

Table S1 The designed primers for qPCR

Internal ID/gene	Primer Sequence	
	Forward	Reverse
mRNAs		
EVM0003971	cGAATATGAGCCTGGAGAT	CGACCTTAGAATCCTTGT
EVM0004814	GATTCTTCGCCGTTCAAG	ACATAAGGGTCTGGTATTCC
EVM0009373	CTCATTGCTGGTGTGTAT	GTATTACGGTCAAGGATAGAAC
EVM0008905	GACGGACAAGTATGTAATGG	AATGGAAGGAAGTTGAACAG
EF1	CGATACCTCCCTCCGCCAG	ACAGGCGGAACGACCACAAC

Table S2 Repeative sequence statistic of *Conidiobolus obscurus*

Type	Number	Length (bp)	Percentage (%)
Class I	20,908	4,509,867	11.99
Class I/LINE	26	1,523	0.00
Class I/LTR	2	171	0.00
Class I/LTR/Copia	18	1,760	0.00
Class I/LTR/Gypsy	152	304,211	0.81
Class I/PLE/LARD	20,710	4,225,460	11.24
Class II	5,304	968,376	2.57
Class II/MITE	3,362	476,389	1.27
Class II/Maverick	1,527	295,252	0.79
Class II/TIR	193	129,689	0.34
Class II/Unknown	222	93,467	0.25
Potential Host Gene	1,351	259,385	0.69
SSR	25	10,926	0.03
Unknown	9,816	2,088,534	5.55
Total	27,588	6,558,671	17.44

Table S3 Gene number of the protein-encoding genes annotated in different databases

Database	Number
GO	2,375
KEGG	4,321
KOG	6,465
Pfam	7,710
Swissprot	6,460
TrEMBL	8,195
Nr	8,270
CAZyme	392
TCDB	97
PHI	2,888
all	8,566

Table S4 the sequencing data and alignment statistics

Samples	Clean reads	Clean bases	GC Content*	%≥Q30^Ψ	Mapped reads
C-1	56,539,926	16,803,169,322	37.10%	94.29%	81,354,935 (71.94%)
C-2	58,566,590	17,455,882,080	37.23%	94.56%	85,057,246 (72.62%)
C-3	60,759,696	18,028,324,124	37.37%	94.66%	75,783,626 (62.36%)
Pre-C-1	21,365,220	6,395,062,008	37.54%	94.11%	35,882,293 (83.97%)
Pre-C-2	20,596,396	6,165,534,548	37.57%	94.24%	34,729,506 (84.31%)
Pre-C-3	21,521,034	6,447,217,940	37.37%	93.94%	36,143,008 (83.79%)
Post-C-1	22,055,956	6,606,661,946	36.81%	94.13%	36,498,667 (82.74%)
Post-C-2	20,455,959	6,128,162,266	36.45%	93.73%	33,753,277 (82.5%)
Post-C-3	22,409,737	6,710,299,490	36.78%	94.48%	37,116,052 (82.81%)

* GC content: GC content percentage of Clean Data, namely the percentage of Clean Data base G and C;

^Ψ %≥Q30: percentage of Clean Data which quality value is greater than or equal to Q30 (an error rate of 1 in 1000).

Table S5 Differential expression of selected genes putatively related to transcription factors (TF) during conidiation.

Internal ID	FPKM*			Log2(FC) [†]		PHI	Annotation
	Pre-C	C	Post-C	C vs. pre-C	C vs. post-C		
EVM0007139	0.25	5.57	2.88	3.89	1.21	PHI:287	GATA-4/5/6 TF
EVM0007072	16.24	41.74	23.84	1.39	1.07	/	Histone-like TF
EVM0006849	44.03	101.27	57.09	1.23	1.09	/	Transcription initiation factor
Co_242	0.00	18.18	2.89	7.70	2.82	/	TFIIA
EVM0006123	0.92	4.69	0.97	2.33	2.35	PHI:2128	Homeobox phx1 TF
EVM0003245	0.00	2.34	0.13	6.15	3.79	PHI:2039	Homeobox phx1 TF
EVM0001087	1.34	5.91	1.52	2.09	2.12	PHI:2039	C2H2 finger domain TF
EVM0004983	0.06	2.99	0.31	4.95	3.40	PHI:232	C2H2 finger domain TF
EVM0008462	1.93	18.15	5.54	3.19	1.90	PHI:1405	STE-like TF
EVM0002148	0.11	2.13	0.24	3.90	3.18	PHI:3315	SteA TF
EVM0007454	0.33	3.78	0.19	3.44	4.45	PHI:1921	Activator of gluconeogenesis TF
EVM0000062	12.39	25.68	11.54	1.09	1.43	PHI:2930	RNA polymerase II-specific TF
EVM0010146	0.13	1.47	0.32	3.10	2.23		Cutinase TF
EVM0000205	18.17	41.06	15.94	1.22	1.63	PHI:1742	Fungal specific TF
EVM0003677	9.24	111.30	38.21	3.56	1.80	PHI:2565	Fungal specific TF
EVM0008905	38.21	269.52	11.23	2.83	4.76	PHI:2406	Heat shock TF
Co_1230	1.00	4.90	0.65	2.16	2.96	/	Heat shock TF
EVM0008509	28.60	61.05	19.28	1.13	1.93	/	Pcc1 TF
EVM0006858	21.95	71.91	36.99	1.74	1.22	/	e(y)2 TF
EVM0002806	13.05	34.55	11.79	1.44	1.82	PHI:1295	Transcription initiation factor
EVM0000750	98.92	204.70	46.81	1.10	2.36	PHI:3808	TFIID
							Asexual reproduction regulation TF
							CREB family TF

* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

† FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01 .

Table S6 The DEGs associated with the main GO terms

Internal ID	FPKM*			Log2(FC) [†]		Pfam annotation
	Pre-C	C	Post-C	C vs. pre-C	C vs. post-C	
Biological Process:carbohydrate metabolic process (GO:0005975)						
EVM0003314	0.30	21.02	0.00	5.88	9.51	Glycosyl hydrolases family 16
EVM0005673	0.77	2.40	0.06	1.62	5.33	Glycosyl hydrolases family 31
EVM0009297	25.90	59.04	16.88	1.23	2.07	Glycogen debranching enzyme
EVM0009626	31.33	65.56	20.27	1.11	1.96	Glycogen debranching enzyme
EVM0000365	10.12	47.79	0.87	2.27	5.99	Glycosyl hydrolases family 16
EVM0001373	10.45	48.78	0.90	2.25	5.97	Glycosyl hydrolases family 16
EVM0008569	22.33	49.64	27.33	1.18	1.12	Ribulose-phosphate 3 epimerase family
EVM0007041	76.64	161.17	57.15	1.11	1.76	Ribulose-phosphate 3 epimerase family
EVM0008158	0.00	1.55	0.07	6.09	4.10	Glycosyl hydrolases family 18
EVM0004064	3.64	133.52	22.28	5.14	2.81	Glycosyl hydrolases family 18
EVM0001249	6.24	148.22	24.14	4.48	2.84	Glycosyl hydrolases family 18
EVM0004020	1.58	206.41	17.19	6.98	3.82	Glycosyl hydrolases family 18
EVM0004131	8.18	131.74	23.17	3.99	2.74	Glycosyl hydrolases family 18
Biological Process: transport (GO:0006810)						
EVM0004058	5.71	11.80	5.54	1.08	1.36	ABC transporter
EVM0002255	0.02	3.49	0.42	5.89	2.85	Major intrinsic protein
EVM0006467	0.04	5.42	0.12	4.52	5.47	Sugar (and other) transporter
EVM0007330	2.86	54.35	4.28	4.26	3.92	Sulfate permease family; STAS domain
EVM0006243	1.22	10.98	1.37	3.14	3.23	Sulfate permease family
EVM0009518	12.87	35.39	12.83	1.47	1.68	Sulfate permease family
EVM0009164	7.66	21.62	12.07	1.53	1.10	STAS domain
EVM0002273	4.98	55.02	17.55	3.46	1.92	Sodium/hydrogen

EVM0004950	23.24	65.43	33.45	1.53	1.24	exchanger family
EVM0003315	7.42	16.96	6.98	1.18	1.50	Mitochondrial carrier
EVM0000187	9.02	20.94	8.40	1.26	1.59	Mitochondrial carrier
EVM0003819	10.66	20.92	11.24	1.01	1.17	ABC transporter
Biological Process: cellular process (GO:0009987)						Nucleoside transporter
EVM0006180	0.21	7.20	1.11	4.70	2.91	Glucanosyltransferase; X8 domain
EVM0007333	0.14	2.54	0.44	3.80	2.66	Glucanosyltransferase; X8 domain
EVM0004067	86.45	544.69	301.14	2.67	1.12	Cellulase (glycosyl hydrolase family 5)
EVM0010061	3.07	6.70	1.20	1.16	2.68	Protein tyrosine kinase
EVM0008877	8.02	16.60	3.22	1.09	2.61	Protein tyrosine kinase
Co_2537	2.56	5.06	3.09	1.02	1.68	Response regulator receiver domain
EVM0002403	3.76	20.76	10.86	2.48	1.21	Lipase (class 3)
EVM0001310	6.53	15.93	6.64	1.28	1.51	Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2)
EVM0006252	0.00	5.03	0.97	7.84	2.50	Protein tyrosine kinase; Kinase-like
EVM0004435	4.02	24.39	7.19	2.61	2.02	Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
EVM0003992	3.91	23.47	6.92	2.59	2.02	Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
EVM0003677	9.24	111.30	38.21	3.56	1.80	HSF-type DNA-binding
EVM0002806	13.05	34.55	11.79	1.44	1.82	Cell pattern formation-associated
EVM0003907	0.03	3.64	0.03	3.66	5.64	Peptidase inhibitor I9
EVM0001805	1.07	2.90	0.15	1.44	4.24	Peptidase inhibitor I9
Cellular Component: membrane (GO:0016020)						
EVM0004514	47.08	91.44	40.78	1.01	1.44	Glucanosyltransferase; X8 domain
EVM0002472	2.21	9.34	1.72	2.11	2.71	1,3-beta-glucan synthase
EVM0003159	0.75	7.38	0.34	3.23	4.44	--
EVM0000484	2.27	9.24	1.73	2.06	2.68	1,3-beta-glucan synthase
EVM0004224	2.86	10.57	2.08	1.93	2.61	1,3-beta-glucan synthase
EVM0001764	6.32	21.13	4.13	1.78	2.62	1,3-beta-glucan synthase
EVM0005934	0.01	1.64	0.06	5.13	4.43	Fibronectin type II domain
EVM0004067	86.45	544.69	301.14	2.67	1.12	Cellulase
EVM0010219	126.01	321.21	52.74	1.38	2.87	Fatty acid hydroxylase

EVM0003064	35.03	189.63	16.33	2.47	3.80	superfamily ABC transporter
EVM0004058	5.71	11.80	5.54	1.08	1.36	ABC transporter
EVM0000865	0.02	1.09	0.01	5.23	6.10	E1-E2 ATPase
EVM0001785	0.02	1.12	0.01	5.10	6.13	E1-E2 ATPase
EVM0001357	1.69	7.84	0.42	2.22	4.40	E1-E2 ATPase
EVM0005475	23.17	766.40	1.97	5.06	8.74	NADH-ubiquinone reductase complex 1 MLRQ subunit
EVM0006467	0.04	5.42	0.12	4.52	5.47	Major Facilitator Superfamily
EVM0010232	11.82	36.07	3.93	1.65	3.45	Sugar (and other) transporter
EVM0004950	23.24	65.43	33.45	1.53	1.24	Mitochondrial carrier protein
EVM0004653	50.58	124.17	52.37	1.28	1.47	Mitochondrial carrier protein
EVM0003315	7.42	16.96	6.98	1.18	1.50	Mitochondrial carrier protein
EVM0004218	2.40	11.34	3.28	2.17	1.98	Heavy-metal-associated domain
EVM0005466	28.92	90.54	17.56	1.69	2.64	EamA-like transporter family
EVM0006025	11.59	27.57	5.91	1.29	2.49	EamA-like transporter family
EVM0000187	9.02	20.94	8.40	1.26	1.59	ABC transporter
EVM0005299	69.05	137.92	39.23	1.01	2.08	Cytochrome c oxidase subunit VIc
EVM0002609	3.71	22.25	7.96	2.61	1.75	Glycosyl hydrolase family 47
EVM0003938	19.16	94.08	24.69	2.30	2.17	NADH-ubiquinone oxidoreductase MWFE subunit
Cellular Component: cytosol (GO:0005829)						
EVM0001685	0.23	10.18	0.19	5.06	5.52	Ubiquitin-conjugating enzyme
Co_1850	7.65	24.25	8.56	1.54	1.61	LSM domain
EVM0005642	6.97	27.14	10.29	1.98	1.65	LSM domain
EVM0002852	11.65	33.69	11.81	1.56	1.77	Ubiquitin family
EVM0000395	72.33	192.18	69.85	1.44	1.73	Ubiquitin family
EVM0010225	12.44	29.32	6.67	1.25	2.33	U1 zinc finger
EVM0002141	7.76	15.95	4.99	1.07	1.93	Cytidine and deoxycytidylate deaminase zinc-binding region

EVM0009693	2.90	18.26	3.28	2.54	2.62	Uncharacterised protein family
EVM0005733	887.99	2628.51	612.76	1.60	2.36	Ribosomal L29 protein
EVM0006554	50.75	259.70	60.76	2.38	2.35	Thioredoxin; AhpC/TSA family
EVM0002020	99.80	266.43	113.85	1.44	1.49	Thioredoxin; AhpC/TSA family
EVM0002444	252.14	506.80	158.18	1.03	1.94	Thioredoxin; AhpC/TSA family
EVM0003561	89.95	228.12	117.78	1.36	1.21	EF-hand domain
EVM0004218	2.40	11.34	3.28	2.17	1.98	Heavy-metal-associated domain
EVM0006741	4.89	11.72	5.87	1.25	1.23	Urm1 (Ubiquitin related modifier)
EVM0000925	15.56	44.95	18.82	1.57	1.53	Acyl transferase
EVM0001674	12.36	34.64	13.94	1.53	1.59	Acyl transferase
EVM0001137	10.84	25.60	9.36	1.26	1.72	Acyl transferase
Cellular Component: nucleus (GO:0005634)						
EVM0001685	0.23	10.18	0.19	5.06	5.52	Ubiquitin-conjugating enzyme
EVM0002852	11.65	33.69	11.81	1.56	1.77	Ubiquitin family
EVM0000395	72.33	192.18	69.85	1.44	1.73	Ubiquitin family
EVM0009693	2.90	18.26	3.28	2.54	2.62	Uncharacterised protein family
EVM0006554	50.75	259.70	60.76	2.38	2.35	Thioredoxin
EVM0002020	99.80	266.43	113.85	1.44	1.49	Thioredoxin
EVM0002444	252.14	506.80	158.18	1.03	1.94	Thioredoxin
EVM0003561	89.95	228.12	117.78	1.36	1.21	EF-hand domain
EVM0004218	2.40	11.34	3.28	2.17	1.98	Heavy-metal-associated domain
EVM0010037	177.80	1749.36	115.71	3.31	4.18	Acyl CoA binding protein
EVM0008569	22.33	49.64	27.33	1.18	1.12	Ribulose-phosphate 3 epimerase
EVM0007041	76.64	161.17	57.15	1.11	1.76	Ribulose-phosphate 3 epimerase
EVM0004983	0.06	2.99	0.31	4.95	3.40	STE like transcription factor
EVM0002148	0.11	2.13	0.24	3.90	3.18	Fungal Zn(2)-Cys(6) binuclear cluster domain
Molecular Function: hydrolase activity (GO:0016787)						
EVM0009290	5.10	251.35	26.34	5.64	3.50	Cellulase
EVM0007726	28.46	63.04	8.57	1.19	3.13	Glycosyl hydrolase family
EVM0004067	86.45	544.69	301.14	2.67	1.12	Cellulase)
EVM0003971	42.26	105.31	50.33	1.36	1.34	Beta-glucan synthesis-

						associated protein (SKN1)
Co_1182	0.00	0.47	0.11	6.18	2.22	Platelet-activating factor acetylhydrolase
EVM0002220	1.39	6.54	1.47	2.26	2.41	Amidohydrolase family
EVM0000082	0.02	0.65	0.00	4.10	6.64	Subtilase family
EVM0001805	1.07	2.90	0.15	1.44	4.24	Subtilase family
EVM0008226	9.05	53.10	1.22	2.57	5.63	Trypsin
EVM0005001	21.39	88.68	1.10	2.08	6.55	Trypsin
EVM0009772	2.42	5.80	0.08	1.27	5.66	Trypsin
EVM0001721	48.83	147.41	19.30	1.63	3.20	Trypsin
EVM0000789	0.02	2.06	0.01	5.13	6.18	Glycosyl hydrolases family 18
EVM0000088	0.47	10.13	0.64	4.38	4.18	Glycosyl hydrolases family 18
EVM0007380	0.00	1.05	0.01	5.72	5.23	Glycosyl hydrolases family 18
EVM0000612	0.46	8.30	0.60	4.13	4.00	Glycosyl hydrolases family 18
EVM0008574	0.11	0.87	0.27	2.72	1.88	Glycosyl hydrolases family 18
EVM0006427	0.11	0.84	0.32	2.68	1.63	Glycosyl hydrolases family 18
EVM0003563	0.11	0.84	0.25	2.64	1.89	Glycosyl hydrolases family 18
Molecular Function: catalytic activity (GO:0003824)						
EVM0006541	0.06	220.04	63.88	9.69	2.04	Polysaccharide deacetylase
EVM0008805	0.00	10.70	0.00	8.66	9.19	Glycosyl hydrolases family 16
EVM0008271	0.00	9.93	0.00	8.44	8.98	Glycosyl hydrolases family 16
EVM0004224	2.86	10.57	2.08	1.93	2.61	1,3-beta-glucan synthase
EVM0000444	0.88	28.13	1.34	5.02	4.65	Chitin synthase
EVM0006157	0.01	6.72	0.74	5.96	3.32	Pyridoxal-dependent decarboxylase
EVM0009297	25.90	59.04	16.88	1.23	2.07	Glycogen debranching enzyme
EVM0009626	31.33	65.56	20.27	1.11	1.96	Glycogen debranching enzyme
EVM0003949	0.92	6.97	2.76	2.80	1.56	HD domain
EVM0003025	10.15	24.96	14.34	1.31	1.05	AMP-binding enzyme
Co_102	0.03	4.79	0.04	6.32	6.31	Eukaryotic aspartyl protease
EVM0007192	43.88	125.58	33.11	1.56	2.17	Aminotransferase class I and II

EVM0007255	6.16	17.73	7.03	1.55	1.60	Glycerophosphoryl diester phosphodiesterase family
EVM0004087	7.96	49.50	7.38	2.57	2.99	Aminotransferase class I and II
Molecular Function: serine-type peptidase activity (GO:0008236)						
EVM0007218	0.00	6.15	0.01	7.49	7.29	Subtilase family
EVM0000403	0.67	25.11	1.45	3.77	3.65	Subtilase family
EVM0005632	0.41	10.97	1.22	3.70	2.98	Subtilase family
EVM0004644	147.47	970.44	12.14	2.74	6.57	Subtilase family
EVM0008109	0.06	14.77	0.12	6.93	4.37	Trypsin
EVM0006838	4.46	290.36	7.64	5.96	5.43	Trypsin
EVM0008156	0.47	36.30	3.51	5.95	3.56	Trypsin
EVM0007680	0.16	8.65	0.04	5.14	6.88	Trypsin
EVM0006920	10.03	255.93	10.92	4.64	4.76	Trypsin
Co_2766	2.87	42.32	0.45	3.87	6.62	Trypsin
EVM0009083	5.02	36.42	0.99	2.87	5.41	Trypsin
EVM0003166	6.32	27.37	6.54	2.15	2.33	Trypsin

* The transcript level is expressed in fragments per kilobase per million fragments (FPKM) values. C: mycelia at sporulating stage; Pre-C: mycelia before sporulating stage; Post-C: mycelia after sporulating stage.

† FC is the fold change of differentially expressed genes between the three libraries of C, Pre-C and PostC. There are genes expressing with significant difference (a fold change ≥ 2 and a false discovery rate < 0.001).

Table S7 The DEGs associated with the main KEGG pathway

Internal ID	FPKM*			Log2(FC) †		Pfam annotation
	Pre-C	C	Post-C	C vs. pre-C	C vs. post-C	
Oxidative phosphorylation (ko00190)						
EVM0009508	19.49	101.99	24.80	2.40	2.30	ATP synthase subunit H
EVM0004390	11.36	41.00	12.96	1.86	1.91	Vacuolar (H+)-ATPase G subunit
EVM0000869	11.09	39.75	12.80	1.85	1.88	Vacuolar (H+)-ATPase G subunit
EVM0000557	85.43	262.37	75.67	1.65	2.05	Vacuolar (H+)-ATPase G subunit
EVM0005475	23.17	766.40	1.97	5.06	8.74	NADH-ubiquinone reductase complex 1
EVM0007673	82.11	222.07	41.72	1.45	2.65	NADH-ubiquinone oxidoreductase B18
EVM0004399	40.00	104.82	37.18	1.39	1.73	NADH:ubiquinone oxidoreductase,
EVM0001245	45.65	241.07	37.97	2.42	2.92	Cytochrome oxidase c subunit VIb
EVM0008584	20.72	62.39	11.85	1.61	2.64	Cytochrome c oxidase subunit VIIc
EVM0004161	50.11	185.06	101.63	1.87	1.11	Cytochrome oxidase assembly protein
EVM0006582	254.08	559.04	183.56	1.17	1.88	Cytochrome c oxidase subunit VIa
EVM0005299	69.05	137.92	39.23	1.01	2.08	Cytochrome c oxidase subunit VIc
EVM0008956	8.39	39.48	8.45	2.20	2.44	Ubiquinol-cytochrome C reductase hinge protein
EVM0007884	9.44	36.04	10.39	1.93	2.04	Ubiquinol-cytochrome C reductase hinge protein
EVM0008409	9.62	34.39	10.52	1.81	1.93	Ubiquinol-cytochrome C reductase hinge protein
EVM0002948	16.20	66.97	14.73	2.02	2.41	Ubiquinol-cytochrome C reductase
EVM0003754	11.42	47.32	10.64	1.99	2.35	Ubiquinol-cytochrome C reductase
EVM0009982	11.29	26.73	13.52	1.25	1.22	Ubiquinol-cytochrome-

						c reductase complex subunit (QCR10)
EVM0005826	37.87	139.64	36.72	1.89	2.19	ATP synthase complex subunit h
EVM0008514	58.16	164.13	46.60	1.52	2.07	ATP synthase complex subunit h
EVM0000544	63.03	231.60	29.49	1.88	3.20	Mitochondrial ATP synthase epsilon chain
EVM0001330	39.78	120.09	32.18	1.61	2.15	Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain
EVM0005601	42.32	109.17	29.39	1.37	2.13	ATP synthase E chain
Amino sugar and nucleotide sugar metabolism (ko00520)						
EVM0000444	0.88	28.13	1.34	5.02	4.65	Chitin synthase
EVM0004669	3.74	36.43	11.22	3.31	1.97	Chitin synthase
EVM0001244	48.91	588.98	30.89	3.63	4.52	Glycosyl hydrolase family 20
EVM0005566	74.65	342.19	19.81	2.23	4.37	Glycosyl hydrolase family 20
EVM0007277	20.04	42.44	11.52	1.12	2.14	Acetyltransferase (GNAT) family
EVM0008158	0.00	1.55	0.07	6.09	4.10	Glycosyl hydrolases family 18
EVM0000789	0.02	2.06	0.01	5.13	6.18	Glycosyl hydrolases family 18
EVM0007628	1.09	27.49	0.76	4.65	5.38	Glycosyl hydrolases family 18
EVM0000088	0.47	10.13	0.64	4.38	4.18	Glycosyl hydrolases family 18
EVM0007380	0.00	1.05	0.01	5.72	5.23	Glycosyl hydrolases family 18
EVM0004064	3.64	133.52	22.28	5.14	2.81	Glycosyl hydrolases family 18
EVM0001249	6.24	148.22	24.14	4.48	2.84	Glycosyl hydrolases family 18
EVM0004020	1.58	206.41	17.19	6.98	3.82	Glycosyl hydrolases family 18
EVM0004131	8.18	131.74	23.17	3.99	2.74	Glycosyl hydrolases family 18
EVM0002377	3.67	21.22	3.63	2.56	2.81	Glycosyl hydrolases family 18
EVM0000612	0.46	8.30	0.60	4.13	4.00	Glycosyl hydrolases family 18
EVM0008574	0.11	0.87	0.27	2.72	1.88	Glycosyl hydrolases

EVM0006427	0.11	0.84	0.32	2.68	1.63	family 18 Glycosyl hydrolases
EVM0003563	0.11	0.84	0.25	2.64	1.89	family 18 Glycosyl hydrolases
EVM0005693	69.41	186.04	94.25	1.45	1.25	family 18 GDP-mannose 4,6 dehydratase
MAPK signaling pathway - yeast (ko04011)						
EVM0008074	0.21	1.79	0.08	2.84	4.10	1,3-beta-glucan synthase component
EVM0002472	2.21	9.34	1.72	2.11	2.71	1,3-beta-glucan synthase component
EVM0003159	0.75	7.38	0.34	3.23	4.44	1,3-beta-glucan synthase component
EVM0007566	4.93	23.19	3.05	2.26	3.18	1,3-beta-glucan synthase component
EVM0000484	2.27	9.24	1.73	2.06	2.68	1,3-beta-glucan synthase component
EVM0004224	2.86	10.57	2.08	1.93	2.61	1,3-beta-glucan synthase component
EVM0001764	6.32	21.13	4.13	1.78	2.62	1,3-beta-glucan synthase component
EVM0005361	18.15	309.79	148.14	4.10	1.32	Catalase-related immune-responsive
EVM0009987	4.35	71.98	34.28	4.02	1.33	Catalase-related immune-responsive
EVM0007860	6.31	102.14	50.99	3.99	1.26	Catalase-related immune-responsive
EVM0001653	22.96	61.12	33.62	1.45	1.13	Variant SH3 domain
EVM0004983	0.06	2.99	0.31	4.95	3.40	STE like transcription factor
EVM0001126	5.85	71.98	23.78	3.62	1.86	GGL domain
EVM0008649	126.30	916.02	323.30	2.89	1.77	GGL domain
EVM0000750	98.92	204.70	46.81	1.10	2.36	bZIP transcription factor
Ribosome (ko03010)						
EVM0000242	815.77	2264.82	654.09	1.51	2.06	S25 ribosomal protein
EVM0002937	950.39	3871.05	526.06	2.05	3.14	Ribosomal protein S28e
EVM0005588	1245.76	3090.38	851.98	1.34	2.13	Ribosomal protein S27
EVM0009766	3.72	12.37	5.28	1.69	1.46	Ribosomal protein L36
EVM0009938	4.64	13.08	6.88	1.46	1.16	Ribosomal protein L34
EVM0003011	1717.35	7151.17	1263.06	2.09	2.77	Ribosomal protein L44
Co_61	110.67	363.52	56.75	1.74	2.93	Ribosomal L38e protein family

EVM0005733	887.99	2628.51	612.76	1.60	2.36	Ribosomal L29 protein
Co_2197	79.87	185.90	47.97	1.25	2.22	Ribosomal L39 protein
Co_3023	210.28	485.31	155.24	1.24	1.91	Ribosomal L38e protein family
EVM0008541	286.98	658.84	211.23	1.23	1.91	Ribosomal L38e protein family
EVM0001436	2710.86	6189.85	1919.84	1.23	1.96	Ribosomal protein L32
EVM0007727	124.99	359.92	71.21	1.56	2.60	Ribosomal protein S27a
EVM0002763	750.10	1656.68	494.70	1.17	2.01	Ribosomal protein S27a

* The transcript level is expressed in fragments per kilobase per million fragments (FPKM) values. C: mycelia at sporulating stage; Pre-C: mycelia before sporulating stage; Post-C: mycelia after sporulating stage.

† FC is the fold change of differentially expressed genes between the three libraries of C, Pre-C and Post-C. There are genes expressing with significant difference (a fold change ≥ 2 and a false discovery rate < 0.001).

Table S8 Differential expression of selected genes related to cell wall/membrane/envelope biogenesis during conidiation.

Internal ID	FPKM*			Log2(FC) [†]		PHI
	Pre-C	C	Post-C	C vs. pre-C	C vs. post-C	
1,3-beta-glucan synthase						
EVM0008074	0.21	1.79	0.08	2.84	4.10	PHI:2533
EVM0002472	2.21	9.34	1.72	2.11	2.71	PHI:2533
EVM0003159	0.75	7.38	0.34	3.23	4.44	PHI:2533
EVM0007566	4.93	23.19	3.05	2.26	3.18	PHI:2533
EVM0000484	2.27	9.24	1.73	2.06	2.68	PHI:2533
EVM0004224	2.86	10.57	2.08	1.93	2.61	PHI:2533
EVM0001764	6.32	21.13	4.13	1.78	2.62	PHI:2533
EVM0003971	42.26	105.31	50.33	1.36	1.34	/
Glucanotransferase						
EVM0006180	0.21	7.20	1.11	4.70	2.91	PHI:33
EVM0007333	0.14	2.54	0.44	3.80	2.66	PHI:33
EVM0004514	47.08	91.44	40.78	1.01	1.44	PHI:33
Glycosyl hydrolase						
EVM0007001	4.14	54.19	23.03	3.73	1.51	/
EVM0007042	32.83	87.13	11.42	1.45	3.19	PHI:748
EVM0007726	28.46	63.04	8.57	1.19	3.13	PHI:748
EVM0005673	0.77	2.40	0.06	1.62	5.33	PHI:1071
EVM0003793	0.10	1.22	0.03	3.10	4.73	/
Chitin synthase/chitinase						
EVM0000444	0.88	28.13	1.34	5.02	4.65	PHI:3048
EVM0004669	3.74	36.43	11.22	3.31	1.97	PHI:3050
EVM0008158	0.00	1.55	0.07	6.09	4.10	PHI:2388
EVM0000789	0.02	2.06	0.01	5.13	6.18	PHI:2388
EVM0007628	1.09	27.49	0.76	4.65	5.38	PHI:2388
EVM0000088	0.47	10.13	0.64	4.38	4.18	PHI:2388
Cellulase						
EVM0009290	5.10	251.35	26.34	5.64	3.50	PHI:323
EVM0004067	86.45	544.69	301.14	2.67	1.12	PHI:323
Ergosterol						
EVM0010219	126.01	321.21	52.74	1.38	2.87	PHI:3035
Mannan biosynthesis/mannoprotein assembly						
EVM0006408	0.47	277.15	40.64	8.94	2.98	/
EVM0003767	0.95	5.10	2.14	2.35	1.48	PHI:2482

* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

† FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01 .

Table S9 The DEGs associated with PHI database*

DEG ID	PHI
EVM0001654	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0003421	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0006252	PHI:1221 FGSG_03146 I1RJM9 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Lethal
EVM0004341	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0004394	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0007784	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0007218	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0009119	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0004379	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0004020	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0008109	PHI:653 GIP2 AAL11721 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0008303	PHI:2321 SidI Q4WR83 746128 Aspergillus_fumigatus Reduced_virulence
EVM0009549	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0002185	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0000830	PHI:1180 (Sc_Sat4) I1RS32 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0003125	PHI:2042 ABC3 Q3Y5V5 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0002496	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0009502	PHI:438 BcBOT1_(related:_CND5) AAQ16576 40559 Botrytis_cinerea Reduced_virulence
EVM0004492	PHI:397 LAC2 AAV64894 5207 Cryptococcus_neoformans Unaffected_pathogenicity
EVM0008865	PHI:429 CIPLS1 CAD43407 290576 Colletotrichum_lindemuthianum Loss_of_pathogenicity
EVM0001751	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence

EVM0003245	PHI:2039 Con7p Q069J4 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0008158	PHI:2388 Chi2 0 5530 Metarhizium_anisopliae Mixed_outcome
EVM0006838	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0006157	PHI:177 ODC CAB56523 13684 Stagonospora_nodorum Reduced_virulence
EVM0008156	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0000614	PHI:697 ugt51E1 AAM81358 5022 Leptosphaeria_maculans Unaffected_pathogenicity
EVM0001824	PHI:1161 MgMfs1 A4ZGP3 54734 Mycosphaerella_graminicola_(related:_Zymoseptoria_triticii) Chemistry_target
EVM0007380	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0009290	PHI:323 VFGLU1 AAO63562 93591 Verticillium_fungicola Reduced_virulence
EVM0004016	PHI:511 CaNAG4 EAK93098 5476 Candida_albicans Reduced_virulence
EVM0008454	PHI:1541 GzF1bD I1RE42 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0000952	PHI:777 MGG_00883 EDK02450 318829 Magnaporthe_oryzae Loss_of_pathogenicity
EVM0002960	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0007590	PHI:2021 Pac2 MGG_06564 5270 Ustilago_maydis Reduced_virulence
EVM0005882	Ktr1 PHI:3095 J5JDI1 176275 Beauveria_bassiana unaffected_pathogenicity_
EVM0001943	PHI:577 NoxB BAE72682 35717 Epichloe_festucae Wild-type_mutualism
EVM0000865	PHI:440 PMR1 CAB87245 5476 Candida_albicans Reduced_virulence
EVM0007554	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0004064	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0007680	PHI:653 GIP2 AAL11721 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0000789	PHI:2388 Chi2 0 5530 Metarhizium_anisopliae Mixed_outcome
EVM0001785	PHI:440 PMR1 CAB87245 5476 Candida_albicans Reduced_virulence
EVM0000444	CSMA PHI:3048 Q4X0H6 746128 Aspergillus_fumigatus mixed_outcome_
EVM0004983	PHI:232 STE12a AAG49739 5207 Cryptococcus_neoformans Reduced_virulence

EVM0005502	PHI:1511 GzHOME009 I1RXF3 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0007786	PHI:1221 FGSG_03146 I1RJM9 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Lethal
EVM0003715	PHI:2357 CYP52X1 E2EAF6 475271 Beauveria_bassiana Reduced_virulence
EVM0009373	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0006180	PHI:33 PHR1 AAA68196 5476 Candida_albicans Reduced_virulence
EVM0007628	PHI:2388 Chi2 0 5530 Metarhizium_anisopliae Mixed_outcome
EVM0006920	PHI:653 GIP2 AAL11721 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0006467	PHI:2968 Hxs1 J9VQA5 5207 Cryptococcus_neoformans Reduced_virulence
EVM0001249	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0001327	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0004130	PHI:1434 GzC2H103 I1S8Y5 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0000088	PHI:2388 Chi2 0 5530 Metarhizium_anisopliae Mixed_outcome
EVM0008112	PHI:2839 RED1 Q8NJQ2 5016 Cochliobolus_heterostrophus Reduced_virulence
EVM0000612	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0003018	PHI:2839 RED1 Q8NJQ2 5016 Cochliobolus_heterostrophus Reduced_virulence
EVM0005361	PHI:106 CAT1 AAC39448 5476 Candida_albicans Reduced_virulence
EVM0007723	PHI:104 CaMNT1 CAA67930 5476 Candida_albicans Reduced_virulence
EVM0009987	PHI:106 CAT1 AAC39448 5476 Candida_albicans Reduced_virulence
EVM0004131	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0007860	PHI:106 CAT1 AAC39448 5476 Candida_albicans Reduced_virulence
EVM0001410	PHI:1310 GzbHLH011 I1RQC1 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0010093	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0002148	conx1 PHI:3315 G4MT41 318829 Magnaporthe_oryzae reduced_virulence
EVM0007672	PHI:2839 RED1 Q8NJQ2 5016 Cochliobolus_heterostrophus Reduced_virulence

EVM0007139	PHI:287 CLNR1 AAN65464 290576 Colletotrichum_lindemuthianum Loss_of_pathogenicity
EVM0007333	PHI:33 PHR1 AAA68196 5476 Candida_albicans Reduced_virulence
EVM0000403	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0007619	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0005600	PHI:2920 FET3-1 E3QRA4 31870 Colletotrichum_graminicola Reduced_virulence
EVM0004577	PHI:383 SOD5 EAL00626 5476 Candida_albicans Loss_of_pathogenicity
EVM0005632	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0006099	PHI:213 CPA1 AAF69795 5207 Cryptococcus_neoformans Reduced_virulence
EVM0003907	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0001001	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0003677	PHI:2565 Q5APJ0 Q5APJ0 5476 Candida_albicans Reduced_virulence
EVM0003126	PHI:1161 MgMfs1 A4ZGP3 54734 Mycosphaerella_graminicola_(related:_Zymoseptoria_triticii) Chemistry_target
EVM0009891	PHI:674 Can2 AAZ30051 178876 Cryptococcus_neoformans Increased_virulence_(Hypervirulence)
EVM0001772	PHI:2839 RED1 Q8NJQ2 5016 Cochliobolus_heterostrophus Reduced_virulence
EVM0009087	PHI:2128 MoHox1 MGG_04853 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) reduced_virulence
EVM0006347	PHI:2844 BRM2 O93802 5599 Alternaria_alternata Unaffected_pathogenicity
EVM0005592	AKT7 PHI:4194 V5XZS6 5599 Alternaria_alternata increased_virulence_(Hypervirulence)
EVM0002733	PHI:2844 BRM2 O93802 5599 Alternaria_alternata Unaffected_pathogenicity
EVM0000479	PHI:419 CSH1 AAP93915 5476 Candida_albicans Reduced_virulence
EVM0007454	PHI:1921 GzZC236 I1RCH8 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0002401	PHI:2100 Spf1 MGG_12005 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Mixed_outcome
EVM0001521	PHI:1511 GzHOME009 I1RFX3 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0004669	CHSF PHI:3050 Q4WC58 746128 Aspergillus_fumigatus mixed_outcome

EVM0004891	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0003159	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0008462	PHI:1405 GzC2H069 I1RWW2 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0001555	PHI:881 MGG_04556 EDJ96020 318829 Magnaporthe_oryzae Reduced_virulence
EVM0003299	PHI:578 NoxR BAF36501 35717 Epichloe_festucae Enhanced_antagonism
EVM0004556	PHI:2266 Ptr2 0 13684 Phaeosphaeria_nodorum_(related:_Stagonospora_nodorum) Unaffected_pathogenicity
EVM0008074	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0004814	PHI:2534 ERG11A Q4WNT5 746128 Aspergillus_fumigatus Mixed_outcome
EVM0008905	PHI:2406 MoSKN7 G4N7Y2 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0006845	PHI:2086 Moatg24 MGG_03638 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0003041	PHI:2158 MoCMK1 EU_984498 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0010231	PHI:511 CaNAG4 EAK93098 5476 Candida_albicans Reduced_virulence
EVM0004644	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0003276	PHI:2042 ABC3 Q3Y5V5 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0004948	PHI:2293 cycA B0XTA5 746128 Aspergillus_fumigatus Reduced_virulence
EVM0008574	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0005176	PHI:2293 cycA B0XTA5 746128 Aspergillus_fumigatus Reduced_virulence
EVM0002621	PHI:881 MGG_04556 EDJ96020 318829 Magnaporthe_oryzae Reduced_virulence
EVM0006427	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0004067	PHI:323 VFGLU1 AAO63562 93591 Verticillium_fungicola Reduced_virulence
EVM0003563	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0001189	PHI:267 MLT1 AAD51594 5476 Candida_albicans Reduced_virulence
EVM0003856	PHI:1564 GzOB004 Q4IPZ1 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity

EVM0004435	PHI:249 CYP1 AAG13968 318829 Magnaporthe_oryzae Reduced_virulence
EVM0002609	PHI:2488 Man1 G4ND25 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0003992	PHI:249 CYP1 AAG13968 318829 Magnaporthe_oryzae Reduced_virulence
EVM0008226	PHI:653 GIP2 AAL11721 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0006512	C14DM PHI:3258 Q4QGX0 5664 Leishmania_major reduced_virulence_
EVM0002377	PHI:144 CHT42 AAC05829 29875 Trichoderma_virens Reduced_virulence
EVM0000213	PHI:1506 GzHOME001 I1RC01 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0002403	PHI:2081 Moatg15 MGG_12828 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0003064	PHI:267 MLT1 AAD51594 5476 Candida_albicans Reduced_virulence
EVM0008611	PHI:397 LAC2 AAV64894 5207 Cryptococcus_neoformans Unaffected_pathogenicity
EVM0000693	GGT PHI:3146 O25743 210 Helicobacter_pylori unaffected_pathogenicity_
EVM0008849	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0001903	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0006554	PHI:2644 thioredoxin_1 P0AA28 90371 Salmonella_enterica_serovar_Typhimurium Reduced_virulence
EVM0001722	PHI:432 FGL1 AAQ23181 5518 Fusarium_graminearum Reduced_virulence
EVM0003767	PHI:2482 AIHK1 Q09JB7 160389 Alternaria_longipes Increased_virulence_(Hypervirulence)
EVM0006123	PHI:2128 MoHox1 MGG_04853 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) reduced_virulence
EVM0007566	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0002356	PHI:1494 MAT1-1-3 I1RX41 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0003636	PHI:811 MGG_10510 EDK06580 318829 Magnaporthe_oryzae Reduced_virulence
EVM0008542	PHI:2545 TIF35 Q4X1I3 746128 Aspergillus_fumigatus Mixed_outcome
EVM0001357	PHI:440 PMR1 CAB87245 5476 Candida_albicans Reduced_virulence
EVM0003013	PHI:2128 MoHox1 MGG_04853 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) reduced_virulence

EVM0008015	PHI:1161 MgMfs1 A4ZGP3 54734 Mycosphaerella_graminicola_(related : _Zymoseptoria_triticii) Chemistry_target
EVM0009816	PHI:2510 msdS/AfmsdC Q6PWQ1 746128 Aspergillus_fumigatus Unaffected_pathogenicity
EVM0003166	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0009054	ssp PHI:3418 Q5DPX0 29385 Staphylococcus_saprophyticus mixed_outcome_
EVM0003445	PHI:1052 PHL1 ACB38886 135779 Cercospora_zeae-maydis Unaffected_pathogenicity
EVM0002682	PHI:2400 Fgp2 IIS215 5518 Gibberella_zeae_(related: _Fusarium_graminearum) Unaffected_pathogenicity
EVM0002472	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0001087	PHI:2039 Con7p Q069J4 148305 Magnaporthe_oryzae_(related: _Magnaporthe_grisea) Loss_of_pathogenicity
EVM0005001	Vsp PHI:3018 B7VSJ8 212663 Vibrio_splendidus reduced_virulence_
EVM0000484	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0007607	PHI:1816 GzZC131 I1RRS3 5518 Gibberella_zeae_(related: _Fusarium_graminearum) Unaffected_pathogenicity
EVM0006745	PHI:2272 CpkB A9Z1V6 13684 Phaeosphaeria_nodorum_(related: _Stagonospora_nodorum) Unaffected_pathogenicity
EVM0004713	Pop1 PHI:3209 A4KTQ9 312341 Ceratocystis_populicola reduced_virulence_
EVM0002111	PHI:816 MGG_04582 EDJ95999 318829 Magnaporthe_oryzae Reduced_virulence
EVM0008189	PHI:811 MGG_10510 EDK06580 318829 Magnaporthe_oryzae Reduced_virulence
EVM0004224	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal
EVM0007154	PHI:1301 GzbHLH002 I1RB45 5518 Gibberella_zeae_(related: _Fusarium_graminearum) Unaffected_pathogenicity
EVM0004161	PHI:503 COX15 AAB64668 4932 Saccharomyces_cerevisiae Reduced_virulence
EVM0002963	PHI:1301 GzbHLH002 I1RB45 5518 Gibberella_zeae_(related: _Fusarium_graminearum) Unaffected_pathogenicity
EVM0001554	PHI:438 BcBOT1_(related: _CND5) AAQ16576 40559 Botrytis_cinerea Reduced_virulence
EVM0009437	PHI:1343 GzC2H003 I1RAF0 5518 Gibberella_zeae_(related: _Fusarium_graminearum) Reduced_virulence
EVM0000556	PHI:881 MGG_04556 EDJ96020 318829 Magnaporthe_oryzae Reduced_virulence
EVM0007007	PHI:871 MGG_12656 EDK01997 318829 Magnaporthe_oryzae Reduced_virulence
EVM0001764	PHI:2533 FKS1 Q4WLT4 746128 Aspergillus_fumigatus Lethal

EVM0006956	PHI:373 PLD1 EAK93902 5476 Candida_albicans Reduced_virulence
EVM0004888	PHI:2349 VE1_(VEA)_(velvet) G8CYZ6 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0005411	PHI:881 MGG_04556 EDJ96020 318829 Magnaporthe_oryzae Reduced_virulence
EVM0000067	PHI:881 MGG_04556 EDJ96020 318829 Magnaporthe_oryzae Reduced_virulence
EVM0004407	PHI:2519 LYS9 Q4WQ27 746128 Aspergillus_fumigatus Lethal
EVM0005673	PHI:1071 Gas1 CAF05793 5270 Ustilago_maydis Loss_of_pathogenicity
EVM0008273	PHI:1541 GzFlbD I1RE42 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0009965	PHI:871 MGG_12656 EDK01997 318829 Magnaporthe_oryzae Reduced_virulence
EVM0000925	PHI:96 FAS2 AAA34345 5476 Candida_albicans Loss_of_pathogenicity
EVM0003286	PHI:2544 PAB1 Q4WK03 746128 Aspergillus_fumigatus Mixed_outcome
EVM0004950	PHI:2038 Mir1 MGG_02370 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0009621	PHI:601 orf48 AAL20303 216597 Salmonella_enterica Unaffected_pathogenicity
EVM0001674	PHI:96 FAS2 AAA34345 5476 Candida_albicans Loss_of_pathogenicity
EVM0007332	PHI:2601 Oligopeptidase_B Q94795 5693 Trypanosoma_cruzi Reduced_virulence
EVM0001689	PHI:1506 GzHOME001 I1RC01 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0005693	PHI:274 USX1 AAM22494 5207 Cryptococcus_neoformans Loss_of_pathogenicity
EVM0001653	PHI:2222 Sho1 XP_759303 5270 Ustilago_maydis Mixed_outcome
EVM0007042	PHI:748 um00446 Not_available 5270 Ustilago_maydis Unaffected_pathogenicity
EVM0002020	PHI:2644 thioredoxin_1 P0AA28 90371 Salmonella_enterica_serovar_Typhimurium Reduced_virulence
EVM0001805	PHI:2117 SPM1 P58371 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0002806	PHI:1295 FgStuA I1S0A8 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0006840	PHI:2490 MCA E9B636 5665 Leishmania_mexicana Mixed_outcome
EVM0010219	FgERG3A PHI:3035 I1RFM2 5518 Fusarium_graminearum reduced_virulence_
EVM0003076	PHI:2976 CgOPT1 C6ZRH8 29905 Colletotrichum_gloeosporioides_f._s.p._aeschynomenes Reduced_virulence
EVM0005568	PHI:2008 HST1 EDJ98541 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity

EVM0003561	PHI:2109 CNB MGG_06933 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Mixed_outcome
EVM0001631	PHI:871 MGG_12656 EDK01997 318829 Magnaporthe_oryzae Reduced_virulence
EVM0007761	PHI:2510 msdS/AfmsdC Q6PWQ1 746128 Aspergillus_fumigatus Unaffected_pathogenicity
EVM0000122	Pop1 PHI:3209 A4KTQ9 312341 Ceratocystis_populicola reduced_virulence_
EVM0003025	PHI:2321 SidI Q4WR83 746128 Aspergillus_fumigatus Reduced_virulence
EVM0008744	PHI:1180 (Sc_Sat4) I1RS32 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Reduced_virulence
EVM0004653	PHI:2038 Mir1 MGG_02370 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0005770	PHI:419 CSH1 AAP93915 5476 Candida_albicans Reduced_virulence
EVM0009772	PHI:652 GIP1 AAL11720 67593 Phytophthora_sojae Effector_(plant_avirulence_determinant)
EVM0010134	PHI:2544 PAB1 Q4WK03 746128 Aspergillus_fumigatus Mixed_outcome
EVM0001137	PHI:96 FAS2 AAA34345 5476 Candida_albicans Loss_of_pathogenicity
EVM0000187	PHI:2042 ABC3 Q3Y5V5 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0004080	Pop1 PHI:3209 A4KTQ9 312341 Ceratocystis_populicola reduced_virulence_
EVM0004025	PHI:871 MGG_12656 EDK01997 318829 Magnaporthe_oryzae Reduced_virulence
EVM0008974	PHI:2552 NOP4 Q4WNM3 746128 Aspergillus_fumigatus Mixed_outcome
EVM0000205	PHI:1742 GzZC057 I1S7H5 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0007726	PHI:748 um00446 Not_available 5270 Ustilago_maydis Unaffected_pathogenicity
EVM0003315	PHI:2038 Mir1 MGG_02370 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Unaffected_pathogenicity
EVM0010224	PHI:2643 CFAS A4HTK3 5671 Leishmania_infantum Reduced_virulence
EVM0010061	PHI:1255 FGSG_07745 I1RQ67 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0006879	PHI:438 BcBOT1_(related:_CND5) AAQ16576 40559 Botrytis_cinerea Reduced_virulence
EVM0008470	PHI:2158 MoCMK1 EU_984498 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Reduced_virulence
EVM0000351	PHI:871 MGG_12656 EDK01997 318829 Magnaporthe_oryzae Reduced_virulence

EVM0007277	PHI:174 GNA1 BAA36496 5476 Candida_albicans Reduced_virulence
EVM0001968	PHI:2510 msdS/AfmsdC Q6PWQ1 746128 Aspergillus_fumigatus Unaffected_pathogenicity
EVM0000750	Atf1 PHI:3808 IIS0C0 5518 Fusarium_graminearum_(related:_Gibberella_zeae) effector_(plant_avirulence_determinant)
EVM0000062	PHI:2930 ctf2 J9MFF7 59765 Fusarium_oxysporum_f._sp._Lycopersici Reduced_virulence
EVM0008877	PHI:1255 FGSG_07745 IIRQ67 5518 Gibberella_zeae_(related:_Fusarium_graminearum) Unaffected_pathogenicity
EVM0004058	PHI:2042 ABC3 Q3Y5V5 148305 Magnaporthe_oryzae_(related:_Magnaporthe_grisea) Loss_of_pathogenicity
EVM0002444	PHI:2644 thioredoxin_1 P0AA28 90371 Salmonella_enterica_serovar_Typhimurium Reduced_virulence
EVM0004514	PHI:33 PHR1 AAA68196 5476 Candida_albicans Reduced_virulence

*DEGs were significantly upregulated in both S vs. pre-S and S vs. post-S.

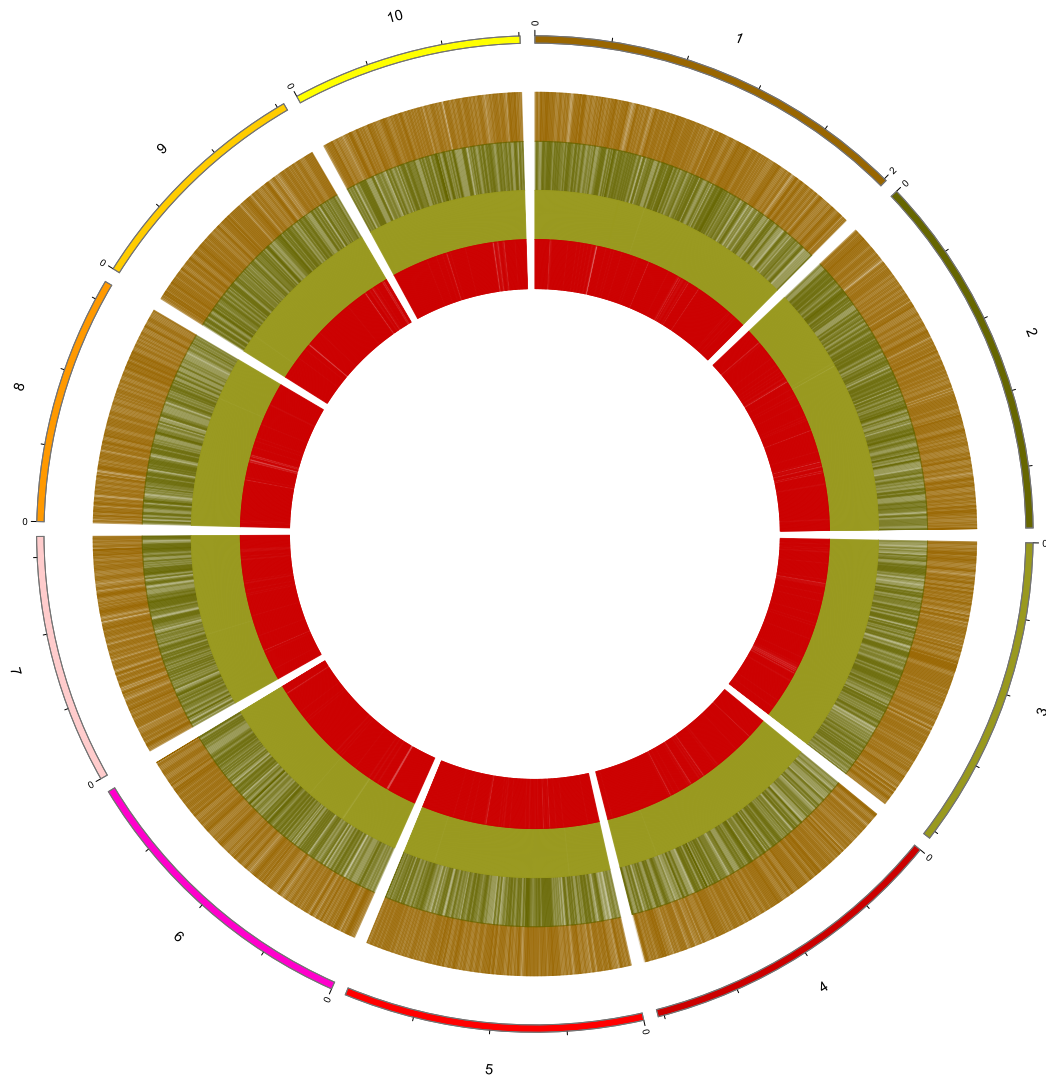
Table S10 Differential expression of selected genes related to secondary metabolite biosynthesis, transport, and catabolism during conidiation.

Internal ID	FPKM*			Log2(FC) [†]		PHI
	Pre-C	C	Post-C	C vs. pre-C	C vs. post-C	
ABC transporter						
EVM0003125	0.00	3.00	0.00	6.51	7.05	PHI:2042
EVM0004058	5.71	11.80	5.54	1.08	1.36	PHI:2042
EVM0000187	9.02	20.94	8.40	1.26	1.59	PHI:2042
EVM0003276	0.48	3.21	0.46	2.74	3.05	PHI:2042
EVM0003064	35.03	189.63	16.33	2.47	3.80	PHI:267
EVM0001189	34.69	210.88	36.30	2.64	2.80	PHI:267
Alcohol dehydrogenase GroES-like						
EVM0001555	0.21	2.13	0.03	3.10	5.26	PHI:881
EVM0002621	0.30	2.22	0.10	2.68	4.23	PHI:881
EVM0000556	0.49	1.78	0.06	1.80	4.61	PHI:881
EVM0000067	0.31	1.06	0.02	1.72	4.86	PHI:881
EVM0005411	1.27	4.32	0.44	1.72	3.31	PHI:881
Cytochrome P450						
EVM0003715	0.08	3.17	0.42	4.84	3.10	PHI:2357
EVM0002185	0.04	73.62	4.56	6.53	4.22	PHI:4194
EVM0006879	10.31	22.53	9.59	1.16	1.49	PHI:438
Co_147	6.23	12.54	6.30	1.06	1.26	/
EVM0009502	0.02	3.72	0.33	6.30	3.43	PHI:438
EVM0001327	0.03	1.65	0.17	4.48	3.19	PHI:4194
EVM0004394	0.04	14.15	2.03	7.69	3.01	PHI:4194
EVM0009549	0.08	10.82	3.89	6.73	1.73	PHI:4194
EVM0001554	18.15	64.35	27.86	1.86	1.48	PHI:438
Co_423	0.03	1.76	0.14	4.97	3.49	/
EVM0005592	0.28	3.49	0.52	3.46	2.88	PHI:4194
EVM0002960	0.27	13.76	6.94	5.49	1.25	PHI:4194
EVM0003421	0.00	12.09	0.08	8.77	6.96	PHI:4194
EVM0004379	0.00	3.30	0.24	7.10	3.77	PHI:4194
EVM0004814	14.66	103.77	31.34	2.84	1.98	PHI:2534
Co_207	0.07	1.37	0.44	2.72	1.49	/
Multicopper oxidase						
EVM0004492	0.13	14.31	0.52	6.28	4.77	PHI:397
EVM0008611	0.34	1.85	0.68	2.40	1.68	PHI:397
EVM0005600	0.53	7.57	0.41	3.73	4.37	PHI:2920

* The transcript level is expressed as fragments per kilobase per million mapped reads (FPKM).

[†] FC is the fold change (FC) of DEGs based on a FC of ≥ 2 and an FDR of < 0.01 .

Figure S2. Characteristics of the de novo genome assembly. From the outside to the inside are as follows: I scaffolds, the different colors represent different scaffolds (the top10 scaffolds were chosen); II GC content; III gene density; IV miRNA; V tRNA.



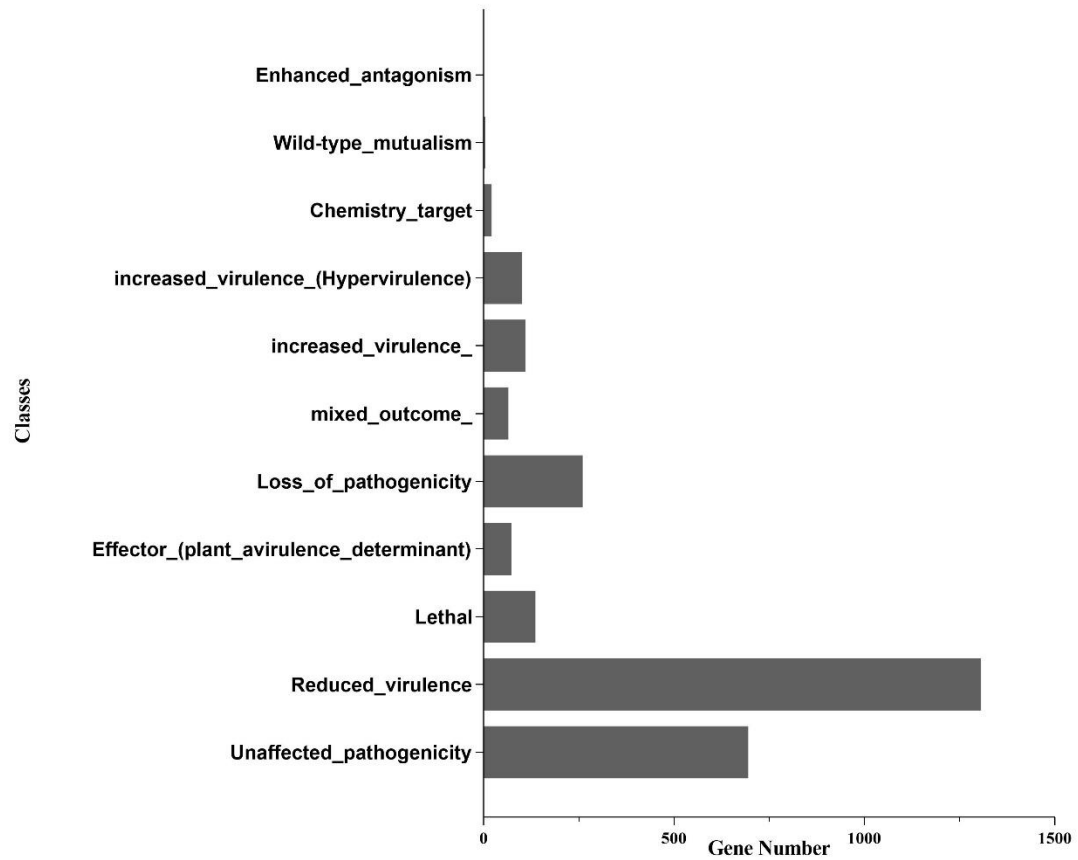


Figure S3. the PHI-annotated categories of the predicted protein-encoding genes of the *Conidiobolus obscurus* genome.

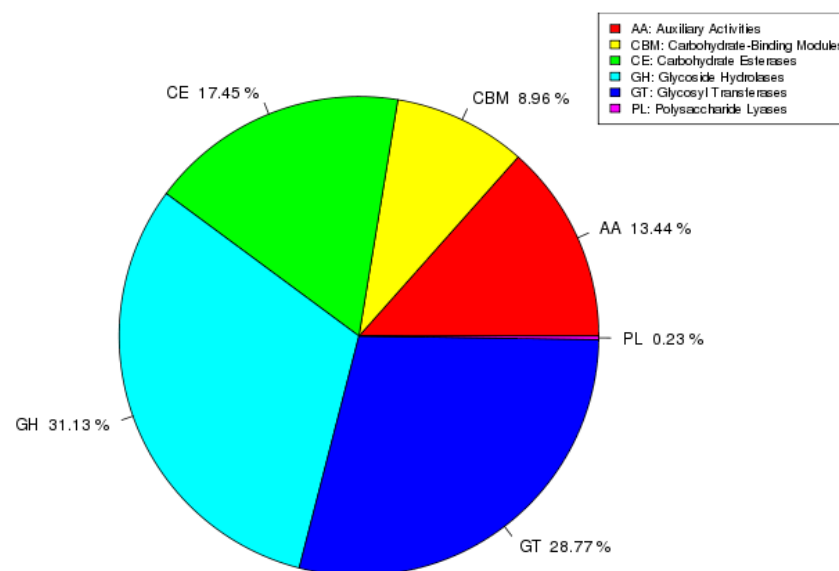


Figure S4. the CAZyme-coding genes in *Conidiobolus obscurus*.

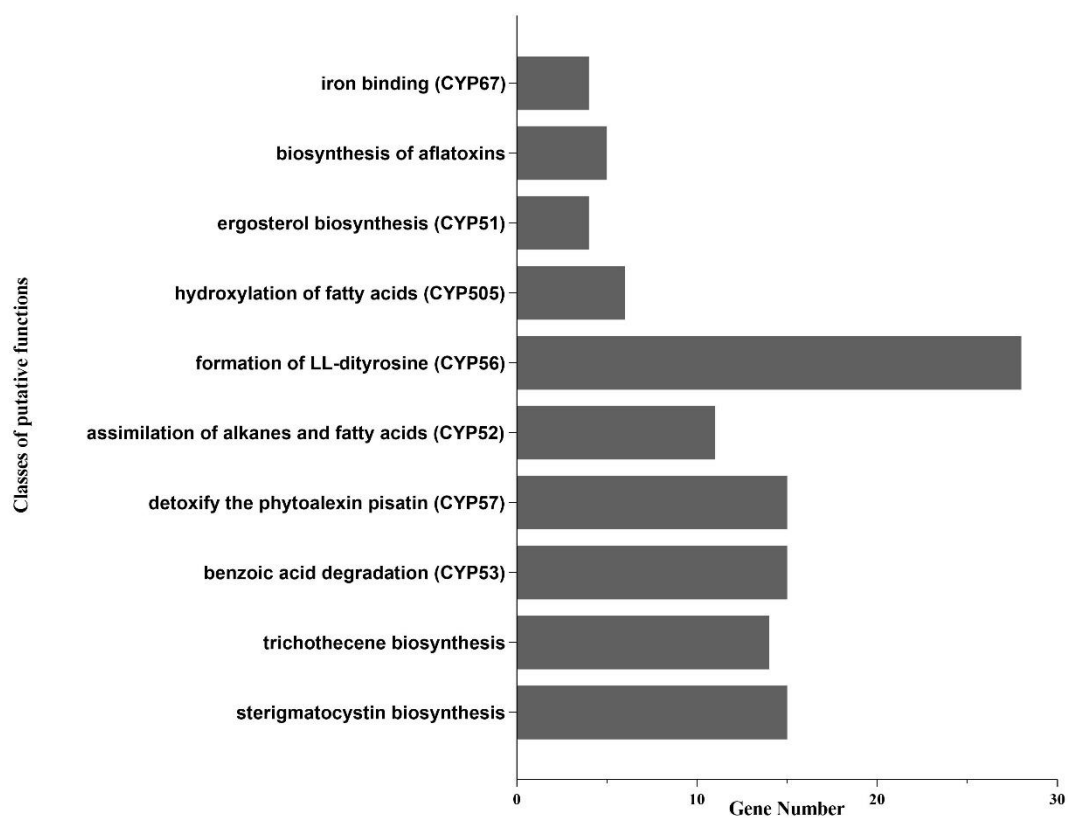


Figure S5. The putative functions and gene number of main P450 classes in the *Conidiobolus obscurus* genome.

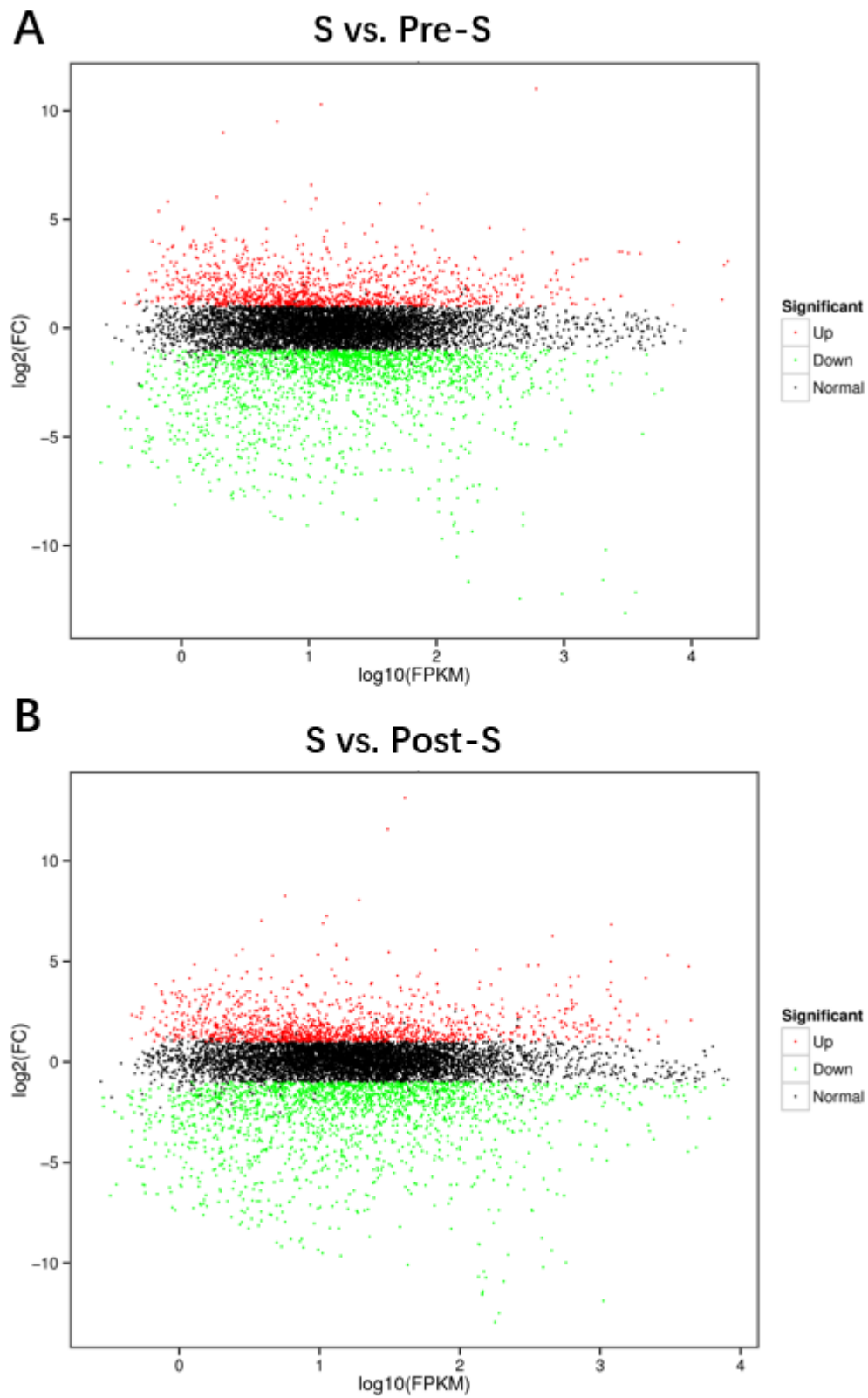
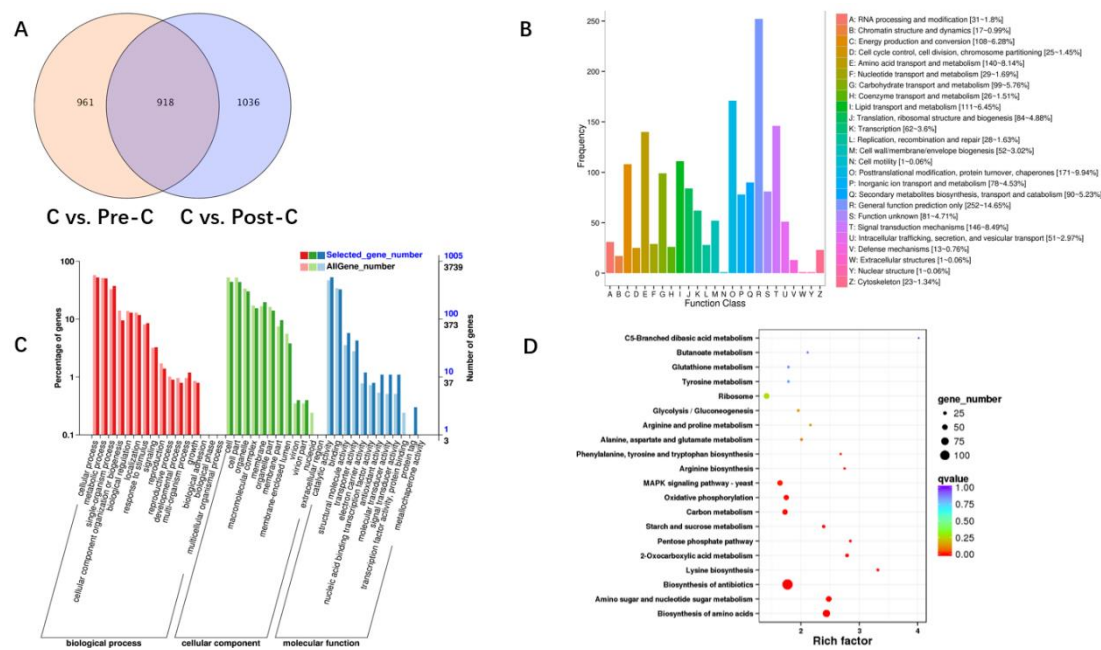


Figure S6. the MA plots of DEGs in C vs. Pre-C and C vs. Post-C.

Figure S7. Classification of upregulated genes in C stage vs. pre-C stage or C stage vs. post-C stage. (A) Number of upregulated genes putatively related to conidiation; (B) NCBI eukaryotic orthologous groups of proteins (KOG) functional annotation; (C) Gene Ontology (GO) functional annotation; (D) KEGG enrichment analysis. A smaller q value indicated a more significant enrichment, considering a $FDR \leq 0.01$ as the threshold.



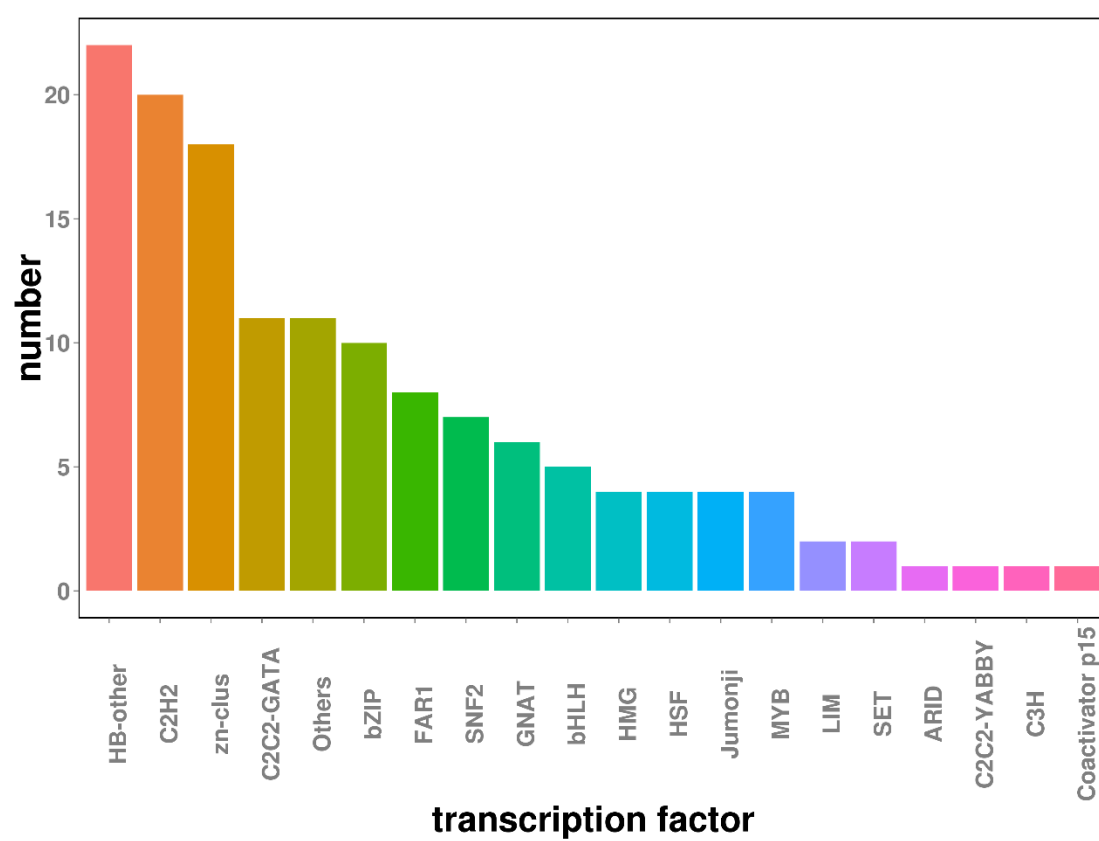


Figure S8. Transcription factor families

Figure S9. Validation of four differentially expressed transcripts at pre-C, C, and post-C stages of *C. obscurus* using RT-qPCR. (A) Heat shock transcription factor (EVM0008905); (B) Cytochrome P450 (EVM0004814); (C) β -glucan synthesis-associated protein (EVM0003971); (D) Trypsin-like serine proteinase (EVM0009373). Relative fold changes of C, post-C, were compared to the pre-C stage, which was set to a fold change of 1. Error bars are expressed as SEM from three biological replicates. Different lowercase letters marked on the bars indicated significant differences based on Fisher's least significant difference test following one-way ANOVA, with $P < 0.05$. The primers used are listed in Table S1.

