Table 6. Gene set 1 (46 genes): Continuous red light (Rc)-induced genes defined as both robustly Rc-light-induced and moderately to robustly dependent on PIF3 for this Rc-light-induction.

AGI LOCUS	DESCRIPTION	MFI(WT) (R1/D1)	MFI(pif3) (R1/D1)	MFIR (WT/pif3)	BIN
Transcription (TX)					
AT5G24120	RNA polymerase sigma subunit SigE (sigE)	23.28	11.98	1.94	B
AT3G02380	zinc finger protein CONSTANS-LIKE 2 (COL2)	11.25	4.40	2.55	A
AT5G47610	zinc finger (C3HC4-type RING finger)	4.45	2.70	1.65	B
AT4G26150	zinc finger (GATA type)	3.36	1.69	1.99	B
AT5G56860	zinc finger (GATA type)	2.45	1.33	1.84	B
AT1G07050	Zinc finger protein Constans-like 15 (COL15)	2.42	1.54	1.56	B
Photosynthesis/Chloroplast (P/C)					
AT4G14690	**chlorophyll A-B binding family protein/ELIP**	**13.73**	**5.51**	**2.49**	**A**
AT3G22840	chlorophyll A-B binding family protein/ ELIP	13.47	5.89	2.29	A
AT4G27030	expressed protein	3.85	2.35	1.64	B
AT2G05100	**chlorophyll A-B binding protein / LHCII type II**	**3.76**	**1.35**	**2.79**	**A**
AT1G14345	expressed protein	3.45	2.01	1.72	B
AT3G17040	Psbs maturation factor	3.10	1.89	1.64	B
AT1G44446	chlorophyll a oxygenase (CAO) / chlorophyll b synthase	3.06	1.99	1.53	B
AT1G44000	expressed protein	3.05	1.74	1.75	B
AT5G54270	chlorophyll A-B binding protein / LHCII type III	3.02	1.07	2.81	A
AT3G54890	**chlorophyll A-B binding protein / LHCI type I**	**2.84**	**1.19**	**2.39**	**A**
AT5G13630	**magnesium-chelatase subunit chloroplast, putative (CHLH)**	**2.73**	**1.32**	**2.06**	**A**
AT1G80130	expressed protein	2.68	1.32	2.04	A
AT2G34430	chlorophyll A-B binding protein / LHCII type I	2.46	1.21	2.03	A
AT3G59400	genomes uncoupled 4 (GUN4)	2.42	1.12	2.16	A
AT1G50250	**FTSH1, chloroplast**	**2.42**	**1.48**	**1.63**	**B**
AT5G57345	expressed protein	2.32	1.41	1.65	B
AT2G23670	expressed protein	2.28	1.31	1.74	B
AT4G33010	**glycine decarboxylase**	**2.23**	**1.14**	**1.96**	**B**
AT5G08050	expressed protein	2.08	1.23	1.69	B
AT2G21330	fructose-bisphosphate aldolase	2.03	0.78	2.61	A
AT2G33250	expressed protein	2.01	1.18	1.71	B
Cellular Metabolism (CM)					
AT5G49730	ferric reductase-like	3.44	2.19	1.57	B
AT3G21560	UDP-glucosyltransferase	3.36	1.74	1.93	B
AT2G01290	ribose 5-phosphare isomerase	2.50	1.58	1.58	B
AT1G27480	lecithin:cholesterol acyltransferase family protein / LACT	2.40	1.23	1.94	B
AT3G23530	cyclopropane fatty acid synthase, chalcone synthase (CHSY)	2.35	1.03	2.27	A
AT5G13930	chalcone synthase / naringenin-putative / CPA-FA synthase	2.05	1.23	1.67	B

Signaling (S)					
AT5G24850	cryptochrome dash (CRYD)	6.55	4.05	1.62	B
AT5G23730	transducin family protein / WD-40 repeat	3.76	2.21	1.70	B
Transport (TR)					
AT1G17100	SOUL heme-binding family protein	5.34	2.57	2.08	A
AT3G21670	nitrate transporter (NTP3)	3.27	2.12	1.54	B
AT1G75460	ATP-dependent protease La (LON) domain-containing protein	3.20	1.79	1.78	B
AT3G27170	chloride channel protein (CLC-b)	2.68	1.58	1.69	B
AT2G03750	sulfotransferase family protein	2.02	1.13	1.79	B
Growth/Development (G/D)					
AT2G36870	xyloglucan:xyloglucosyl transferase	2.45	1.13	2.17	A
Stress/Defense (S/D)					
AT4G09350	DNAJ heat shock N-terminal domain-containing protein	2.37	1.48	1.60	B
Hypothetical/Unknown (H/U)					
AT5G55620	expressed protein	3.77	1.80	2.10	A
AT5G42760	O-methyltransferase N-terminus domain-containing protein	2.67	1.43	1.86	B
AT1G42550	expressed protein	2.42	1.58	1.53	B
AT1G49660	expressed protein	2.07	1.30	1.59	B

This set comprises genes displaying a 2-fold or greater increase in expression in response to 1 h Rc in WT from Bins A and B of Figure 3 combined. The genes in Bins A and B of Figure 3 display a 1.5-fold or greater increase in expression in WT compared to *pif3* in response to 1 h Rc.

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 A: genes with MFIR(WT/*pif3*) of $\geq$ 2. Bin B: genes with a MFIR(WT/*pif3*) of 1.5-2.

Genes in bold-face type were identified as being phyB-regulated at 1 h of Rc in a previous study using the 8000-gene Affymetrix array (1). 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.