

1 **Supplemental material**

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3 **TABLE S1** Proteins identified in knobs and mycelia of *M. haptotylum* using LC-MS/MS.

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5 **TABLE S2** Features of all genes with the Pfam domain WSC in *M. haptotylum*.

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7 **FIG S1** SDS-PAGE analysis of extracted proteins.

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9 **FIG S2** Sequence logo of the WSC domain.

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11 **FIG S3** Distribution of proteins and transcripts in different KOG categories.

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13 **FIG S4** Phylogeny of 173 WSC Pfam domains from six fungal genomes.

14 **TABLE S1** Proteins identified in knobs and mycelia of *M. haptotylum* using LC-MS/MS.

NCBI Locus ID ^a	Matching peptides ^b	Knob ^c	Mycelium ^c	Uniprot ID ^d	Description	PHI-base ^e	Phylogeny ^f
H072_8026	3	3	0	-	-		ss ^g
H072_7202	3	3	0	-	-		ss ^g
H072_2504	1	2	0	-	-		ls
H072_4225	1	2	0	-	-		ls
H072_6857	1	1	0	-	-		ss ^g
H072_8717	1	1	0	-	-		ss ^g
H072_8137	4	3	0	B8M6K0	1,3-beta-glucanosyltransferase, putative	PHR1	core
H072_11580	1	1	0	F2S3Q3	26S proteasome regulatory subunit RPN11		core
H072_2306	1	1	0	A6RMK3	3-hydroxyacyl-CoA dehydrogenase		core
H072_4821	1	1	0	C1GSE0	40S ribosomal protein S16		core
H072_858	1	1	0	B8MZ16	40S ribosomal protein S25, putative		core
H072_9322	2	3	0	E3QCX3	6,7-dimethyl-8-ribityllumazine synthase		core
H072_6833	4	4	0	A3LSL7	Agglutinin-like protein 2		core
H072_7564	2	3	0	A1CHW0	Alpha-glucosidase AgdA	Gas1	core
H072_10654	1	2	0	E4USH8	Arginine permease		core
H072_3167	1	1	0	A7EH61	Argininosuccinate synthetase		core
H072_5606	1	1	0	C1GKS3	ARP2/3 complex 20 kDa subunit		core
H072_6336	1	3	0	E9E375	ATP-dependent Zn protease	PEX6	core
H072_3089	1	1	0	B6QPL5	BAR domain protein		core
H072_8969	1	1	0	Q68KY1	Beta-glucosidase	um00446	core
H072_8828	2	1	0	B2VYL4	cAMP-dependent protein kinase regulatory subunit	RPK1	core
H072_5305	1	1	0	O94255	Carbonic anhydrase	Can2	core
H072_7670	1	1	0	A5AB21	Carboxypeptidase Y	um01886	core

H072_11090	4	2	0	B6JV38	Cell agglutination protein mam3		core
H072_4865	1	1	0	B2WKN9	Chaperone protein dnaK		core
H072_5869	1	1	0	B2W796	Chitin biosynthesis protein CHS5	MRB1	core
H072_5258	1	1	0	B9R282	'Cold-shock' DNA-binding domain protein		core
H072_5249	1	1	0	Q9TYL3	C-type lectin protein 122		ls
H072_11420	3	2	0	Q19AS3	Cuticle-degrading serine protease		core
H072_10767	1	1	0	C5PDZ1	Cyclophilin B, putative	CPA1	core
H072_9166	1	1	0	Q4WTN4	D-3-phosphoglycerate dehydrogenase		core
H072_11462	1	1	0	C5PC30	Dihydrolipoamide acetyltransferase, putative		core
H072_8843	1	1	0	B6QTM2	Dihydrolipoamide succinyltransferase		core
H072_777	1	1	0	G3J6B0	DUF543 domain protein		core
H072_9522	1	2	0	B6QSL6	Endo alpha-1,4 polygalactosaminidase		core
H072_6866	1	1	0	B2WFL9	Eukaryotic translation initiation factor 3 subunit M		core
H072_5927	1	1	0	C8VQV2	Exo-beta-1,3-glucanase		core
H072_1293	2	3	0	B0XYK6	Extracellular serine-rich protein, putative		core
H072_8109	1	1	0	A1CAW6	Extracellular serine-threonine rich protein		core
H072_3103	1	1	0	C5FMX2	FAD binding domain-containing protein		core
H072_1852	1	1	0	A1CG01	Ferulic acid esterase (FaeA), putative		core
H072_6764	2	1	0	Q5USB2	Gas1-like protein	GAS1	core
H072_4513	1	1	0	E3QVC3	Gelsolin		core
H072_7455	1	1	0	Q5B093	Glucose-6-phosphate isomerase		core
H072_10613	1	1	0	B2WFA1	Glucosidase 2 subunit beta		core
H072_5488	1	2	0	A1CUX5	Glutathione S-transferase family protein		core
H072_10458	1	2	0	A8N6M0	Glycine-rich RNA binding protein		core
H072_8800	1	1	0	F0XIB2	GPI anchored cell wall protein		core
H072_10737	1	1	0	C0P137	Isocitrate dehydrogenase		core

H072_4751	1	1	0	C5DIY2	KLTH0E16082p		core
H072_7185	1	1	0	E3QQL9	LSM domain-containing protein		core
H072_9427	6	4	0	B8MP05	Maltose phosphorylase		core
H072_8764	2	1	0	F2RLV9	Metallopeptidase domain protein		ss
H072_5236	1	1	0	B8MQJ3	Mitochondrial ATPase subunit ATP4, putative		core
H072_9628	1	1	0	B0XTW8	Mitochondrial F1F0 ATP synthase subunit Atp18		core
H072_1845	1	1	0	Q4CTP5	Mucin TcMUCI, putative		ss
H072_8860	1	1	0	E3QMN8	Myosin regulatory light chain cdc4		core
H072_4934	1	1	0	A1CM74	NADH-ubiquinone oxidoreductase B14 subunit		core
H072_9492	1	1	0	B6Q1W8	Nascent polypeptide-associated complex		core
H072_462	1	1	0	B6QBA6	Nuclear segregation protein (Bfr1), putative		core
H072_9167	2	1	0	B6QGR2	Nucleosome assembly protein Nap1, putative		core
H072_10638	1	1	0	E9EEH8	Outer membrane autotransporter		core
H072_2342	1	2	0	F9WZR8	Peptidase aspartic	MGG_01748	core
H072_7530	1	1	0	E9DTG2	Pre-mRNA splicing factor (Srp1), putative		core
H072_448	2	2	0	Q5BCF8	Probable feruloyl esterase B		core
H072_10254	4	2	0	Q9P6S0	Putative cell agglutination protein		core
H072_973	1	1	0	Q9P6S0	Putative cell agglutination protein		core
H072_6835	2	4	0	E9F139	Putative glyoxal oxidase		core
H072_10205	3	3	0	E9F139	Putative glyoxal oxidase		core
H072_10940	1	2	0	E9F139	Putative glyoxal oxidase		core
H072_8804	3	2	0	E9F139	Putative glyoxal oxidase		core
H072_5095	2	1	0	E9F139	Putative glyoxal oxidase		core
H072_1462	2	1	0	B6Q9R4	Ran-specific GTPase-activating protein		core
H072_5796	1	1	0	A1DDD5	RNA annealing protein Yra1, putative		core
H072_5208	4	2	0	B2WDQ6	RNA binding domain containing protein		core

H072_5543	1	1	0	G2XUB8	Similar to small nuclear ribonucleoprotein g		core
H072_2885	1	1	0	G3FEJ1	Snodprot		core
H072_6341	1	1	0	G3FEJ1	Snodprot		core
H072_3765	2	2	0	C5JF23	Sorbitol utilization protein SOU1	Mdh1	core
H072_3441	1	3	0	Q4WUB7	SsDNA binding protein, putative		core
H072_8460	1	1	0	C9S9J0	Superoxide dismutase	CPSOD1	core
H072_9501	1	2	0	C0S9X0	Synaptobrevin		core
H072_9252	2	1	0	B6QND5	Transformer-SR ribonucleoprotein		core
H072_6884	2	2	0	A6SFQ6	Translation initiation factor 3 subunit B		core
H072_5716	1	1	0	B0CYE6	Translationally-controlled tumor protein		core
H072_1264	1	2	0	Q4WZQ6	Translocon-associated protein, alpha subunit		core
H072_4515	2	1	0	F2T0M7	Tyrosinase		core
H072_1932	1	1	0	B8LVZ5	Ubiquinol-cytochrome c reductase complex		core
H072_4699	1	1	0	Q2ULC1	Ubiquitin-like protein		core
H072_251	1	1	0	D5GA29	Uroporphyrinogen decarboxylase		core
H072_333	1	1	0	B2VXC9	WLM domain containing protein		core
H072_9053	3	1	0	B2VYM4	von Willebrand domain containing protein		core
H072_8456	2	1	0	C5FVD1	Woronin body major protein	HEX1	core
H072_7321	1	1	0	B6QLH9	Yapsin, putative	SAP6	core
H072_10839	2	1	0	A1CXU2	YCII-related domain protein		core
H072_8040	3	0	1	-	-		ss ^g
H072_11421	1	0	1	-	-		ls
H072_2442	1	0	1	-	-		ls
H072_2849	1	0	1	-	-		ss
H072_4969	1	0	1	-	-		ls
H072_5071	2	0	1	A1CNN3	3-isopropylmalate dehydrogenase	LEU2	core

H072_7212	1	0	1	Q0CA00	40S ribosomal protein S1		core
H072_4824	2	0	2	Q2H733	40S ribosomal protein S14		core
H072_8904	2	0	2	C1G810	40S ribosomal protein S4		core
H072_1819	1	0	2	A7TI44	40S ribosomal protein S8		core
H072_4551	2	0	1	C8VP37	5'-methylthioadenosine phosphorylase		core
H072_8358	1	0	1	G2XEJ2	60S ribosomal protein L10-B		core
H072_9155	2	0	2	A7E5M3	60S ribosomal protein L2		core
H072_400	2	0	1	E4UV03	60S ribosomal protein L23a		core
H072_1346	1	0	1	B2VUF3	60S ribosomal protein L33		core
H072_3115	1	0	1	E9EVG2	60S ribosomal protein L9		core
H072_4920	3	0	1	A1DLW3	Actin		core
H072_9171	1	0	1	G0S4P9	Adenosine kinase-like protein		core
H072_8285	1	0	1	B2W768	ADP-ribose pyrophosphatase		core
H072_10361	2	0	2	A8NWX9	ADP-ribosylation factor Arf1		core
H072_9057	1	0	1	C0NAM8	Alpha-mannosidase		core
H072_2059	1	0	1	B2WB98	Aspartyl aminopeptidase		core
H072_3661	1	0	1	Q8X213	Beta-galactosidase		core
H072_8897	10	0	4	Q8X213	Beta-galactosidase		core
H072_4124	1	0	1	Q1WMR7	Beta-lactamase class C binding protein-like protein		core
H072_7033	2	0	1	B8LYB6	Cell division control protein Cdc48	PEX6	core
H072_11288	1	0	2	A0DNP7	Chromosome undetermined scaffold_58		ls
H072_6958	1	0	2	F2SN81	Cleavage and polyadenylation specific factor 5		core
H072_4161	2	0	2	C9SY92	Copper transport protein ctr4		core
H072_11173	2	0	2	Q4ING3	Cytochrome c peroxidase, mitochondrial		core
H072_1410	7	0	2	D5GGN7	Dihydrolipoyl dehydrogenase		core
H072_250	2	0	1	C4JLH5	Dipeptidyl-peptidase 5		core

H072_7618	1	0	1	E9EAV3	DUF614 domain protein		core
H072_10773	6	0	2	C0NAB0	Enolase		core
H072_2097	1	0	1	A1CAU1	Esterase, putative		core
H072_5189	5	0	1	Q2US06	F0F1-type ATP synthase	ssaN	core
H072_2712	1	0	1	F2SC85	Gamma-cysteine synthetase regulatory subunit		core
H072_5254	1	0	1	G2X076	Glucan 1,3-beta-glucosidase		core
H072_9382	1	0	1	E3Q9B8	Glucose sorbosone dehydrogenase		core
H072_7720	1	0	1	C5GQQ5	Glucose transporter		core
H072_1348	1	0	1	D5GIU9	Glucose-6-phosphate 1-dehydrogenase		core
H072_1331	1	0	1	B8MNR3	Glutamate carboxypeptidase, putative		core
H072_6620	1	0	1	A1CKI7	Glutathione S-transferase GstA		core
H072_10870	2	0	1	F0XM66	GPI-anchored cell wall organization protein ecm33		core
H072_4845	1	0	1	C1MGF5	Helicase		core
H072_3332	3	0	3	B6Q8V9	High affinity zinc ion transporter, putative		core
H072_10799	2	0	2	A1CNS2	Homoserine acetyltransferase family protein		core
H072_9059	2	0	2	E3Q4C4	Hsp70-like protein		core
H072_8071	1	0	1	A6SAG8	Leukotriene A-4 hydrolase homolog		core
H072_7269	2	0	2	A6SA55	Malic enzyme		core
H072_8642	1	0	1	C1GPN6	Membrane biogenesis protein Yop1		core
H072_10242	2	0	1	Q4WQK0	MFS transporter, putative		core
H072_2171	2	0	1	A7EHB2	Mitochondrial peroxiredoxin PRX1	TSA1	core
H072_9406	2	0	2	A7ELH5	Mitochondrial processing peptidase beta subunit		core
H072_1954	1	0	1	E9DJ65	Oxidoreductase		core
H072_11032	1	0	1	B6H9J0	Pc16g11390 protein		core
H072_9235	1	0	1	E5R1Z9	Peroxiredoxin DOT5		core
H072_2638	1	0	1	E3QLI7	Pfs domain-containing protein		core

H072_5807	2	0	2	A8N9Z6	Pirin domain-containing protein		core
H072_4573	2	0	1	B2AQR4	Predicted CDS Pa_4_3430		core
H072_6567	1	0	2	Q4WFK4	Probable 1,4-beta-D-glucan cellobiohydrolase		core
H072_740	1	0	1	Q8X077	Probable proteasome subunit alpha type-2		core
H072_7191	1	0	1	E3S7K9	Probable Xaa-Pro aminopeptidase P		core
H072_3324	2	0	1	B6QRG8	Proteasome component Prs3, putative		core
H072_10716	1	0	1	E3RUA8	Proteasome subunit alpha type		core
H072_3320	1	0	1	D5GBG2	Proteasome subunit beta type		core
H072_8855	1	0	2	B2WMI6	Purine permease		core
H072_7459	3	0	1	C4YFN5	Rab GDP-dissociation inhibitor		core
H072_4618	1	0	1	B8MRE3	RAS small monomeric GTPase Rab6	CLPT1	core
H072_2692	1	0	2	O93856	Ras-like protein	RAS1	core
H072_2657	1	0	1	Q6CFH4	Ribose-5-phosphate isomerase		core
H072_5782	1	0	2	C5JD38	Ribosomal protein L7a		core
H072_560	1	0	1	C1GBD3	RNP domain-containing protein		core
H072_5386	1	0	1	B6K4U6	S-adenosylmethionine synthetase	MGG_00383	core
H072_8873	1	0	1	E4ZH33	Similar to 40S ribosomal protein S17		core
H072_3146	2	0	1	E4ZLT6	Similar to delta 1-pyrroline-5-carboxylate dehydrogenase		core
H072_10966	1	0	1	E4ZWH5	Similar to DUF814 domain-containing protein		core
H072_8300	7	0	3	E5A5S8	Similar to fatty acid oxygenase	PPOA	core
H072_10791	2	0	2	G2YT91	Similar to peptidase		core
H072_5468	2	0	1	G2Y7Z4	Similar to proteasome subunit alpha type 1		core
H072_3012	1	0	1	G2Y153	Similar to ras-related protein ypt1	CLPT1	core
H072_2935	2	0	2	G2Y4X7	Similar to tyrosinase		core
H072_5183	1	0	1	D5MTF9	Succinate dehydrogenase subunit A		core
H072_9165	1	0	2	C4JNC6	Succinyl-CoA ligase alpha-chain		core

H072_6019	1	0	1	B0DN92	Thioredoxin		core
H072_6985	2	0	1	C5JW14	Transcription factor RfeF		core
H072_1506	1	0	1	Q0CN96	Tubulin alpha-1 chain	beta-tubulin	core
H072_9647	1	0	1	E9EUM6	Urea transporter		core
H072_9474	3	0	2	A7EJU4	Vacuolar ATP synthase subunit E		core
H072_1656	3	2	4	-	-		ls
H072_11515	7	4	4	-	-		ls
H072_10061	4	2	4	A6S5A2	14-3-3 protein		core
H072_1296	1	1	1	C5FLK4	2,3-bisphosphoglycerate-independent phosphoglycerate mutase		core
H072_9511	7	1	1	C5NZN9	2-methylcitrate dehydratase, putative		core
H072_5591	2	3	2	C5P2T9	40S ribosomal protein S15, putative		core
H072_613	3	3	2	E9F0G2	40S ribosomal protein S18		core
H072_1619	1	1	1	A7E5C7	40S ribosomal protein S19		core
H072_4705	2	1	1	Q86ZG1	40S ribosomal protein S24		core
H072_10413	1	3	3	E9CZU1	40S ribosomal protein S3		core
H072_2214	1	1	1	F0X7C8	40S ribosomal protein s5		core
H072_10410	3	2	1	G3JBG0	40S ribosomal protein S7		core
H072_9617	4	2	1	C5JCK9	40S ribosomal protein S9		core
H072_3423	7	4	3	C8VMU4	4-aminobutyrate aminotransferase		core
H072_297	2	1	2	A7E5G0	60S ribosomal protein L1		core
H072_11562	2	1	1	F2SCD3	60S ribosomal protein L26		core
H072_5408	1	2	3	F2S9H0	60S ribosomal protein L35		core
H072_758	3	4	4	E3KFB8	60S ribosomal protein L40		core
H072_10336	3	2	2	C1GY65	60S ribosomal protein L6		core
H072_7449	3	4	2	Q4W9S6	60S ribosomal protein L7		core
H072_8772	3	2	3	B6GWT7	6-phosphogluconate dehydrogenase, decarboxylating		core

H072_10403	6	4	3	A1D489	ADP,ATP carrier protein		core
H072_111	1	1	1	C0NKH9	ADP-ribosylation factor		core
H072_11540	15	3	3	P40108	Aldehyde dehydrogenase		core
H072_2170	1	1	1	A1CHK2	Aldose 1-epimerase, putative		core
H072_11516	7	3	4	C1GDQ9	Alkaline phosphatase		core
H072_6410	2	1	1	D8DUI6	Alpha-1,6-glucosidase, pullulanase-type		core
H072_10095	2	1	1	Q9HG00	Alpha-galactosidase		core
H072_4639	14	4	2	C8V659	Aminopeptidase		core
H072_3011	4	1	2	Q4WEV5	Aminopeptidase, putative		core
H072_9479	3	4	2	E9EJ64	ATP synthase D chain		core
H072_940	7	4	3	C1GIF6	ATP synthase subunit 5		core
H072_9367	16	4	4	F0XTF0	ATP synthase subunit beta	ssaN	core
H072_7513	7	3	3	C5JQV8	ATP-dependent molecular chaperone HSC82	HSP90	core
H072_227	2	1	2	A1CJT5	ATP-dependent RNA helicase eIF4A	VAD1	core
H072_8474	8	4	4	B6QEB0	Autophagic serine protease Alp2		core
H072_7037	1	1	1	E9DJF7	Beta-1,3-glucanosyltransferase	GAS1	core
H072_10514	6	4	4	A7F2T8	Brt1		core
H072_6432	2	1	1	E9DY83	Calcofluor white hypersensitive protein		ls
H072_5152	6	2	2	B2WDE1	Calreticulin		core
H072_1143	2	1	2	G2QFL8	Carbohydrate-binding module family 48 protein		core
H072_11104	4	2	1	F2PH15	Carboxypeptidase	um01888	core
H072_4030	5	3	2	B6HPP6	Carboxypeptidase Y homolog A	um01886	core
H072_6416	7	4	2	C8VRG6	Carnitine acetyl transferase		core
H072_1531	5	1	2	C5JTH3	Chaperonin GroL		core
H072_3717	9	1	4	C0NIW4	Cobalamin-independent methionine synthase	MSY1	core
H072_8961	2	3	1	C8VCM2	Cyanate hydratase		core

H072_512	1	1	1	E3QDN0	DJ-1/PfpI family protein		core
H072_6484	14	4	4	A6RVB0	DnaK-type molecular chaperone BiP		core
H072_283	4	4	1	Q873Z5	Elongation factor 1 beta subunit		core
H072_2534	9	3	3	Q96X45	Elongation factor 2		core
H072_8326	14	2	3	B2VV92	Endothelin-converting enzyme 1		core
H072_3998	1	1	1	B0Y8Q4	FKBP-type peptidyl-prolyl isomerase, putative	BcPIC5	core
H072_4602	9	4	3	Q4WY39	Fructose-bisphosphate aldolase, class II		core
H072_2750	3	1	1	E5R0W2	Fumarylacetoacetase		core
H072_5604	7	1	3	F9XAN5	Glucokinase	HXK1	core
H072_2327	5	3	3	C5GQQ5	Glucose transporter	FRT1	core
H072_6630	6	3	1	C6HB15	Glutaminase A		core
H072_1102	3	3	3	Q873E8	Glutathione reductase		core
H072_6664	2	1	2	B2W2A7	Glutathione S-transferase		core
H072_7628	5	2	1	Q2UAA3	Glutathione S-transferase		core
H072_6088	4	1	3	Q6B960	Glyceraldehyde 3-phosphate dehydrogenase		core
H072_2385	4	2	3	D4DGP3	Glycosyl hydrolase, putative		core
H072_8798	1	1	1	F0XIB2	GPI anchored cell wall protein		core
H072_8801	1	1	3	F0XIB2	GPI anchored cell wall protein		core
H072_8797	5	4	4	F0XIB2	GPI anchored cell wall protein		core
H072_3286	1	1	4	B1NNU0	GPI anchored CFEM domain protein		ls
H072_10064	3	3	3	B1NNT9	GPI anchored CFEM domain protein		ls
H072_8802	3	1	2	E9F4I8	GPI anchored protein, putative		core
H072_5177	3	2	3	A1C3X6	GPI anchored protein, putative		ls
H072_4162	1	3	2	E9F4I8	GPI anchored protein, putative		core
H072_2629	5	3	1	G2WQ85	Heat shock protein		core
H072_9974	7	4	4	C8VJN8	Histone H1		core

H072_6094	1	4	3	P04909	Histone H2A-alpha		core
H072_6093	8	4	4	D5G562	Histone H2B		core
H072_4460	2	3	4	F9XD44	Histone H3		core
H072_4461	6	4	4	P04914	Histone H4		core
H072_5895	6	4	4	Q76MU7	Histone H4		core
H072_3464	3	1	1	B8MGP9	HMG box protein, putative		ls
H072_1514	15	4	4	C1GLI2	Hsp70-like protein		core
H072_3209	10	3	4	C5GFP7	Immunogenic protein		core
H072_1384	1	1	1	D2JY86	Initiation factor 5a		core
H072_1583	1	4	2	B2W290	Integral membrane protein		core
H072_684	3	1	1	B8M2D7	Isocitrate dehydrogenase, NAD-dependent	LEU2	core
H072_10483	3	2	1	G0ZGS9	Isopentenyl-diphosphate isomerase		core
H072_5292	1	2	1	A6YIY0	Major ampullate spidroin 2		core
H072_10207	11	2	4	Q7ZA65	Malate dehydrogenase		core
H072_4910	4	1	3	B8MTP1	Malate dehydrogenase, NAD-dependent		core
H072_9486	2	1	1	B8M532	Malate synthase AcuE	MLS1	core
H072_5154	10	3	3	Q0CT17	Methylmalonate-semialdehyde dehydrogenase		core
H072_5302	2	1	2	Q4WQ50	Mn superoxide dismutase SodB	SOD2	core
H072_3247	1	2	3	Q5G5B5	Mucin-like protein		core
H072_7115	1	1	2	A1C671	NAD dependent epimerase/dehydratase family protein		core
H072_6117	2	1	4	C1GGT1	Naringenin 3-dioxygenase		core
H072_4754	2	3	3	C4JZ26	Nonhistone chromosomal protein 6A	MNH6	core
H072_8576	9	4	4	A4QSA2	Nucleoside diphosphate kinase		core
H072_1095	7	4	4	F2TUB3	Outer mitochondrial membrane protein porin 1		core
H072_9845	6	2	2	A1D617	Palmitoyl-protein thioesterase		core
H072_3494	7	3	4	Q5ASX5	Peptidyl-prolyl cis-trans isomerase	CPA1	core

H072_8871	2	4	2	B4VX45	Peptidyl-prolyl cis-trans isomerase, FKBP-type	BcPIC5	core
H072_10420	1	1	1	E7R805	Peptidylprolyl-cis/trans-isomerase		core
H072_8	7	1	2	A1DAN6	Phosphate-repressible phosphate permease		core
H072_7752	1	1	3	A1DM57	Phosphomannomutase		core
H072_7290	8	3	3	C5JTE5	Plasma membrane ATPase	PMR1	core
H072_10672	3	4	4	D4NXD9	Poly-ubiquitin		core
H072_7877	11	4	4	Q2TXY5	Predicted protein		ls
H072_8183	3	1	3	Q5USB0	Profilin-like protein		core
H072_1780	14	4	4	B2W8Q8	Protein disulfide-isomerase		core
H072_11591	3	1	1	C9SWZ1	Putative uncharacterized protein		core
H072_6859	7	4	4	E3S5J5	Putative uncharacterized protein		core
H072_8078	5	4	4	A1D8M5	Putative uncharacterized protein		core
H072_6761	8	4	3	E3QM16	Quinone oxidoreductase		core
H072_806	4	2	2	E3QPZ4	Ras family protein	CLPT1	core
H072_1995	1	4	3	B2W104	Retrograde transporter		core
H072_2182	2	2	2	Q2TXA3	RIB40 DNA, SC010		core
H072_812	4	3	2	E3QDU7	Ribosomal L22e family protein		core
H072_8438	2	2	3	E3QT71	Ribosomal protein L18		core
H072_1429	6	2	2	E3QA16	RNA recognition domain-containing protein		core
H072_1800	2	1	1	D5GBM8	Serine hydroxymethyltransferase		core
H072_4069	4	1	3	E3QHC9	Short chain dehydrogenase	Mdh1	core
H072_9515	5	2	2	E9EAF9	Short-chain dehydrogenase/reductase family	MGG_00056	core
H072_2823	8	4	4	G2YTP4	Similar to 14-3-3 protein		core
H072_1894	11	1	4	G2YDI7	Similar to 3-oxoacyl-(Acyl-carrier-protein) reductase	THR1	core
H072_10253	3	4	3	E4ZUZ7	Similar to 60s acidic ribosomal protein		core
H072_11308	6	3	2	G7X964	Similar to An01g05370		core

H072_4898	6	3	3	E5A7F8	Similar to elongation factor 1-gamma	core
H072_10868	1	2	1	E4ZVM0	Similar to fumarylacetoacetate hydrolase domain-containing protein 1	core
H072_2522	1	3	2	E5A638	Similar to glycolipid transfer protein HET-C2	core
H072_1471	1	1	1	F2T6A3	Small nuclear ribonucleoprotein Sm D3	core
H072_5601	4	4	4	C9SD45	Spherulin-1A	core
H072_1786	3	3	2	E9E1Q2	Sphingolipid long chain base-responsive protein PIL1	core
H072_5132	2	3	4	F2S9K7	Structural toxin protein RtxA	core
H072_10037	2	2	1	F0X9V8	Subtilisin-like protease	core
H072_7045	5	1	3	C5PFN7	Succinyl-CoA:3-ketoacid-coenzyme A transferase	core
H072_10021	5	4	4	Q9Y783	Superoxide dismutase	SOD2 core
H072_2181	1	1	1	F2STR3	Syntaxin	core
H072_6843	5	3	1	E3Q9F0	Tannase and feruloyl esterase	core
H072_1708	1	2	2	F2PKU8	Telomere and ribosome associated protein Stm1	core
H072_3033	4	3	1	E4V0A3	Thioredoxin domain-containing protein	core
H072_5104	8	4	4	Q6C7L4	Thioredoxin reductase	core
H072_1118	2	3	1	C5NZ58	TPR Domain containing protein	core
H072_6506	19	4	4	D5G4P9	Transaldolase	core
H072_7551	2	4	4	B6JZ05	Transcription factor tau subunit sfc4	core
H072_10376	3	2	2	F0XLR6	Transketolase	core
H072_4738	5	2	3	A1D3Y8	Translation elongation factor EF-1 alpha	core
H072_1444	3	1	1	E3S053	Triosephosphate isomerase	core
H072_6869	3	4	2	C1HDY0	Tropomyosin-1	core
H072_8125	4	2	1	C5JXN6	Tyrosinase	core
H072_4094	3	4	4	B0CQN3	Ubiquitin	core
H072_9895	3	4	4	A7E993	Ubiquitin fusion protein	core
H072_6217	5	4	1	A1C4U0	Vacuolar aspartyl aminopeptidase Lap4	core

H072_3605	14	4	4	E9EY37	Vacuolar protease A	ugt51E1	core
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16 ^a Gene models matching the peptide sequences. Models in bold were considered to be significantly upregulated in knobs (see Table 1).

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18 ^b Number of unique peptides matching a single protein.

19

20 ^c Number of replicates that the protein was found in.

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22 ^d Hits of the gene model in the Uniprot database (1). Searches were performed using the Blastp algorithm (2) with an e-value threshold of 1e-10. Fungal
23 sequences are shown among the top hits.

24

25 ^e Homologs of the gene model identified in the pathogen–host interaction (PHI) protein database (3).

26

27 ^f Indicated if the gene model is shared with other fungi (core), shared between *M. haptotylum* and *A. oligospora* (lineage specific, ls) or unique in *M. haptotylum*
28 (species specific, ss) (T. Meerupati, K-M. Andersson, E. Friman, D. Kumar, A. Tunlid, and D. Ahrén, submitted for publication).

29

30 ^g Protein that is an orphan, e.i. they had no homologues in the NCBI database (4) and lacked Pfam domains (5).

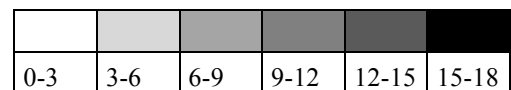
31 **TABLE S2** Features of all proteins with the Pfam domain WSC in *Monacrosporium haptotylum*

ID	Proteome ^a	Transcriptome ^b	Exp ^c	Length (aa)	Sec ^d	O-Glyc ^e	N-Glyc ^e	TM ^f	RADAR ^g
H072_10205	up	up	■	559	SiP	55	2	-	130 (4)
H072_6833	up	up	■	999	SiP	156	3	-	804 (14)
H072_6835	up	up	■	392	SiP	1	2	-	85 (3)
H072_8804	up	up	■	546	SiP	50	1	-	113 (5)
H072_973	up	up	■	877	SiP*	60	4	-	737 (9)
H072_10940	iden	up	■	330	SiP	15	-	-	106 (3)
H072_5095	iden	up	■	772	SiP	29	1	-	438 (6)
H072_22		up	■	313	SiP	9	-	-	198 (3)
H072_4229		up	■	828	SiP	113	3	-	641 (10)
H072_4501		up	■	492	SiP	70	3	-	342 (5)
H072_4641		up	■	223	SiP	1	-	-	176 (3)
H072_4974		up	■	330	SiP	10	2	-	104 (2)
H072_694		up	■	271	SiP	-	-	-	142 (4)
H072_10165			■	1263	SiP	95	9	-	370 (4)
H072_10524			■	320	SiP	37	1	-	118 (4)
H072_10626			■	2282	SiP	181	12	-	398 (10)
H072_10675			■	920	-	16	4	7	128 (2)
H072_10905			■	3063	SiP	28	6	-	3103 (47)
H072_1433			■	386	-	43	3	2	89 (3)
H072_1809			■	1581	SiP	93	10	-	1023 (11)
H072_196			■	1159	SiP	2	1	-	738 (6)
H072_2046			■	1836	SiP	271	11	-	456 (10)
H072_2543			■	1142	-	81	7	-	295 (8)
H072_311			■	849	SiP	47	-	-	153 (3)
H072_4477			■	364	SiP	-	5	-	101 (3)
H072_4490			■	643	SiP	100	1	-	205 (6)
H072_5385			■	1102	SiP	60	5	-	995 (11)
H072_654			■	414	SiP	43	-	-	362 (3)
H072_6644			■	2659	SiP	237	16	-	1625 (11)
H072_7616			■	2882	SiP*	90	7	-	2814 (29)
H072_7637			■	727	SiP	14	1	-	501 (3)
H072_8090			■	1707	SiP	211	3	-	496 (10)
H072_8104			■	1279	SiP*	483	6	-	537 (5)

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36 ^a Proteins identified using mass spectrometry. “up” denotes protein that was at least two-fold upregulated in knobs
37 versus mycelia. “iden” indicates proteins that were uniquely identified in knobs.

38

39 ^b “up” indicates gene that was more than two-fold upregulated (infected hyphae versus knob, $P < 0.01$) in the
40 transcriptome (T. Meerupati, K-M. Andersson, E. Friman, D. Kumar, A. Tunlid, and D. Ahrén, submitted for
41 publication).

42

43 ^c “Exp” denotes the total transcriptional normalized expression levels (\log_2 values) according to the scale.

44

45 ^d “SiP” indicates that the protein has a predicted secretion signal using the SignalP 4.1 server (6), asterisk indicates
46 protein with GPI anchor signal using PredGPI (7).

47

48 ^e Number of *O*- and *N*-glycosylation sites using NetOGlyc 3.1 (8) and NetNGlyc 1.0
49 (<http://www.cbs.dtu.dk/services/NetNGlyc/>).

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51 ^f Number of transmembrane (TM) regions predicted using Phobius (9).

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53 ^g Max score and in brackets the number of repeats using RADAR (10).

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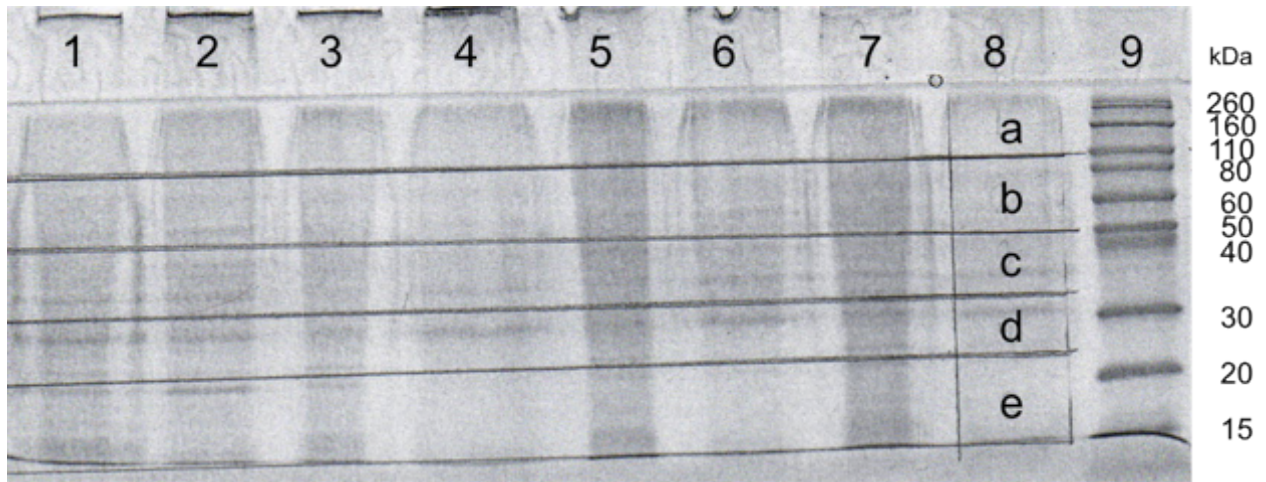
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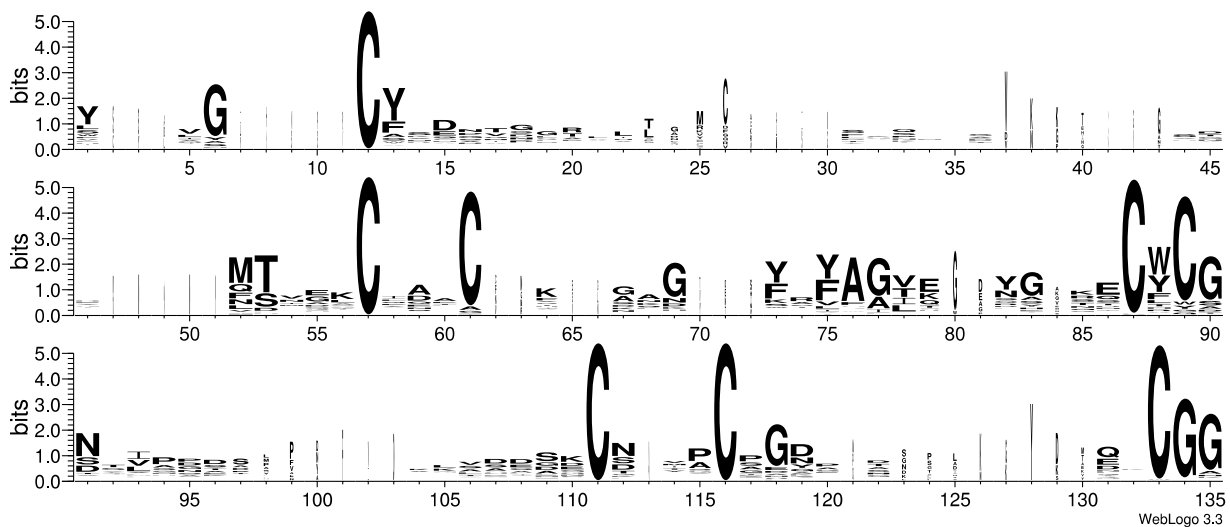
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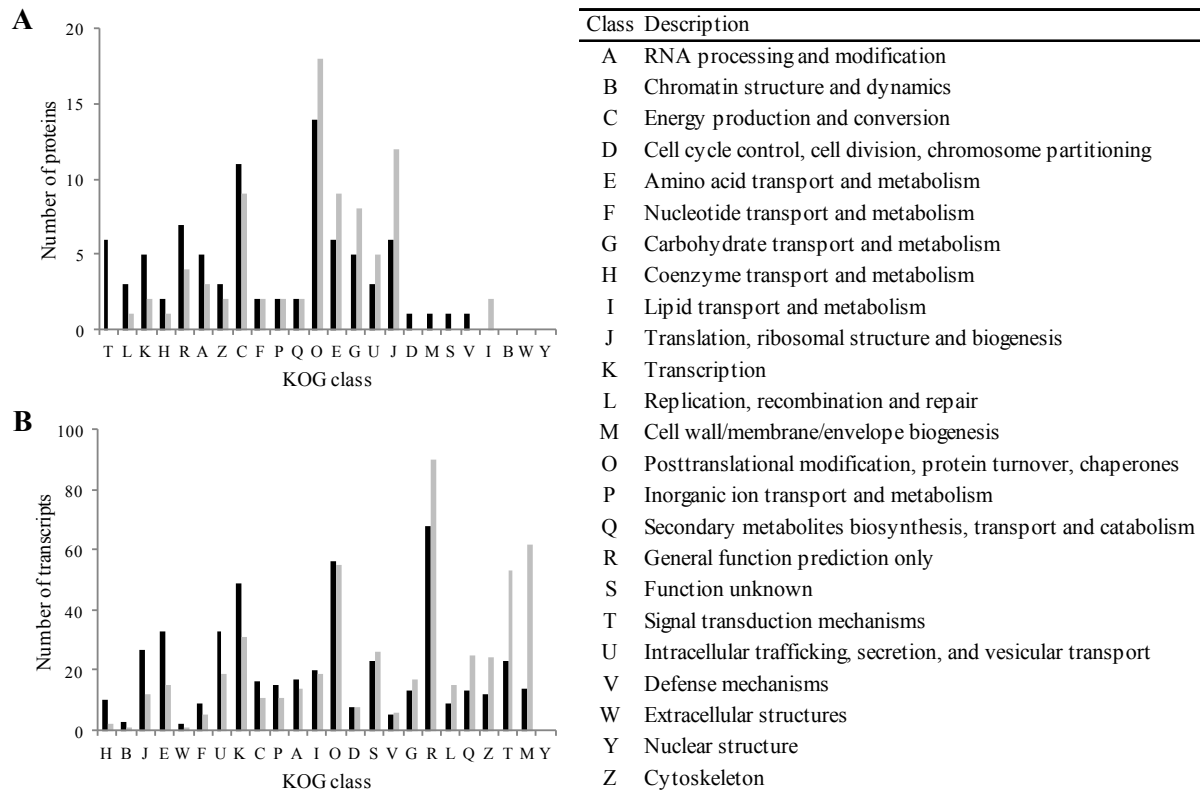
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 64 **FIG S1** SDS-PAGE analysis of the proteins extracted from mycelia and knobs of *M. haptotylum*.
 65 Lane 1, 3, 5 and 7 are replicates from mycelia and lane 2, 4, 6 and 8 are replicates from knob.
 66 Lane 9 is the molecular weight marker. Following electrophoresis and staining each lane was cut
 67 into five slices (a-e).



70
 71 **FIG S2** Sequence logo of the WSC domain. The logo was derived from the alignment that Fig. 3
 72 is based on. The prevalence of amino acids at specific positions is shown. The sequence logo was
 73 created with WebLogo version 3.3 (11).

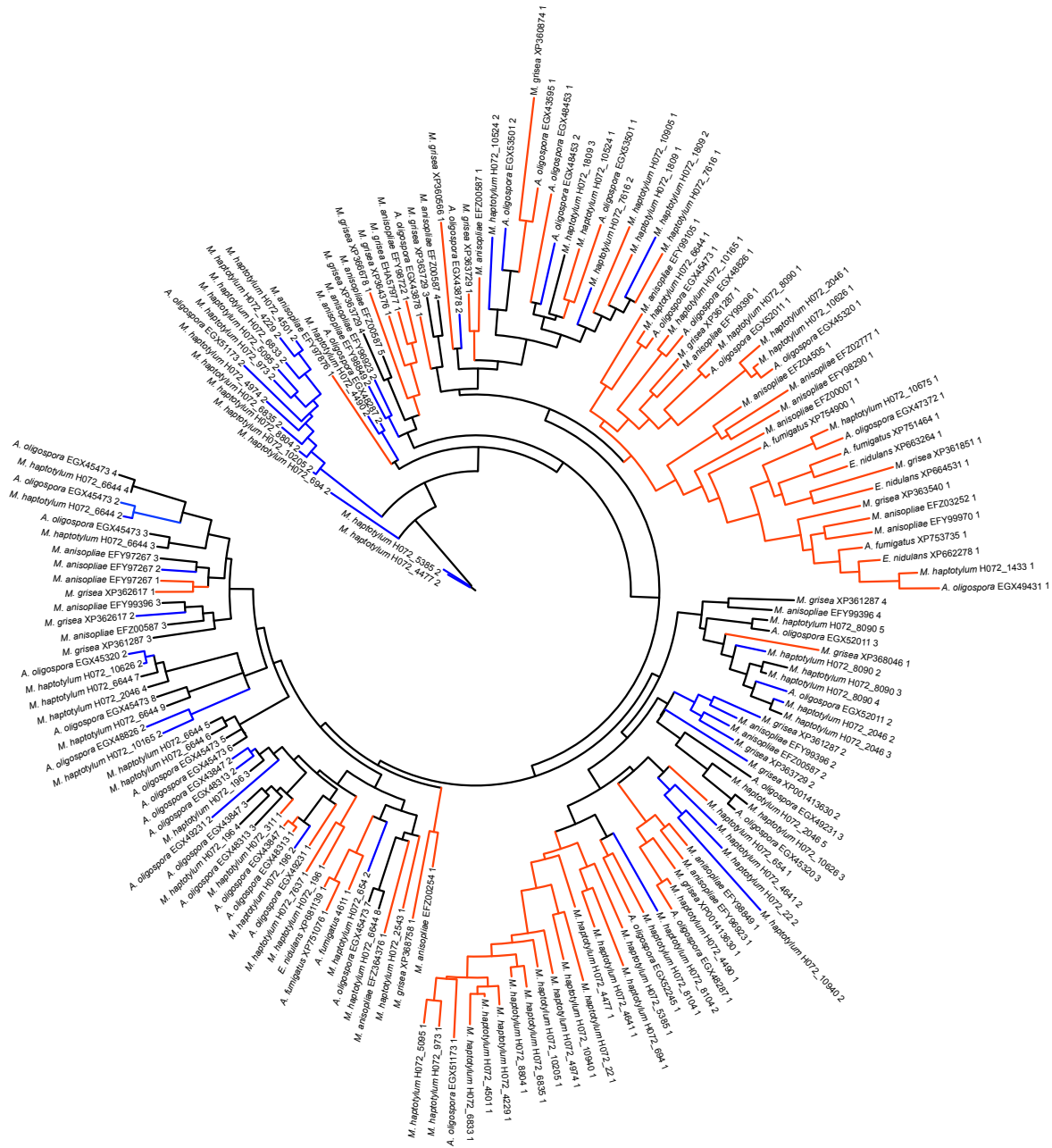


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76 **FIG S3** Distribution of proteins and transcripts in different KOG categories in the knobs (black
 77 bars) and mycelia (grey bars) of *Monacrosporium haptotylum*. The categories are listed in
 78 descending order of enrichment in the knobs, i.e. the categories with the highest values of the
 79 ratio of abundance in knobs versus mycelia are found to the left of the figures. (A) KOG
 80 categories in the proteome. The total number of proteins that were mapped to KOG categories
 81 was 82 and 86 for knobs and mycelia, respectively. The data include both the significantly
 82 upregulated proteins and the proteins that were uniquely present in either knobs or mycelia. (B)
 83 KOG categories in the transcriptome. A total of 478 genes were upregulated and mapped to a
 84 KOG category in knobs and 522 were upregulated and mapped to a KOG category in mycelia.

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88 **FIG S4** Phylogeny of 173 WSC Pfam domains from six fungal genomes. Branches of the first
 89 WSC domain counted from the N-terminus in each protein are colored in red. Branches of the
 90 second WSC domain in each protein are colored in blue. The number following each protein ID
 91 refers to the order of the Pfam domain in the protein counted from the N-terminus. Proteins
 92 containing the WSC domain were retrieved from the genomes of *Monacrosporium haptotylum*

93 (33 proteins) (T. Meerupati, K-M. Andersson, E. Friman, D. Kumar, A. Tunlid, and D. Ahrén,
94 submitted for publication), *Arthrotrrys oligospora* (16 proteins) (12), *Metarhizium anisopliae*
95 (16 proteins) (13), *Aspergillus fumigatus* (5 proteins) (14), *Emericella nidulans* (4 proteins) (15)
96 and *Magnaporthe grisea* (13 proteins) (16). In total, 87 sequences were retrieved and regions
97 corresponding to 173 WSC domains were extracted using the extractseq program from the
98 EMBOSS package (17). Sequences was aligned using the MAFFT multiple alignment program
99 (18). An unrooted maximum likelihood (ML) tree was reconstructed from the 173 WSC domains
100 using PhyML 3.0 version (19). The phylogenetic tree was visualized in iTOL (20).

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