

Supplemental Table S2A: Functional enrichment analysis for genes significantly differentially expressed between genotypes under varied light conditions, based on results in Table S1.

Light condition*	Comparison**	Numbers of genes	FunCat***	hits	P value	
Dark	<i>wt</i> > Δ <i>phy-1</i>	570	FunCat ID	category		
			20	cellular transport, transport facilitation and transport routes	34	0.009742033
			11	transcription	51	0.012154446
			14	protein fate (folding, modification, destination)	31	0.023879067
			34	interaction with the environment	14	0.025798119
	10	cell cycle and dna processing	43	0.029836814		
	<i>wt</i> < Δ <i>phy-1</i>	34	1.05	C-compound and carbohydrate metabolism	7	0.002044641
			1.25	extracellular metabolism	2	0.005460742
			42.27	extracellular / secretion proteins	1	0.039196902
	<i>wt</i> > Δ <i>phy-2</i>	30	01.05.03	polysaccharide metabolism	3	0.004452304
			16.19.05	GTP binding	2	0.012907326
			01.03.07	deoxyribonucleotide metabolism	1	0.025362670
			01.05.02	sugar, glucoside, polyol and carboxylate metabolism	2	0.041317302
	<i>wt</i> < Δ <i>phy-2</i>	374	1	metabolism	57	0.003016224
14			protein fate (folding, modification, destination)	10	0.005855991	
16			protein with binding function or cofactor requirement	21	0.007508537	
12			protein synthesis	2	0.010987566	
11			transcription	10	0.045926619	
<i>wt</i> > Δ <i>phy-1phy-2</i>	91	10.01	DNA processing	5	0.036402992	
		1.03	nucleotide/nucleoside/nucleobase metabolism	4	0.037770441	
<i>wt</i> < Δ <i>phy-1phy-2</i>	251	14	protein fate (folding, modification, destination)	2	9.16E-06	
		1	metabolism	47	0.000355600	
		11	transcription	5	0.009030819	
		10	cell cycle and dna processing	4	0.013944346	
		12	protein synthesis	1	0.020063531	
		2	energy	12	0.041220991	
Short-light (5–30 minutes)	<i>wt</i> > Δ <i>phy-1</i>	868	11	transcription	102	8.32E-09
			2	energy	13	0.000119794

			10 cell cycle and dna processing	76	0.000273360
			12 protein synthesis	47	0.001366762
			32 cell rescue, defense and virulence	34	0.012764613
	<i>wt < Δphy-1</i>	729	14 protein fate (folding, modification, destination)	11	7.55e-10
			10 cell cycle and dna processing	6	1.53e-08
			16 protein with binding function or cofactor requirement	37	1.89e-06
			11 transcription	13	4.19e-06
			20 cellular transport, transport facilitation and transport routes	69	0.000465769
			30 cellular communication/signal transduction mechanism	3	0.000530156
			40 cell fate	2	0.000956294
			12 protein synthesis	6	0.001294734
			1 metabolism	104	0.007145111
			18 regulation of metabolism and protein function	3	0.008979217
			43 cell type differentiation	5	0.009189262
			42 biogenesis of cellular components	15	0.022263649
	<i>wt > Δphy-2</i>	47	12 protein synthesis	6	0.000987466
			1 metabolism	2	0.033551134
			16 protein with binding function or cofactor requirement	9	0.048508082
	<i>wt < Δphy-2</i>	2435	16 protein with binding function or cofactor requirement	175	8.09e-11
			10 cell cycle and dna processing	63	2.79e-09
			11 transcription	82	4.41e-08
			12 protein synthesis	35	4.34e-06
			14 protein fate (folding, modification, destination)	113	1.00e-05
			40 cell fate	21	3.18e-05
			42 biogenesis of cellular components	62	3.59e-05
			43 cell type differentiation	27	5.53e-05
			1 metabolism	366	6.90e-05
			18 regulation of metabolism and protein function	19	0.000124549
			30 cellular communication/signal transduction mechanism	29	0.000129588
	<i>wt > Δphy-1phy-2</i>	165	16 protein with binding function or cofactor requirement	27	0.007256799
			11 transcription	17	0.008902073
			12 protein synthesis	9	0.042823408
	<i>wt < Δphy-1phy-2</i>	1010	14 protein fate (folding, modification, destination)	15	7.64e-12

			11 transcription	14	5.44e-09
			16 protein with binding function or cofactor requirement	45	8.20e-09
			1 metabolism	146	2.03e-06
			10 cell cycle and dna processing	16	9.17e-06
			12 protein synthesis	6	3.17e-05
			42 biogenesis of cellular components	14	0.000142166
			40 cell fate	3	0.000176486
			43 cell type differentiation	6	0.001890744
			18 regulation of metabolism and protein function	5	0.012975309
			30 cellular communication/signal transduction mechanism	9	0.022183862
Medium-light (45-90 minutes)	<i>wt</i> > Δ <i>phy-1</i>	1672	11 transcription	143	7.96e-07
			12 protein synthesis	73	0.000413473
			20 cellular transport, transport facilitation and transport routes	102	0.000796570
			2 energy	32	0.001610322
			1 metabolism	207	0.003619794
			14 protein fate (folding, modification, destination)	97	0.017054629
			10 cell cycle and dna processing	103	0.031781590
	<i>wt</i> < Δ <i>phy-1</i>	258	16 protein with binding function or cofactor requirement	10	7.54e-05
			10 cell cycle and dna processing	2	0.000593475
			14 protein fate (folding, modification, destination)	6	0.002773060
			12 protein synthesis	1	0.013021562
			20 cellular transport, transport facilitation and transport routes	27	0.020119186
	<i>wt</i> > Δ <i>phy-2</i>	142	11 transcription	6	0.022447518
			01.05.02 sugar, glucoside, polyol and carboxylate metabolism	4	0.026105816
	<i>wt</i> < Δ <i>phy-2</i>	973	32.01.04 pH stress response	1	0.029112861
			10 cell cycle and dna processing	19	3.08E-06
			16 protein with binding function or cofactor requirement	66	1.90E-05
			14 protein fate (folding, modification, destination)	36	6.11E-05
			11 transcription	29	0.000137743
			18 regulation of metabolism and protein function	6	0.006501374
30 cellular communication/signal transduction mechanism			11	0.023450994	
40 cell fate			9	0.028843913	
<i>wt</i> > Δ <i>phy-1phy-2</i>	112	34.05 cell motility	2	0.010287373	

			42.05 centrosome	1	0.024434886
	<i>wt < Δphy-1phy-2</i>	3651	12 protein synthesis	80	9.63E-06
			11 transcription	185	1.25E-05
			16 protein with binding function or cofactor requirement	383	1.32E-05
			30 cellular communication/signal transduction mechanism	109	0.035985731
Long-light (120-240 minutes)	<i>wt > Δphy-1</i>	769	11 transcription	94	3.80e-11
			2 energy	12	0.002452591
			12 protein synthesis	38	0.006037258
			32 cell rescue, defense and virulence	25	0.006225415
			16 protein with binding function or cofactor requirement	112	0.018803074
			14 protein fate (folding, modification, destination)	45	0.040435595
	<i>wt < Δphy-1</i>	222	14 protein fate (folding, modification, destination)	2	3.88e-06
			1 metabolism	52	1.75e-05
			10 cell cycle and dna processing	1	8.06e-05
			20 cellular transport, transport facilitation and transport routes	29	0.006909646
			12 protein synthesis	2	0.044138580
	<i>wt > Δphy-2</i>	109	20.03 transport facilities	6	0.017921697
			20.01 transported compounds (substrates)	10	0.018788153
			42.01 cell wall	4	0.023392619
	<i>wt < Δphy-2</i>	768	16 protein with binding function or cofactor requirement	50	1.28e-05
			1 metabolism	133	4.54e-05
			11 transcription	21	8.23e-05
			12 protein synthesis	6	8.86e-05
10 cell cycle and dna processing			21	0.003021290	
<i>wt > Δphy-1phy-2</i>	35	10.01.05 DNA recombination and DNA repair degradation / modification of foreign (exogenous)	3	0.009963034	
		32.10.07 polysaccharides	1	0.033454990	
		01.20.01 metabolism of primary metabolic sugar derivatives	1	0.043542186	
		01.25.01 extracellular polysaccharide degradation	1	0.048549810	
<i>wt < Δphy-1phy-2</i>	2126	11 transcription	56	1.38e-09	
		14 protein fate (folding, modification, destination)	77	4.08e-08	
		16 protein with binding function or cofactor requirement	143	5.97e-08	
		1 metabolism	314	1.21e-07	

			12	protein synthesis	22	2.08e-07
			40	cell fate	17	0.000322911
			18	regulation of metabolism and protein function	15	0.000687948
			10	cell cycle and dna processing	67	0.003103874
			42	biogenesis of cellular components	56	0.006589054
			43	cell type differentiation	27	0.013984022
			30	cellular communication/signal transduction mechanism	29	0.029583682

Table S2B. Sequences used in Figure 4.

No.	Name	GeneBank Accessions
1	<i>Aspergillus clavatus fphA</i>	XP_001274979
2	<i>Aspergillus flavus fphA</i>	XP_002380144
3	<i>Aspergillus fumigatus fphA</i>	XP_746476
4	<i>Aspergillus fumigatus fphA?</i>	XP_750813
5	<i>Aspergillus nidulans fphA</i>	XP_682277
6	<i>Aspergillus niger fphA</i>	CAK46534
7	<i>Aspergillus oryzae fphA</i>	XP_001818729
8	<i>Aspergillus terreus fphA</i>	XP_001216524
9	<i>Botrytis cinerea phy-1</i>	AAR30111
10	<i>Botrytis cinerea phy-2</i>	AAR30112
11	<i>Cochliobolus heterostrophus phy-1</i>	AAR29900
12	<i>Cryptococcus neoformans</i>	XP_567913
13	<i>Cyanothece sp.</i>	YP_003137260
14	<i>Gibberella moniliformis phy-1</i>	AAR30124
15	<i>Magnaporthe grisea phy-1</i>	XP_001412165
16	<i>Nectria haematococca phy-1</i>	XP_003052512
17	<i>Neosartorya fischeri fphA</i>	XP_001262526
18	<i>Neosartorya fischeri fphA?</i>	XP_001258043
19	<i>Neurospora crassa Phy1</i>	XP_960393
20	<i>Neurospora crassa Phy2</i>	AAZ57421
21	<i>Nostoc azollae</i>	YP_003723286
22	<i>Penicillium chrysogenum fphA</i>	XP_002556620
23	<i>Penicillium marneffeii fphA</i>	XP_002144720
24	<i>Phaeosphaeria nodorum phy-1</i>	XP_001802722
25	<i>Podospora anserine phy-1</i>	XP_001905870
26	<i>Podospora anserine phy-2</i>	XP_001903686
27	<i>Pseudomonas putida</i>	YP_001748669
28	<i>Pyrenophora tritici-repentis phy-1</i>	XP_001936957
29	<i>Sclerotinia sclerotiorum phy-1</i>	XP_001585628
30	<i>Sclerotinia sclerotiorum phy-2</i>	XP_001596430
31	<i>Sordaria macrospora phy-1</i>	XP_003353153
32	<i>Talaromyces stipitatus fphA</i>	XP_002340762
33	<i>Ustilago maydis</i>	XP_761879
34	<i>Verticillium albo-atrum phy-1</i>	XP_003000814

Supplemental Table S2C. Phytochromes and phytochrome-like proteins identified from published ascomyceteous genomes at the JGI fungal genome database.

Taxonomy	Sequences	Genomes	
Dothideomycetes	Altbr1 5093 AB05093.1	<i>Alternaria brassicicola</i> ¹	
	Aurpu var mel1 16610 gw1.15.168.1	<i>Aureobasidium pullulans</i> var. <i>melanogenum</i> ²	
	Aurpu var nam1 44080 e gw1.6.315.1	<i>Aureobasidium pullulans</i> var. <i>namibiae</i> ²	
	Aurpu var pull 268792 e gw1.4.150.1	<i>Aureobasidium pullulans</i> var. <i>pullulans</i> ²	
	Aurpu var subl 285445 CE171331 21132	<i>Aureobasidium pullulans</i> var. <i>subglaciale</i> ²	
	Bauco1 60611 gw1.2.1892.1	<i>Baudoinia compniacensis</i> ¹	
	Clafu1 186523 scf7180000128495 G13856	<i>Cladosporium fulvum</i> ³	
	Coccal 4297 gm1.4297 g	<i>Cochliobolus carbonum</i> ⁴	
	CocheC4 1 50370 estExt Genemark1.C 110317	<i>Cochliobolus heterostrophus</i> ¹	
	CocheC5 3 105834 CocheC5 1.estExt Genewise1Plus.C 90602	<i>Cochliobolus heterostrophus</i> ¹	
	Cocmil 6573 gm1.6573 g	<i>Cochliobolus miyabeanus</i> ⁴	
	Cocsal 325851 CE121292 3167	<i>Cochliobolus sativus</i> ¹	
	Cocvil 27376 gm1.5980 g	<i>Cochliobolus victoria</i> ⁴	
	Dotse1 121759 e gw1.1.2683.1	<i>Dothistroma septosporum</i> ³	
	Hyspu1 1 113029 NODE 352 length 279204 cov 25.g4723.t1	<i>Hysterium pulicare</i> ¹	
	Lepmu1 5196 Lema T112210.1	<i>Leptosphaeria maculans</i> ⁵	
	Macph1 11133 MPH 11376m.01	<i>Macrophomina phaseolina</i> ⁶	
	Mycgr3 41717 e gw1.5.15.1	<i>Mycosphaerella graminicola</i> ⁷	
	Pyrtr1 152306 PRTT 06624	<i>Pyrenophora teres</i> ⁸	
	Pyrtr1 10762 PTTG 19668.1	<i>Pyrenophora tritici-repentis</i> ⁹	
	Rhyru1 1 110678 NODE 2590 length 41030 cov 38.g8259.t1	<i>Rhynchostroma rufulum</i> ¹	
	Sepmu1 145583 estExt fgenesh1 kg.C 1 t10067	<i>Septoria musiva</i> ¹	
	Seppo1 16291 gm1.1898 g	<i>Septoria populicola</i> ¹	
	Settu1 149644 estExt Genewise1Plus.C 16 t10294	<i>Setosphaeria turcica</i> ¹	
	Settu1 512716 CE512715 20088	<i>Setosphaeria turcica</i> ¹	
	Stano2 5862 SNOG 12501.3	<i>Stagonospora nodorum</i> ¹⁰	
	Venpi1 211056 VP.s180.g11759.t1	<i>Venturia pirina</i> ¹¹	
	Zymar1 774380 Za111 scaffold 730 0005	<i>Zymoseptoria ardabiliae</i> ¹²	
Zymps1 801330 Zp221 scaffold 379 00001	<i>Zymoseptoria pseudotritici</i> ¹²		
Eurotiomycetes	Aspbr1 24753 fgenesh1 pg.1 # 285	<i>Arthroderma benhamiae</i> ¹³	
	Aspcl1 2057 7000001156840358	<i>Aspergillus clavatus</i> ¹⁴	
	Aspfl1 25661 7000001155852047	<i>Aspergillus flavus</i> ¹⁴	
	Aspfo1 34706 fgenesh1 pg.9 # 267	<i>Aspergillus fumigatus</i> ¹⁵	
	Aspfu A1163 1 108889 CADAFUBT00009918m.01	<i>Aspergillus fumigatus</i> ¹⁵	
	Aspful 4844 Afu4g02900 mRNA	<i>Aspergillus fumigatus</i> ¹⁵	
	Aspka1 1 16595 AKAW 05123m.01	<i>Aspergillus kawachii</i> ¹⁶	
	Aspni bvT 1 320165 estExt fgenesh1 pm.C 10211	<i>Aspergillus niger</i> ¹⁷	
	Aspni DSM 1 166081 An14g02970m.01	<i>Aspergillus niger</i> ¹⁷	
	Aspni NRRL3 1 845 NRRL3 00845	<i>Aspergillus niger</i> ¹⁷	
	Aspni7 1080634 e gw1.102.829.1	<i>Aspergillus niger</i> ¹⁸	
	Aspnid1 6870 AN9008	<i>Aspergillus nidulans</i> ¹⁴	
	Aspor1 2197 AO090001000178 mRNA	<i>Aspergillus oryzae</i> ¹⁴	
	Aspte1 2041 ATET 07903	<i>Aspergillus terreus</i> ¹⁴	
	Eurhel 461233 e gw1.24.337.1	<i>Eurotium rubrum</i> ¹⁹	
	Neofi1 5305 7000001156986890	<i>Neosartorya fishcheri</i> ¹⁴	
	Penac1 381296 estExt Genewise1.C 1 t60270	<i>Paracoccidioides brasiliensis</i> ²⁰	
	Pench1 80760 e gw1.4.2264.1	<i>Penicillium chrysogenum</i> ²¹	
	PenchWiscl 1 136770 PCH Pc06g00040	<i>Penicillium chrysogenum</i> ²¹	
	Pendi1 4281 PDIG 49920m.01	<i>Penicillium digitatum</i> ²²	
	Penox1 1288 EPS26357	<i>Penicillium oxalicum</i> ²³	
	Leotiomyces	Ascsa1 2610 2610 t	<i>Ascocoryne sarcoides</i> ²⁴
		Blugr1 20670 BGHDH14 bgh02766	<i>Blumeria graminis</i> ²⁵
Blugr1 21444 BGHDH14 bgh01671		<i>Blumeria graminis</i> ²⁵	
Botci1 10642 BC1T 08283		<i>Botrytis cinerea</i> ²⁶	
Botci1 8154 BC1T 01106		<i>Botrytis cinerea</i> ²⁶	
Glalo1 10114 GLAREA 02630m.01		<i>Glarea lozoyensis</i> ²⁷	
Glalo1 2390 GLAREA 10892m.01		<i>Glarea lozoyensis</i> ²⁷	
Marbr1 2324 MBM 05870		<i>Marssonina brunnea</i> ²⁸	
Marbr1 2839 MBM 06385		<i>Marssonina brunnea</i> ²⁸	
Oidma1 163689 estExt Genewise1Plus.C 7 t30127		<i>Oidiodendron maius</i> ²⁹	
Scslc1 7405 SS1G 12828T0		<i>Sclerotinia sclerotiorum</i> ³⁰	
Scslc1 8089 SS1G 13512T0		<i>Sclerotinia sclerotiorum</i> ³⁰	

	Sclsc1 9235 SS1G_02650T0	<i>Sclerotinia sclerotiorum</i> ³⁰
Orbiliomycetes	Artol1 10601 AOL_s00215g48m.01	<i>Arthrobotrys oligospora</i> ³¹
	Monha1 4440 H072_4535m.01	<i>Monacrosporium haptotylum</i> ^{32,33}
Pezizomycetes	Pyrco1 5746 PCON_06747m.01	<i>Pyronema confluens</i> ³⁴
	Tubme1 4182 GSTUMT00007042001	<i>Tuber melanosporum</i> ³⁵
Sordariomycetes	Beaba1 2816 BBA_02816m.01	<i>Beauveria bassiana</i> ³⁶
	Colgr1 10012 GLRG_10611T0	<i>Colletotrichum graminicola</i> ³⁷
	Colhi1 8988 CH063_11183T0	<i>Colletotrichum higginsianum</i> ³⁷
	Cormil 4450 CCM_04461m.01	<i>Cordyceps militaris</i> ³⁸
	Eutla1 4740 UCREL1_9450m.01	<i>Eutypa lata</i> ³⁹
	Fusfu1 8568 FFUJ_05887m.01	<i>Fusarium fujikuroi</i> ⁴⁰
	Fusgr1 9632 FGSG_08608T0	<i>Fusarium graminearum</i> ⁴¹
	Fusox1 11092 FOXG_03424	<i>Fusarium oxysporum</i> f. sp. <i>Lycopersici</i> ⁴²
	Fusox2 17584 FOXG_03424T0	<i>Fusarium oxysporum</i> ⁴²
	Fusox2 17585 FOXG_03424T1	<i>Fusarium oxysporum</i> ⁴²
	Fusve1 7054 FVEG_02296T0	<i>Fusarium verticillioides</i> ⁴²
	Fusve2 10239 FVEG_02296T0	<i>Fusarium verticillioides</i> ⁴²
	Fusve2 10240 FVEG_02296T1	<i>Fusarium verticillioides</i> ⁴²
	Maggr1 120527 MGG_12377T0	<i>Magnaporthe grisea</i> ⁴³
	Metac1 4734 MAC_04734m.01	<i>Metarhizium acridum</i> ⁴⁴
	Metan1 2298 MAA_02298m.01	<i>Metarhizium robertsii</i> ⁴⁴
	Necha2 91733 fgenesh1_pm.sca_2_chr3_3_0000133	<i>Nectria haematococca</i> ⁴⁵
	Neucr_trp3_1 10659 Neucr2.NCU05790T0	<i>Neurospora crassa</i> ⁴⁶
	Neucr_trp3_1 1269615 fgenesh1_pg.7_#_80	<i>Neurospora crassa</i> ⁴⁷
	Neucr2 10659 NCU05790T0	<i>Neurospora crassa</i> ⁴⁷
	Neucr2 8817 NCU04834T0	<i>Neurospora crassa</i> ⁴⁷
	Neute_mat_a1 131250 fgenesh2_pm.6_#_120	<i>Neurospora tetrasperma</i> ⁴⁸
	Neute_mat_a1 96894 estExt_Genewise1.C_72170	<i>Neurospora tetrasperma</i> ⁴⁸
	Neute_matA2 46279 e_gw1.5.55.1	<i>Neurospora tetrasperma</i> ⁴⁸
	Neute_matA2 87274 estExt_Genewise1Plus.C_60544	<i>Neurospora tetrasperma</i> ⁴⁸
	Phaal1 1267 UCRPA7_2680m.01	<i>Phaeoacremonium aleophilum</i> ⁴⁹
	Podan2 5532 Pa_4_890	<i>Podospora anserine</i> ⁵⁰
	Podan2 5984 Pa_4_9540	<i>Podospora anserina</i> ⁵⁰
	Thiar1 702547 e_gw1.3.1052.1	<i>Thielavia terrestris</i> ⁵¹
	Triat2 319399 estExt_Genemark.C_contig_250425	<i>Trichoderma atroviride</i> ⁵²
	Trire2 77764 estExt_GeneWisePlus.C_80856	<i>Trichoderma reesei</i> ⁵³
	TrireRUTC30_1 98151 estExt_Genewise1Plus.C_7_t10008	<i>Trichoderma reesei</i> ⁵³
	TriviGv29_8_2 190601 fgenesh1_pm.5_#_361	<i>Trichoderma virens</i> ⁵²
	Veral1 3365 VDBG_09309T0	<i>Verticillium alfalfa</i> ⁵⁴
	Verdal1 2980 VDAG_07462T0	<i>Verticillium dahlia</i> ⁵⁴
	Taphrinomycetes	Tapde1_1 1672 TAPDE_002075g.01

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- 3 de Wit, P. J. G. M. *et al.* The Genomes of the Fungal Plant Pathogens *Cladosporium fulvum* and *Dothistroma septosporum* Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. *Plos Genetics* **8**, doi:ARTN e1003088; 10.1371/journal.pgen.1003088 (2012).
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