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Supplemental information

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running title: Mitochondrial retrograde signalling

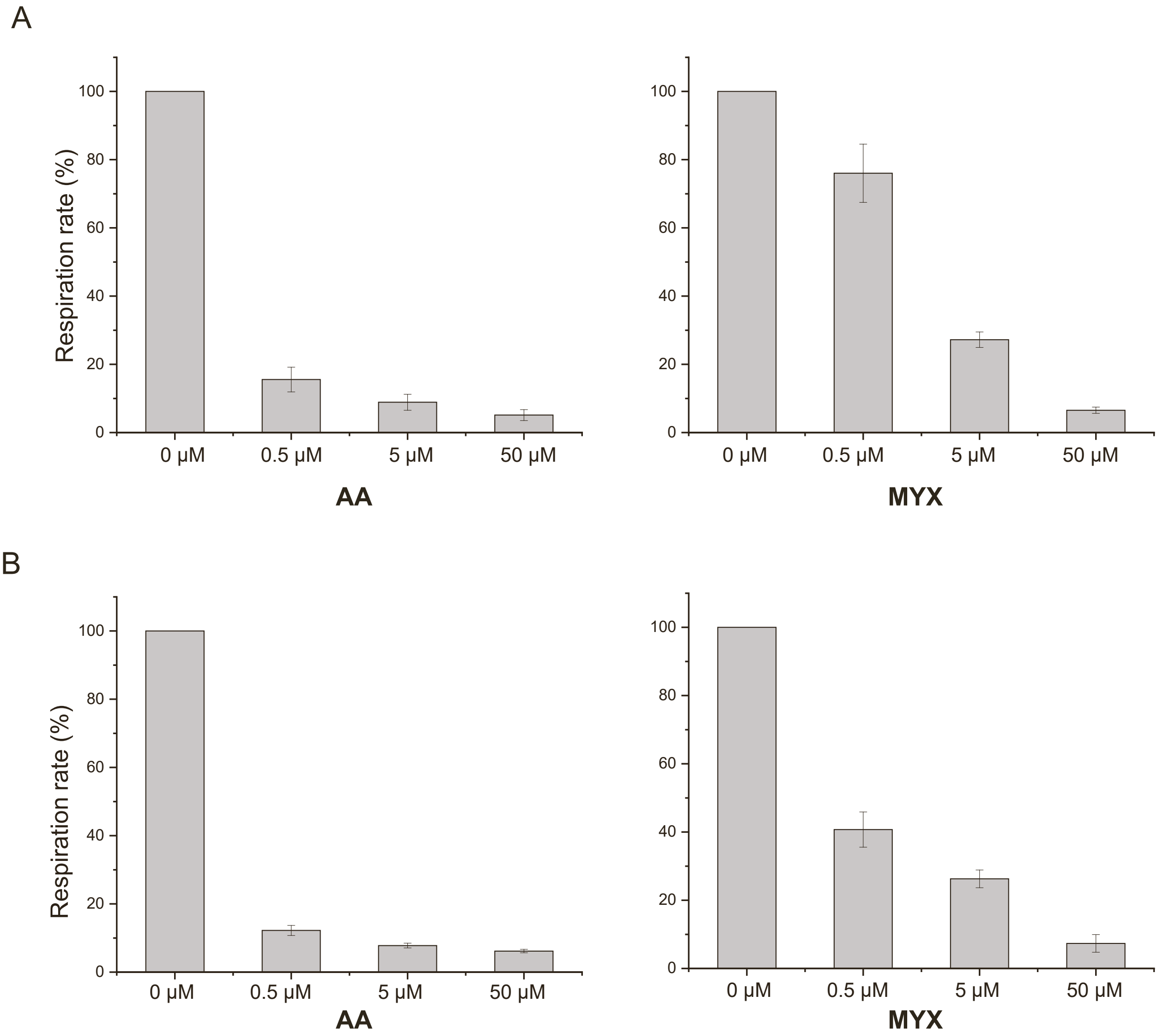
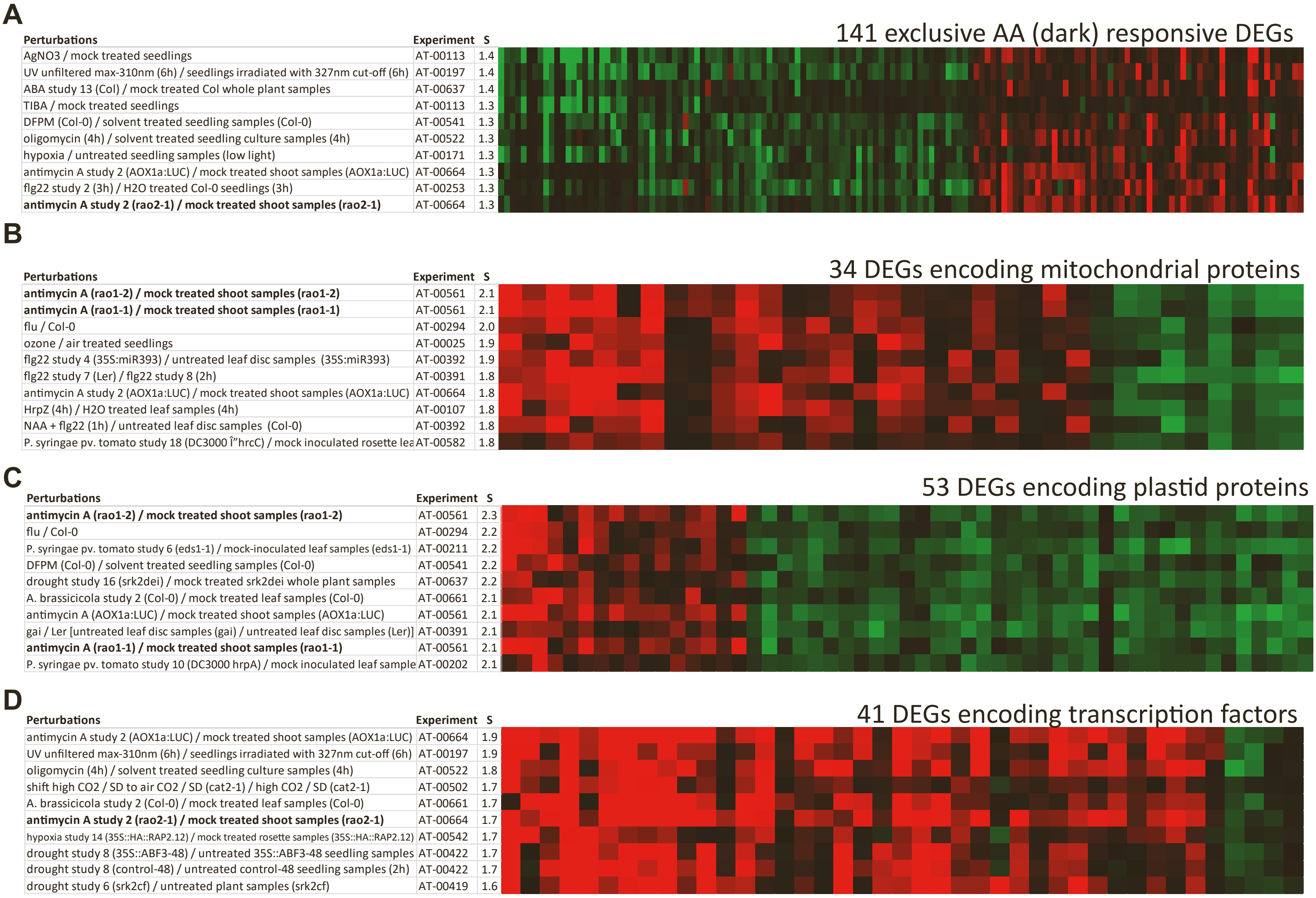


Figure S1. Oxygen consumption of mitochondria or leaf discs from wild type plants after addition of antimycin A (AA) or myxothiazol (MYX).

(A) Purified mitochondria isolated from 12-day old plants (Col-0) after treatment with antimycin A (AA) or myxothiazol (MYX) at concentrations of 0, 0.5, 5, and 50 µM.

(B) Leaf discs from four weeks old plants (Col-0) after treatment with antimycin A (AA) and myxothiazol (MYX) at concentrations of 0, 0.5, 5, and 50 µM.



A

141 exclusive AA (dark) responsive DEGs

Perturbations	Experiment	S
AgNO3 / mock treated seedlings	AT-00113	1.4
UV unfiltered max-310nm (6h) / seedlings irradiated with 327nm cut-off (6h)	AT-00197	1.4
ABA study 13 (Col) / mock treated Col whole plant samples	AT-00637	1.4
TIBA / mock treated seedlings	AT-00113	1.3
DFPM (Col-0) / solvent treated seedling samples (Col-0)	AT-00541	1.3
oligomycin (4h) / solvent treated seedling culture samples (4h)	AT-00522	1.3
hypoxia / untreated seedling samples (low light)	AT-00171	1.3
antimycin A study 2 (AOX1a:LUC) / mock treated shoot samples (AOX1a:LUC)	AT-00664	1.3
flg22 study 2 (3h) / H2O treated Col-0 seedlings (3h)	AT-00253	1.3
antimycin A study 2 (rao2-1) / mock treated shoot samples (rao2-1)	AT-00664	1.3

B

34 DEGs encoding mitochondrial proteins

Perturbations	Experiment	S
antimycin A (rao1-2) / mock treated shoot samples (rao1-2)	AT-00561	2.1
antimycin A (rao1-1) / mock treated shoot samples (rao1-1)	AT-00561	2.1
flu / Col-0	AT-00294	2.0
ozone / air treated seedlings	AT-00025	1.9
flg22 study 4 (35S:miR393) / untreated leaf disc samples (35S:miR393)	AT-00392	1.9
flg22 study 7 (Ler) / flg22 study 8 (2h)	AT-00391	1.8
antimycin A study 2 (AOX1a:LUC) / mock treated shoot samples (AOX1a:LUC)	AT-00664	1.8
HrpZ (4h) / H2O treated leaf samples (4h)	AT-00107	1.8
NAA + flg22 (1h) / untreated leaf disc samples (Col-0)	AT-00392	1.8
P. syringae pv. tomato study 18 (DC3000 Î”hrcC) / mock inoculated rosette lea	AT-00582	1.8

C

53 DEGs encoding plastid proteins

Perturbations	Experiment	S
antimycin A (rao1-2) / mock treated shoot samples (rao1-2)	AT-00561	2.3
flu / Col-0	AT-00294	2.2
P. syringae pv. tomato study 6 (eds1-1) / mock-inoculated leaf samples (eds1-1)	AT-00211	2.2
DFPM (Col-0) / solvent treated seedling samples (Col-0)	AT-00541	2.2
drought study 16 (srk2dei) / mock treated srk2dei whole plant samples	AT-00637	2.2
A. brassicicola study 2 (Col-0) / mock treated leaf samples (Col-0)	AT-00661	2.1
antimycin A (AOX1a:LUC) / mock treated shoot samples (AOX1a:LUC)	AT-00561	2.1
gai / Ler [untreated leaf disc samples (gai) / untreated leaf disc samples (Ler)]	AT-00391	2.1
antimycin A (rao1-1) / mock treated shoot samples (rao1-1)	AT-00561	2.1
P. syringae pv. tomato study 10 (DC3000 hrpA) / mock inoculated leaf sample	AT-00202	2.1

D

41 DEGs encoding transcription factors

Perturbations	Experiment	S
antimycin A study 2 (AOX1a:LUC) / mock treated shoot samples (AOX1a:LUC)	AT-00664	1.9
UV unfiltered max-310nm (6h) / seedlings irradiated with 327nm cut-off (6h)	AT-00197	1.9
oligomycin (4h) / solvent treated seedling culture samples (4h)	AT-00522	1.8
shift high CO2 / SD to air CO2 / SD (cat2-1) / high CO2 / SD (cat2-1)	AT-00502	1.7
A. brassicicola study 2 (Col-0) / mock treated leaf samples (Col-0)	AT-00661	1.7
antimycin A study 2 (rao2-1) / mock treated shoot samples (rao2-1)	AT-00664	1.7
hypoxia study 14 (35S::HA::RAP2.12) / mock treated rosette samples (35S::HA::RAP2.12)	AT-00542	1.7
drought study 8 (35S::ABF3-48) / untreated 35S::ABF3-48 seedling samples	AT-00422	1.7
drought study 8 (control-48) / untreated control-48 seedling samples (2h)	AT-00422	1.7
drought study 6 (srk2cf) / untreated plant samples (srk2cf)	AT-00419	1.6

Figure S2. Characterisation of the antimycin A (AA) specific response in dark conditions.
(A) Genes exclusively differentially expressed in response to antimycin A in the dark were analysed using the signature tool within Genevestigator to identify studies (perturbations) that showed the most similar fold-change responses. Similarity score (S) is indicated. The top 10 studies in which similar fold-change responses were observed for these genes are shown.
(B) Fold-changes for antimycin A responsive genes in the dark encoding 34 mitochondrial proteins. Similarity score (S) and the top 10 studies showing greatest similarity to these are indicated.
(C) Fold-changes for antimycin A responsive genes in the dark encoding 53 chloroplast proteins. Similarity score (S) and the top 10 studies showing greatest similarity to these are indicated.
(D) Fold-changes for antimycin A responsive genes in the dark encoding 41 transcription factors. Similarity score (S) and the top 10 studies showing greatest similarity to these are indicated.
Each subset contained antimycin A treated rao mutant studies (indicated in bold).

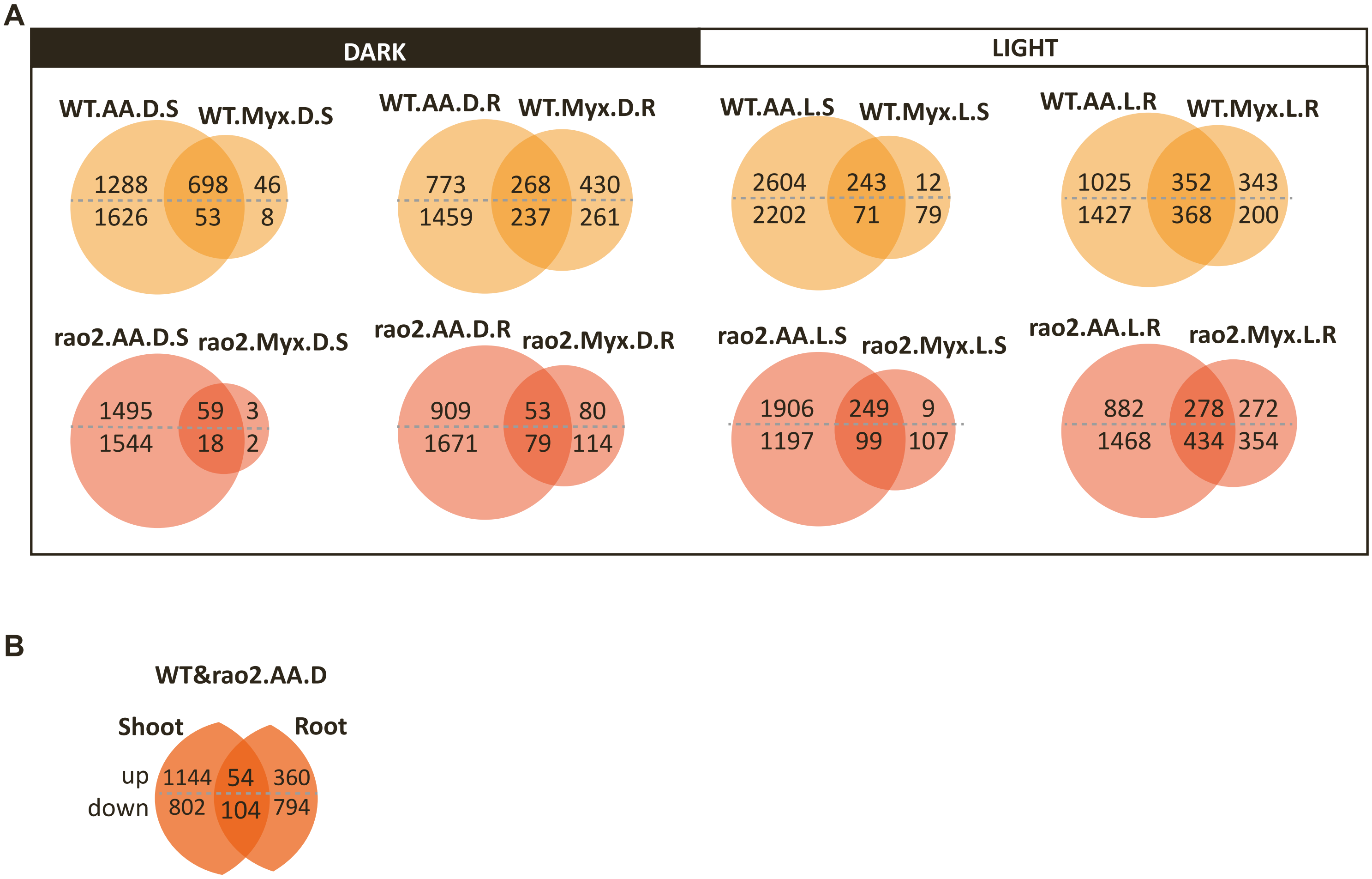


Figure S3. Venn diagrams showing the response to antimycin A (AA) and myxothiozol (MYX) treatments in light and dark.
(A) Overlapping number of differentially expressed genes between Col-0 wild type (WT) and ANAC017 mutant line (*rao2)* following antimycin A (AA) and myxothiazol (Myx) treatment in the light (L) and dark (D) in shoot (S) and roots (R).
(B) Overlapping number of differentially expressed genes between shoot and root that were also overlapping between Col-0 wild type (WT) and an ANAC017 mutant line (*rao2*) in response to AA treatment in the dark.

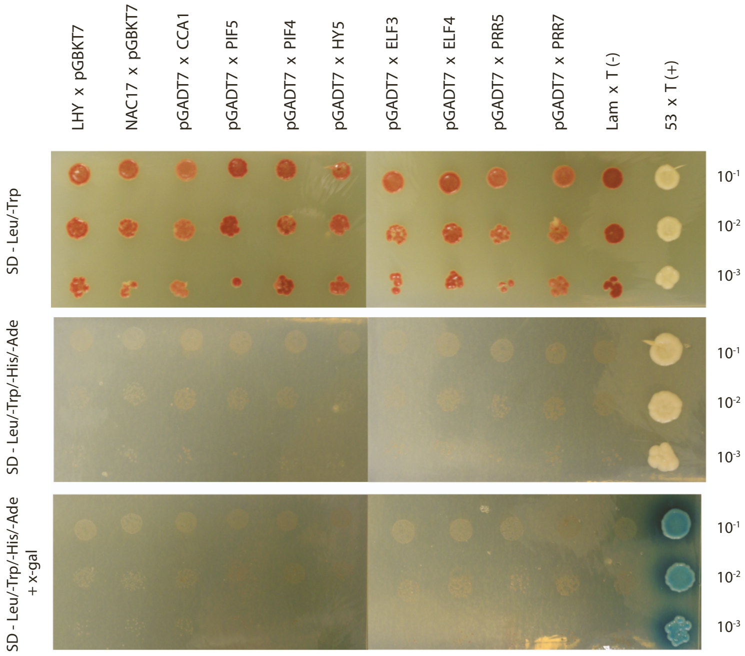


Figure S4. Self-activation test for protein-protein interactions shown in Figure 6. ANAC017 and circadian genes were cloned into pGBKT7 and pGADT7, followed by transformation into Y2HGold strain or Y187 strain separately. Mating was performed between each clone with empty vectors to test for self-activation. Successful mating was confirmed by growth on SD/-leu/-trp media. Self-activation was determined by growth on SD/-Leu/-Trp/-His/-Ade (with or without x-gal) with serial dilutions shown. pGBKT7-53 and pGBKT7-Lam transformed in Y2HGOLD strain were mated with pGADT7-T in Y187 strain as positive and negative controls.

Table S1: Binding sites of transcription factors regulating clock- and light-dependent processes in the AOX1a and ANAC013 promoter regions (Figure 4A,B) (data retrieved form the ReMap 2022, https://remap.univ-amu.fr/)

target gene	chr	start	end	TF	score	strand	peak start	peak end
AOX1a	3	7905282	7905587	ELF3	5	.	7905453	7905454
AOX1a	3	7906287	7906822	LHY	2	.	7906531	7906532
AOX1a	3	7906321	7906736	CCA1	2	.	7906536	7906537
AOX1a	3	7906340	7906807	GI	1	.	7906574	7906575
AOX1a	3	7906344	7906859	PIF5	1	.	7906637	7906638
AOX1a	3	7906344	7906956	PIF4	1	.	7906574	7906575
AOX1a	3	7906425	7906949	HY5	6	.	7906670	7906671
AOX1a	3	7906452	7906743	ELF3	6	.	7906591	7906592
AOX1a	3	7906456	7906825	APRR7	1	.	7906638	7906639
AOX1a	3	7906494	7906783	APRR5	1	.	7906616	7906617
ANAC013	1	11908415	11908698	HY5	1	.	11908596	11908597
ANAC013	1	11908612	11909067	ELF3	6	.	11908862	11908863
ANAC013	1	11909102	11909526	PIF3	1	.	11909354	11909355
ANAC013	1	11909152	11909860	LHY	2	.	11909610	11909611
ANAC013	1	11909342	11909674	GI	1	.	11909369	11909370
ANAC013	1	11909394	11909621	HY5	1	.	11909497	11909498
ANAC013	1	11909417	11909720	CCA1	3	.	11909581	11909582
ANAC013	1	11909422	11909764	RVE4	1	.	11909590	11909591
ANAC013	1	11909433	11909769	RVE6	1	.	11909607	11909608
ANAC013	1	11909503	11909716	RVE5	1	.	11909611	11909612
ANAC013	1	11909520	11909682	RVE7	1	.	11909605	11909606
ANAC013	1	11910472	11910882	ELF3	1	.	11910667	11910668
ANAC013	1	11911130	11911716	LHY	1	.	11911533	11911534
ANAC013	1	11911375	11911756	HY5	3	.	11911578	11911579

Table S2. Top50 enriched TFs sharing binding sites with ANAC017 (Figure

TF	nb.overlaps	random.average	mapped.peaks.ratio	effect.size	p.significance	p.value	q.significance	q.value	e.significance
SPT6	1600	17.67	0.0508	6.501	2447.900	0	2446.516	0	2445.29
AGO1	1349	18.83	0.0497	6.162	1928.639	0	1927.259	0	1926.02
ARR1	1298	18.33	0.0384	6.146	1849.391	0	1848.015	0	1846.78
AT2G14045	1028	8.67	0.0685	6.890	1693.502	0	1692.13	0	1690.89
ARR12	908	5.83	0.0876	7.282	1602.752	0	1601.383	0	1600.14
WRKY33	930	8.67	0.0578	6.746	1492.267	0	1490.902	0	1489.65
WIP2	995	12.67	0.0480	6.296	1462.851	0	1461.49	0	1460.24
WRKY42	903	8.83	0.0677	6.676	1430.187	0	1428.829	0	1427.57
SYD	1063	18.33	0.0375	5.858	1424.355	0	1423.001	0	1421.74
NAC078	693	2.33	0.0771	8.214	1417.959	0	1416.609	0	1415.35
WRKY18-33-40	865	7.67	0.0670	6.818	1406.916	0	1405.569	0	1404.30
ANAC050	670	2.33	0.0840	8.166	1361.231	0	1359.888	0	1358.62
HY5	923	12.17	0.0481	6.245	1343.454	0	1342.115	0	1340.84
MED12	763	5.00	0.1199	7.254	1340.879	0	1339.542	0	1338.26
TT1	840	8.50	0.0523	6.627	1318.419	0	1317.086	0	1315.81
NFYB2	956	17.50	0.0379	5.772	1257.007	0	1255.678	0	1254.39
ANAC13	546	1.17	0.2985	8.870	1225.774	0	1224.448	0	1223.16
WRKY18	752	6.67	0.0642	6.818	1223.529	0	1222.206	0	1220.91
NAC053	556	1.33	0.1037	8.704	1220.299	0	1218.979	0	1217.68
ARR10	719	7.33	0.0722	6.615	1126.579	0	1125.263	0	1123.96
TPR1	797	12.33	0.0339	6.014	1105.749	0	1104.436	0	1103.13
BRM	705	7.17	0.0819	6.620	1105.722	0	1104.412	0	1103.11
WRKY40	633	4.33	0.0751	7.191	1101.116	0	1099.81	0	1098.50
RD26	701	8.50	0.0588	6.366	1046.310	0	1045.008	0	1043.70
ANAC057	520	2.00	0.0950	8.022	1034.993	0	1033.693	0	1032.38
RPS4	386	0.33	0.2885	10.177	1019.856	0	1018.559	0	1017.24
NAC017	385	0.33	0.5086	10.174	1016.791	0	1015.497	0	1014.18
AGO4	804	16.67	0.0343	5.592	1015.052	0	1013.761	0	1012.44
ATHB-6	699	9.33	0.0567	6.227	1014.406	0	1013.119	0	1011.79
ANAC102	585	4.83	0.0814	6.919	970.401	0	969.1175	0	967.79
GBF3	689	10.33	0.0406	6.059	965.617	0	964.3356	0	963.00
ATHB-7	685	10.50	0.0475	6.028	953.627	0	952.3493	0	951.01
CAMTA2	640	7.83	0.0504	6.352	952.993	0	951.7178	0	950.38
AT5G50360	642	8.50	0.0466	6.239	934.301	0	933.0291	0	931.69
EICBP-B	494	2.50	0.0691	7.626	924.704	0	923.4347	0	922.09
SMXL6	562	5.83	0.0650	6.590	877.121	0	875.8547	0	874.51
LHY	575	6.67	0.0453	6.430	869.948	0	868.685	0	867.33
RBOHJ	573	6.83	0.0527	6.390	859.992	0	858.7324	0	857.38
AT5G04760	595	8.17	0.0540	6.187	856.956	0	855.699	0	854.34
ZAT6	622	10.00	0.0462	5.959	853.533	0	852.2787	0	850.92
ABC1K1	455	2.33	0.1022	7.607	849.392	0	848.1407	0	846.78
AGL8	592	8.33	0.0470	6.151	846.238	0	844.9894	0	843.62
MYB44	581	7.83	0.0475	6.213	841.327	0	840.0809	0	838.71
ABF3	601	9.17	0.0574	6.035	838.384	0	837.141	0	835.77
GBF2	568	7.67	0.0493	6.211	822.305	0	821.0645	0	819.69
ANAC016	353	0.67	0.2793	9.048	812.906	0	811.6683	0	810.29
SPCH	605	10.50	0.0418	5.848	810.498	0	809.2636	0	807.88
ELF3	457	3.00	0.0683	7.251	804.278	0	803.0458	0	801.66
MYC3	607	11.17	0.0420	5.764	798.057	0	796.8284	0	795.44
TZP	496	4.67	0.0597	6.732	795.518	0	794.2947	0	792.90

Table S3. Arabidopsis mutant lines used

Name of mutant line	Designation in stock centre o	Gene name	Arabidopsis gene identifie	Mutant background	PubMed ID
toc1-101	*toc1-101 t-DNA*	*TOC1 (TIMING OF CAB EXPRESSION1)*	AT5G61380	Col-0	PMID: 16212608
cca1-1 lhy-11	*cca1-1 lhy-11 t-DNA*	*CCA1 (CIRCADIAN CLOCK-ASSOCIATED 1) / LHY (LATE ELONGATED HYPOCOTYL)*	AT2G46830/AT1G01060	Col-0	PMID: 17540692
elf3-7	*elf3-7 EMS*	*ELF3 (EARLY FLOWERING3)*	AT2G25930	Col-0	PMID: 11402160
elf4-101	*elf4-101 t-DNA*	*ELF4 (EARLY FLOWERING4)*	AT2G40080	Col-0	PMID: 14605220
prr7-3	*SALK_030430C*	*PRR7 (PSEUDO-RESPONSE REGULATOR 7)*	AT5G02810	Col-0	PMID: 15705949
bzip60	*SALK_050203C*	*BASIC REGION/LEUCINE ZIPPER MOTIF 60*	AT1G42990	Col-0	PMID: 18574595
aox1a-1	*SALK_084897*	*AOX1a (ALTERNATIVE OXIDASE 1a)*	AT3G22370	Col-0	PMID: 18424626
rao2-1	*rao2-1 EMS*	*ANAC017 (Arabidopsis NAC domain-containing protein 17)*	AT1G34190	Col:LUC	PMID: 24045017
ANAC017-OE2	*rao2 complementation*	*ANAC017 (Arabidopsis NAC domain-containing protein 17)*	AT1G34191	Col:LUC	PMID: 30872424

Table S4. Binding sites of transcription factors regulating clock- and light-dependent processes to 56 genes that showed enhanced binding of ANAC017 in light upon

seqnames	start	end	log2(Fold)	p.value	FDR	gene	location	Bound by clock component, NACs (IGV)
chr1	1704628	1705028	1.96	4.54E-10	1.59E-07	AT1G05680	promoter	GI, PIF3, LHY, HY5, CCA1, NAC16, PIF4, ELF3, NAC102
chr2	15424916	15425316	1.56	5.48E-07	5.70E-05	AT2G36800	promoter	NAC102, LHY, NAC16, PIF3, CCA1, ELF3, GI
chr5	17176040	17176440	1.49	4.34E-06	1.90E-04	AT5G42830	promoter	PIF3, NAC102, HY5, ELF3
chr4	10349922	10350322	1.39	2.78E-06	1.62E-04	AT4G18880	promoter	HY5, LHY, GI, NAC102, PIF4, CCA1, PIF5, HY5
chr4	8974434	8974834	1.34	5.92E-06	2.12E-04	AT4G15760	promoter	LHY, PIF5, NAC102, GI, HY5, NAC13
chr5	25678321	25678721	1.34	3.03E-05	4.61E-04	AT5G64190	promoter	LHY, GI, PRR5, NAC102, NAC16,
chr2	1339433	1339833	1.33	6.51E-07	5.70E-05	at2g04050	promoter	GI, ELF3, NAC102, PIF3, NAC13, NAC16, NAC17
chr4	17571669	17572069	1.32	6.92E-06	2.12E-04	at4g37370	promoter	ELF3, NAC102, PIF3, ELF3, PIF4, NAC16, HY5
chr3	20633874	20634274	1.32	7.74E-06	2.12E-04	at3g55620	promoter	ELF3, NAC102, CCA1
chr5	17458834	17459234	1.32	3.35E-06	1.67E-04	at5g43450	promoter	NAC102, PIF3, PIF5, PIF4, HY5, GI, CCA1, NAC16, NAC13, NAC17
chr2	7919227	7919627	1.28	7.89E-06	2.12E-04	at2g18193	promoter	GI, PIF5, PIF3, HY5, NAC17
chr2	9254179	9254579	1.28	3.88E-05	4.98E-04	at2g21640	promoter	NAC13, NAC16, PIF4, PIF3, HY5, NAC17
chr1	11668583	11668983	1.27	2.68E-05	4.51E-04	at1g32350	promoter	NAC102, ELF3, PIF3
chr5	4755903	4756303	1.25	3.85E-05	4.98E-04	at5g14730	promoter	LHY, CCA1, PIF5, NAC102, HY5, NAC16, ELF3
chr2	2141171	2141571	1.24	1.34E-05	3.12E-04	at2g05710	promoter	NAC102, GI, LHY, PIF4, HY5, ELF3, PRR7
chr4	9600036	9600436	1.22	1.60E-05	3.29E-04	at4g17080	promoter	HY5, PIF4, NAC16, PIF4, NAC102, PRR7, HY5, PIF5
chr1	27233328	27233728	1.22	5.72E-05	5.72E-04	at1g72330	promoter	HY5, PIF4, GI, PIF3, LHY, NAC102
chr4	9673347	9673747	1.21	1.49E-04	1.11E-03	at4g17260	promoter	PIF3, LHY, NAC16, NAC13
chr2	19316310	19316710	1.21	4.22E-05	5.09E-04	at2g47000	promoter	PIF3, GI, HY5, LHY, NAC13, PIF3, NAC16
chr3	16923206	16923606	1.2	2.16E-04	1.45E-03	at3g46080	promoter	PIF4, HY5, NAC102, PIF3
chr3	9194971	9195371	1.2	2.96E-05	4.61E-04	at3g25250	promoter	GI, PIF4, PIF3, PIF5, HY5, NAC102, LHY, NAC13
chr5	4891405	4891805	1.2	2.70E-05	4.51E-04	at5g15090	promoter	PIF3, NAC13, ELF3, HY5, NAC102, GI
chr1	28745687	28746087	1.18	1.08E-04	8.40E-04	at1g76600	promoter	NAC102, PIF4, HY5, PIF5, PIF3, PRR5, ELF3
chr5	16290458	16290858	1.18	1.33E-05	3.12E-04	at5g40690	promoter	NAC102, PIF3, PIF4, HY5, PIF5, GI, NAC16, NAC17
chr2	8930466	8930866	1.18	2.00E-05	3.68E-04	at2g20720	promoter	HY5, PIF3, NAC012, NAC16, NAC17, ELF3, GI
chr1	11927803	11928203	1.18	5.19E-05	5.68E-04	at1g32920	promoter	PIF5, PRR5, ELF3, PIF3, PRR7, LHY, NAC16, NAC13
chr3	1080736	1081136	1.18	9.68E-05	8.06E-04	at3g04120	promoter	PIF4, LHY, NAC102, PIF5, GI, CCA1, HY5, PRR5, PRR7,
chr2	1150375	1150775	1.17	9.19E-05	7.84E-04	at2g03760	promoter	NAC102, PIF5, NAC13, NAC17,
chr3	2753011	2753411	1.16	9.91E-05	8.07E-04	at3g09020	promoter	NAC102, GI, PIF5, ELF3, PIF4, PIF3, HY5
chr5	2860724	2861124	1.15	5.57E-05	5.72E-04	at5g08790	promoter	ELF3, PIF3, PRR5, LHY, NAC102,
chr1	21887253	21887653	1.15	4.84E-05	5.47E-04	at1g59590	promoter	NAC16, PIF4, HY5, PIF5, NAC102, PIF3, NAC13, LHY
chr5	15631171	15631571	1.14	3.30E-04	1.99E-03	at5g39050	promoter	NAC102, HY5, GI, PIF4, ELF3,
chr5	24101769	24102169	1.13	2.95E-04	1.81E-03	at5g59820	promoter	PIF3, CCA1, LHY, GI, PIF5, NAC16, PRR7,
chr2	6758359	6758759	1.11	2.00E-03	8.24E-03	at2g15480	promoter	LHY, ELF3, GI, PIF4, NAC102, PIF3, HY5,
chr2	13631756	13632156	1.11	3.98E-05	4.98E-04	at2g32020	promoter	LHY, HY5, ELF3, GI, PIF4, PIF5, NAC102PRR7, PIF3, NAC16, NAC13
chr4	2234575	2234975	1.1	4.35E-04	2.49E-03	at4g04490	promoter	PIF3, ELF3, NAC16, NAC102, NAC13, HY5
chr1	16137385	16137785	1.1	8.02E-05	7.39E-04	at1g42990	promoter	NAC102, NAC13, LHY, NAC16, HY5, PIF5, PRR5, PIF3,
chr1	5869467	5869867	1.1	1.54E-03	6.73E-03	at1g17170	promoter	NAC102, HY5, NAC13, ELF3
chr2	1982979	1983379	1.09	3.25E-03	1.19E-02	at2g05420	promoter	NAC17, NC13, ELF3, PIF3, NAC16,
chr5	6597839	6598239	1.09	1.41E-03	6.25E-03	at5g19550	promoter	HY5, ELF3, LHY, PIF3
chr1	8384808	8385208	1.09	1.56E-04	1.12E-03	at1g23710	promoter	LHY, NAC102, PIF5, GI, HY5, PIF4, PRR5, CCA1, PRR7, ELF3, PIF3, NAC13, NAC16
chr2	19010963	19011363	1.09	1.52E-04	1.11E-03	at2g46310	promoter	NAC16, PIF3, PIF5, PIF4, PRR5, PRR7, HY5,
chr2	6761302	6761702	1.08	2.82E-03	1.12E-02	at2g15480	coding	PIF3, HY5, ELF3, PIF4, PIF5,
chr1	3337908	3338308	1.08	2.24E-04	1.48E-03	at1g10170	promoter	PIF3, NAC102, ELF3, GI, PIF4, HY5, NAC16
chr3	4201689	4202089	1.06	5.89E-04	3.06E-03	at3g13080	promoter	ELF3, HY5, PIF3, PIF4, GI, LHYNAC16, PRR5
chr2	17409171	17409571	1.06	1.01E-04	8.07E-04	at2g41730	promoter	NAC16, NAC102, GI, PIF3, LHY, PIF4, NAC13, ELF3, HY5
chr3	3270929	3271329	1.06	4.32E-04	2.49E-03	at3g10500	promoter	LHY, PIF5, ELF3, NAC102, PIF4, HY5, CCA1, PIF3, GI,
chr3	7906346	7906746	1.05	8.94E-05	7.82E-04	at3g22370	promoter	LHY, CCA1, GI, NAC102, GI, PIF4, PIF5, NAC13, HY5, NAC16ELF3, PRR7, PRR5,
chr2	18232564	18232964	1.05	3.49E-04	2.07E-03	at2g44070	promoter	PIF3, CCA1, ELF3, PIF4, HY5, PRR5, PIF5
chr4	5447679	5448079	1.05	1.07E-03	4.94E-03	at4g08555	promoter	PIF3, HY5, NAC16, CCA1, NAC102
chr2	8955716	8956116	1.04	9.47E-04	4.42E-03	at2g20800	promoter	NAC17
chr4	13904123	13904523	1.03	5.01E-04	2.78E-03	at4g27940	promoter	LHY, NAC102, PIF4, HY5, PIF5, ELF3, PRR5, PIF3, NAC13, NAC16, GI, TOC1
chr1	5871422	5871822	1.02	1.29E-02	3.28E-02	at1g17180	promoter	LHY, NAC13, NAC16
chr4	9390778	9391178	1.01	2.39E-04	1.55E-03	at4g16680	promoter	NAC16, PRR5, NAC102, ELF3, GI, NAC13, CCA1, PIF3, PRR7
chr3	11195249	11195649	1.01	5.94E-04	3.06E-03	at3g29250	promoter	PIF4, PIF5, GI, NAC102, LHY, HY5, PIF3, NAC16, PRR5, NAC17,
chr4	7494167	7494567	1	2.81E-04	1.76E-03	at4g12735	promoter	ELF3, NAC102, HY5, PIF4, PIF3, NAC13, NAC16,
chr1	11615929	11616329	1	8.08E-04	3.93E-03	at1g32230	3' UTR region	HY5, PIF5, PIF4, PIF3, GI, ELF3

Table S5. Primers sequences used in this study.

Name	Arabidopsis gene identifier	Sequence (5'- 3')	Use
attB1F_NAC17_linker_noATG_FW	At1g34190	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGGATCCGGAGGTGGAGCGGATTCTTCACCCGATT	gateway cloning of CDS of NAC17
attB2R_NAC17_linker_RV	At1g34190	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCACCTCCGGATCMGTCTTTCAAGAGAAGACTTCTAC	gateway cloning of CDS of NAC17
attB4_2kb PromNAC17_FW	At1g34190	GGGGACAACTTTGTATAGAAAAGTTGCTTGTGTGGATGATACTAAATTTTG	gateway cloning of 2kb promoter of NAC17
attB1r_PromNAC17_Rev	At1g34190	GGGGACTGCTTTTTTGTACAAACTTGCTACGTAACAAATCAAAACCGATC	gateway cloning of 2kb promoter of NAC17
attB1F_GFP_FW		GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGTGAGCAAGGGCGAGGA	gateway cloning of GFP
attB2R_GFP linker_REV		GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCACCTCCGGATCCCTTGTACAGCTCGTCCATGCC	gateway cloning of GFP
UBC_qRT_F	At5g25760	CTGCGACTCAGGGAATCTTCTA	qPCR
UBC_qRT_R	At5g25760	TTGTGCCATTGAATTGAACCC	qPCR
CCA1_QRT_F	AT2G46830	TCGAAAGACGGGAAGTGGAACG	qPCR
CCA1_QRT_R	AT2G46830	GTCGATCTTCATTGGCCATCTCAG	qPCR
LHY_QRT_F	AT1G01060	GAGCTTGGCAACGAATTGAAGAAC	qPCR
LHY_QRT_R	AT1G01060	AAAGCTTGGCAAACAGGGATGC	qPCR
PRR5_QRT_F	AT5G24470	CAGCTTTCACACGGTACGTTCAC	qPCR
PRR5_QRT_R	AT5G24470	TTGGAGGCGGTTCAGATGTATTG	qPCR
PIF4_QRT_F	AT2G43010	TCAGATGCAGCCGATGGAGATG	qPCR
PIF4_QRT_R	AT2G43010	CGACGGTTGTTGACTTTGCTGTC	qPCR
NAC017_QRT_F	At1g34190	GTACTACCATAGCAAAGAAGGG	qPCR
NAC017_QRT_R	At1g34190	AAGACTTCTACCTGAGACTCG	qPCR
AOX1a_qRT_F1	At3g22370	GACGGTCCGTACGGTTTCG	qPCR
AOX1a_qRT_R1	At3g22370	CTTCTGATTCGCGTCCTCCTCCT	qPCR
UGT74E2_RTF	At1g05680	TTTCCCTTCGTTCCCGATGCTG	qPCR
UGT74E2_RTR	At1g05680	TTCGGGTATGAGGACGATTCGC	qPCR
SOT12-qRT-F	AT2G03760	AAGGACTTTGGCACACACAAGC	qPCR
SOT12-qRT-R	AT2G03760	AAGAAACTGGAAACTTGTGTCGG	qPCR
ATAF2-qRT-F	AT5G08790	TTGGGTATCAAGAAAGCACTCGTC	qPCR
ATAF2-qRT-R	AT5G08790	ACCCAATCATCAAGTCGTAGGTTG	qPCR
bzip60-qRT-F	AT1G42990	CGATGATGCTGTGGCTAAAA	qPCR
bzip60-qRT-R	AT1G42990	TCTCAAGCATTCTCTTTCGAGAT	qPCR
qAOX1D for	At1g32350	CTTTCACAACCCAAATGGTACG	qPCR
qAOX1D rev	At1g32351	GCCTCTTCTTCTAAGTATCCAGTG	qPCR
qRT_ANAC053_Fwd	AT3G10500	GGGTTATGCATGAGTATCGGTTGG	qPCR
qRT_ANAC053_Rev	AT3G10500	GCACAAACGCATCTTGGTGAAC	qPCR
NDA1_qRT_Fwd	AT1G07180	GTATCCAACCGGCGATTTCACG	qPCR
NDA1_qRT_Rev	AT1G07180	AGTTACAGTCTCACAATGCACCTC	qPCR
NDB2_qRT_Fwd	AT4G05020	CATCCTGACCATGTTTGACAAGAG	qPCR
NDB2_qRT_Rev	AT4G05020	CTCTCCTCCTTTGGTTTTAGCAG	qPCR
ACO3_qPCR_For	AT2G05710	TGAGTATGGAAGTGGTAGCTCACG	qPCR
ACO3_qPCR_Rev	AT2G05710	AATCACCGCTTTAACACCCTGTAG	qPCR
ACTIN2_ChIP_FWD	AT3G18780	ACTACGAGCAGGAGATGGAAACCT	ChIP-qPCR
ACTIN2_ChIP_REV	AT3G18780	GCAGCTTCCATTCCCACAAACGAG	ChIP-qPCR
AOX1a_ChIP_FWD	AT3G22370	AGCTCTTGGCGACCACGCAA	ChIP-qPCR
AOX1a_ChIP_REV	AT3G22370	CCCTTGTGGTCATGAGAGAGACT	ChIP-qPCR
UGT74E2_ChIP-1F	At1g05680	TTGTCTATGTTCCGTGGCGA	ChIP-qPCR
UGT74E2_ChIP-1R	At1g05680	GCAGTGTCTCTCTCTCAGGG	ChIP-qPCR
DOGT1_ChIP-1F	AT2G36800	AGGATAAGATGCGTGGAGAGT	ChIP-qPCR
DOGT1_ChIP-1R	AT2G36800	GTGAGCCCTCCAAGTTGTTG	ChIP-qPCR
HSFA4A_ChIP-1F	AT4G18880	AGATTGGGTTTGGTGGAATGT	ChIP-qPCR
HSFA4A_ChIP-1R	AT4G18880	ACAACGAATTTTCTTACGGCCA	ChIP-qPCR
AOX1d_ChIP-1F	AT1G32350	TGGAGGAAATGTTTGACACGT	ChIP-qPCR
AOX1d_ChIP-1R	AT1G32350	AGTTGGTGTGTCTATCTCGTGA	ChIP-qPCR
ACO3_ChIP-1F	AT2G05710	GAGAGGGGCTGCGTAGATTA	ChIP-qPCR
ACO3_ChIP-1R	AT2G05710	TTGGGATCGATCATGGAGGA	ChIP-qPCR
ABCB4_ChIP-1F	AT2G47000	AGCAAGAAACACGTCCGAATTT	ChIP-qPCR
ABCB4_ChIP-1R	AT2G47000	TCATTGATTCTGAAAAGGCGCA	ChIP-qPCR
VDAC3_ChIP-1F	AT5G15090	CATGAGTCGGTGTCCCTCTT	ChIP-qPCR
VDAC3_ChIP-1R	AT5G15090	CTAGAGAGTACACGGCCTGC	ChIP-qPCR
SOT12_ChIP-1F	AT2G03760	GTTTGGGTGGTGAAATGGTCA	ChIP-qPCR
SOT12_ChIP-1R	AT2G03760	AGAGTCGTGATTCTCCTTCTTTC	ChIP-qPCR
ANAC081_ChIP-1F	AT5G08790	ACCGTAATCTCCTGCTTCTCA	ChIP-qPCR
ANAC081_ChIP-1R	AT5G08790	TACAACTTCCGCCCCAAGAA	ChIP-qPCR
bZIP60_ChIP-1F	AT1G42990	ATGCTTCCAAATTCCTCCGC	ChIP-qPCR
bZIP60_ChIP-1R	AT1G42990	ACGCGTCCATAATCAACACG	ChIP-qPCR
ANAC053_ChIP-1F	AT3G10500	CGGCTAGGATTACGAATGTGG	ChIP-qPCR
ANAC053_ChIP-1R	AT3G10500	TTGGTTCGCGCAAATGAAGA	ChIP-qPCR
NDB4_ChIP-1F	AT2G20800	AGGGTACGTGAGAGAGAGGT	ChIP-qPCR
NDB4_ChIP-1R	AT2G20800	GGGAACGCGGAACATAATGT	ChIP-qPCR
RCD1_ChIP-1F	AT1G32230	CGTGTATTGACCGCCTCTTC	ChIP-qPCR
RCD1_ChIP-1R	AT1G32230	TTCTTAAGTCGGCGGTTCCT	ChIP-qPCR
CCA1_pgbkpad_F	AT2G46830	CCG GAATTC ATGGAGACAA ATTCG	Y2H cloning
CCA1_pgbkpad_R	AT2G46830	CGC GGATCC TCATGTG GAAGC	Y2H cloning
PIF5_pgbkpgad_F	AT3G59060	ccg GAATTC ATGGAACAAGTGTTTG	Y2H cloning
PIF5_pgbkpgad_R	AT3G59060	cgc GGATCC TCAGCCTATTTTACCC	Y2H cloning
PIF4_pgbkpgad_F	AT2G43010	ggaattc CATATG ATGGAACACCAAGGT	Y2H cloning
PIF4_pgbkpgad_R	AT2G43010	ccg GAATTC CTAGTGGTCCAAACG	Y2H cloning
HY5_pgbkpgad_F	AT5G11260	ccg GAATTC ATGCAGGAACAAGCG	Y2H cloning
HY5_pgbkpgad_R	AT5G11260	cgc GGATCC TCAAAGGCTTGCATC	Y2H cloning
ELF3_pgbkpgad_F	AT2G25930	tcc CCCGGG ATGAAGAGAGGGAAA	Y2H cloning
ELF3_pgbkpgad_R	AT2G25930	cgcGGATCC TTAAGGCTTAGAGGA	Y2H cloning
PRR7_pgbkpgad_F	AT5G02810	ccg GAATTC ATGAATGCTAATGAG	Y2H cloning
PRR7_pgbk_R	AT5G02810	aaaa CTGCAG TTAGCTATCCTCAATG	Y2H cloning
PRR7_pgad_R	AT5G02810	cc ATCGAT TTAGCTATCCTCAATG	Y2H cloning
GI_pgbkpgad_F	AT1G22770	ccg GAATTC ATGGCTAGTTCATCT	Y2H cloning
GI_pgbkpgad_R	AT1G22770	cgc GGATCC TTATTGGGACAAGGA	Y2H cloning
LYH_pgbkpgad_F	AT1G01060	GGAATTCCATATG ATGGATACTA ATACATCTGG	Y2H cloning
LYH_pgbkpgad_R	AT1G01060	CGC GGATCC TCATGTAG AAGCTTC	Y2H cloning
NAC017_ pgbkpgad_F	At1g34190	GGAATTC CATATG ATGGCGGATT CTTCA	Y2H cloning
NAC017_ pgbkpgad_R	At1g34190	TCC CCCGGG CTA ACGGCTGAAGCTA	Y2H cloning