Supp. Table 2. Microarray transcript abundance profiles of selected genes from Table 1. All genes
figures in the manuscript. Each graph is headed by the closest *Arabidopsis* homologue of the *Eucal*
expression on the Y-axis.

Supp. Table 2

***Eucalyptus* EST**	**At Number[a]**	**Description**	**CAZyme Family[b] / Category[c]**
(A)			
Circadian clock- related			
eef1c.pk001.i8	At2g46830	myb-related transcription factor (CCA1) *	TF
eec1c.pk003.d5	At5g57360	Zeitlupe (ZTL)	
(B)			
Starch/sucrose metabolism			
eef1c.pk005.e20	At1g06410	putative trehalose biosynthesis enzyme	
eef1c.pk002.a17	At1g08200	UDP-D-glucuronic acid decarboxylase	
eej1c.pk004.e12	At1g14720	xyloglucan endo-transglycosylase	GH16[b]
eef1c.pk005.b4	At1g19170	Pectinase	GH28[b]
eep1c.pk005.l14	At1g60470	galactinol synthase	GT8[b]/Stress
eep1c.pk005.e16	At2g21730	mannitol dehydrogenase	
eef1c.pk002.l4	At2g28760	UDP-D-glucuronic acid decarboxylase	
eec1c.pk004.e1	At2g36460	fructose bisphosphate aldolase	
eej1c.pk001.l5	At2g36530	phosphopyruvate hydratase	
egx20f08	At2g45290	Transketolase	
eec1c.pk001.n22	At3g04120	GADPH	
eef1c.pk003.d12	At3g15020	malate dehydrogenase	
eea1c.pk005.b13	At3g18080	beta-glucosidase	GH1[b]
eea1c.pk005.p23	At3g21560	UDP-glucosyltransferase *	
egx28e09	At3g23920	β-amylase *	GH14[b]/Stress
eej1c.pk002.g13	At3g43190	sucrose synthase	GT1[b]
eef1c.pk004.d20	At3g52930	fructose bisphosphate aldolase	
eec1c.pk006.c12	At3g52990	pyruvate kinase	
eea1c.pk002.h11	At3g55700	UDP-glucosyl transferase family protein	GT1[b]
eea1c.pk006.h24	At4g02290	endo-1-4-β-glucanase	GH9[b]
eep1c.pk003.f22	At4g17770	putative trehalose biosynthetic enzyme	
egx28b09	At4g19410	Pectinacetylesterase	CE13[b]
eec1c.pk001.m22	At5g20830	sucrose synthase	GT1[b]
egx19g03	At5g49720	endo-1-4-β-glucanase	GH9[b]
eep1c.pk005.e3	At5g59290	UDP-D-glucuronic acid decarboxylase	
eef1c.pk004.h1	At5g64790	glycosyl hydrolase family 17 protein	GH17[b]
eep1c.pk004.f23	At5g66460	endo-1-4-β-glucanase	GH5[b]
egx22b01	At5g67230	glycosyl transferase family 43 protein	GT43[b]
(C)			
Lignin biosynthesis			
eej1c.pk004.j8	At1g72680	cinnamyl-alcohol dehydrogenase (CAD)	

eec1c.pk004.c1	At2g30490	cinnamate-4-hydroxylase (C4H) *	
eea1c.pk007.f7	At2g40890	coumarate-3-hydroxylase (C3H) *	
eec1c.pk003.m8	At3g19450	cinnamyl alcohol dehydrogenase (CAD) *	
eec1c.pk002.f5	At4g34050	caffeoyl-CoA 3-*O* -methyltransferase (CCoAOMT)	
eep1c.pk001.i12	At4g36220	ferulate-5-hydroxylase (F5H)	
(D)			
Water transport			
eec1c.pk002.g8	At3g16240	δ-tonoplast intrinsic protein (δ-TIP)	
eej1c.pk005.l13	At3g53420	plasma membrane intrinsic protein 2B (PIP2B) *	
(E)			
Transcription factor (TF)			
eep1c.pk001.c21	At1g66230	putative transcription factor (MYB20)	
eef1c.pk006.i22	At2g22800	homeobox-leucine zipper protein 9 (HAT9)	
egx28c07	At2g46680	*Arabidopsis thaliana* Homeobox 7 (ATHB7)	Stress
eej1c.pk005.e22	At5g04760	myb family transcription factor	
egx20a08	At5g22570	WRKY transcription factor 38	
(F)			
Hormone- related			
eej1c.pk006.p21	At1g46768	ERF/AP2 transcription factor family member	TF
eej1c.pk001.d7	At1g53910	similar to AP2 domain-containing protein	TF
egx23e06	At1g56220	dormancy/auxin associated family protein *	
eef1c.pk002.l18	At1g60750	auxin-induced aldo reductase family member	
eef1c.pk005.a16	At1g66340	ethylene receptor 1 (ETR1)	
eef1c.pk001.a9	At1g74670	gibberellin-regulated protein 4 (GASA4) *	
eea1c.pk006.o13	At2g04160	auxin-induced subtilisin-like serine protease *	
eej1c.pk007.g5	At3g02885	gibberellin-regulated protein 5 (GASA5)	
egx20b09	At3g14230	ERF/AP2 transcription factor family member	TF
egx22d11	At3g15730	ABA mediated stomatal movement regulator	
egx18a08	At4g27410	NAC TF in ABA-mediated dehydration response	TF/Stress
eef1c.pk003.c18	At5g42650	cytochrome p450 in the JA biosynthetic pathway *	
eej1c.pk003.o24	At5g56030	auxin-induced heat shock protein 90 *	Stress

(G)			
Calcium signalling- related			
eej1c.pk002.l21	At1g62820	calmodulin, contains calcium-binding domain	
eer1c.pk001.o22	At2g02010	glutamate decarboxylase (GAD1)	Stress
eea1c.pk002.d4	At4g27280	calcium-binding EF hand family protein	
(H)			
Stress response			
eea1c.pk004.k20	At1g08830	copper/zinc superoxide dismutase	
eef1c.pk005.c1	At1g20030	pathogenesis-related thaumatin family protein	
eea1c.pk004.b17	At1g46264	heat stress transcription factor family member	TF
egx06h08	At1g52560	26.5 kDa class I small heat shock protein-like	
egx20a06	At1g54050	17.4 kDa class III heat shock protein	
eec1c.pk006.m17	At1g56070	cold-induced translation elongation factor	
eej1c.pk006.l24	At1g69450	early-responsive to dehydration (ERD 15)	
egx06b05	At2g18150	peroxidase	
egx25e11	At2g41430	dehydration-induced protein (ERD 4) *	
eea1c.pk007.n4	At3g09640	L-ascorbate peroxidase 1	
eec1c.pk006.k23	At3g12580	heat shock protein 70 *	
eef1c.pk002.h5	At3g12610	DNA-damage repair/toleration protein	
egx06a11	At4g10250	22.0 kDa small heat shock protein *	
egx25g03	At5g12020	17.6 kDa class II heat shock protein	
egx18g03	At5g52640	81 kDA heat shock protein *	
eej1c.pk002.f18	At5g56000	heat shock protein 81-4 (HSP81-4)	
egx18d10	At5g58070	temperature stress-induced lipocalin *	

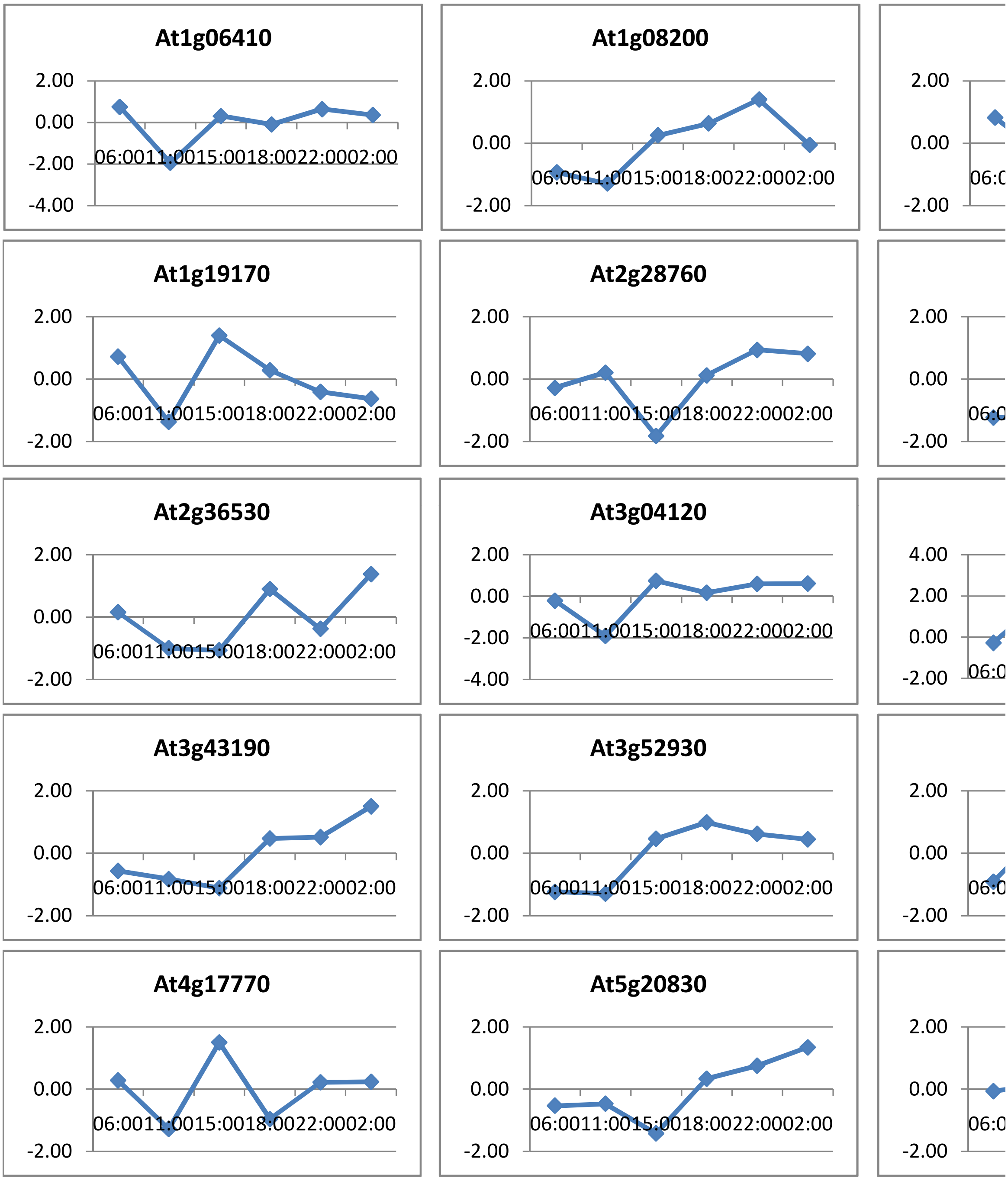
* Circadianly regulated in *Arabidopsis* (Covington and Harmer, 2007)

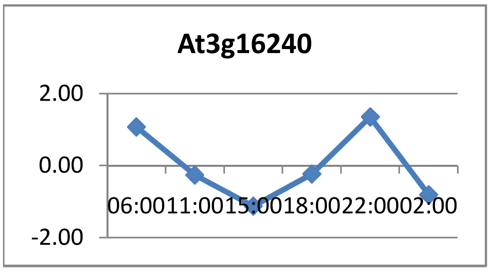
[a] At No. of *Arabidopsis* sequence with best hit to *Eucalyptus* microarray target

[b] As defined in Coutinho et al. (2003)

[c] Additional characterization for genes falling within multiple categories

mentioned in the discussion section of Solomon et al., 2009 are illustrated, excluding those with their o
yptus microarray target. Time of sampling is shown on the X-axis and standardised least square means c

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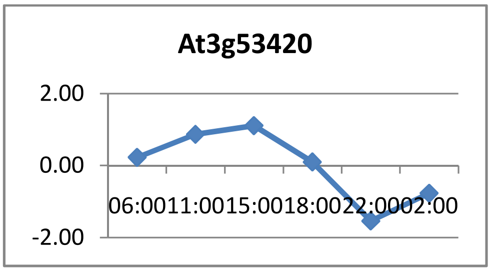
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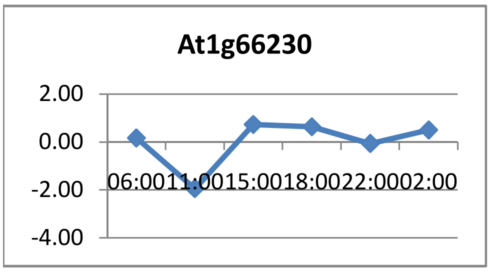
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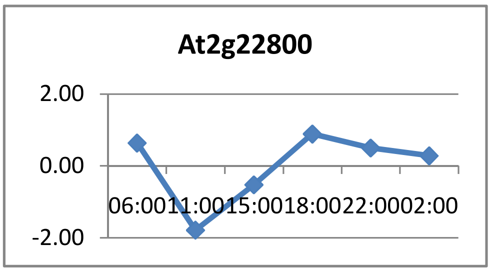
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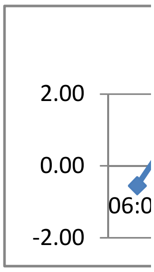
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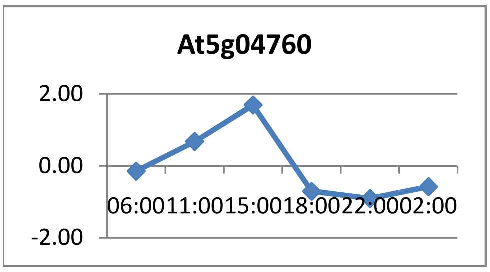
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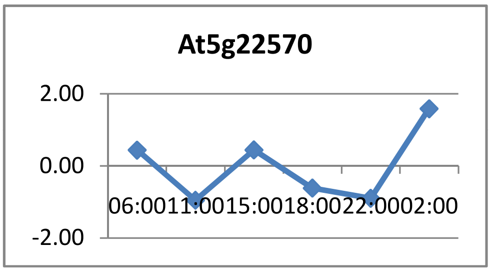
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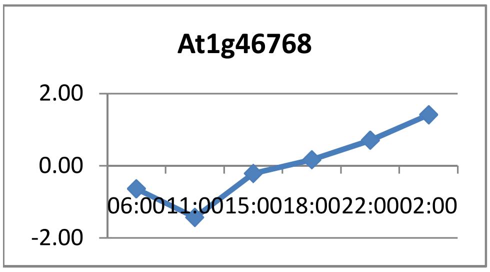
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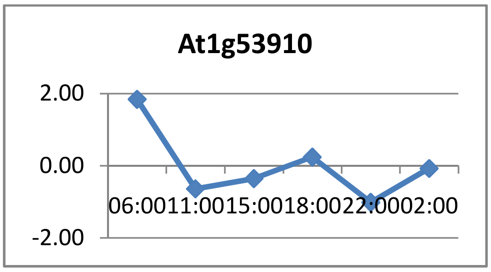
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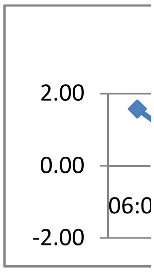
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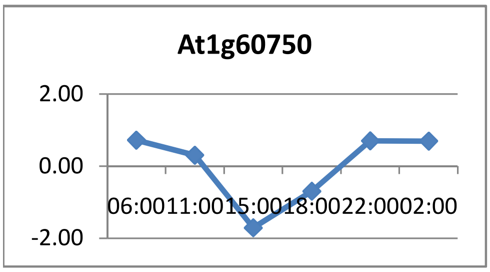
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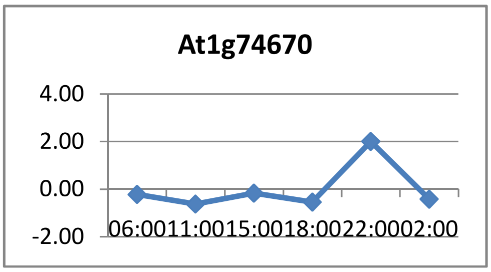
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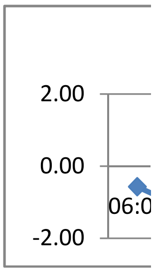
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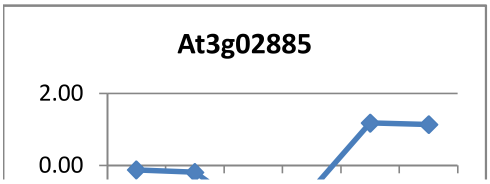
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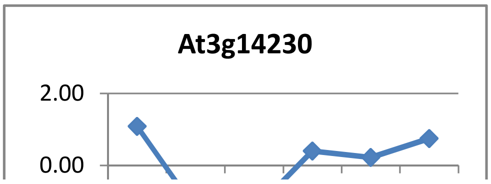
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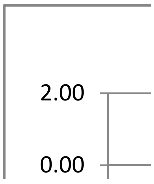
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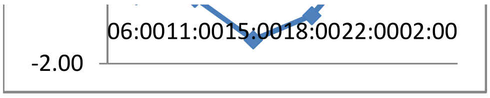

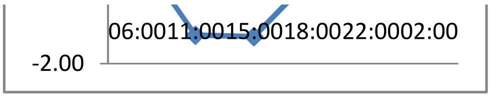

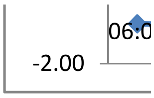

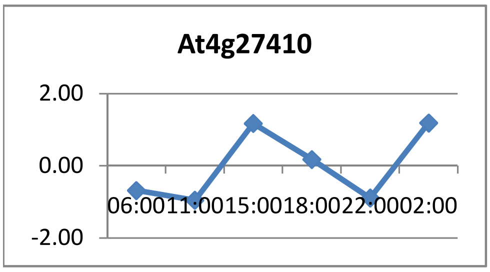
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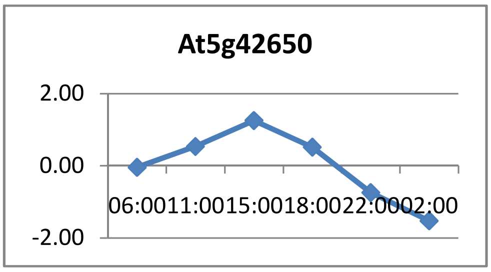
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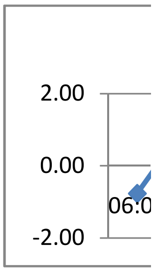

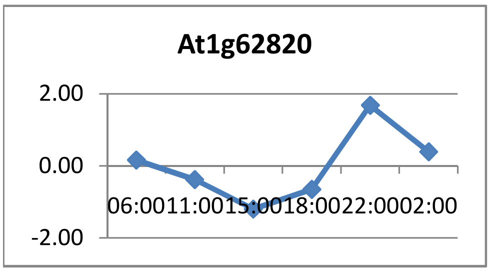
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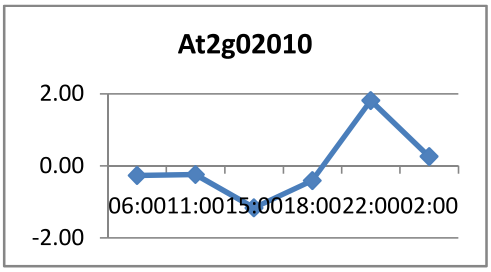
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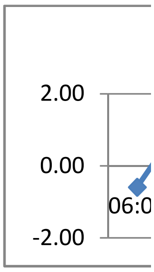

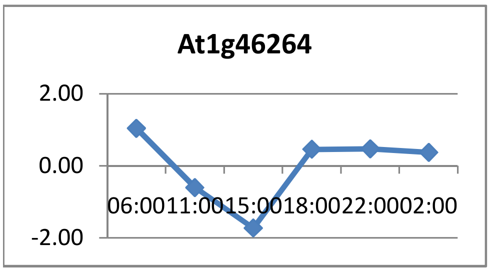
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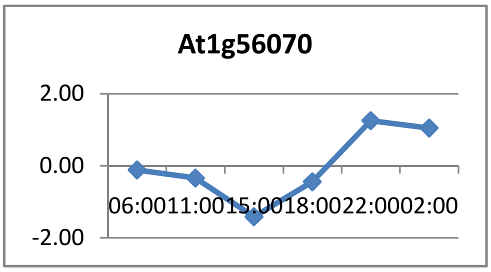
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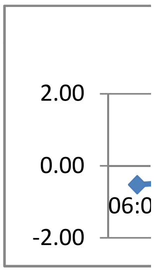

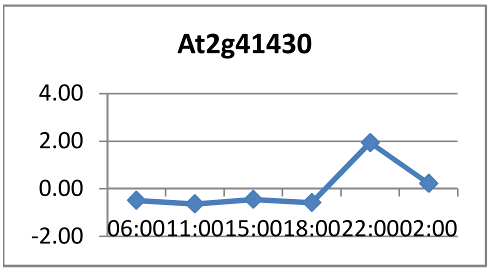
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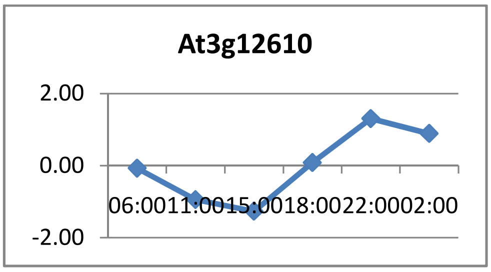
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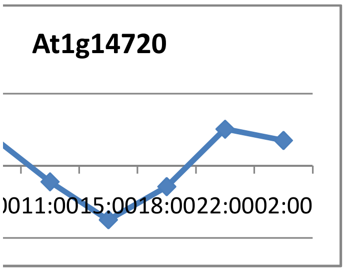

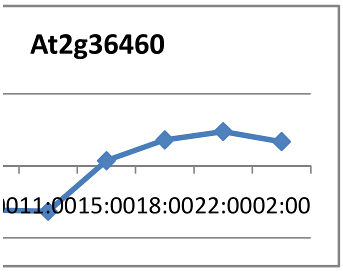

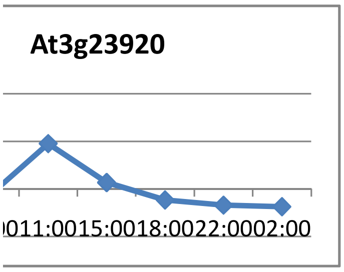

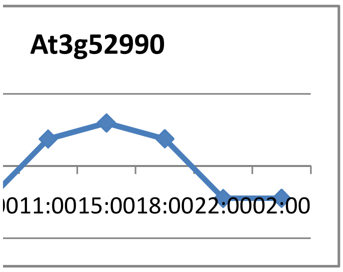

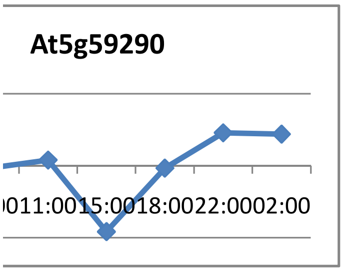

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At1g06410	Encodes a	0.75	-1.95	0.31
At1g06570	4-hydroxyp	-1.01	1.45	-0.13
At1g08200	Encodes a	-0.94	-1.30	0.25
At1g08830	Encodes a	0.83	0.88	-0.29
At1g09140	similar to p	-0.02	0.91	1.29
At1g11860	aminometh	0.49	-0.42	-0.07
At1g12820	transport ir	0.83	-1.65	-0.34
At1g12910	WD repeat	-0.02	0.92	-1.12
At1g13950	AF296082	0.11	-0.45	-1.73
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At1g14720	member of	0.82	-0.45	-1.50
At1g15740	leucine-rich	0.74	1.12	0.84
At1g18260	suppressor	1.69	0.46	-1.07
At1g19170	glycoside h	0.72	-1.37	1.40
At1g20030	pathogene	0.50	0.42	1.00
At1g20630	catalase 1,	0.24	-1.96	0.28
At1g20696	similar to h	0.10	-0.71	-1.59
At1g23820	spermidine	-0.42	-1.11	-0.07
At1g29980	expressed	0.03	1.00	1.19
At1g30230	elongation	-0.24	-0.66	-0.76
At1g43220	pseudogen	-0.60	-1.28	1.60
At1g46264	member of	1.04	-0.61	-1.73
At1g46768	encodes a	-0.63	-1.43	-0.21
At1g52020	pseudogen	0.01	1.79	-0.52
At1g52260	Encodes a	-1.40	-0.13	-0.76
At1g52560	26.5 kDa c	0.16	0.47	0.80
At1g52560	26.5 kDa c	0.30	0.22	0.78
At1g53910	similar to A	1.84	-0.64	-0.35
At1g54050	17.4 kDa c	-0.10	1.64	0.54
At1g54630	similar to a	-0.16	-1.58	0.05
At1g55310	similar to S	-0.26	-1.14	1.64
At1g56070	encodes a	-0.11	-0.34	-1.41
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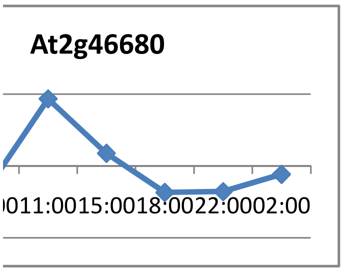
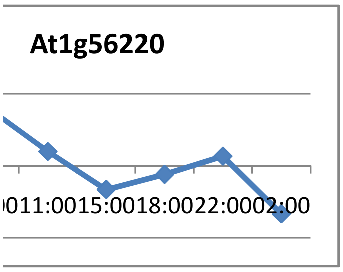
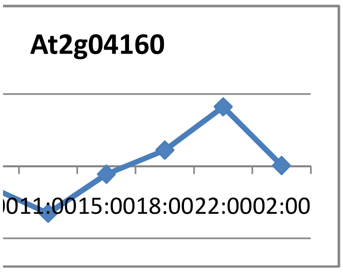
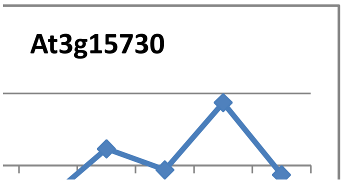
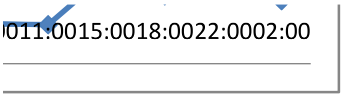


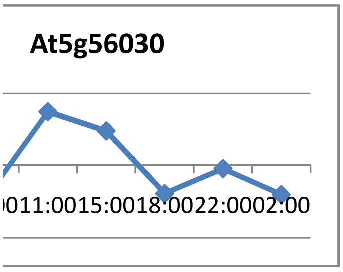


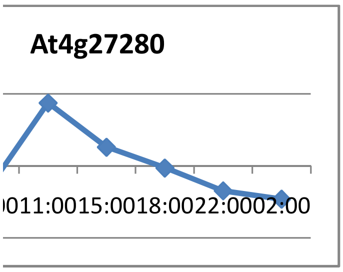


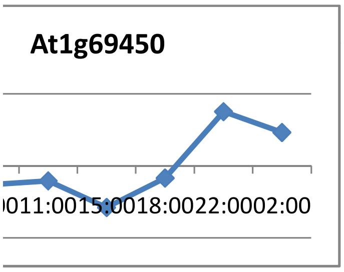


At1g56700	pyrrolidone	-0.01	-1.77	0.93
At1g60420	DC1 doma	-0.62	0.41	1.71
At1g60420	DC1 doma	-0.76	0.57	1.66
At1g60420	DC1 doma	-1.02	0.52	1.02
At1g60420	DC1 doma	-0.85	0.31	1.68
At1g60470	galactinol s	1.69	-0.92	0.31
At1g60470	galactinol s	1.78	-0.69	-0.10
At1g60750	pseudogen	0.72	0.30	-1.71
At1g61000	Nuf2 family	-0.41	-0.41	1.49
At1g61065	expressed	-0.79	-1.07	1.15
At1g61340	F-box famil	-0.43	1.86	0.36
At1g62820	calmodulin	0.16	-0.38	-1.20
At1g63770	peptidase I	-0.88	-1.42	0.96
At1g65930	isocitrate d	-0.59	-1.75	0.32
At1g66230	putative tra	0.16	-1.95	0.73
At1g66340	ethylene re	0.34	-1.88	0.52
At1g68360	zinc finger	-0.42	-0.11	-1.50
At1g69450	early-respo	-0.52	-0.41	-1.15
At1g69620	60S riboso	0.15	-0.38	-1.07
At1g72680	cinnamyl-a	0.89	-0.61	1.19
At1g72680	cinnamyl-a	1.07	-1.25	0.89
At1g74670	gibberellin-	-0.23	-0.63	-0.17
At1g77120	The protein	-0.67	-0.28	1.14
At1g78880	balbiani rin	1.14	-0.93	-1.43
At1g79590	similar to s	0.25	-0.64	-1.01
At2g02010	glutamate	-0.26	-0.24	-1.16
At2g04160	isolated fro	-0.57	-1.31	-0.22
At2g05630	in the Arab	-0.68	1.52	-0.44
At2g06490	CACTA-like	-0.67	0.34	1.55
At2g18150	peroxidase	0.18	-1.37	1.63
At2g19400	protein kina	-1.33	-0.51	1.50
At2g21660	glycine-rich	0.05	-1.31	-1.07
At2g21660	glycine-rich	-0.37	-1.53	0.20
At2g21730	mannitol de	0.54	0.56	1.47
At2g22800	homeobox-	0.64	-1.79	-0.52
At2g23220	member of	0.04	1.52	0.56
At2g26080	glycine deh	-0.57	-0.84	-0.21
At2g26510	permease	1.37	-0.46	-1.58
At2g28760	NAD-deper	-0.31	-0.42	-1.45
At2g28760	NAD-deper	-0.28	0.21	-1.82
At2g29210	splicing fac	0.24	-0.97	-1.27
At2g30490	Encodes a	-0.71	-1.02	1.35
At2g30600	similar to B	0.39	0.17	1.04
At2g33850	expressed	0.28	-0.23	-1.37
At2g33850	expressed	0.15	0.00	-1.48
At2g36460	fructose-bis	-1.23	-1.26	0.14
At2g36530	Involved in	0.16	-1.00	-1.06




At5g56030


At4g27280


At1g69450

At2g39730	ribulose bis	0.70	1.06	0.41
At2g40290	similar to e	-0.22	0.13	-0.70
At2g40890	encodes co	-0.91	-1.47	0.91
At2g41430	dehydration	-0.49	-0.64	-0.45
At2g45290	transketola	-0.06	-1.87	-0.07
At2g46680	Arabidopsi	-0.55	1.87	0.35
At2g46830	myb-relate	1.37	1.12	-0.50
At2g47060	similar to s	-0.03	-1.81	-0.23
At2g47140	short-chain	-0.18	0.45	1.18
At3g02885	gibberellin-	-0.12	-0.19	-1.34
At3g03780	Encodes a	-0.42	-1.30	-0.66
At3g04120	encodes cy	-0.21	-1.91	0.74
At3g04840	40S riboso	0.31	-0.57	-1.37
At3g06035	expressed	-0.03	-1.69	-0.33
At3g06720	importin al	0.40	-0.44	-1.21
At3g06720	importin al	0.59	-1.12	-1.01
At3g09480	histone H2	-0.40	-1.22	-0.69
At3g09640	similar to L	0.42	-0.58	-1.22
At3g10410	serine carb	1.16	-1.01	-1.23
At3g12580	heat shock	-0.80	0.92	1.55
At3g12610	Plays role i	-0.07	-0.94	-1.27
At3g13390	multi-coppe	-0.20	-0.53	-1.42
At3g14230	encodes a	1.09	-1.21	-1.25
At3g15020	malate deh	0.91	-1.90	-0.13
At3g15480	expressed	-0.52	-1.41	1.21
At3g15730	Encodes p	-0.90	-0.92	0.46
At3g16050	A37 (A37)	-0.23	1.36	1.04
At3g16240	Delta tonop	1.07	-0.26	-1.12
At3g18080	glycosyl hy	-0.70	0.39	1.53
At3g18280	protease in	0.27	0.93	-1.42
At3g19450	Encodes a	-0.09	-1.68	1.32
At3g21560	UDP-gluco	0.63	-1.07	-1.19
At3g23810	adenosylho	-0.34	-1.67	-0.19
At3g23920	beta-amyla	-0.27	1.90	0.27
At3g24170	similar to g	-0.40	-1.06	-0.43
At3g25230	Encodes a	0.82	-1.54	0.12
At3g26340	20S protea	-0.25	-1.09	0.06
At3g43190	sucrose sy	-0.56	-0.82	-1.11
At3g43810	EF hand do	-0.39	-0.22	-1.33
At3g48990	AMP-depe	0.56	1.38	-0.70
At3g51670	SEC14 cyto	-0.04	-0.08	-1.49
At3g52220	expressed	0.32	0.14	-1.91
At3g52930	fructose-bis	-1.24	-1.30	0.47
At3g52990	pyruvate ki	-0.91	0.75	1.20
At3g53020	Arabidopsi	0.56	-0.63	0.34
At3g53230	cell division	-0.11	-1.01	-0.87

At3g53420	similar to p	0.23	0.87	1.11
At3g53980	protease i	-0.46	-0.48	1.90
At3g54420	encodes a	0.06	1.59	0.31
At3g55700	UDP-gluco	0.16	0.21	1.05
At3g56050	protein kin	0.25	1.59	-0.52
At3g56800	encodes a	-0.76	-0.32	-1.06
At3g56800	encodes a	-0.48	-0.70	-0.96
At3g56800	encodes a	-0.68	-0.47	-1.06
At3g57610	adenylosu	-0.85	-1.31	1.09
At3g57680	peptidase	0.40	1.59	-0.45
At3g60540	sec61beta	-0.34	-1.78	0.65
At4g00430	plasma me	1.03	1.38	-0.84
At4g00430	plasma me	1.20	-0.73	-1.16
At4g00680	actin-depol	0.40	1.51	0.02
At4g02290	glycosyl hy	-0.11	1.53	-1.41
At4g04350	leucyl-tRN	0.85	0.44	0.69
At4g05530	short-chair	0.51	0.18	-1.94
At4g10250	22.0 kDa E	-0.20	-0.06	1.33
At4g10250	22.0 kDa E	-0.50	0.21	1.25
At4g12340	expressed	-0.57	-0.19	1.76
At4g13930	glycine hyd	-0.23	-1.23	-0.74
At4g15120	VQ motif-c	0.40	-0.43	-0.85
At4g17770	Encodes a	0.28	-1.28	1.50
At4g18640	Required f	0.05	-1.34	1.30
At4g18810	expressed	-0.31	0.03	1.10
At4g19410	pectinacety	-0.14	-0.87	-0.70
At4g22180	F-box fami	-0.53	-1.77	0.68
At4g24160	hydrolase,	-0.36	-1.69	-0.29
At4g25200	AtHSP23.6	-0.83	0.78	1.41
At4g27130	eukaryotic	0.73	-1.26	0.99
At4g27280	calcium-bir	-0.59	1.74	0.52
At4g27410	Encodes a	-0.69	-0.96	1.17
At4g27960	ubiquitin-c	0.72	-1.87	-0.04
At4g28390	Encodes a	1.69	-0.71	-1.14
At4g29160	SNF7 fami	0.18	-0.63	-1.49
At4g29350	Encodes p	-0.03	-0.53	-1.26
At4g29410	60S riboso	-0.01	-0.53	-1.16
At4g32685	expressed	0.72	-0.22	-1.25
At4g34050	caffeoyl-C	-0.43	-1.56	-0.20
At4g35090	similar to c	-0.57	-1.29	-0.21
At4g35090	similar to c	-0.35	-1.45	-0.44
At4g36220	encodes fe	-0.45	-0.43	1.86
At4g36750	quinone re	0.25	1.37	0.20
At4g39230	encodes a	-0.28	0.60	1.49
At5g04760	myb family	-0.15	0.67	1.69
At5g06600	ubiquitin-s	-0.93	-1.42	0.79
At5g09810	Member of	0.40	0.98	0.45

At5g12020	17.6 kDa	0.18	0.10	1.07
At5g13710	SMT1 cont	-0.37	-0.21	-1.55
At5g14670	A member	0.36	-0.83	-1.56
At5g15950	similar to a	1.75	0.07	-0.93
At5g17920	Encodes a	0.32	-0.40	-1.40
At5g17920	Encodes a	-0.66	-1.24	-0.46
At5g17920	Encodes a	-0.03	-1.18	-0.76
At5g18170	encodes th	0.54	0.14	0.85
At5g20830	similar to s	-0.53	-0.47	-1.42
At5g20830	similar to s	-0.61	-0.47	-1.32
At5g22300	nitrilase 4	0.51	1.50	-0.64
At5g22570	member of	0.44	-0.95	0.44
At5g23250	succinyl-C	-0.52	-1.63	-0.21
At5g23750	remorin fa	0.54	0.89	-1.73
At5g25880	The malic	0.06	0.48	-1.36
At5g42050	expressed	-0.96	0.13	1.69
At5g42650	Encodes a	-0.04	0.53	1.26
At5g42650	Encodes a	1.20	0.22	0.43
At5g45430	protein kin	1.47	0.14	-1.22
At5g49720	Encodes a	-0.50	-1.58	1.19
At5g51550	phosphate-	0.58	-0.32	-1.87
At5g52640	Arabidopsi	-0.52	0.25	1.76
At5g52640	Arabidopsi	-0.55	-0.57	-0.73
At5g54770	thiazole bi	-0.22	-1.26	0.54
At5g54960	pyruvate d	-0.95	0.32	1.39
At5g56000	heat shock	-0.97	1.37	0.68
At5g56030	a member	-0.77	1.49	0.95
At5g57360	F-box fami	0.28	0.74	1.17
At5g58070	lipocalin, p	-0.11	0.71	-1.71
At5g59290	Encodes a	-0.06	0.16	-1.83
At5g59890	actin-depol	-0.27	-0.85	-1.17
At5g60390	similar to e	-0.77	0.33	1.66
At5g60390	similar to e	-0.39	-0.11	-0.86
At5g62890	similar to x	-0.16	-1.47	-0.75
At5g64790	glycosyl hy	0.21	1.16	0.83
At5g66460	(1-4)-beta-	-0.47	-0.03	-0.19
At5g66920	multi-copp	-0.20	-0.05	-1.39
At5g67230	glycosyl tr	-0.75	-0.76	1.92
NA	No BlastX	-0.52	0.88	-1.22
NA	No BlastX	0.42	-0.26	-1.87

18:00	22:00	02:00
0.38	-1.79	-0.15
-0.03	-1.37	-1.03
0.11	1.89	-1.02
-0.10	0.64	0.36
0.42	0.47	-1.20
0.63	1.40	-0.05
-0.31	-1.73	0.62
-0.01	-1.36	-0.81
-0.25	-1.38	1.62
-0.42	0.61	0.96
-0.34	1.42	-0.86
0.22	0.89	0.96
-0.44	0.42	1.82
-0.58	1.02	0.70
-0.92	-1.05	-0.74
-0.75	-0.44	0.12
0.29	-0.41	-0.63
-0.39	-1.83	0.30
0.37	0.14	0.93
0.70	0.35	1.16
-0.46	1.82	0.25
0.04	-0.99	-1.27
-0.83	0.96	1.53
-0.37	0.09	0.56
0.46	0.47	0.37
0.16	0.70	1.41
0.37	-0.78	-0.88
0.20	0.71	1.39
0.89	-0.60	-1.72
1.03	-0.67	-1.66
0.24	-1.01	-0.08
-0.07	-0.97	-1.04
-0.33	0.61	1.41
0.71	-0.48	-0.47
-0.44	1.25	1.05
-0.63	1.67	0.72
-0.24	0.27	-1.34

-0.32	0.25	0.92
0.19	-0.63	-1.05
0.07	-0.49	-1.05
0.65	0.29	-1.47
0.27	-0.31	-1.10
0.30	-0.39	-0.99
0.41	-0.41	-1.00
-0.70	0.70	0.69
1.01	-0.76	-0.91
0.03	-0.57	1.26
-0.42	-0.91	-0.47
-0.65	1.68	0.39
0.82	0.74	-0.22
0.44	0.66	0.92
0.63	-0.07	0.50
-0.37	0.72	0.66
-0.21	1.15	1.10
-0.34	1.50	0.93
-0.96	1.46	0.80
-0.10	-1.54	0.16
0.47	-1.14	-0.04
-0.55	2.01	-0.42
1.08	0.14	-1.41
-0.03	0.73	0.52
0.38	1.70	-0.69
-0.41	1.81	0.26
0.44	1.64	0.02
0.66	0.18	-1.24
0.55	-0.63	-1.15
-0.51	-0.26	0.33
0.73	0.06	-0.45
0.36	1.18	0.79
-0.35	1.39	0.66
-0.71	-0.97	-0.89
0.89	0.50	0.28
-0.18	-1.45	-0.50
0.39	1.84	-0.61
0.04	-0.01	0.64
-0.01	0.74	1.44
0.12	0.94	0.82
-0.18	1.04	1.14
1.15	-0.31	-0.47
-0.17	-1.87	0.44
-0.60	1.59	0.33
-0.43	1.61	0.15
0.72	0.95	0.67
0.90	-0.37	1.38

0.19	-1.62	-0.74
1.36	0.82	-1.39
0.94	0.00	0.55
-0.58	1.94	0.22
0.61	0.40	0.99
-0.73	-0.71	-0.23
-0.66	-1.04	-0.29
0.80	0.31	0.96
0.85	-1.15	-1.15
-0.67	1.18	1.14
0.19	0.73	1.46
0.17	0.59	0.61
-0.47	1.42	0.67
0.05	0.86	1.14
-0.79	1.52	0.52
0.33	1.48	-0.28
-0.02	0.90	1.43
-0.08	1.71	-0.25
0.66	-0.35	0.77
-0.19	-0.72	-0.75
0.08	1.31	0.89
-0.14	1.02	1.27
0.40	0.22	0.75
0.23	0.22	0.67
0.01	-0.36	1.07
-0.12	1.74	-0.26
-0.28	-1.22	-0.67
-0.23	1.35	-0.81
0.59	-0.82	-1.00
-1.07	0.82	0.46
0.12	-0.26	0.60
-0.27	1.25	0.65
0.84	0.22	1.15
-0.46	-0.68	-0.75
-0.40	1.76	0.53
-0.71	1.18	0.14
-0.93	0.65	1.56
0.48	0.52	1.51
-0.42	0.97	1.38
0.36	-1.46	-0.14
-0.41	1.55	0.47
0.00	0.45	1.01
0.99	0.62	0.45
0.76	-0.90	-0.89
0.94	0.52	-1.74
-0.03	1.77	0.25

0.10	-1.54	-0.77
-0.09	-0.96	0.09
0.16	-0.86	-1.26
-0.57	-1.68	0.82
-0.55	0.50	-1.26
-0.26	1.57	0.82
-0.36	1.49	1.01
-0.12	1.64	0.69
0.67	-0.44	0.85
-0.64	-1.26	0.35
0.17	0.18	1.11
-0.61	-0.97	0.01
-0.62	1.13	0.17
0.11	-1.51	-0.54
-0.66	0.25	0.41
-0.36	-1.85	0.23
-0.05	0.88	0.42
1.01	-0.92	-1.16
1.05	-0.97	-1.05
0.56	-0.88	-0.68
1.18	-0.18	1.20
-0.28	1.84	-0.68
-0.96	0.22	0.23
-0.44	-0.57	1.00
1.25	-1.12	-0.94
-0.71	1.57	0.86
0.87	0.60	0.15
1.03	0.75	0.56
0.40	-0.97	-0.79
-0.96	0.90	-0.40
-0.06	-0.69	-0.92
0.18	-0.89	1.19
-0.12	0.42	0.89
-0.41	0.41	0.16
-0.04	0.57	1.42
-0.05	1.76	0.11
-0.51	1.67	0.55
-1.07	1.06	0.76
1.04	1.12	0.03
0.07	1.70	0.29
0.23	1.51	0.50
0.19	-1.06	-0.11
0.43	-1.51	-0.73
0.18	-0.58	-1.41
-0.71	-0.91	-0.58
1.07	0.58	-0.10
0.47	-0.52	-1.79

0.96	-0.84	-1.48
-0.08	1.06	1.14
0.22	0.77	1.05
-0.74	-0.59	0.44
-0.67	1.03	1.13
0.17	0.66	1.53
0.85	1.48	-0.36
-0.33	-1.85	0.66
0.33	0.75	1.34
0.15	0.88	1.36
0.16	-0.09	-1.44
-0.62	-0.90	1.59
0.48	1.11	0.76
-0.62	0.20	0.72
-0.96	1.35	0.43
0.49	-0.48	-0.86
0.52	-0.74	-1.52
0.25	-1.78	-0.32
-0.61	-0.56	0.79
0.84	0.27	-0.22
0.28	0.89	0.43
0.23	-0.76	-0.96
-0.24	1.94	0.15
1.67	-0.25	-0.48
0.21	-1.36	0.40
-0.33	0.44	-1.18
-0.78	-0.09	-0.81
0.23	-1.33	-1.09
-0.35	1.16	0.30
-0.07	0.92	0.88
0.42	1.60	0.27
0.34	-0.46	-1.10
-1.00	1.58	0.78
0.33	0.95	1.11
0.01	-1.60	-0.60
-1.20	1.81	0.09
-0.59	1.40	0.84
0.04	-0.44	-0.01
-0.88	1.17	0.58
0.19	0.56	0.96