Table 8. Gene set 2 (143 genes): Continuous red light (Rc)-induced genes defined as robustly Rc-light-responsive, but not, or only marginally, depending on 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) / (TOC1-L1)	25.50	33.19	0.77	X
AT2G31380	zinc finger (B-box type) family protein (ZF3)	13.67	11.08	1.23	D
AT5G44190	myb family transcription factor (GLK2)	8.11	6.06	1.34	C
AT2G30520	signal transducer of phototropic response (RPT2)	8.11	5.55	1.46	C
AT3G21890	zinc finger (B-box type) family protein	7.21	8.51	0.85	X
AT5G24470	pseudo-response regulator 5 (APRR5)	7.21	7.48	0.96	X
AT5G17300	myb family transcription factor	6.21	5.73	1.08	X
AT3G17609	bZIP transcription factor family protein / HY5-like protein (HYH) nearly	5.90	4.71	1.25	X
AT5G11260	bZIP protein HY5 (HY5)	5.61	6.62	0.85	X
AT3G47500	Dof-type zinc finger domain-containing protein (DOF)	5.32	5.10	1.04	X
AT2G21320	zinc finger (B-box type) family protein (ZF6)	5.30	4.02	1.32	C
AT2G46830	myb-related transcription factor (CCA1)	4.18	3.87	1.08	X
AT5G15850	zinc finger protein CONSTANS-LIKE 1 (COL1)	4.10	3.05	1.35	C
AT1G18330	myb family transcription factor	4.07	4.06	1.00	X
AT3G54990	AP2 domain-containing transcription factor	3.95	2.93	1.35	C
AT2G39250	AP2 domain-containing transcription factor	3.85	3.51	1.10	X
AT4G25470	DRE-binding protein (DREB1C) / CRT/DRE-binding factor 2 (CBF2)	3.67	4.90	0.75	X
AT1G06040	zinc finger (B-box type) family protein / salt-tolerance protein (STO) (ZF2)	3.61	3.51	1.03	X
AT1G01520	myb family transcription factor	3.46	3.98	0.87	X
AT5G54470	zinc finger (B-box type) family protein	3.32	3.01	1.10	X
AT5G37260	myb family transcription factor	3.00	2.92	1.03	X
AT3G16350	myb family transcription factor ;	2.97	2.07	1.43	C
AT1G43160	AP2 domain-containing protein RAP2.6 (RAP2.6)	2.92	3.67	0.79	E
AT2G28550	AP2 domain-containing transcription factor RAP2.7 (RAP2.7) nearly	2.89	2.35	1.23	D
AT5G35970	DNA-binding protein	2.82	1.94	1.45	C
AT4G38960	zinc finger (B-box type) family protein zinc finger protein-- Oryza sativa	2.45	2.14	1.15	X
AT1G62030	DC1 domain-containing protein	2.41	2.31	1.05	X
AT1G15100	zinc finger (C3HC4-type RING finger) family protein (RHA2a)	2.40	2.33	1.03	X
AT3G02150	TCP family transcription factor	2.38	2.13	1.12	X
AT4G11360	zinc finger (C3HC4-type RING finger) family protein (RHA1b)	2.35	2.35	1.00	X
AT3G09600	myb family transcription factor	2.32	2.78	0.83	X
AT4G00050	basic helix-loop-helix (bHLH) family protein	2.31	2.02	1.14	X
AT1G01060	myb family transcription factor (LHY)	2.30	2.06	1.12	D
AT1G78600	zinc finger (B-box type) family protein	2.26	2.87	0.79	E
AT3G23210	basic helix-loop-helix (bHLH) family protein	2.25	1.57	1.43	C
AT1G70000	DNA-binding family protein	2.21	1.56	1.42	C
AT1G26790	Dof-type zinc finger domain-containing protein	2.20	1.59	1.39	C
AT2G36080	DNA-binding protein	2.17	1.74	1.24	D
AT1G67030	zinc finger (C2H2 type) family protein (ZFP6)	2.16	2.41	0.90	X
AT1G72030	GCN5-related N-acetyltransferase (GNAT) family protein	2.12	1.64	1.29	C
AT3G10910	zinc finger (C3HC4-type RING finger) family protein	2.03	1.94	1.05	X
AT1G06180	myb family transcription factor	2.00	1.40	1.43	X

Photosynthesis/Chloroplast (P/C)

AT4G17090	beta-amylase (CT-BMY) / 1	3.71	4.95	0.75	E
AT1G78510	solanesyl diphosphate synthase (SPS)	3.00	2.43	1.23	D
AT1G17050	geranyl diphosphate synthase	2.66	2.36	1.13	D
AT1G10960	ferredoxin	2.20	1.54	1.43	C
AT1G76570	chlorophyll A-B binding family protein	2.03	1.69	1.20	D

Cellular Metabolism (CM)

AT3G51240	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H)	11.51	8.91	1.29	C
AT5G15950	adenosylmethionine decarboxylase family protein	4.80	3.54	1.36	C
AT5G17050	UDP-glucoronosyl/UDP-glucosyl transferase family protein	4.63	4.50	1.03	X
AT1G73480	hydrolase	4.62	4.39	1.05	X
AT1G06000	UDP-glucoronosyl/UDP-glucosyl transferase family protein	4.41	3.25	1.36	C
AT5G64170	dentin sialophosphoprotein-related	4.30	4.69	0.92	X
AT5G20070	MutT/nudix family protein low	3.87	3.40	1.14	D
AT4G17670	senescence-associated protein-related	3.21	2.37	1.35	C
AT4G12310	cytochrome P450	3.06	2.92	1.05	X
AT5G11110	sucrose-phosphate synthase	2.93	3.38	0.87	X
AT1G48100	glycoside hydrolase family 28 protein / polygalacturonase	2.90	2.99	0.97	X
AT5G43450	2-oxoglutarate-dependent dioxygenase	2.83	3.99	0.71	E
AT1G07010	calcineurin-like phosphoesterase family protein	2.80	2.51	1.11	X
AT3G21760	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2.69	2.21	1.22	D
AT1G66330	senescence-associated family protein	2.69	2.31	1.16	X
AT4G20860	FAD-binding domain-containing protein	2.69	2.89	0.93	X
AT4G04840	methionine sulfoxide reductase domain-containing protein	2.66	2.06	1.29	C
AT2G29340	short-chain dehydrogenase/reductase (SDR) family protein	2.59	2.16	1.20	X
AT3G47430	peroxisomal biogenesis factor 11 family protein / PEX11 family protein	2.55	2.01	1.27	C
AT4G37760	squalene monooxygenase	2.49	2.20	1.13	X
AT3G62410	CP12 domain-containing protein	2.42	1.99	1.22	D
AT5G58770	dehydrodolichyl diphosphate synthase	2.39	2.75	0.87	X
AT1G66130	oxidoreductase N-terminal domain-containing protein	2.37	2.10	1.13	X
AT1G61890	MATE efflux family protein	2.26	2.58	0.87	X
AT4G11570	haloacid dehalogenase-like hydrolase family protein	2.22	2.35	0.95	X
AT1G72500	inter-alpha-trypsin inhibitor heavy chain-related low	2.19	1.88	1.17	X
AT1G12240	beta-fructosidase (BFRUCT4) / beta-fructofuranosidase/ invertase	2.17	1.70	1.28	C
AT4G10040	cytochrome c	2.14	2.78	0.77	E
AT5G59750	riboflavin biosynthesis protein	2.14	1.79	1.20	D
AT5G03555	permease	2.12	1.79	1.18	D
AT3G57020	strictosidine synthase family protein	2.12	2.69	0.79	X
AT1G23740	oxidoreductase	2.11	1.79	1.18	D
AT4G18010	inositol polyphosphate 5-phosphatase II (IP5PII) nearly	2.11	2.09	1.01	X
AT5G67030	zeaxanthin epoxidase (ZEP) (ABA1)	2.08	1.99	1.04	X
AT3G17790	acid phosphatase type 5 (ACP5)	2.08	1.72	1.20	D
AT4G22100	glycosyl hydrolase family 1 protein	2.03	2.13	0.95	X
AT5G54960	pyruvate decarboxylase	2.03	2.30	0.88	X

Signaling (S)

AT2G02950	phytochrome kinase substrate 1 (PKS1)	7.21	5.14	1.40	C
AT2G30040	protein kinase family protein	6.43	6.10	1.05	X
AT2G46340	phytochrome A supressor spa1 (SPA1)	4.79	4.95	0.97	X
AT5G52250	transducin family protein / WD-40 repeat family protein	4.59	3.91	1.17	D

AT2G24540	kelch repeat-containing F-box family protein	4.43	3.28	1.35	C
AT5G58760	transducin family protein / WD-40 repeat family protein	3.42	2.47	1.39	C
AT1G22770	gigantea protein (GI)	2.99	2.60	1.15	D
AT5G59730	exocyst subunit EXO70 family protein leucine zipper-containing protein	2.92	3.77	0.78	E
AT1G78070	WD-40 repeat family protein	2.51	3.39	0.74	X
AT1G07150	protein kinase family protein	2.50	2.41	1.04	X
AT1G53090	WD-40 repeat family protein / phytochrome A-related	2.12	2.20	0.96	X
Transport (TR)					
AT5G44110	ABC transporter family protein	13.89	10.52	1.32	C
AT5G02270	ABC transporter family protein NBD-like protein POP	8.89	7.53	1.18	D
AT2G37970	SOUL heme-binding family protein weak	6.22	4.44	1.40	C
AT2G29650	inorganic phosphate transporter	2.60	2.26	1.15	D
AT5G64940	ABC1 family protein	2.49	1.74	1.43	C
AT5G64840	ABC transporter family protein	2.40	1.96	1.23	D
AT3G47950	ATPase	2.20	1.60	1.37	C
AT3G24190	ABC1 family protein	2.03	1.62	1.25	C
Growth/Development (G/D)					
AT1G69530	expansin	2.06	1.75	1.18	D
Hormones (H)					
AT1G78440	gibberellin 2-oxidase / GA2-oxidase (GA2OX1)	7.94	6.51	1.22	D
AT4G03400	auxin-responsive GH3 family protein	3.50	4.06	0.86	X
AT2G38210	ethylene-responsive protein	2.35	1.57	1.49	C
AT4G38840	auxin-responsive protein	2.35	1.69	1.39	C
Stress/Defense (S/D)					
AT1G64500	glutaredoxin family protein	9.04	6.72	1.34	C
AT5G58750	wound-responsive protein-related	4.85	3.92	1.24	X
AT1G76080	thioredoxin family protein low	3.04	2.16	1.41	C
AT3G22830	heat shock transcription factor family protein	2.78	2.85	0.98	X
AT1G19670	coronatine-responsive protein / coronatine-induced protein 1 (CORI1)	2.68	1.98	1.36	C
AT5G36910	thionin (THI2.2)	2.38	1.64	1.46	C
AT2G29450	glutathione S-transferase (103-1A)	2.36	3.48	0.68	E
AT2G16365	F-box family protein	2.34	1.72	1.36	C
AT4G21870	26.5 kDa class P-related heat shock protein (HSP26.5-P)	2.14	1.64	1.30	C
AT2G21970	stress enhanced protein 2 (SEP2) nearly	2.01	1.82	1.11	D
Hypothetical/Unknown (H/U)					
AT3G02910	expressed protein	8.38	6.69	1.25	C
AT3G56290	expressed protein	6.99	4.87	1.43	C
AT3G12320	expressed protein	6.47	8.21	0.79	E
AT3G05800	expressed protein	5.54	4.83	1.15	D
AT2G40080	expressed protein	5.01	4.24	1.18	X
AT4G24700	expressed protein	3.60	2.78	1.29	X
AT4G27657	expressed protein	3.59	4.48	0.80	X
AT1G13670	expressed protein	3.23	3.09	1.05	X
AT4G35660	expressed protein	3.19	2.99	1.07	X
AT1G75100	expressed protein	3.17	2.51	1.26	C
AT4G26850	expressed protein	2.98	2.12	1.41	C
AT1G16720	expressed protein	2.95	2.11	1.40	C
AT1G32690	expressed protein	2.82	2.55	1.10	X
AT5G06980	expressed protein	2.81	3.49	0.80	X
AT2G46420	expressed protein	2.66	2.09	1.27	C

AT1G79510	expressed protein	2.60	2.07	1.26	C
AT1G70420	expressed protein	2.57	3.79	0.68	E
AT4G12000	expressed protein	2.56	2.74	0.93	X
AT1G50020	expressed protein	2.33	2.00	1.17	D
AT3G23170	expressed protein	2.29	3.28	0.70	E
AT3G45210	expressed protein	2.13	1.99	1.07	X
AT4G28290	expressed protein	2.09	2.08	1.01	X
AT4G33660	expressed protein	2.03	1.53	1.33	C
AT3G02140	expressed protein	2.01	2.03	0.99	X

This set comprises genes that (*i*) display a 2-fold or greater, and statistically significant, increase in expression in response to 1 h Rc in WT seedlings, but (*ii*) display a smaller than 1.5-Fold (bins C-E, in Fig. 3), or statistically non-significant (Table 2) 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 hour 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: Bins C-E 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. Bin X: genes that display a 2-fold or greater, and statistically significant, increase in expression in response to 1 h Rc in WT seedlings, but a statistically insignificant difference in the increase in expression in WT compared to *pif3* in response to 1 h Rc.

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.