Table 9. Gene set 4 (35 genes): Continuous red light (Rc)-induced genes defined as robustly Rc-light-responsive but not robustly dependent on either phyB or PIF3 for this Rc-light responsiveness

AGI LOCUS	DESCRIPTION	MFI(WT) (R1/D1)	MFI(*pif3*) (R1/D1)	MFIR (WT/*pif3*)	BIN
Transcription (TX)					
AT2G46790	pseudo-response regulator 9 (APRR9)	25.50	33.19	0.77	E
AT5G11260	bZIP protein HY5 (HY5)	5.61	6.62	0.85	E
AT3G47500	Dof-type zinc finger domain (DOF)	5.32	5.10	1.04	D
AT2G46830	myb-related transcription factor (CCA1)	4.18	3.87	1.08	D
AT5G15850	zinc finger protein CONSTANS-LIKE 1 (COL1)	4.10	3.05	1.35	C
AT4G25470	DRE-binding protein (DREB1C) (CBF2)	3.67	4.90	0.75	E
AT1G06040	zinc finger (B-box type) family protein (ZF2)	3.61	3.51	1.03	D
AT1G43160	AP2 domain (RAP2.6)	2.92	3.67	0.79	E
AT2G28550	AP2 domain (RAP2.7)	2.89	2.35	1.23	D
AT1G15100	zinc finger (C3HC4-type RING finger) family protein (RHA2A)	2.40	2.33	1.03	D
AT4G11360	zinc finger (C3HC4-type RING finger) family protein (RHA1b)	2.35	2.35	1.00	E
Photosynthesis/Chloroplast (P/C)					
AT4G17090	ß-amylase (CT-BMY)	3.71	4.95	0.75	E
Cellular Metabolism (CM)					
AT3G51240	naringenin 3-dioxygenase (F3H)	11.51	8.91	1.29	C
AT4G20860	FAD-binding domain	2.69	2.89	0.93	E
AT2G29340	short-chain dehydrogenase	2.59	2.16	1.20	D
AT4G37760	squalene monooxygenase (SQE)	2.49	2.20	1.13	D
AT4G10040	cytochrome c,	2.14	2.78	0.77	E
AT1G23740	oxidoreductase, zinc-binding dehydrogenase family protein	2.11	1.79	1.18	D
AT5G54960	pyruvate decarboxylase,	2.03	2.30	0.88	E
Signaling (S)					
AT2G02950	phytochrome kinase substrate 1 (PKS1)	7.21	5.14	1.40	C
AT2G30040	protein kinase family protein protein kinase domain	6.43	6.10	1.05	D
AT2G46340	phytochrome A supressor spa1 (SPA1)	4.09	3.02	1.35	C
Transport (TR)					
AT5G44110	ABC transporter family protein	13.89	10.52	1.32	C
AT2G37970	SOUL heme-binding family protein	6.22	4.44	1.40	C
AT1G61890	MATE efflux family protein	2.26	2.58	0.87	E
Growth/Development (G/D)					
AT1G69530	expansin (EXP1)	2.06	1.75	1.18	D
Hormones (H)					
AT4G03400	auxin-responsive GH3 family protein	3.50	4.06	0.86	E
AT4G38840	auxin-responsive protein,	2.35	1.69	1.39	C
Stress/Defense (S/D)					
AT1G74310	heat shock protein 101 (HSP101)	2.37	13.17	0.18	G
AT2G29450	glutathione S-transferase (103-1A)	2.36	3.48	0.68	E

AT3G09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	2.16	3.26	0.66	F
AT5G52640	heat shock protein 81-1 (HSP81-1)	2.15	12.11	0.18	G
AT2G21970	stress enhanced protein 2 (SEP2) nearly	2.01	1.82	1.11	D
Hypothetical/Unknown (H/U)					
AT2G40080	expressed protein	5.01	4.24	1.18	D
AT1G13930	expressed protein	3.56	2.34	1.52	B

This is a subset of Gene set 2 that was defined previously by Tepperman et al. (1) as not, or only marginally, dependent on phyB for Rc-responsiveness.

Column-heading definitions:
AGI locus: AGI locus number.
Description: Brief gene description or name derived primarily from current TIGR and TAIR websites.
MFI(WT)(R1/D1): Mean Fold Induction of expression in wild-type (WT) Arabidopsis seedlings exposed to 1 h Rc (R1) over the level in dark control seedlings (D1).
MFI(*pif3*)(R1/D1): Mean Fold Induction of expression in *pif3* mutant seedlings exposed to 1 h Rc (R1) over the levels in dark control seedlings (D1).
MFIR(WT/*pif3*): Mean Fold Induction Ratio = [MFI(WT)(R1/D1)] ÷ [MFI(*pif3*)(R1/D1)].
Bin: From Fig. 3. Bin C: genes with MFIR(WT/*pif3*) of 1.25-1.5. Bin D: genes with MFIR(WT/*pif3*) of 1-1.25; Bin E genes with MFIR(*pif3*/WT) of 1-1.50.

Genes are grouped into functional categories as indicated and arrayed within these categories by magnitude of Rc-responsiveness in WT (MFI(WT)(R1/D1)) in descending order.

1. Tepperman, J. M., Hudson, M. E., Khanna, R., Zhu, T., Chang, H.-S., Wang, X. & Quail, P. H. (2004) *Plant J.* **38**, 725-739.