```
s61 - gctgagtctgaacaagcttgACGGTGGGAATATTCCctcgagtcagagcgtcg
s11 +         cgacgctctgactcgaggGGAATATTCCGCTAGCcaagcttgttcagactcagc
s51 -      gctgagtctgaacaagcttgAGGAATATTCCGTGCCctcgagtcagagcgtcg
z41 +       gctgagtctgaacaagcttgGGAATATTCTCACAGCctcgagtcagagcgtcg
z32 -     gctgagtctgaacaagcttgGCGGAATATTCTGACCctcgagtcagagcgtcg
s12 +       cgacgctctgactcgaggGGGGAATATTCGTGCGcaagcttgttcagactcagc
z40 +         cgacgctctgactcgaggGGAATATACTCGCCTcaagcttgttcagactcagc
s62 -   gctgagtctgaacaagcttgGGGAGGAATATACGGCCctcgagtcagagcgtcg
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z38 + gctgagtctgaacaagcttgGAGTACCGAATATACCctcgagtcagagcgtcg
s16 +        cgacgctctgactcgaggGGGAATATGCCGTACCcaagcttgttcagactcagc
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s9  -  gctgagtctgaacaagcttgACCGCAGAATATCCCCcctcgagtcagagcgtcg
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z77 -       gctgagtctgaacaagcttgAGAATAATCCCCGATAcctcgagtcagagcgtcg
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s14 -   gctgagtctgaacaagcttgCCAGAGAATAATGCCCcctcgagtcagagcgtcg
s46 - gctgagtctgaacaagcttgGAATAGGGAATAACCGcctcgagtcagagcgtcg
s3  -      gctgagtctgaacaagcttgAAGAATAACCCAGTGCcctcgagtcagagcgtcg
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z42 -         cgacgctctgactcgaggGGAATAAACGTACTAAcaagcttgttcagactcagc
s6  -      gctgagtctgaacaagcttgAGGAATAAACACGGGCcctcgagtcagagcgtcg
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s5  -          cgacgctctgactcgaggGGATAATTCCGGACCCcaagcttgttcagactcagc
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s43 -      gctgagtctgaacaagcttgAAGAATGTTCTCGGGCcctcgagtcagagcgtcg
z28 +     gctgagtctgaacaagcttgAAAGAATGTGCGCAGGcctcgagtcagagcgtcg
s8  -  cgacgctctgactcgaggGGACAATCGAATGTGAcaagcttgttcagactcagc
z25 -         cgacgctctgactcgaggGGAATGATATAGCGGAcaagcttgttcagactcagc
z37 -       gctgagtctgaacaagcttgGGAATTAATATGTCCGcctcgagtcagagcgtcg
s18 +        gctgagtctgaacaagcttgGTATTACTCAATTCCCcctcgagtcagagcgtcg
consensus                        GnATdw
```
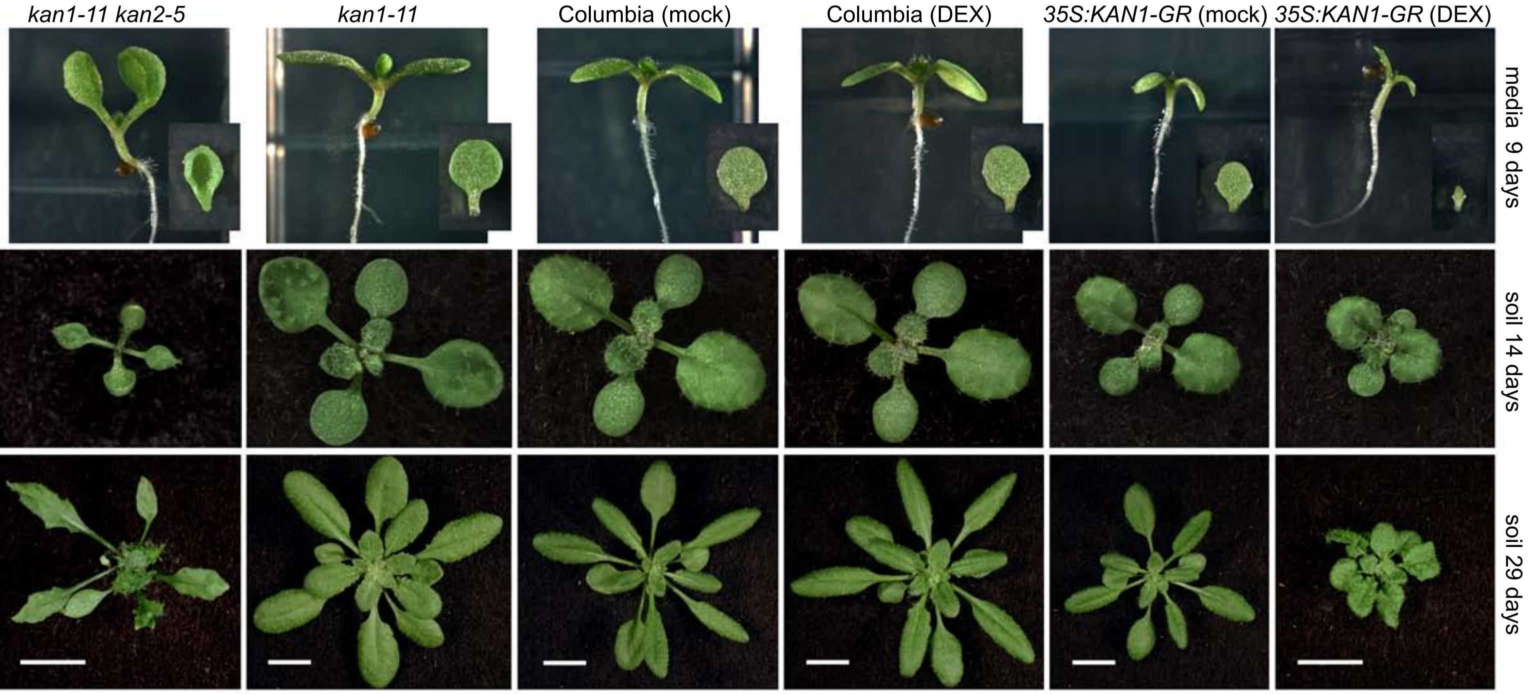
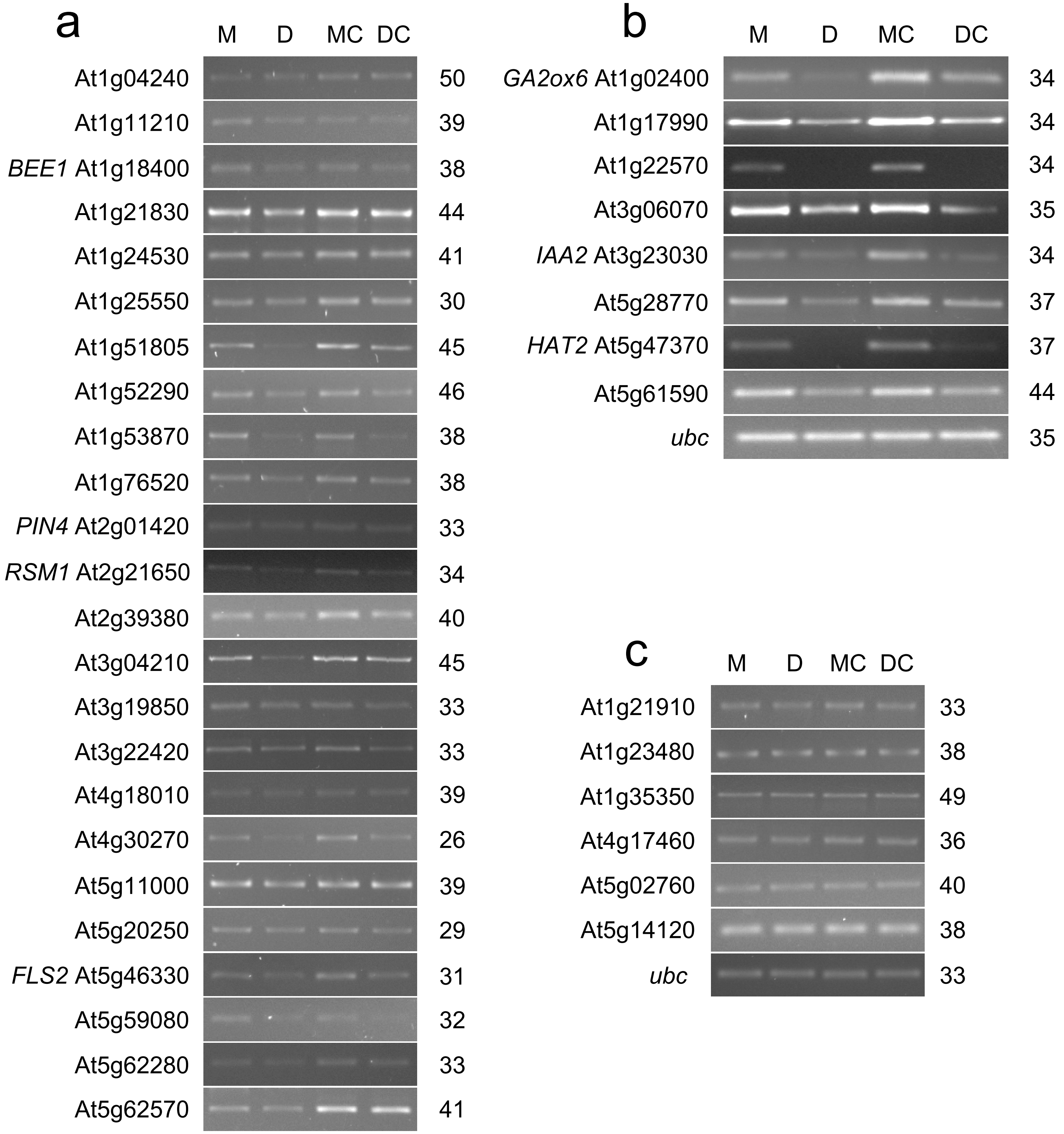
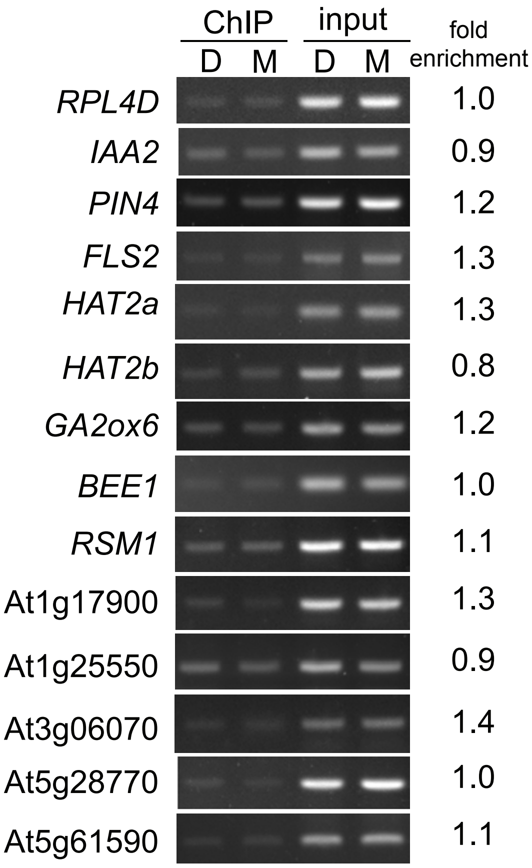

Supplemental Figure 1: Alignment of 50 sequences obtained from PCR-assisted binding site selection. The DNA sequences of fifty unique clones derived from two independent PCR-assisted binding site selection experiments were manually aligned to identify the consensus DNA binding site. Each oligonucleotide contained at least one instance of GNATDW (where N is any nucleotide, D is A, G, or T, and W is A or T) and 28 oligonucleotides contained a second potential binding site. S indicates clones from DNA EMSA selection, Z indicates clones from protein EMSA selection; + & - the clone orientation. Consensus GAATAW sites are red and complementary (often overlapping) WTATTC sites are orange except where they overlap with red nucleotides.



Supplemental Figure 2: Table of phenotypes in loss of function mutants and post-translationally activated *KAN-GR* plants. Top row, *kan1-11*, *kan1-11 kan2-5,* wild-type (Col), and *KAN-GR* seeds were germinated and grown for 9 days on media containing mock or DEX supplementation (as indicated). Cotyledons (inset photos, first row) of *kan1-11 kan2-5* are strongly cupped and DEX-treated *KAN1-GR* cotyledons are narrow and pointed in contrast to Col or mock-treated *KAN-GR* seedlings that form normal cotyledons and first leaves. Intermittent DEX application has different effects on morphogenesis of soil-grown *KAN-GR* plants than continuous exposure in media. Whole 14-day old (second row) and 29-day old (third row) rosettes display effects of loss of *kan* function and ectopic expression of *KAN-GR*. Soil-grown DEX-treated *KAN-GR* plants formed leaves with short petioles and asymmetric leaf blades, which were not observed in mock-treated plants. (Bar = 1 cm)

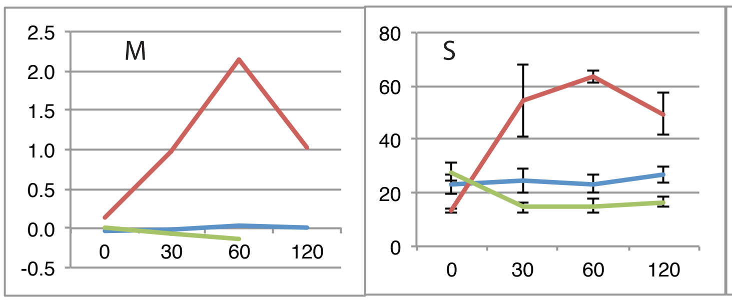


Supplemental Figure 3: Expression of candidate KAN1 target genes was confirmed using RT PCR at limiting numbers of cycles. Reverse-transcription PCR was used to confirm microarray results for select candidate KANT genes. Most putative KANT genes displayed reduced expression in DEX (D) and DEX+CHX (DC) compared to mock (M) and mock+CHX (MC) treated seedlings (a and b). A few genes showed no detectable expression differences (c) in RT-PCR and may represent false discovery. For each template-primer combination, the number of PCR cycles was determined empirically and is shown to the right of each gel image. At least two biologicalreplicates and two technical replicates were performed and a single representative gel image is shown.

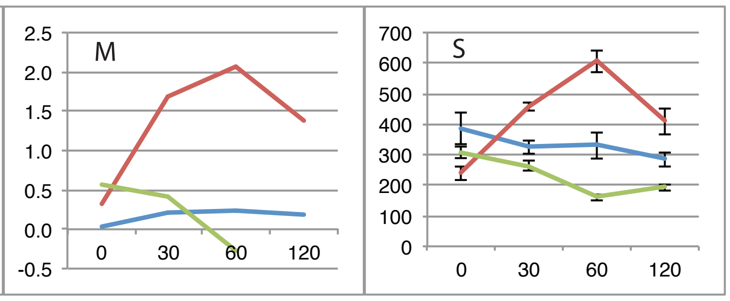


Supplemental Figure 4: Chromatin immunoprecipitation experiments on mock- and DEX-treated Col seedlings reveal no enrichment. ChIP was performed on Col seedlings lacking the KAN-GR transgene as a control for potential non-specific immunoprecipitation effects. None of the promoter fragments tested showed enrichment in DEX- versus mock-treated Col samples indicating that enrichment depends on the KAN-GR transgene. Fold enrichment was calculated as in Fig. 5.

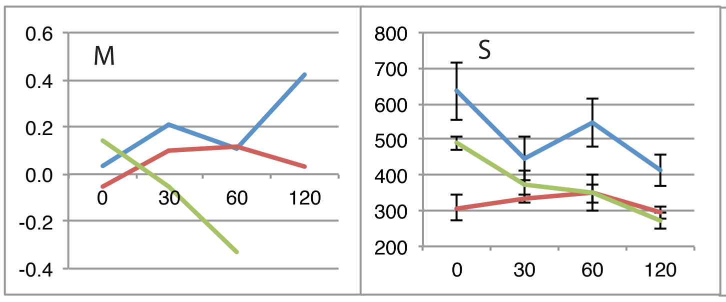
YUC5/ AT5g43890; p=1.5E-2 (GR-REV vs KAN1-GR)



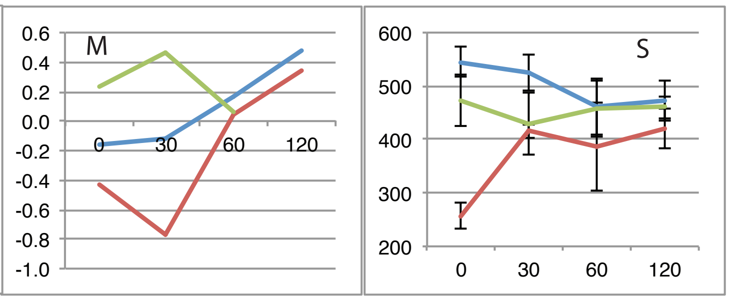
TAA1/ AT1g70560; p=5.5E-5 (GR-REV vs KAN1-GR)



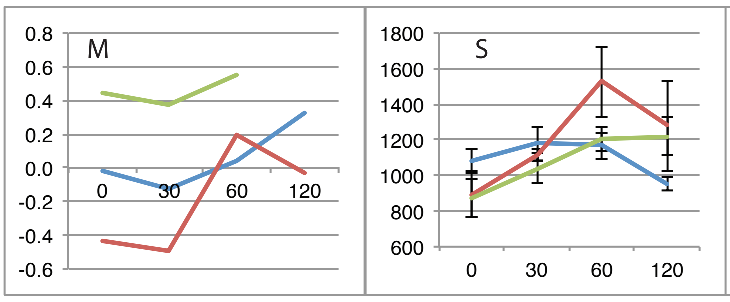
LAX1/AT5g01240; p=2.9E-2 (GR-REV vs KAN1-GR)



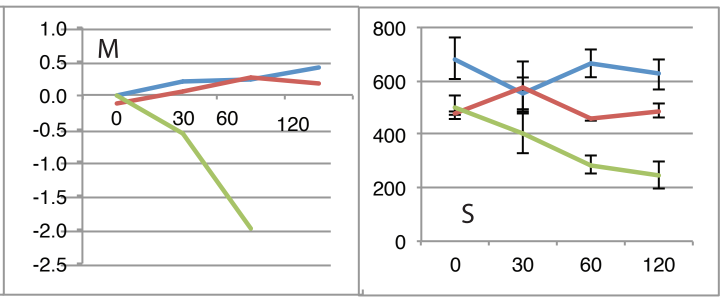
LAX2/AT2g21050; p=3.5E-2 (GR-REV vs KAN1-GR)



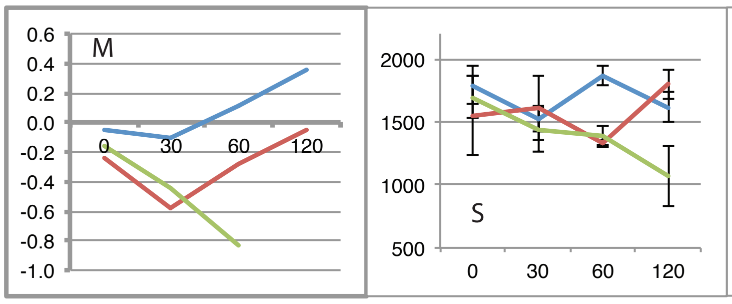
LAX3/AT1g77690; p=2.0E-2 (GR-REV vs KAN1-GR)



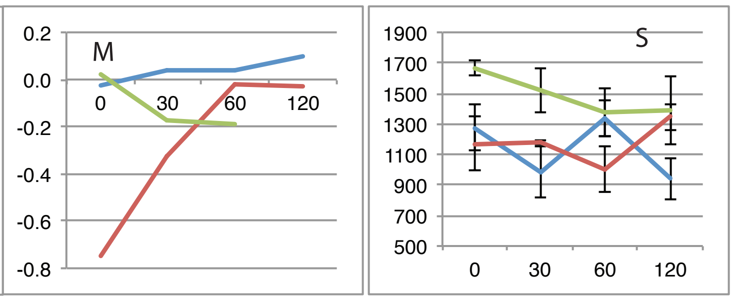
PIN4/AT2g01420; p=8.4E-4 (KAN1-GR vs COL)



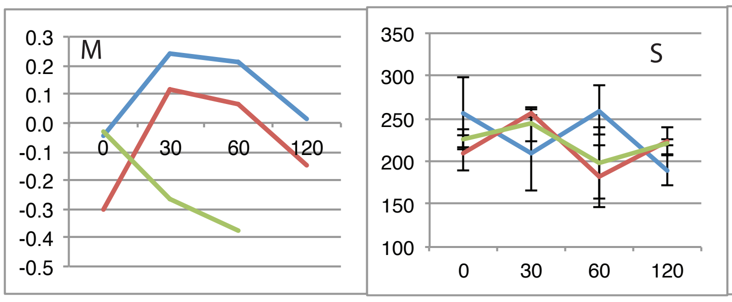
PIN3/AT1g70940; 9=4.7E-2 (GR-REV vs KAN1-GR)



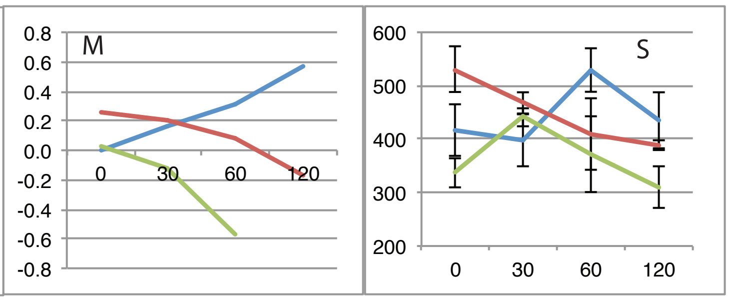
PGP19/ AT3g28860; p=2.8E-3 (GR-REV vs COL)



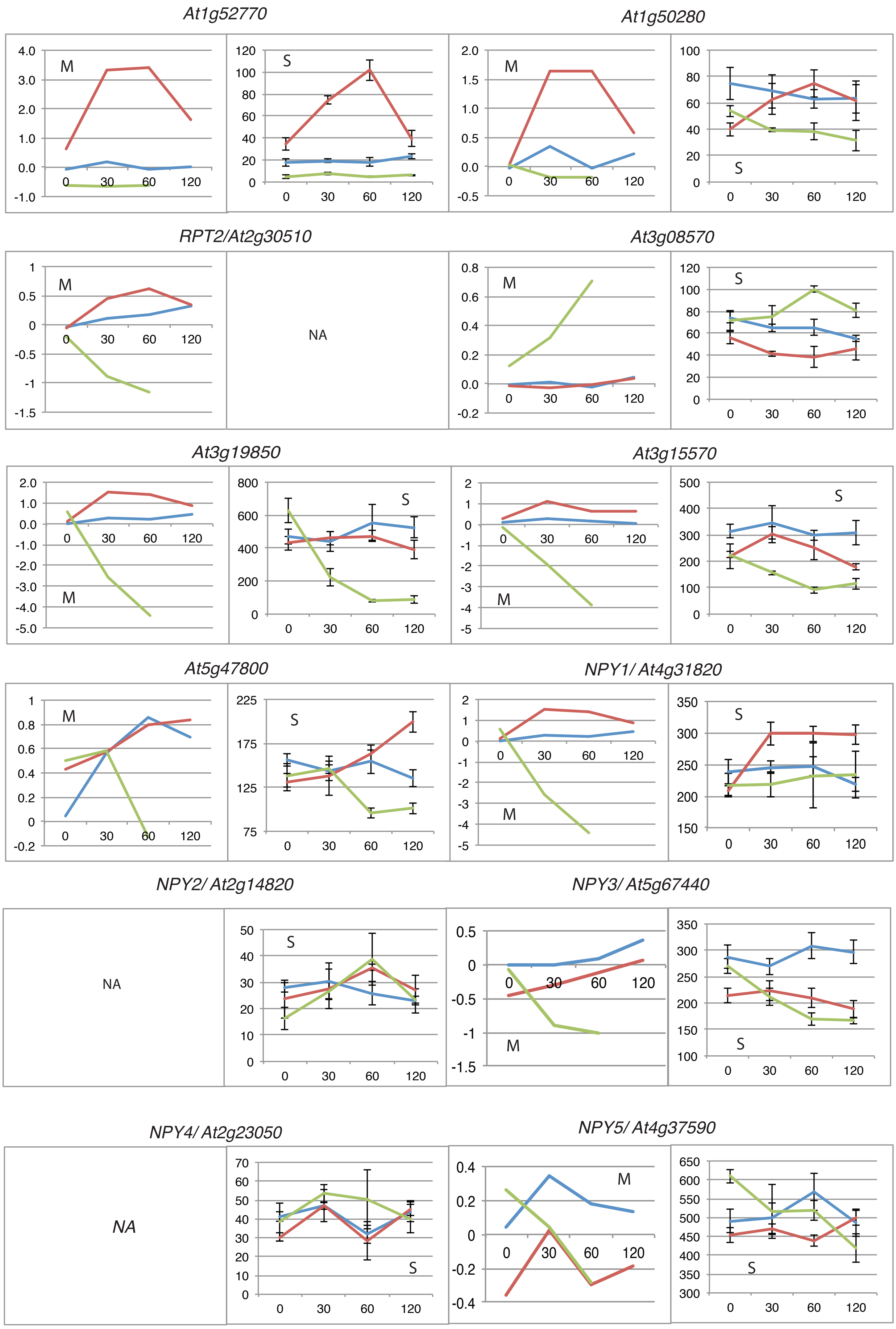
PGP6/ AT2g39480; p=3.6E-2 (GR-REV vs KAN1-GR)



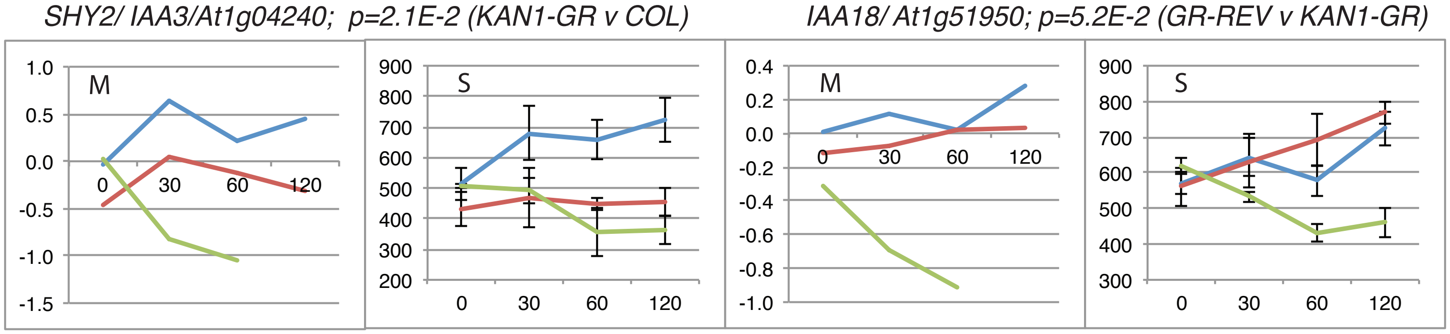
PGP21/ AT3g62150; p=2.7E-2 (GR-REV vs COL) and 2.5E-2 (KAN1-GR vs COL)



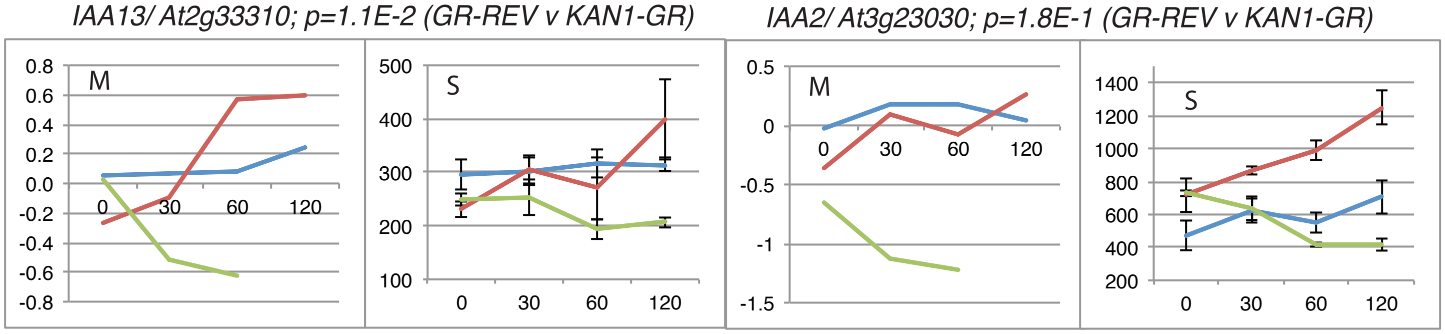
Supplemental Figure 5: Transcript levels for Arabidopsis genes encoding auxin biosynthetic enzymes (YUC5 and TAA1) and auxin transporters in response to DEX treatment of GR-REV and KAN1-GR transgenic plants. M: transcript levels measured by microarray, Y-axis: Normalized transcript levels log(2). X-axis: time after treatment in minutes. S: transcript levels measured by RNA-SEQ, Y-axis: normalized counts, X-axis: time after treatment in minutes. Microarray measurements and P-values (genotype by treatment interaction, adjusted for multiple hypothesis testing) are from Reinhart et al. (2013). GR-REV - red; KAN1-GR - green; Wild-type Columbia - blue. Error bars are standard error of the mean. In all cases, wild type data points are based on 6 biological replicates. Data points for transgenics are based on 3 biological replicates except GR-REV 30 minutes which is based on two biological replicates.



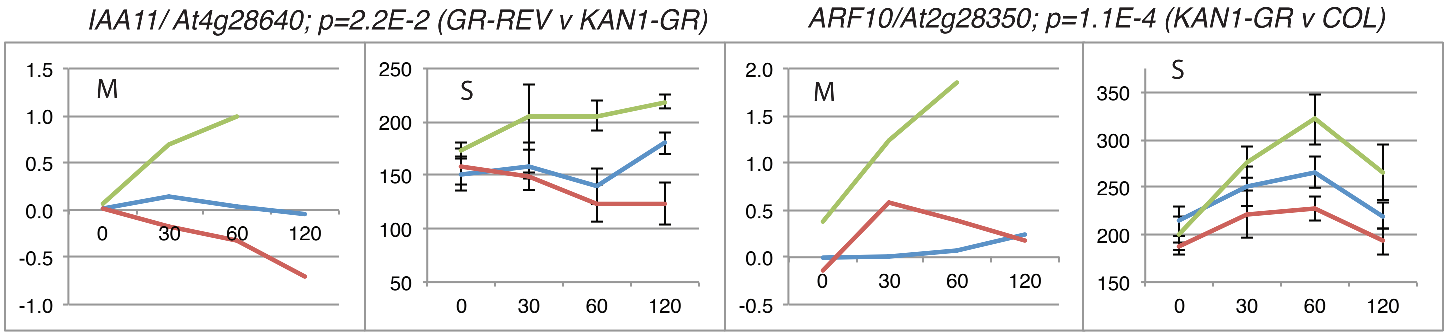
Supplemental Figure 6: Transcript levels for Arabidopsis genes encoding members of the NPH3 family of BTB-POZ domain proteins in response to DEX treatment of GR-REV and KAN1-GR transgenic plants. M: transcript levels measured by microarray, Y-axis: Normalized transcript levels log(2). X-axis: time after treatment in minutes. S: transcript levels measured by RNA-SEQ, Y-axis: normalized counts, X-axis: time after treatment in minutes. Microarray measurements and P-values (genotype by treatment interaction, adjusted for multiple hypothesis testing) are from Reinhart et al. (2013). GR-REV - red; KAN1-GR - green; Wild-type Columbia - blue. Error bars are standard error of the mean. In all cases, wild type data points are based on 6 biological replicates. Data points for transgenics are based on 3 biological replicates except GR-REV 30 minutes which is based on two biological replicates.


SHY2/ IAA3/At1g04240; p=2.1E-2 (KAN1-GR v COL)

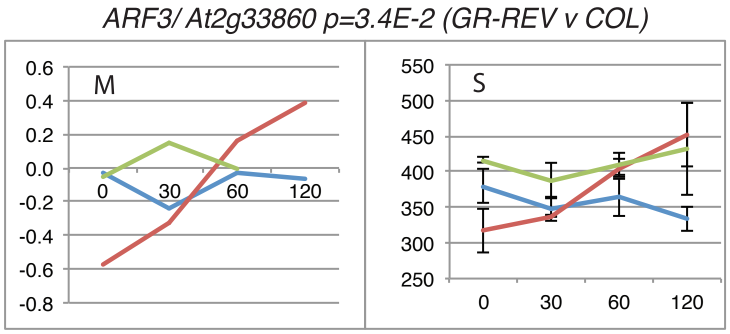
IAA18/ At1g51950; p=5.2E-2 (GR-REV v KAN1-GR)


IAA13/ At2g33310; p=1.1E-2 (GR-REV v KAN1-GR)

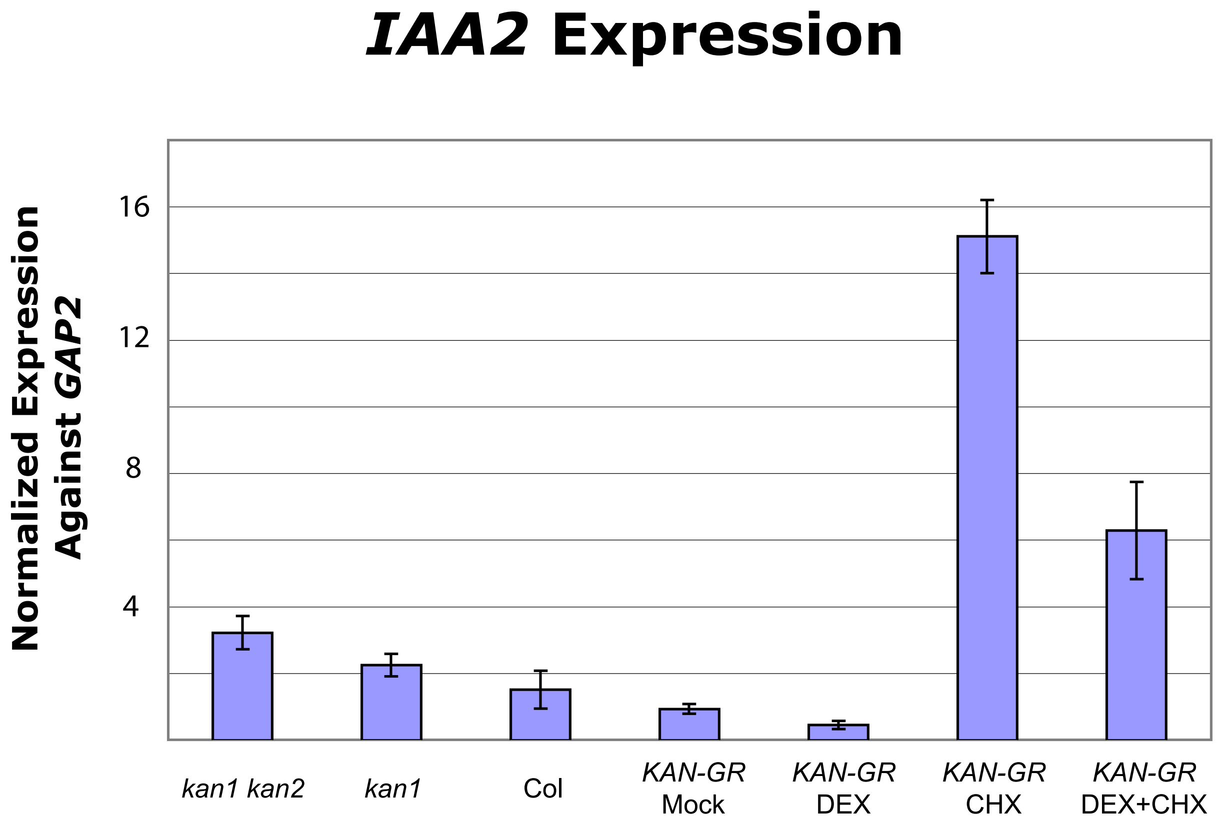
IAA2/ At3g23030; p=1.8E-1 (GR-REV v KAN1-GR)


IAA11/ At4g28640; p=2.2E-2 (GR-REV v KAN1-GR)

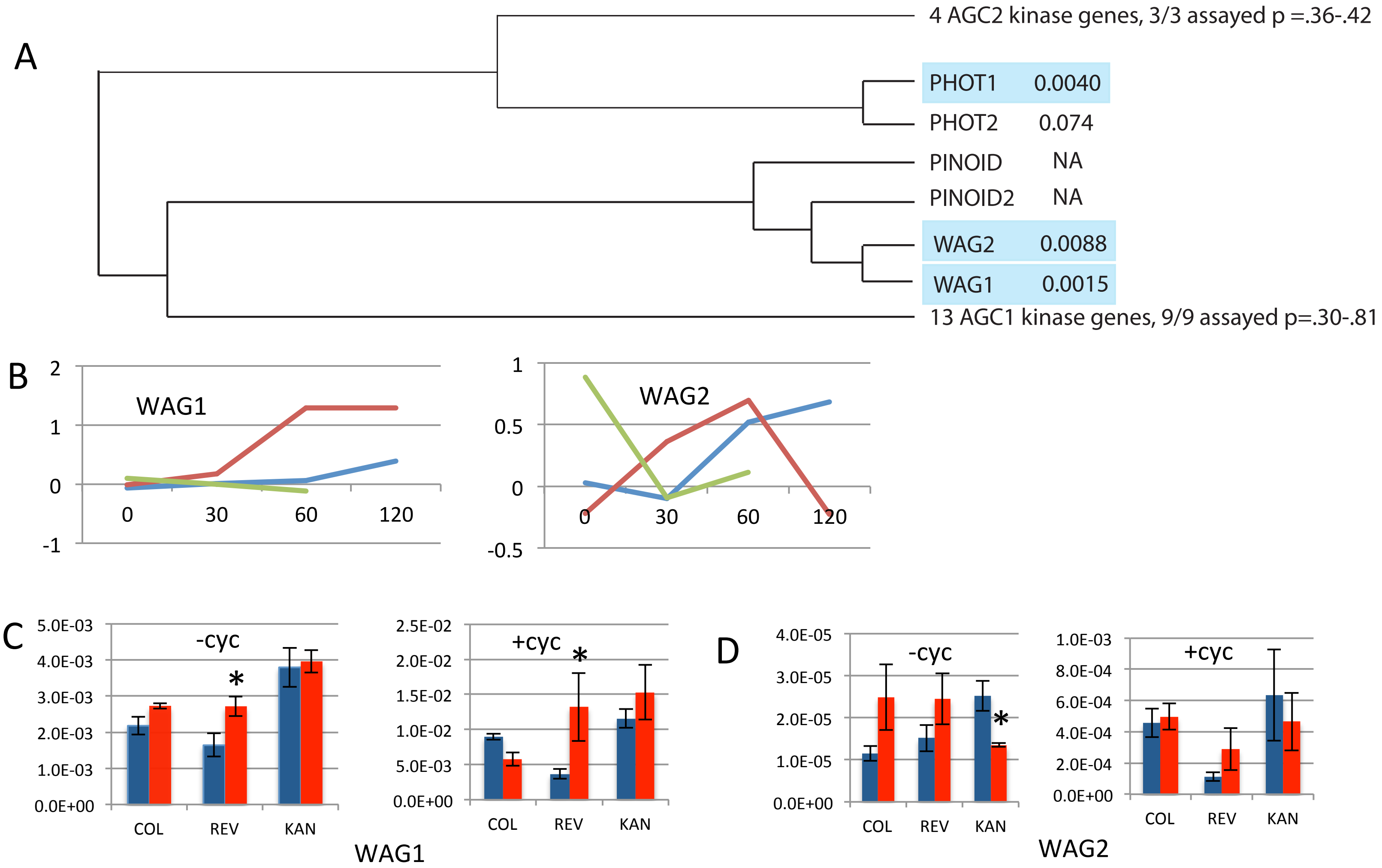
ARF10/At2g28350; p=1.1E-4 (KAN1-GR v COL)


ARF3/ At2g33860 p=3.4E-2 (GR-REV v COL)

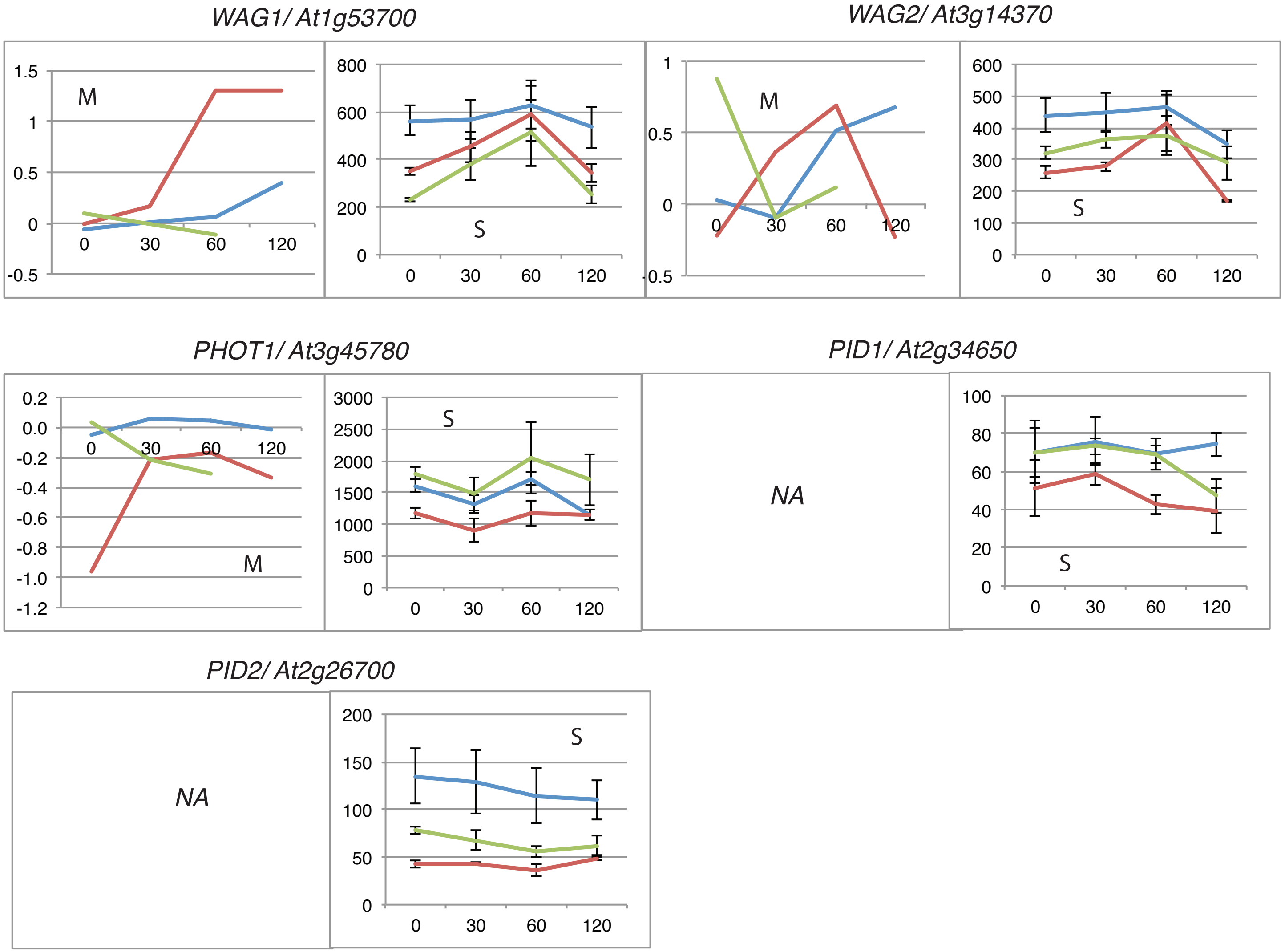
Supplemental Figure 7: Transcript levels for Arabidopsis genes encoding auxin responsive transcriptional regulators. M: transcript levels measured by microarray, Y-axis: Normalized transcript levels log(2). X-axis: time after treatment in minutes. S: transcript levels measured by RNA-SEQ, Y-axis: normalized counts, X-axis: time after treatment in minutes. Microarray measurements and P-values (genotype by treatment interaction, adjusted for multiple hypothesis testing) are from Reinhart et al. (2013). GR-REV - red; KAN1-GR - green; Wild-type Columbia - blue. Error bars are standard error of the mean. In all cases, wild type data points are based on 6 biological replicates. Data points for transgenics are based on 3 biological replicates except GR-REV 30 minutes which is based on two biological replicates.



Supplemental Figure 8: IAA2 expression is up-regulated in loss-of-function kan mutants and down-regulated in posttranslationally activated KAN-GR. Quantitative RT-PCR was used to assay expression levels of IAA2 in the following genotypes: kan1-11 kan2-5, kan1-11, wild-type (Col), and KAN-GR treated with mock- or DEX in the absence and presence of CHX. Results were normalized to GAP2 with the results of KAN-GR mock arbitrarily set to 1. Error bars are standard errors of the mean.



Supplemental Figure 9. Differential regulation of members of the AGC3 gene family by REVOLUTA and KANADI A. Phylogenetic tree of AGC3 kinases (after Bögre et al., 2003). Values are probabilities for interaction between genotype and time of treatment in a 2 way ANOVA comparing GR-REVOLUTA lines treated with dexamethasone to KANADI1-GR lines treated with dexamethasone. **B.** Graphs of transcript levels for wild-type (blue); GR-REVOLUTA (red) and KANADI1-GR (green) lines treated with dexamethasone. Y axis = normalized transcript levels (log base 2). X axis = time in minutes after dexamethasone treatment. **C.** Q-RT-PCR experiments on cDNAs made from mock (blue) and dexamethasone treated (red) seedlings for one hour in the presence and absence of cycloheximide (REV=GR-REV; KAN=KAN1-GR). Three biological replicates were tested for each bar. Asterisk shows values that are different from untreated control at p<.05 (t test). Error bars are standard errors of the mean.



Supplemental Figure 10: Transcript levels for Arabidopsis genes encoding AGC kinases in response to DEX treatment of GR-REV and KAN1-GR transgenic plants. M: transcript levels measured by microarray, Y-axis: Normalized transcript levels log(2). X-axis: time after treatment in minutes. S: transcript levels measured by RNA-SEQ, Y-axis: normalized counts, X-axis: time after treatment in minutes. Microarray measurements and P-values (genotype by treatment interaction, adjusted for multiple hypothesis testing) are from Reinhart et al. (2013). GR-REV - red; KAN1-GR - green; Wild-type Columbia - blue. Error bars are standard error of the mean. In all cases, wild type data points are based on 6 biological replicates. Data points for transgenics are based on 3 biological replicates except GR-REV 30 minutes which is based on two biological replicates.

Supplemental Table 1. Fold enrichment (1) in KAN1-GR CHIP experiment

Gene (2)	Exp1	Exp2	Mean
RPL4D	0.78	1.11	0.95
IAA2	3.21	3.33	3.27
PIN4	4.29	3.46	3.87
FLS2	4.47	3.81	4.14
HAT2a	0.90	1.06	0.98
HAT2b	2.80	2.63	2.71
GA2ox6	3.81	2.70	3.25
BEE1	4.38	4.44	4.41
AtRL2	3.61	2.66	3.14
At1g17990	3.22	2.98	3.10
At1g25550	3.12	3.03	3.07
At3g06070	2.99	2.68	2.84
At5g28770	3.44	2.97	3.20
At5g61590	5.14	4.04	4.59

(1) Fold enrichment was calculated by normalizing PCR product intensities to a negative control, the RIBOSOMAL PROTEIN L4D (RPL4D) coding region, followed by calculating the ratio DEX IP/input to mock IP/input.
(2) Gene adjacent to KAN1 binding site. See Figure 5 for position of KAN1 binding sites and PCR fragments amplified.

Supplemental Table 2. Auxin regulated genes by REV and KAN.

Gene Title	Transcript ID(Array Design)	Probe Set ID	Corrected p-value(Time-Genotype)GR-REV vs KAN1-GR	Corrected p-value(Time-Genotype) GR-REV vs COL	Corrected p-value(Time-Genotype)KAN1-GR vs COL	[0min, GRKAN](normalized)	[0min, GRREV](normalized)	[30min, GRKAN](normalized)	[30min, GRREV](normalized)	[60min, GRKAN](normalized)	[60min, GRREV](normalized)
AUXIN BIOSYNTHETIC ENZYME GENES											
YUCCA8	AT4G28720	253794_at	4.48E-01	5.34E-01	6.98E-01	-0.3168	-0.3397	-0.2312	-0.1345	-0.3803	-0.0059
YUCCA5	At5g43890	249094_at	1.54E-02	1.06E-02	8.41E-01	0.0139	0.1363	-0.0734	0.9701	-0.1355	2.1363
TAA1	AT1G70560	260364_at	5.47E-05	6.34E-03	7.49E-02	0.5605	0.3232	0.4108	1.6899	-0.2738	2.0675
TAR2	AT4G24670	254125_at	7.82E-02	3.88E-01	3.96E-01	0.1358	-0.4146	-0.1180	-0.2069	-0.3463	0.2226
AUX1 FAMILY OF INFLUX TRANSPORTERS											
LAX1	AT5G01240	251133_at	2.91E-02	5.42E-01	1.43E-01	0.1392	-0.0552	-0.0500	0.0986	-0.3296	0.1188
AUX1	At2g38120	267092_at	1.75E-01	9.60E-01	3.24E-01	0.1598	-0.4130	-0.0231	-0.4080	-0.1177	-0.1442
LAX2	AT2G21050	264025_at	3.53E-02	8.90E-01	7.57E-01	0.2358	-0.4321	0.4590	-0.7699	0.0623	0.0489
LAX3	AT1G77690	259680_at	2.03E-02	3.10E-01	9.91E-01	0.4441	-0.4347	0.3737	-0.4968	0.5542	0.1901
PIN FAMILY of AUXIN TRANSPORT FACILITATORS											
PIN7	At1g23080	264900_at	8.14E-02	3.85E-01	5.27E-01	0.3428	-0.4238	0.1547	-0.0719	0.3054	0.1650
PIN3	At1g70940	262263_at	4.69E-02	8.73E-01	1.26E-01	-0.1640	-0.2339	-0.4424	-0.5820	-0.8321	-0.2833
PIN1	At1g73590	259845_at	4.12E-01	9.36E-01	8.63E-01	0.1173	0.0852	0.1713	-0.2966	0.0269	-0.1288
PIN4	At2g01420	266300_at	5.12E-04	9.65E-01	8.43E-04	-0.0001	-0.1373	-0.5678	0.0545	-1.9815	0.2473
PIN2	At5g57090	247947_at	7.52E-01	9.05E-01	9.32E-01	0.5659	-0.3895	0.6134	-0.7129	0.6710	-0.2834
PGP FAMILY OF AUXIN TRANSPORT FACILITATORS											
PGP1	AT2G36910	263865_at	4.40E-01	3.49E-01	7.22E-01	-0.0134	0.1452	-0.0159	-0.0785	0.3653	0.0622
PGP2	AT4G25960	254034_at	8.33E-02	8.98E-01	6.07E-02	0.0983	-0.0576	-0.3446	-0.1781	-0.5291	0.1334
PGP4	AT2G47000	266752_at	5.57E-01	9.05E-01	9.97E-01	0.1921	-0.9628	0.0142	-1.1064	0.3611	-1.1427
PGP6	At2g39480	266964_at	3.62E-02	9.69E-01	1.46E-01	-0.0339	-0.3023	-0.2666	0.1142	-0.3767	0.0661
PGP9	At4g18050	254710_at	9.32E-01	7.03E-01	9.37E-01	-0.0845	-0.1996	-0.1003	-0.1509	0.0125	-0.0269
PGP14	AT1G28010	259579_at	3.43E-01	8.98E-01	6.85E-01	-0.5969	-0.2826	-0.0531	-0.1606	0.0696	-0.2358
PGP19	AT3G28860	257137_at	1.59E-02	2.75E-03	4.53E-01	0.0224	-0.7476	-0.1699	-0.3245	-0.1889	-0.0231
PGP20	AT3G55320	251781_at	2.44E-01	9.67E-01	5.30E-01	-0.0833	-0.3177	-0.2921	0.1280	-0.0657	-0.2181
PGP21	At3g62150	251248_at	2.64E-01	2.73E-02	2.48E-02	0.0267	0.2530	-0.1189	0.2052	-0.5718	0.0757
NPH3 like BTB-POZ domain proteins											
AT1G30440	AT1G30440	261796_at	5.24E-02	6.70E-01	2.68E-01	-0.1160	-0.1403	-0.5560	0.0665	-0.6548	0.2536
AT1G52770	AT1G52770	260146_at	8.21E-05	1.25E-07	9.69E-01	-0.6386	0.6284	-0.6510	3.3257	-0.6280	3.4012
AT1G50280	AT1G50280	262464_at	7.81E-03	5.72E-03	4.60E-01	0.0280	0.0261	-0.1846	1.6325	-0.1719	1.6348
RPT2	At2g30510	267517_at	1.79E-03	6.39E-01	3.08E-02	-0.2003	-0.0562	-0.8914	0.4487	-1.1562	0.6242
RPT2	At2g30520	267516_at	4.02E-02			0.3203	-0.8113	-0.4336	0.8247	-1.3741	0.9188
AT2G47860	AT2G47860	266507_at	8.23E-01	6.86E-01	7.93E-01	0.3261	-0.0161	0.1874	-0.1663	0.2306	0.0309
AT3G08570	AT3G08570	258672_at	1.58E-01	5.93E-01	3.44E-02	0.1232	-0.0111	0.3174	-0.0271	0.7033	-0.0055
AT3G49900	AT3G49900	252227_at	7.03E-01	6.13E-01	8.35E-01	0.2098	0.2016	0.1745	0.1832	-0.0682	0.2349
AT3G19850	AT3G19850	257964_at	4.22E-05	1.06E-01	2.27E-07	0.5945	0.1165	-2.5562	1.4999	-4.4263	1.4226
AT3G22104	AT3G22104	257260_at	3.71E-01	7.57E-01	8.56E-01	0.0640	-0.0488	-0.1276	0.1511	-0.0276	0.0543
AT3G44820	AT3G44820	246331_at	1.10E-01	2.45E-01	8.84E-02	-0.0974	-0.0228	-0.1557	-0.0080	-0.4345	-0.0904
AT3G15570	AT3G15570	257294_at	2.98E-05	7.43E-01	5.97E-06	-0.1093	0.2655	-1.9051	1.0836	-3.8841	0.6506
AT3G26490	AT3G26490	256872_at	5.82E-01	2.07E-01	2.17E-01	0.0148	-0.0173	-0.0771	0.3329	0.4144	0.6708
ENP1/NPY1	At4g31820	253493_at	2.55E-02	4.17E-01	5.23E-02	0.0085	-0.1721	-0.5496	0.6333	-0.9713	0.8172
NPY5	AT4G37590	253062_at	1.12E-02	8.81E-01	5.45E-03	0.2631	-0.3577	0.0474	0.0215	-0.2834	-0.2929
NPY3	AT5G67440	246999_at	4.70E-02	9.19E-01	3.98E-03	-0.0673	-0.4557	-0.9055	-0.3003	-1.0171	-0.1195
AT5G47800	AT5G47800	248772_at	1.73E-02	9.24E-01	2.42E-01	0.4968	0.4290	0.5834	0.5706	-0.1281	0.7932
NPH3	At5g64330	247288_at	2.28E-01	7.26E-01	4.58E-01	0.1821	-0.1226	0.0536	0.2180	0.3748	0.1794
AT5G66560	AT5G66560	247048_at	1.19E-01	8.35E-01	2.45E-01	0.2248	-0.0649	-0.1845	-0.4910	-0.4722	0.0838
AGC KINASE encoding genes											
	AT1G51170	265144_at	3.64E-01	8.01E-01	5.04E-01	0.3380	-0.0240	-0.0777	-0.1126	0.1313	0.0159
WAG1	At1g53700	259961_at	1.54E-03	2.05E-05	4.25E-01	0.0983	-0.0096	-0.0042	0.1766	-0.1187	1.2985
AT2G36350	AT2G36350	263962_at	3.61E-01	4.67E-01	8.94E-01	-0.3042	0.3402	-0.0724	-0.1410	0.0346	0.5829
AT2G44830	AT2G44830	266812_at	4.92E-01	8.64E-01	2.69E-01	0.3920	0.1858	0.0829	0.1234	-0.1323	0.1880
AT3G12690	AT3G12690	257696_at	5.10E-01	6.69E-01	8.05E-01	0.1571	0.1836	0.2107	0.0101	0.3645	0.0969

Gene Title	**Transcript ID(Array Design)**	**Probe Set ID**	**Corrected p-value(Time-Genotype)GR-REV vs KAN1-GR**	**Corrected p-value(Time-Genotype) GR-REV vs COL**	**Corrected p-value(Time-Genotype)KAN1-GR vs COL**	**[0min, GRKAN](normalized)**	**[0min, GRREV](normalized)**	**[30min, GRKAN](normalized)**	**[30min, GRREV](normalized)**	**[60min, GRKAN](normalized)**	**[60min, GRREV](normalized)**
AT3G20830	AT3G20830	257975_at	**4.17E-01**	**3.73E-01**	**7.73E-01**	0.1995	**-0.4459**	-0.1100	**-0.0536**	0.1421	**-0.3763**
AGC2-1	At3g25250	257840_at	**3.93E-01**	**9.59E-01**	**5.24E-01**	0.0078	**-0.0182**	0.3191	**0.0056**	0.2313	**-0.0198**
WAG2	At3g14370	258367_at	**8.83E-03**	**1.61E-01**	**1.87E-01**	0.8853	**-0.2164**	-0.0924	**0.3638**	0.1152	**0.6939**
ATPK7	At3g27580	258029_at	**8.14E-01**	**6.55E-01**	**2.43E-01**	0.1125	**0.5025**	0.2488	**0.6177**	0.6156	**0.8301**
PHOT1	At3g45780	252543_at	**3.96E-03**	**3.60E-02**	**2.21E-01**	0.0325	**-0.9598**	-0.2189	**-0.2175**	-0.3078	**-0.1643**
AT3G44610	AT3G44610	252646_at	**4.56E-01**	**9.02E-01**	**4.94E-01**	0.1579	**-0.1772**	0.5519	**-0.1617**	0.4526	**-0.1919**
KIPK	At3g52890	251994_at	**6.51E-01**	**6.94E-01**	**9.53E-01**	0.2580	**0.2031**	0.1941	**0.3655**	0.3308	**0.5677**
AT4G26610	AT4G26610	253976_at	**3.08E-01**	**3.70E-01**	**5.47E-01**	-0.0632	**0.1990**	-0.0229	**-0.0632**	-0.1601	**0.0792**
PHOT2	At5g58140	247853_at	**7.42E-02**	**6.45E-01**	**8.23E-01**	0.2823	**0.2582**	0.5427	**0.1881**	0.6905	**0.1551**
TIR1 Auxin receptor gene											
TIR1	At3g62980	251199_at	**8.78E-02**	**8.10E-01**	**4.41E-01**	-0.0497	**0.1352**	0.2281	**-0.1253**	0.1975	**-0.1154**
IAA protein coding genes											
IAA10	At1g04100	264328_at	**9.17E-01**	**6.55E-01**	**5.94E-01**	0.1427	**0.1337**	-0.0130	**-0.0769**	0.0576	**0.0920**
BDL/IAA12	At1g04550	264605_at	**1.95E-01**	**8.55E-01**	**9.59E-01**	0.2067	**0.0823**	0.1988	**0.3639**	0.1712	**0.6136**
SHY2/IAA3	At1g04240	263656_at	**3.57E-02**	**8.84E-01**	**2.10E-02**	0.0231	**-0.4670**	-0.8270	**0.0545**	-1.0473	**-0.1249**
AXR3/IAA17	At1g04250	263664_at	**5.73E-01**	**5.38E-01**	**8.82E-01**	0.0310	**-0.5721**	-0.2121	**-0.6577**	-0.2376	**-0.5513**
IAA18	At1g51950	246376_at	**5.23E-02**	**8.00E-01**	**9.87E-02**	-0.3177	**-0.1175**	-0.6971	**-0.0749**	-0.9123	**0.0185**
IAA8	At2g22670	265319_at	**6.32E-01**	**9.13E-01**	**9.63E-01**	0.2723	**-0.1269**	0.2671	**-0.0072**	0.3197	**-0.1232**
IAA13	At2g33310	255788_at	**1.10E-02**	**5.09E-02**	**2.87E-01**	0.0207	**-0.2669**	-0.5216	**-0.0993**	-0.6244	**0.5680**
IAA16	At3g04730	258797_at	**5.63E-02**	**1.69E-01**	**6.42E-01**	-0.0978	**-0.6153**	-0.1858	**-0.5105**	-0.3079	**-0.0510**
IAA19	At3g15540	258399_at	**4.23E-01**	**9.64E-01**	**4.49E-01**	0.2183	**-0.2099**	0.0998	**-0.1750**	-0.0807	**0.0003**
IAA2	At3g23030	257766_at	**1.85E-01**	**8.35E-01**	**3.65E-01**	-0.6442	**-0.3616**	-1.1198	**0.0889**	-1.2216	**-0.0726**
IAA7	At3g23050	257769_at	**5.44E-02**	**9.81E-01**	**1.41E-01**	0.0697	**-0.3769**	-0.3159	**-0.0702**	-0.2680	**-0.0053**
IAA14	At4g14550	245593_at	**2.08E-01**	**7.30E-01**	**9.82E-01**	-0.0959	**-0.4847**	-0.2435	**-0.9137**	-0.1563	**-0.3299**
IAA1	At4g14560	245397_at	**1.18E-01**	**1.23E-01**	**3.06E-02**	0.0757	**-0.0638**	-0.1399	**-0.1999**	-0.4601	**0.2333**
PAP2/IAA27	At4g29080	253749_at	**3.30E-01**	**7.62E-01**	**6.34E-01**	-0.0074	**-0.3523**	0.1346	**-0.4615**	0.2163	**-0.5651**
IAA11	At4g28640	253791_at	**2.20E-02**	**9.96E-02**	**3.42E-02**	0.0673	**0.0211**	0.6931	**-0.1727**	0.9908	**-0.3219**
IAA28	At5g25890	246861_at	**2.98E-01**	**8.81E-01**	**7.77E-01**	-0.3820	**-0.7368**	-0.8656	**-0.4449**	-0.3752	**-0.5091**
ATAUX2-11/IAA4	At5g43700	249109_at	**7.08E-01**	**7.88E-01**	**5.73E-01**	-0.0413	**-0.0465**	-0.2066	**-0.0099**	-0.3207	**-0.0858**
IAA9	At5g65670	247148_at	**4.25E-01**	**7.63E-01**	**8.35E-01**	-0.0258	**0.0089**	0.0742	**-0.2066**	0.1832	**-0.0682**
Auxin Response Factor genes											
ARF19	At1g19220	256010_at	**7.01E-01**	**7.51E-01**	**8.88E-01**	0.1762	**-0.0976**	0.1077	**0.0482**	0.0021	**0.0381**
MP/ARF5	At1g19850	255782_at	**2.69E-01**	**2.89E-01**	**9.12E-01**	0.3153	**0.5389**	0.4002	**0.0178**	0.2044	**0.1089**
ARF6	At1g30330	256311_at	**4.40E-01**	**6.91E-02**	**6.76E-01**	0.2501	**0.0579**	0.1611	**0.1150**	0.1032	**-0.3268**
ARF12	At1g34310	262566_at	**4.03E-01**	**8.80E-01**	**9.62E-01**	0.0861	**0.1587**	0.0846	**-0.2172**	0.0703	**0.0071**
ARF1	At1g59750	262914_at	**1.81E-01**	**6.41E-01**	**8.77E-01**	-0.0025	**-0.4024**	-0.1054	**0.0304**	-0.1689	**-0.1216**
ARF17	At1g77850	262136_at	**1.16E-01**	**9.82E-01**	**6.21E-01**	-0.3101	**0.4030**	-0.2243	**0.0413**	-0.4592	**0.3957**
ARF10	At2g28350	265272_at	**6.14E-02**	**7.48E-02**	**1.14E-04**	0.3780	**-0.1455**	1.2363	**0.5780**	1.8560	**0.3911**
ARF11	At2g46530	265454_at	**3.83E-01**	**5.10E-01**	**6.60E-01**	0.0777	**-0.0071**	0.0566	**-0.3777**	-0.0258	**0.2381**
ETT/ARF3	At2g33860	267452_at	**3.08E-02**	**3.45E-02**	**4.48E-01**	-0.0539	**-0.5726**	0.1443	**-0.3306**	-0.0053	**0.1657**
ARF18	At3g61830	251289_at	**2.31E-01**	**9.67E-01**	**7.16E-01**	0.2843	**0.4201**	0.5603	**0.3375**	0.7802	**0.2191**
ARF16	At4g30080	253662_at	**5.18E-01**	**9.72E-01**	**7.89E-01**	0.0039	**-0.3530**	0.0550	**-0.4597**	0.5012	**-0.2403**
ARF9	At4g23980	254194_at	**2.70E-01**	**2.62E-01**	**9.66E-01**	0.1328	**-0.5181**	-0.1033	**-0.4119**	0.0485	**-0.7721**
NPH4/ARF7	At5g20730	245971_at	**7.39E-01**	**3.74E-01**	**4.27E-01**	0.3258	**0.0331**	0.0198	**0.0024**	0.0757	**-0.1631**
ARF8	At5g37020	249651_at	**9.00E-01**	**6.42E-01**	**9.68E-01**	0.4158	**0.0856**	0.6122	**0.1071**	0.6936	**0.2882**
ARF2	At5g62000	247508_at	**1.10E-01**	**9.34E-01**	**3.82E-01**	1.0147	**-2.1363**	0.8950	**1.0372**	0.3372	**1.0751**
ARF2	At5g62010	247468_at	**5.82E-01**			0.1158	**-0.1651**	0.2248	**0.0375**	0.2435	**-0.1632**
ARF4	At5g60450	247643_at	**6.88E-01**	**3.60E-01**	**3.20E-01**	0.2567	**-0.1409**	0.1152	**-0.0110**	-0.1490	**-0.4370**

Degree of yellow shading indicates values that are statistically significant at varying levels.

Supplemental Table 3: Oligonucleotide sequences

Primers for Oligonucleotide Selection and EMSA

Oligo Name	Sequence (forward strand)
BSSlong	gctgagtctgaacaagcttgNNNNNNNNNNNNNNNcctcgagtcagagcgtcg
BSSr	cgacgctctgactcgagg
BSSf	gctgagtctgaacaagcttg
GS13	gctgagtctgaacaagcttgG**GAATAA**AAACGTGCCcctcgagtcagagcgtcg
GS15	gctgagtctgaacaagcttgG**cAATAA**AAACGTGCCcctcgagtcagagcgtcg
GS17	gctgagtctgaacaagcttgG**GtATAA**AAACGTGCCcctcgagtcagagcgtcg
GS18	gctgagtctgaacaagcttgG**GAtTAA**AAACGTGCCcctcgagtcagagcgtcg
GS19	gctgagtctgaacaagcttgG**GAAaAA**AAACGTGCCcctcgagtcagagcgtcg
GS20	gctgagtctgaacaagcttgG**GAATtA**AAACGTGCCcctcgagtcagagcgtcg
GS28	gctgagtctgaacaagcttgG**GAATAg**AAACGTGCCcctcgagtcagagcgtcg
GS21	gctgagtctgaacaagcttgG**GAATATTC**ACGTGCCcctcgagtcagagcgtcg
GS35 (ARR10 binding	gctgagtctgaacaagcttgC**AATCT**AAAACGTGCCcctcgagtcagagcgtcg
GS14	gctgagtctgaacaagcttgG**tAATAA**AAACGTGCCcctcgagtcagagcgtcg
GS16	gctgagtctgaacaagcttgG**aAATAA**AAACGTGCCcctcgagtcagagcgtcg
GS29	gctgagtctgaacaagcttgG**GAATAc**AAACGTGCCcctcgagtcagagcgtcg
GS32	gctgagtctgaacaagcttgG**GAATcA**AAACGTGCCcctcgagtcagagcgtcg
GS33	gctgagtctgaacaagcttgG**GAATgA**AAACGTGCCcctcgagtcagagcgtcg

Primers for RT-PCR

Gene	forward	reverse
At1g02400	gtttcggagaacattctgaccctca	gccgacatacgtggcttctttg
At1g04240	gaggctgggattaccgggaaca	catccaacaatctgagcctttcgag
At1g11210	aggagccggaggttgtgtatgaa	caacggaagcgttgacttgttgc
At1g17990	tcccgccattgtcaacgactttag	tgcaaatggcgagagtctgattcc
At1g18400	tgcccggatgttataaggctatgg	ctgcatggaatcaactgcatctgtc
At1g21830	cagcctccctaagatattcgccttg	ttgcgccatctaagcgatgact
At1g21910	cctacttcatcagccgtctcgt	catcgagcatcgtcgtcgagt
At1g22570	cgtggtcgggaactgcctctatac	gaccctctcgctattacctccttcg
At1g23480	ccctgagctccaagttcctaaatgg	cgtcctgcctctagtaacccgatg
At1g24530	atcttcctcactcagcgacgtaacc	acggcgagacaagttacaggaagac
At1g25550	tcaccggagttacaccgcagattc	actgccgttgttgtggattttcacc
At1g35350	ccgcttcttcttcctcatggttcta	agtgctttgcctctgcttgaagtc
At1g51805	ggagagtcatcgtgtgttcgttgc	ggtgtcacggctcacgtttaagttg
At1g52290	acccgcggttagagaatgattttg	ttcgatctcctgcgttgtacgttg
At1g53870	cggagcaagagaggttcacgatt	cttgattgcgaaaactgatccacga
At1g76520	gcacttgtgatcgggctcattactc	gcaaccaagacgccgataatactgg
At2g01420	ccggtacgggtgtttcaactaaacc	ggcggcatatgtgttccgttgt
At2g21650	gcacaatgttgctagagctgttgg	ttgcttcttgtctcactgcagctt
At2g39380	agatgaacacaacaaccacgcagt	ttgcagcgtagcttctgagttttg
At3g04210	tgcctgaatgagttggcactga	ccatcccaactaagtcgctgaaatc
At3g06070	tctctttccagggtttgttcagagg	gggataaaggaaccgatgaatctcc
At3g19850	ggggtttacgatgtggatttggtga	tcctcggatgatagtttcggatgag
At3g22420	gacgtgtaggctaacggcattgg	gccgtctcaaacgggaagtaaatgt
At3g23030	gcaatggcgtacgagaaagtcaac	gtcaaactccgatccgaatcaaacc
At4g17460	tccgcagttctcgaagacactttc	ccgccgattctcttccgttaatttc
At4g18010	ttatggattgccggaagatttggtg	ttgtggccggaagttaagtgtgag
At4g30270	aaccgccaatttccacacttactca	cctcatcggcttgttctttggaaac
At5g02760	gaatcagggccgcttacattcaac	cctaccctcggacgcaaacttct
At5g11000	atccagaagcagaggaggtttgtg	cgaaatcgaagacgacgaagaact
At5g14120	ccgagctcgttgtcagggacta	gggccatccgtacgcaaagaatatg
At5g20250	gcgattgtttgttcgctgatcct	ctcgtgctcacggattttgagtg
At5g28770	tcactggtcggttaatggaatgacg	tgctcatcattggtgtagctttgga
At5g46330	ctcacgtaagcgattttggaactgc	ctcacgtaagcgattttggaactgc
At5g47370	agactcccatggaaccaaacattcg	ctcttcccgctaatggtgcttga
At5g59080	aaacatggctcacaagctcaacgta	gggttctgtccattagcgtcgtc
At5g61590	tgatattgatgctgcaagggctta	ttgttgttccttgaggctgtggta

Primers for RT-PCR

Gene	forward	reverse
At5g62280	ggtctgctgagaatgctactaaagc	gcgattagtgcaacgagtatgtcg
At5g62570	tggaaagcatctagcaggcatca	cacgggaagcgatagattgttcaag
ubc/At5g25760	ctgagccggacagtcctcttaactg	cggcgaggcgtgtatacatttgtg
act2/At3g18780	tggtcgtacaaccggtattgtgctgg	tgtctcttacaatttcccgctctgctg
NPY1/ENP	gcttcttaaagctgcttcagggtca	tcgcctcaaaaaccagtcgctgc
NPY2	ccccagaccagcacatgatgca	gcagctgcgtagctcccttcc
NPY3	cacgatggtgtgtatcgtgcca	cacggcgtgagcacaagcct
NPY4	tcccaagacactctcacgacgtg	tgttcacacgcttccgcggat
NPY5	acttgcggaaatggtctcgagct	gttttgaaccgcgtgagcgca
WAG1	accggaaaaatggaagacgacgg	tggagtgttgttgccgcgga
WAG2	aggctaggatgcgccagggg	cgtgagacagccttaaacgcgt
PID	acctcaccggcgattctccct	tcgtcgcggtgaacggagttg
PID2	gcctccgccaaccgtctaaacg	ggtcacggtcgttgtcgctgag

Primers for Chromatin Immunoprecipitation

Gene	left primer	right primer
RPL4D/At5g02870	tgtgtttgttcattactgtgctatgc	ataaagctggcggttcgagt
IAA2/At3g23030	cgggtcggccgatagaat	tcggaagcatgaaaggcaag
PIN4/At2g01420	aacggtccaacagtggcttg	gttttctggagggacgtgga
FLS2/At5g46330	cgctcaaaactaaatcggaaa	agggatcatgtcacggatgt
HAT2a/At5g47370	ttggccatcttatttgttttgga	tggtaatgaagaagagaggggatt
HAT2b/At5g47370	tgttttgtaccaaccactccaatta	tggataacgcaatttgcactactt
GA2ox6/At1g02400	ggttaggcaagaatgttgacaataaa	catcctacaaatcgcgtaaggtg
BEE1/At1g18400	gcattggccatttggaagtt	tggtcgtgggttccattagg
RSM1/At2g21650	ttgatatggttttcatggcagaga	acgtgctcgcggaaaattac
At1g17990	gaaatggggtgagacagagatgat	aagacgtgcacaaatgcttaaggt
At1g25550	ttttctggttacatatcttgattccaa	cggattttacttgggaaagggtag
At3g06070	tttttaatggatgcgaatgcaaat	ggaattcctaactaccttatccaatga
At5g28770	cgttgtaactgtaggcgaatctca	taatggccccgacaagagtc
At5g61590	caagacaaccctacaagacaagca	cacaaaccaaaaccaaaaagacttg

Other Primers

UASf	CTTcctaggcaattgGTCGGAGTACTGTCCTCC
UASr	TCCcctagggaattcGTCGTCCTCTCCAAATGAAA
KBDf	ATTCggatCcAAGATGCCGACAAAGCGAAGC
KBDr	AAGCgaattcCTTGTTAGTGGTCTTAACAGTTCG

Supplemental Data References

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