family protein similar		-2.21
BR6OX2/CYP85A2 (BRASSINOSTEROID-6-	BR6OX2	-2.31
Arabidopsis thaliana uncharacterized		-2.36
U-box domain-containing protein	PUB25	-2.55
expressed protein [At3g01516.1]		-2.62
1,2-diacylglycerol 3-beta-	MONOGALACT	-2.71
Arabidopsis thaliana SAUR-like auxin-		-2.74
expressed protein [At5g01015.1]		-2.82
expressed protein contains Pfam profile		-2.88
JAS1/JAZ10/TIFY9 (JASMONATE-ZIM-	JAZ10	-3.23
ethylene-responsive element-binding	EREBP; ERF13	-3.32
UDP-glucoronosyl/UDP-glucosyl	UDP-GLUCOSYL	-3.33
exostosin family protein contains Pfam	F8H	-3.33
xyloglucan:xyloglucosyl transferase /	XTR2	-3.37
Arabidopsis thaliana peroxidase 62		-3.44
Arabidopsis thaliana uncharacterized		-3.45
methionine sulfoxide reductase domain-	MSRB9	-3.58
disease resistance-responsive protein-		-3.59
invertase/pectin methylesterase		-3.63
DC1 domain-containing protein contains		-3.64
DNAJ heat shock N-terminal domain-		-3.65
myb family transcription factor similar to	MYB112	-3.73
protease inhibitor/seed storage/lipid		-3.79
ANAC102 (Arabidopsis NAC domain	NAC102	-3.79
Arabidopsis thaliana tolB-related protein		-3.79
AAA-type ATPase family protein contains		-3.82
expressed protein contains Pfam profile		-3.82
heavy-metal-associated domain-		-3.85
WRKY59 (WRKY DNA-binding protein 59);	WRKY59	-3.88
expressed protein [At1g68440.1]		-3.88
Arabidopsis thaliana cystathionine beta-		-3.90
hydroxyproline-rich glycoprotein family		-3.91
SKS5 (SKU5 Similar 5); copper ion binding	sks5	-3.95
Arabidopsis thaliana peroxidase 9		-3.96
germin-like protein (GLP9) identical to	GLP9	-4.06
Arabidopsis thaliana putative chitinase		-4.08
expressed protein contains Pfam profile		-4.10
succinyl-CoA ligase [GDP-forming] beta-		-4.11
xyloglucan:xyloglucosyl transferase,		-4.12
metal transporter, putative (ZIP9)		-4.16
Arabidopsis thaliana Proline-rich		-4.16
DNAJ heat shock N-terminal domain-		-4.26
ovate family protein 59% similar to	OFP1	-4.37
Arabidopsis thaliana bifunctional		-4.39

WRKY family transcription factor DNA-	WRKY70	-4.43
PBS3 (AVRPPHB SUSCEPTIBLE 3);	PBS3	-4.43
expressed protein [At5g49100.1]		-4.46
expressed protein [At1g72240.1]		-4.46
multi-copper oxidase type I family	sks2	-4.50
AGP13 (ARABINOGALACTAN PROTEIN	AGP13	-4.53
Arabidopsis thaliana PAK-box/P21-Rho-		-4.62
expressed protein [At5g59510.1]; DEVIL	DVL18; RTFL5	-4.62
transferase family protein similar to		-4.64
GDSL-motif lipase/hydrolase family		-4.67
trehalose-6-phosphate phosphatase,	TPPF	-4.68
expressed protein [At4g14450.1]		-4.72
Arabidopsis thaliana uncharacterized		-4.75
amino acid permease, putative similar to	LAX3	-4.80
glycosyl hydrolase family 17 protein		-4.82
4CL1 (4-COUMARATE:COA LIGASE 1); 4-	4CL1	-4.85
root cap 1 (RCP1) identical to	RCP1	-5.03
AtNUDT7 (ARABIDOPSIS THALIANA	NUDT7	-5.04
expressed protein [At3g60650.1]		-5.10
Arabidopsis thaliana transcription factor		-5.12
Arabidopsis thaliana plastocyanin-like		-5.16
cytochrome P450, putative	CYP96A1	-5.18
F-box family protein contains		-5.22
protein phosphatase 2C family protein /		-5.30
expressed protein [At5g65300.1]		-5.37
Arabidopsis thaliana uncharacterized		-5.43
expansin, putative (EXP12) similar to	ATEXPA12;	-5.45
expressed protein [At5g66985.1]		-5.56
UDP-glucoronosyl/UDP-glucosyl	UDP-GLUCOSYL	-5.74
DC1 domain-containing protein contains		-5.75
expressed protein contains Pfam profile		-5.87
cytochrome P450, putative	PHYB	-5.89
receptor-like protein kinase-related		-5.89
expansin family protein (EXPL2) contains	1-AMINO-	-5.93
expressed protein [At1g29270.1]		-5.97
remorin family protein contains Pfam		-5.99
AP2 domain-containing transcription	PUCHI	-6.06
extracellular dermal glycoprotein-related		-6.31
auxin-responsive GH3 family protein	GH3.1	-6.33
xyloglucan:xyloglucosyl transferase,	XTR8	-6.37
BLH6 (BELL1-LIKE HOMEODOMAIN 5);	BLH6	-6.47
expressed protein contains Pfam profile		-6.58
glycosyl transferase family 2 protein	CSLA14	-6.61
Arabidopsis thaliana uncharacterized		-6.79
adenylate isopentenyltransferase 3 /	IPT3	-6.97

annexin 3 (ANN3) nearly identical to	ANN3	**-7.01**
protease inhibitor/seed storage/lipid		**-7.06**
AP2 domain-containing transcription	ATERF53;ERF	**-7.12**
cytochrome P450, putative similar to	CYP90D1	**-7.16**
glycosyl hydrolase family 9 protein	GH9B8	**-7.30**
RNA cyclase family protein contains		**-7.37**
short-chain dehydrogenase/reductase	AtHSD4	**-7.57**
short-chain dehydrogenase/reductase		**-7.82**
expressed protein ; expression		**-7.88**
U-box domain-containing protein similar	PUB29	**-8.46**
ankyrin repeat family protein contains		**-8.50**
meprin and TRAF homology domain-		**-8.72**
zinc finger (C3HC4-type RING finger)		**-8.84**
inositol-3-phosphate synthase isozyme 1	MIPS1	**-9.05**
PHI-1 (PHOSPHATE-INDUCED 1)	PHI-1	**-9.35**
TCH3 (TOUCH 3)	TCH3	**-9.53**
peroxidase, putative similar to		**-9.86**
cytochrome P450, putative similar to	BR6OX1	**-9.92**
auxin-responsive family protein similar		**-9.92**
U-box domain-containing protein low		**-10.34**
CBL-interacting protein kinase 13	CIPK13;	**-10.77**
leucine-rich repeat family protein	RLP29	**-10.85**
expressed protein [At5g22580.1]		**-12.29**
universal stress protein (USP) family		**-12.54**
UGT73B4; UDP-glycosyltransferase/	UGT73B4	**-12.69**
expressed protein [At5g15120.1]		**-12.78**
expressed protein similar to myo-inositol	CIL	**-13.25**
arabinogalactan-protein, putative	AGP22	**-17.04**
pyruvate decarboxylase, putative strong	ATZIP9; ZIP9	**-17.36**
xyloglucan:xyloglucosyl transferase /	XTH22; TCH4	**-18.85**
proline oxidase, putative / osmotic stress-		**-20.08**
strictosidine synthase family protein		**-26.37**
expressed protein similar to unknown		**-26.55**
pentacyclic triterpene synthase, putative	THAS1	**-36.83**
expressed protein wound-inducible		**-48.95**
similar to unknown protein [Arabidopsis		**-50.13**

color key	
downregulated	unchanged
lown-regulation increased	
own-regulation decreased	
p/down-regulation lost	

Genes involved in BR-response

Gene_ID	Representative Public ID	0% Glc + 100 nM BR vs 0% Glc	3% Glc vs 0% Glc	3% Glc + 100 nM BR vs 0% Glc
A_84_P15205|838	AT1G16390	1.37	-13.36	-12.57
A_84_P19941,A_8	AT1G17060	1.24	2.37	1.63
A_84_P21523|838	AT1G18400	1.43	-2.51	-6.98
A_84_P12404|842	AT1G55610	-1.32	1.90	1.50
A_84_P786180,A_	AT1G75750	-1.03	-2.58	-7.41
A_84_P23744,A_8	AT1G78300	1.22	-2.15	-1.40
A_84_P20128,A_8	AT2G03760	-1.02	2.36	-15.34
A_84_P14435|817	AT2G26710	2.22	-3.39	-3.67
A_84_P12582,A_8	AT2G30980	1.25	1.03	1.73
A_84_P10829|820	AT3G13730	-6.01	2.47	1.15
A_84_P826388,A_	AT3G30180	-4.26	-2.54	-1.95
A_84_P869611,A_	AT3G50660	-8.48	-1.18	-7.55
A_84_P268280|82	AT3G50750	-1.34	-3.70	-12.63
A_84_P18482|825	AT3G61460	-1.96	-1.25	-5.09
A_84_P15668|828	AT4G03080	1.18	-1.69	-2.02
A_84_P208608|82	AT4G18890	1.18	3.57	2.46
A_84_P11031|829	AT4G30610	1.07	1.37	2.51
A_84_P123562,A_	AT4G36540	-1.02	-3.80	-3.00
A_84_P162603|82	AT4G36780	-2.38	-1.30	-18.27
A_84_P11316|830	AT5G04240	1.11	-1.90	-18.45
A_84_P813697,A_	AT5G05690	-1.74	-2.40	-11.17
A_84_P795619,A_	AT5G08130	-1.41	1.77	2.20
A_84_P20630|833	AT5G38970	-14.60	-1.44	-4.69
A_84_P17859|835	AT5G57560	3.36	-12.77	-15.49
A_84_P19773|836	AT5G62380	1.05	8.49	5.87
A_84_P811115,A_	AT5G65430	1.10	-1.95	-1.42

Gene Title	Gene Symbol
carbohydrate transmembrane transporter/ sugar:hydrogen ion	ATOCT3
cytochrome P450, family 72, subfamily C, polypeptide 1; oxygen	CYP72C1
BR ENHANCED EXPRESSION 1; transcription factor	BEE1
BRI 1 LIKE; kinase	BRL1
GAST1 PROTEIN HOMOLOG 1	GASA1
GENERAL REGULATORY FACTOR 2; protein phosphorylated amino	GRF2
sulfotransferase	SOT12
PHYB ACTIVATION TAGGED SUPPRESSOR 1; oxygen binding /	BAS1
shaggy-related protein kinase delta / ASK-delta / ASK-dzeta (ASK4)	SKdZeta
CYTOCHROME P450, FAMILY 90, SUBFAMILY D, POLYPEPTIDE 1;	CYP90D1
BRASSINOSTEROID-6-OXIDASE 2; monooxygenase/ oxygen	BR6OX2
DWARF 4	DWF4
brassinosteroid signalling positive regulator-related	
BRASSINOSTEROID-RESPONSIVE RING-H2; protein binding / zinc	BRH1
kelch repeat-containing serine/threonine phosphoesterase family	
brassinosteroid signalling positive regulator-related	BEH3
BRI1 SUPPRESSOR 1	BRS1
BR ENHANCED EXPRESSION 2; DNA binding / transcription factor	BEE2
brassinosteroid signalling positive regulator-related	
EARLY FLOWERING 6; transcription factor	ELF6
CPD (CABBAGE 3); oxygen binding	CPD
BES1-interacting Myc-like protein 1; DNA binding / transcription	BIM1
BRASSINOSTEROID-6-OXIDASE; oxygen binding	BR6OX1
xyloglucan:xyloglucosyl transferase	TCH4
VASCULAR-RELATED NAC-DOMAIN 6; transcription factor	VND6
GENERAL REGULATORY FACTOR 8; protein phosphorylated amino	GRF8

upregulated

color key	
downregulated	unchanged

BR-Glc regulated genes involved in various phytohormone respon

Hormone category	*AGI*	*0% Glc+100 nM BR vs 0% Glc*	*3% Glc vs 0% Glc*	*3% Glc+100 nM BR vs 0% Glc*
Auxin	AT1G53700	2.39	3.58	14.54
	AT2G04550	-7.04	-18.33	-9.28
	AT2G14960	8.03	-1.06	1.7
	AT2G28085	3.22	-1.75	1.37
	AT2G37030	-4.6	-5.16	5.32
	AT3G15540	2.75	-1.22	2.26
	AT4G14560	-2.67	-3.41	-16.52
	AT4G36110	3.89	-3.21	2.18
	AT5G13320	6.22	-1.18	1.79
	AT5G18560	-9.13	1.07	-3.07
	AT5G57560	3.36	-12.77	-15.49
Cytokinin	AT1G75450	-2.79	-3.05	-3.22
	AT3G63110	-2.27	5.7	4.69
	AT5G65800	4.67	1.29	7.77
	AT2G15120	2.85	6.2	6.94
ABA	AT4G11890	2.23	-1.07	2.47
	AT5G01540	3.3	5.35	13.06
	AT5G01550	3.22	6.5	20.39
	AT5G13320	6.22	-1.18	1.79
Ethylene	AT5G18560	-9.13	1.07	-3.07
	AT1G01480	-2.83	1.67	-1.04
	AT2G44840	7.3	1.99	3.98
	AT4G05100	-2.06	2.07	-2.37
	AT4G37770	3.46	-1.06	4.19
	AT5G25190	2.87	3.07	19.1
	AT5G51190	2.21	-1.54	1.03
	AT5G65800	4.67	1.29	7.77
JA	AT4G05100	-2.06	2.07	-2.37
	AT5G13220	2.07	-2.59	-1.16
	AT3G56400	2.48	-3.09	-1.95

ses.

Gene Title	*Gene Symbol*
protein kinase	WAG1
dual specificity protein phosphatase family protein	IBR5
auxin-responsive GH3 family protein	GH3.1
auxin-responsive family protein	
auxin-responsive family protein	
auxin-responsive protein	IAA19
auxin-responsive protein	IAA1
SAUR-like auxin-responsive protein	
auxin-responsive GH3 family protein	PBS3
AP2 domain-containing transcription factor, putative	PUCHI
xyloglucan:xyloglucosyl transferase	TCH4
cytokinin oxidase family protein	CKX5
adenylate isopentenyltransferase 3	ATIPT3
1-aminocyclopropane-1-carboxylate synthase	ACS5
secretory protein	
protein kinase family protein	
lectin protein kinase	
lectin protein kinase	
auxin-responsive GH3 family protein	PBS3
AP2 domain-containing transcription factor	PUCHI
1-aminocyclopropane-1-carboxylate synthase 2	ACS2
ethylene-responsive element-binding protein	ATERF13
myb family transcription factor	AtMYB74
1-aminocyclopropane-1-carboxylate synthase	ACS8
ethylene-responsive element-binding protein	
AP2 domain-containing transcription factor	ERF105
1-aminocyclopropane-1-carboxylate synthase	ACS5
myb family transcription factor	AtMYB74
JASMONATE-ZIM-DOMAIN PROTEIN 10	JAZ10
WRKY family transcription factor	WRKY70

BR-regulated genes involved in stress responses.

Gene_ID	Representative Public ID	0% Glc + 100 nM BR vs 0% Glc	3% Glc vs 0% Glc	3% Glc + 100 nM BR vs 0% Glc
A_84_P251265,A_84	AT1G63720	-4.14	1.26	-1.79
A_84_P21159|81955	AT3G04010	-3.75	1.90	1.07
A_84_P22215|82412	AT3G49630	-3.12	-1.35	-1.54
A_84_P816739,A_84	AT1G44970	-2.67	-1.28	1.29
A_84_P511454|8343	AT5G43570	-2.67	-15.35	-24.80
A_84_P18845|84121	AT1G48000	-2.37	1.88	1.37
A_84_P20724,A_84_	AT5G63790	-2.31	4.19	1.48
A_84_P262520|8356	AT5G55620	-2.31	10.48	24.24
A_84_P19256|82007	AT3G09220	-2.29	-9.86	-20.91
A_84_P12484|84218	AT1G58170	-2.22	10.87	1.37
A_84_P16321|81656	AT2G20420	-2.17	1.49	1.95
A_84_P22388|82944	AT4G33070	-2.16	17.22	15.20
A_84_P10949|82585	AT4G05100	-2.06	2.07	-2.37
A_84_P15423|81689	AT2G23620	-2.05	-9.34	-24.54
A_84_P824506,A_84	AT1G51680	-2.05	1.88	2.80
A_84_P16948|83670	AT5G65730	-2.02	-110.66	-36.27
A_84_P16807|83164	AT5G17760	-2.01	4.79	1.80
A_84_P302000|8354	AT5G53250	2.01	-14.19	-15.03
A_84_P853187,A_84	AT4G34150	2.03	1.93	4.42
A_84_P12725|82248	AT3G28510	2.04	19.37	21.18
A_84_P16848,A_84_	AT5G39580	2.05	-2.19	-1.39
A_84_P14776|82841	AT4G23180	2.07	2.21	4.29
A_84_P524680,A_84	AT5G13220	2.07	-2.59	-1.16
A_84_P807670	AT3G53990	2.07	1.28	-10.47
A_84_P13482|81845	AT2G38760	2.08	3.63	-4.93
A_84_P528136,A_84	AT4G23190	2.09	3.83	3.61
A_84_P16226|83801	AT1G14540	2.14	3.86	5.06
A_84_P17749|83136	AT5G15120	2.15	1.01	-10.63
A_84_P233559|8375	AT1G10340	2.17	-9.80	-6.34
A_84_P12547|81762	AT2G30750	2.19	32.94	11.97
A_84_P12960|82711	AT4G14630	2.20	-3.61	-1.86
A_84_P22181|82244	AT3G28210	2.21	23.22	25.81
A_84_P296724,A_84	AT5G51190	2.21	-1.54	1.03
A_84_P19534|82905	AT4G29340	2.22	4.04	3.89
A_84_P827321,A_84	AT4G11890	2.23	-1.07	2.47
A_84_P18119|84274	AT1G64400	2.23	1.00	1.80
A_84_P22847|83801	AT1G14550	2.24	12.93	6.45
A_84_P13130|83582	AT5G57220	2.25	12.62	5.10
A_84_P74914|81825	AT2G36840	2.26	2.23	3.36
A_84_P15464|82119	AT3G03670	2.32	-27.10	-7.54
A_84_P19706|83453	AT5G45000	2.32	1.55	2.39
A_84_P23919|81817	AT2G35980	2.40	17.21	10.99
A_84_P16571|82480	AT3G56400	2.48	-3.09	-1.95

A_84_P15741|82883	AT4G27280	2.49	-1.31	2.07
A_84_P801239,A_84	AT1G02920	2.53	4.53	5.73
A_84_P90109|81974	AT3G05800	2.53	1.49	4.42
A_84_P17597|82762	AT4G18880	2.62	7.74	11.60
A_84_P15946|83521	AT5G51440	2.64	37.76	3.92
A_84_P12956|83014	AT4G39830	2.66	-1.29	3.15
A_84_P22053,A_84_	AT2G41100	2.68	-4.04	-6.85
A_84_P20237|83918	AT1G26420	2.74	10.06	10.35
A_84_P157715|8436	AT1G72930	2.74	20.54	26.13
A_84_P812454,A_84	AT1G02930	2.80	4.12	4.90
A_84_P61660|81601	AT2G15220	2.85	6.20	6.94
A_84_P813874,A_84	AT4G12720	2.87	1.33	-2.17
A_84_P20998,A_84_	AT1G35140	2.92	-20.48	-6.43
A_84_P825802,A_84	AT5G25250	2.93	2.20	3.20
A_84_P556555|8318	AT5G02490	3.10	5.86	9.32
A_84_P19294,A_84_	AT1G26380	3.10	41.95	40.12
A_84_P16369|81687	AT2G23380	3.14	4.26	8.05
A_84_P13393|84292	AT1G66090	3.16	9.50	10.06
A_84_P23380|83172	AT5G01540	3.30	5.35	13.06
A_84_P17859|83586	AT5G57560	3.36	-12.77	-15.49
A_84_P11613|81805	AT2G34930	3.37	1.85	10.71
A_84_P11694,A_84_	AT3G01830	3.38	6.39	9.64
A_84_P17815|83455	AT5G45200	3.38	2.48	6.84
A_84_P79989|82907	AT4G29520	3.43	7.41	15.46
A_84_P19231|81715	AT2G26150	3.66	75.17	91.66
A_84_P13475|81565	AT2G11810	3.74	2.05	2.00
A_84_P13077,A_84_	AT5G42380	3.98	10.22	15.09
A_84_P10559|83952	AT1G01560	4.05	8.02	5.59
A_84_P786490,A_84	AT2G46400	4.23	2.63	5.39
A_84_P10627|81662	AT2G20880	5.02	-3.87	-2.10
A_84_P18737|83386	AT5G38710	5.65	-10.48	-14.44
A_84_P23478,A_84_	AT5G41750	5.86	7.00	9.52
A_84_P17343|81909	AT2G44840	7.30	1.99	3.98
A_84_P16097|83902	AT1G24140	10.84	13.42	24.87

GeneName	GeneSymbol
hypothetical protein	
glycosyl hydrolase family 17	
2-oxoacid-dependent oxidase,	
peroxidase 9	
serine protease inhibitor, potato	
myb family transcription factor	
NAC domain-containing protein	NAC102
expressed protein similar to	
laccase family protein / diphenol	
disease resistance-responsive	
succinyl-CoA ligase [GDP-	
pyruvate decarboxylase, putative	
myb family transcription factor	
esterase, putative similar to	
4-coumarate--CoA ligase 1	4CL1
xyloglucan:xyloglucosyl	
AAA-type ATPase family protein	
arabinogalactan-protein, putative	
calcium-dependent lipid-binding	
AAA-type ATPase family protein	
peroxidase 62	
receptor-like protein kinase 4,	
protein TIFY 9	JAZ10
universal stress protein (USP)	
annexin 3 (ANN3) nearly identical	
cysteine-rich receptor-like	CRK11
anionic peroxidase, putative	
expressed protein [At5g15120.1]	
ankyrin repeat family protein	
cytochrome P450 71A12,	
germin-like protein (GLP9)	
zinc finger (AN1-like) family	
ethylene-responsive transcription	
profilin 3 (PRO3) (PFN3) identical	
ABA- AND OSMOTIC-STRESS-	ARCK1
long-chain-fatty-acid--CoA ligase,	
anionic peroxidase, putative	
cytochrome P450, putative	
ACT domain-containing protein	
peroxidase, putative similar to	
Toll-Interleukin-Resistance (TIR)	
harpin-induced family protein	
WRKY family transcription factor	

color key	
upregulated	**downregulated**

calcium-binding EF hand family	
glutathione S-transferase 11	GSTF7
expressed protein [At3g05800.1]	
heat shock transcription factor 21	
23.5 kDa mitochondrial small	
L-ascorbate oxidase, putative	
calmodulin-like protein 12	TCH3
FAD-binding domain-containing	
Toll-Interleukin-Resistance (TIR)	
glutathione S-transferase 1	GSTF6
secretory protein, putative	
nudix hydrolase 7	NUDT7
Phosphate-responsive 1-like	PHI-1
Flotillin-like protein 1	
heat shock cognate 70 kDa	
FAD-binding and BBE domain-	
curly leaf protein (CURLY LEAF) /	
disease resistance protein (TIR-	
lectin protein kinase, putative	
xyloglucan:xyloglucosyl	
disease resistance family protein	
putative calcium-binding protein	
disease resistance protein (TIR-	
expressed protein [At4g29520.1]	
heat shock transcription factor	
1,2-diacylglycerol 3-beta-	
calcium-binding protein CML37	CML37
mitogen-activated protein kinase,	
putative WRKY transcription	WRKY46
AP2 domain-containing	
proline oxidase, putative /	
TIR-NBS-LRR class disease	
ethylene-responsive element-	
matrixin family protein similar to	

unchanged

List of enriched cis-regulatory elements in promoters of BR-regulated and BR-Glc coregulated

Category	Enriched TF sites name	P-value
BR regulated genes (303)	TATA-box motif	$<10^{-10}$
	AtMYC2 BS in RD22	$<10^{-8}$
	MYCATERD1	$<10^{-8}$
	CARGCW8GAT	$<10^{-6}$
	W-box promoter motif	$<10^{-5}$
	GAREAT	$<10^{-4}$
	ARF binding site motif	$<10^{-3}$
	DREB1A/CBF3	$<10^{-3}$
	MYB4 binding site motif	$<10^{-3}$
BR up-regulated genes (190)	TATA-box motif	$<10^{-7}$
	AtMYC2 BS in RD22	$<10^{-5}$
	MYCATERD1	$<10^{-5}$
	CARGCW8GAT	$<10^{-4}$
	W-box promoter motif	$<10^{-4}$
	GAREAT	$<10^{-3}$
	MYB4 binding site motif	$<10^{-3}$
BR down-regulated genes (113)	CACGTGMOTIF	$<10^{-7}$
	ABRE-like binding site motif	$<10^{-5}$
	ABFs binding site motif	$<10^{-3}$
	ABRE binding site motif	$<10^{-3}$
	AtMYC2 BS in RD22	$<10^{-3}$
	GBOXLERBCS	$<10^{-3}$
	MYCATERD1	$<10^{-3}$
	TATA-box motif	$<10^{-3}$
BR regulated genes up- and down-regulated by Glc alone (217)	TATA-box motif	$<10^{-7}$
	GAREAT	$<10^{-5}$
	ABRE binding site motif	$<10^{-4}$
	AtMYC2 BS in RD22	$<10^{-4}$
	CARGCW8GAT	$<10^{-4}$
	MYCATERD1	$<10^{-4}$
	ABFs binding site motif	$<10^{-3}$
Genes synergistically regulated by BR and Glc alone (125)	GAREAT	$<10^{-3}$
	TATA-box motif	$<10^{-3}$
Genes antagonistically regulated by BR and Glc alone (92)	AtMYC2 BS in RD22	$<10^{-4}$
	MYCATERD1	$<10^{-4}$
	TATA-box motif	$<10^{-4}$
BR-regulation of genes affected (2 fold more/less or lost) significantly in presence of Glc (256)	AtMYC2 BS in RD22	$<10^{-7}$
	MYCATERD1	$<10^{-7}$
	TATA-box motif	$<10^{-7}$
	CARGCW8GAT	$<10^{-4}$
	ABRE-like binding site motif	$<10^{-3}$
	ARF binding site motif	$<10^{-3}$
	GAREAT	$<10^{-3}$
	W-box promoter motif	$<10^{-3}$

BR-regulation of genes affected synergistically (2 fold or more up) in presence of Glc (110)	No enriched binding factors found	
Extent of BR regulated genes affected antagonistically (2 fold or more down or lost) in presence of Glc (146)	AtMYC2 BS in RD22	$<10^{-5}$
	MYCATERD1	$<10^{-5}$
	TATA-box motif	$<10^{-5}$
	CARGCW8GAT	$<10^{-4}$

genes in dark grown Arabidopsis seedlings

List of BR-regulated genes involved in hypocotyl growth and development.

Representative Public ID	0% Glc + 100 nM BR vs. 0% Glc	3% Glc vs. 0% Glc	3% Glc + 100 nM BR vs. 0% Glc	Gene Description
AT4G14630	2.20	-3.61	-1.86	germin-like protein (GLP9)
AT4G14560	-2.67	-3.41	-16.52	auxin-responsive protein
AT2G26710	2.22	-3.39	-3.67	cytochrome P450, putative
AT3G20830	-2.36	-2.90	-4.69	cAMP-/ cGMP-dependent protein kinase C
AT5G19110	4.51	-2.77	-1.80	extracellular dermal glycoprotein-related
AT5G62340	2.62	-2.29	-1.00	invertase/pectin methylesterase inhibitor
AT2G39430	-2.23	-2.19	-14.69	disease resistance-responsive protein-
AT3G15540	2.75	-1.22	2.26	auxin-responsive protein
AT3G50660	-8.48	-1.18	-7.55	cytochrome P450 90B1
AT5G65800	4.67	1.29	7.77	ACC synthase, putative
AT4G38410	2.77	1.69	9.57	dehydrin, putative
AT4G22470	-2.70	2.14	1.09	protease inhibitor/seed storage/lipid
AT4G28650	2.91	3.03	9.11	leucine-rich repeat transmembrane protein
AT5G14750	2.93	3.09	9.02	myb family transcription factor
AT5G10970	2.53	7.76	9.74	zinc finger (C2H2 type) family protein
AT4G01630	10.87	32.65	99.38	expansin, putative

Gene Symbol
GLP9
IAA1/AXR5
PHYB
IAA19
DWF4
ETO2
ATEXLA2
ATMYB66
ATEXP17

color key		
upregulated	**downregulated**	**unchanged**