Table 11. Gene set 5 (37 genes): Continuous red light (Rc)-repressed genes defined as robustly Rc-light-repressed and statistically-dependent on PIF3 for Rc-light-repression.

AGI_LOCUS	Description	Function	MFR(WT) (D1/R1)	MFR(pif3) (D1/R1)	MFRR (WT/pif3)	BIN
Bin A						
AT5G02580	expressed protein	H/U	6.11	1.99	3.07	A
AT3G25730	AP2 domain-containing transcription factor	TXN	2.75	0.79	3.49	A
AT4G01250	WRKY family transcription factor	TXN	2.23	0.83	2.68	A
Bin B						
AT2G21910	cytochrome P450, putative	CM	3.49	2.31	1.51	B
AT1G13260	DNA-binding protein RAV1 (RAV1)	TXN	2.69	1.53	1.76	B
AT3G01450	expressed protein	H/U	2.66	1.39	1.91	B
AT3G29370	expressed protein	H/U	2.55	1.66	1.54	B
AT2G28400	expressed protein contains Pfam profile PF04520	H/U	2.11	1.18	1.79	B
Bin C						
AT4G16780	homeobox-leucine zipper protein 4 (HAT4)	TXN	4.54	3.05	1.49	C
AT4G35720	expressed protein contains Pfam profile PF03087	H/U	4.21	2.94	1.43	C
AT5G07010	sulfotransferase family protein similar to steroid sulfotransferase 3	CM	3.95	2.68	1.47	C
AT5G44260	zinc finger (CCCH-type) family protein	TXN	3.71	2.92	1.27	C
AT4G08950	phosphate-responsive protein, putative (EXO) similar to phi-1	SIG	3.31	2.64	1.25	C
AT4G10240	zinc finger (B-box type) family protein	TXN	3.13	2.19	1.43	C
AT4G16670	expressed protein	H/U	2.92	2.32	1.26	C
AT4G14465	DNA-binding protein-related contains AT-hook motif	TXN	2.47	1.79	1.38	C
AT3G57800	basic helix-loop-helix (bHLH) family protein	TXN	2.09	1.59	1.32	C
AT2G37680	phytochrome A specific signal transduction component (FHY1)	SIG	2.08	1.51	1.38	C
AT5G18600	glutaredoxin family protein	TR	2.06	1.41	1.46	C
Bin D						
AT4G36010	pathogenesis-related thaumatin family protein	S/D	4.09	3.37	1.21	D
AT3G60390	homeobox-leucine zipper protein 3 (HAT3)	TXN	2.79	2.48	1.13	D
AT1G14920	gibberellin response modulator (GAI) (RGA2)	H	2.52	2.22	1.14	D
AT5G61440	thioredoxin family protein	S/D	2.13	1.81	1.18	D
AT3G58620	tetratricopeptide repeat (TPR)-containing protein	CM	2.10	1.74	1.21	D
AT1G71970	expressed protein	H/U	2.01	1.79	1.12	D
AT5G60680	expressed protein contains Pfam profile PF04520	H/U	2.01	1.69	1.19	D
Bin E						
AT2G18300	basic helix-loop-helix (bHLH) family protein	TXN	2.08	2.47	0.84	E
AT2G20750	ß-expansin, putative (EXPB1)	G/D	1.64	2.42	0.68	E
AT5G02550	expressed protein	H/U	1.70	2.25	0.75	E
AT3G54770	RNA recognition motif (RRM)-containing protein	TXN	1.66	2.16	0.77	E
AT5G66330	leucine-rich repeat family protein	SIG	1.56	2.11	0.74	E
AT1G15550	gibberellin 3-beta-dioxygenase /hydroxylase (GA4)	H	1.39	2.10	0.66	E
AT4G25420	gibberellin 20-oxidase	H	1.50	2.04	0.73	E
AT1G49200	zinc finger (C3HC4-type RING finger) family protein	TXN	1.57	2.02	0.78	E
AT1G13250	glycosyl transferase family 8 protein	CM	1.68	2.02	0.83	E
Bin F						
AT4G30170	peroxidase, putative identical to peroxidase ATP8a	S/D	1.31	2.17	0.61	F
AT5G02890	transferase family protein contains	CM	1.40	2.37	0.59	F
No Bin G						

This set comprises all genes from Fig. 12 displaying a 2-fold or greater decrease in expression in response to 1 h Rc in WT (Bins A-D in Fig. 12) or in *pif3* (Bins E and F in Fig. 12), arranged according to Bin in Fig. 12.

Column-heading definitions:

AGI locus: AGI locus number.

Description: Brief gene description or name derived primarily from current TIGR and TAIR websites.

Function: Functional category: Transcription (TXN); Cellular Metabolism (CM); Signaling (SIG); Transport (TR); Hormones (H); Growth and Development (G/D); Stress/Defense (S/D); Hypothetical/Unknown (H/U).

MFR(WT)(D1/R1): Mean Fold Repression of expression in wild-type (WT) Arabidopsis seedlings exposed to 1 h Rc (R1) compared to the level in dark control seedlings (D1).

MFR(*pif3*)(D1/R1): Mean Fold Repression of expression in *pif3* mutant seedlings exposed to 1 h Rc (R1) compared to the level in dark control seedlings (D1).

MFRR(WT/*pif3*): Mean Fold Repression Ratio = [MFR(WT)(D1/R1)] ÷ [MFR(*pif3*)(D1/R1)]

Bin: From Fig. 12.