

Supplementary Material online

Supplementary Table S1. Overview of the taxa used in this study and the corresponding data sources.

Supplementary Table S2. Taxon – Gene matrices for the three core ortholog sets *fungi* (A), *basidiomycota* (B), and *pezizomycotina* (C). Only fungal taxa with completely sequenced genomes are represented. Genes highlighted in yellow correspond to loci that have been suggested by the fungal tree of life project (AFTOL2) as candidate genes for fungal phylogeny reconstruction (http://aftol.org/pages/AFTOL2_locib.html).

Supplementary Table S3. Description and sources of the fungal images shown in Fig. 3 and Supplementary Fig. S9.

Supplementary Fig. S1. Saturation plots for the 15 datasets used in this study. The slope of the linear regression line is given in the individual plots.

Supplementary Fig. S2. Supplementary Fig. S2. Bias for slowly evolving genes in EST directed gene selections. To illustrate the effect of EST taxon sampling and EST set size on the bias for selecting slowly evolving genes, we chose two sets of EST taxa from our data. Set A represents 20 taxa for which only 3,800 – 9,900 ESTs are available. Set B represents 20 taxa for which more than 10,000 ESTs each are available (max: 35,000). Both sets have almost all of the 1,206 fungi core orthologs represented (A: 1,161; B: 1,193). From these two core ortholog collections we constructed 20 subsets of genes using inclusion thresholds from 1 to 20. An inclusion threshold of k requires that a gene occur in at least k taxa in either set A or set B. For the resulting collections of genes we plotted the length distribution of the corresponding primer taxa trees. (A) shows the results for set A, and (B) shows the results for set B. The trend is the same for both taxon sets. A gene evolves slower on average the more EST sets it is represented in. However, this bias is alleviated for set B comprising taxa with many ESTs. Larger EST sets facilitate a more comprehensive sampling of genes encoded in a species' genome and have a higher probability to represent also genes that are expressed at lower levels. As a consequence, overlap sets of genes present in different large EST collections will be less biased towards highly expressed, slowly evolving genes.

Supplementary Fig. S3. Copy number of genes in the data set *fungi_1*. The y-axis denotes the maximum number of copies for any of the 121 genes across the 99 analyzed fungal genomes.

Supplementary Fig. S4. GO-overrepresentation graph of the genes in the data sets *fungi_1* (A) and *fungi_2* (B). Shown are only the significantly overrepresented GO terms of the GO sub ontology Biological Process. The color code reflects the nominal p-value of the overrepresented terms from red (lower p-values) to yellow (higher p-values). Entries in the individual fields represent (from top): GO term Id; expected number of genes annotated with this GO term in the data subset, observed number of genes in the subset vs. number of genes in the full gene set annotated with this GO term; nominal p-value of the overrepresentation; term description. The summary of individual terms to complex processes was done by eye. Substantially more GO terms are overrepresented in the data set *fungi_1* (A) than in *fungi_2* (B). Moreover, the

degree of connectivity between the individual terms –a reflection of their functional correlation- is substantially higher in the fungi_1 data set. A re-sampling test indicates that a slightly higher number of genes in fungi_1 cannot explain the difference between the two data sets.

Supplementary Fig. S5. Evolutionary relationships of the fungi derived from data set fungi_1. The maximum likelihood tree and the maximum parsimony tree are shown in **A** and **B**, respectively. Values on the individual branches denote bootstrap support. The Bayesian consensus tree is shown in **C**. This tree is based on partition 3 of the fungi_1 set encompassing 39 genes. Branch support values denote Bayesian posterior probabilities. *Monacrosporium* haptotylum (Orbiliomycetes) is clearly misplaced in this tree and groups within the Basidiomycota. We trust that this effect represents a tree reconstruction artifact and does not reflect a phylogenetic signal in the data. Note that the Bayesian consensus trees from partitions 1 and 2 of fungi_1 show the correct placement of *M. haptotylum* at the base of the Pezizomycotina. We therefore ignored this taxon when collapsing the Bayesian consensus tree for the supernet analysis. **D** shows the MRP supertree based on data set fungi_1A, where again the values on the branches denote bootstrap support in %. A * denotes 100% bootstrap support or a Bayesian posterior probability of 1. Names of taxa represented by genome sequences are written in capital letters, names of taxa represented by EST are in lower case. Note that branch lengths for the trees **A** and **C** reflect the expected numbers of substitutions (branches for the Microsporidia have been shortened by a factor of 10), while they have no meaning for trees **B** and **D**. The color code of the branches follows Fig. 3

Supplementary Fig. S6. Evolutionary relationships of the fungi derived from data set fungi_2. The maximum likelihood tree and the maximum parsimony tree are shown in **A** and **B**, respectively. Values on the individual branches denote bootstrap support. The Bayesian consensus tree is shown in **C**. This tree is based on partition 3 of the fungi_2 set encompassing 39 genes. Branch support values denote Bayesian posterior probabilities. The MRP supertree is shown in **D** where again the values on the branches denote bootstrap support in %. A star denotes 100% bootstrap support or a Bayesian posterior probability of 1. Names of taxa represented by genome sequences are written in capital letters, names of taxa represented by EST are in lower case. Note that branch lengths for the trees **A** and **C** reflect the expected numbers of substitutions (branches for the Microsporidia have been shortened by a factor of 10), while they have no meaning for trees **B** and **D**. The color code of the branches follows Fig. 3.

Supplementary Fig. S7. Evolutionary relationships of the Pezizomycotina inferred from data set pezizomycotina_1. The maximum likelihood tree and the Bayesian consensus trees are shown in **A** and **B**, respectively. The respective values on the individual branches denote bootstrap support and Bayesian posterior probability. A * denotes 100% bootstrap support or a Bayesian posterior probability of 1. Names of taxa represented by genome sequences are written in capital letters, names of taxa represented by EST are in lower case.

Supplementary Fig. S8. EST guided compilation of phylogenomic data sets selects for slowly evolving genes. The histogram shows the lengths of the trees connecting the six primer taxa for the 1,226 single copy genes in the *pezizomycotina* core ortholog set. The values for the subset of genes in pezizomycotina_1 that have been selected due to their abundance in the EST data are colored in green.

Supplementary Fig. S9. The phylogenetic backbone of the fungi based on 15 datasets. The numbers of species represented by each leaf are given in parenthesis for the data sets fungi_1 and fungi_2, respectively. A * denotes those instances where either one or both species are absent from data set fungi_2 and are represented only in the supertree based on fungi_2A. A '-' indicates that a taxon is entirely missing in a data set. Colors highlight major systematic groups of the fungi (Ascomycota: red; Basidiomycota: blue; Mucoromycotina: magenta; Glomeromycota: purple; Entomophthoromycotina: yellow; Blastocladiomycota: marine; Chytridiomycota/Neocallimastigomycota: green). Given the tentativeness in our reconstruction of the basal fungal relationships we keep the network structure for this part of the fungal backbone tree. Contractions of the dashed branches result in the topology that is suggested by our refined analysis of the early branching fungi with data set fungi_3.

Supplementary Table S1. Data sources

Web-Resources:

BaylorCollege: <http://www.hgsc.bcm.tmc.edu>
Broad: <http://www.broad.mit.edu>
CandidaGenomeDatabase: <http://www.candidagenome.org>
Dictybase: <http://dictybase.org>
Ensembl: <http://www.ensembl.org>
Genolevures: <http://www.genolevures.org>
Josephine Bay Paul Center: <http://gmod.mbl.edu>
JGI: <http://genome.jgi-psf.org>
KEGG: http://www.genome.jp/kegg/catalog/org_list.html
NCBI: <http://www.ncbi.nlm.nih.gov/projects>
NCBI/RefSeq: <http://www.ncbi.nlm.nih.gov/RefSeq>
Podospora anserina Genome Project: <http://podospora.igmors.u-psud.fr>
SaccharomycesGenomeDatabase: <http://yeastgenome.org>
TBestDB: <http://tbestdb.bcm.umontreal.ca>
UniGent: <http://bioinformatics.psb.ugent.be/genomes>
Uniprot/Integr8: <http://www.uniprot.org>
www.fungalgenomes.org: <http://www.fungalgenomes.org>
Wormbase: www.wormbase.org
dbEST: <http://www.ncbi.nlm.nih.gov/projects/dbEST>

Genomes	Taxon Name	# Sequences*	Web-Resource
	ALTERNARIA_BRASSICICOLA	10.688	JGI
	AEDES_AEGYPTI	15.419	Ensembl
	AJELLOMYCES_CAPSULATUS	9.349	Broad
	AJELLOMYCES_DERMATITIDIS_ER-3	9.522	Broad
	ANTONOSPORA_LOCUSTAE	2.606	Josephine Bay Paul Center
	ASCOSPHAERA_APIIS	9.103	BaylorCollege
	ASHBYA_GOSSYPII	4.717	Uniprot/Integr8
	ASPERGILLUS_CLAVATUS	9.120	Broad
	ASPERGILLUS_FISCHERI	10.403	Broad
	ASPERGILLUS_FLAVUS	12.587	Broad
	ASPERGILLUS_FUMIGATUS	9.629	Uniprot/Integr8
	ASPERGILLUS_NIDULANS	10.665	Broad
	ASPERGILLUS_NIGER	11.200	JGI
	ASPERGILLUS_ORYZAE	12.056	Uniprot/Integr8
	ASPERGILLUS_TERREUS	10.406	Broad
	BATRACHOCHYTRIUM_DENDROBATIDIS	8.732	JGI
	BOTRYOTINIA_FUCKELIANA	16.448	Broad
	CANDIDA_ALBICANS	6.205	CandidaGenomeDatabase
	CANDIDA_DUBLINIENSIS_CD36	5.860	NCBI/RefSeq
	CANDIDA_GLABRATA	5.199	Uniprot/Integr8
	CANDIDA_PARAPSILOSIS	5.733	Broad
	CANDIDA_TROPICALIS	6.258	Broad
	CAPITELLA_SP_I_ECS-2004	32.415	JGI
	CAPSASPORA_OW CZARZAKI	8.381	Broad
	CHAETOMIUM_GLOBOSUM	11.124	Broad
	CLAVISPORA_LUSITANIAE	5.941	Broad
	COCCIDIOIDES_IMMIS	10.352	Broad
	COCCIDIOIDES_POSADASII	9.897	Broad
	COCHLIOBOLUS_HETEROSTROPHUS	9.633	JGI
	COPRINOPSIS_CINEREA	13.544	Broad
	CRYPHONECTRIA_PARASITICA	11.184	JGI
	CRYPTOCOCCUS_NEOFORMANS_VAR._NEOFORMA	6.440	Uniprot/Integr8
	DANIO_RERIO	21.322	Ensembl
	DEBARYOMYCES_HANSENI	6.242	Uniprot/Integr8
	DICTYOSTELIUM_DISCOIDEUM_AX4	13.328	Dictybase
	DICTYOSTELIUM_PURPUREUM_QSDP1	12.410	JGI
	ENCEPHALITOOZON_CUNICULI	1.909	Uniprot/Integr8
	ENTEROCYTOZON_BIENEUSI_H348	3.632	NCBI/RefSeq
	FUSARIUM_GRAMINEARUM	13.321	Broad
	FUSARIUM_OXYSPORUM_F_SP_LYCOPERSICI	17.608	Broad
	FUSARIUM_VERTICILLIOIDES	14.177	Broad

GALLUS_GALLUS	16.736	Ensembl
HETEROBASIDIUM_ANNOSUM	12.299	JGI
HOMO_SAPIENS	21.673	Ensembl
HYDRA_MAGNIPAPILLATA	17.398	NCBI/RefSeq
KLUYVEROMYCES_LACTIS	5.071	Uniprot/Integr8
KLUYVEROMYCES_THERMOTOLERANS	5.092	Genolevures
KLUYVEROMYCES_WALTII	5.213	KEGG
LACCARIA_BICOLOR	20.614	JGI
LODDEROMYCES_ELONGISPORUM	5.799	Broad
LOTTIA_GIGANTEA	23.851	JGI
MAGNAPORTHE_GRISEA	12.684	Uniprot/Integr8
MALASSEZIA_GLOBOSA_CBS_7966	4.286	NCBI/RefSeq
MELAMPSORA_LARICIS-POPULINA	16.831	JGI
MICROSPORUM_CANIS_CBS_113480	8.765	Broad
MICROSPORUM_GYPSEUM_CBS_118893	8.876	Broad
MONILOPHTHORA_PERNICIOSA_FA553	13.560	NCBI/RefSeq
MONOSIGA_BREVICOLLIS	9.196	JGI
MUCOR_CIRCINELLOIDES	10.930	JGI
MUS_MUSCULUS	23.497	Ensembl
MYCOSPHAERELLA_FIJIENSIS	10.313	JGI
MYCOSPHAERELLA_GRAMINICOLA	11.395	JGI
NECTRIA_HAEMATOCOCCA_MPVI	15.707	JGI
NEMATOSTELLA_VECTENSIS	27.273	JGI
NEUROSPORA_CRASSA	9.827	Uniprot
NEUROSPORA_DISCRETA_FGSC_8579_MAT_A	9.948	JGI
NEUROSPORA_TETRASPERMA_FGSC_2508_MAT_A	10.640	JGI
NOSEMA_CERANAE	2.082	NCBI
ORYZIAS_LATIPES	19.686	Ensembl
PARACOCCIDIOIDES_BRASILIENSIS	9.263	Broad
PEDICULUS_HUMANUS	10.773	VectorBase
PENICILLIUM_CHRYSOGENUM	12.773	Uniprot/Integr8
PENICILLIUM_MARNEFFEI	10.638	NCBI/RefSeq
PHANEROCHAETE_CHRYSOSPORIUM	10.048	JGI
PHYCOMYCES_BLAKEESLEEANUS	14.792	JGI
PICHIA_GUILLIERMONDII	5.920	Broad
PICHIA_PASTORIS	5.313	UniGent
PICHIA_STIPITIS	5.807	JGI
PLEUROTUS_OSTREATUS_PC15	11.603	JGI
PODOSPORA_ANSERINA	10.614	Podospora anserina Genome Project
POSTIA_PLACENTA	9.113	JGI
PRISTIONCHUS_PACIFICUS	29.644	Wormbase
PUCCINIA_GRAMINIS_F_SP_TRITICI	20.566	Broad
PYRENOPHORA_TRITICI	12.169	Broad
RHIZOPUS_ORYZAE	17.467	Broad
SACCHAROMYCES_BAYANUS	6.297	NCBI
SACCHAROMYCES_CASTELLII	4.677	SaccharomycesGenomeDatabase
SACCHAROMYCES_CEREVISIAE	6.698	Ensembl
SACCHAROMYCES_KLUYVERI	5.321	Genolevures
SACCHAROMYCES_KUDRIAVZEVII	7.208	NCBI
SACCHAROMYCES_MIKATAE	6.526	NCBI
SACCHAROMYCES_PARADOXUS	6.174	NCBI
SCHIZOPHYLLUM_COMMUNE	13.210	JGI
SCHIZOSACCHAROMYCES_JAPONICUS	5.167	Broad
SCHIZOSACCHAROMYCES_OCTOSPORUS	4.907	Broad
SCHIZOSACCHAROMYCES_POMBE	4.976	Uniprot/Integr8
SCHIZOSACCHAROMYCES_SP_OY26	5.057	Broad
SCLEROTINIA_SCLEROTIORUM	14.522	Broad
SPIZELLOMYCES_PUNCTATUS	8.804	Broad
SPOROBOLOMYCES_ROSEUS	5.536	JGI
STAGONOSPORA_NODORUM	16.597	Broad
TALAROMYCES_STIPITATUS	13.252	NCBI/RefSeq
THIELAVIA_TERRESTRIS	9.815	JGI
TREMELLA_MESENERICA	8.313	JGI
TRICHODERMA_ATROVIRIDE	11.100	JGI
TRICHODERMA_REESEI	9.143	JGI
TRICHODERMA_VIRENS	11.643	JGI
TRICHOPHYTON_EQUINUM_CBS127.97	8.560	Broad

TRICHOPLAX_ADHAERENS	11.520	JGI
TUBER_MELANOSPORUM	7.496	Genoscope
UNCINOCARPUS_REESII	7.798	Broad
USTILAGO_MAYDIS	6.522	Broad
VANDERWALTOZYMA_POLYSPORA	5.345	Uniprot/Integr8
VERTICILLIUM_ALBO-ATRUM_VAMS.102	10.220	Broad
VERTICILLIUM_DAHLIAE_VDLS.17	10.535	Broad
XENOPUS_TROPICALIS	18.023	Ensembl
YARROWIA_LIPOLYTICA	6.525	Uniprot/Integr8
ZYGOSACCHAROMYCES_ROUXII	4.991	Genolevures

ESTs

Agaricus_bisporus	612	dbEST
Allomyces_macrozynus	2.410	dbEST
Alternaria_alternata	269	dbEST
Amoebidium_parasiticum	1.333	TBestDB
Amorphotheca_resinae	4.289	dbEST
Antrrodia_cinnamomea	5.088	dbEST
Armillariella_tabescens	130	dbEST
Aureobasidium_pullulans	4.705	dbEST
Blastocladiella_emersonii	7.145	dbEST
Blumeria_graminis_f_sp_hordei	7.750	dbEST
Blumeria_graminis_f_sp_hordei_DH14	5.000	dbEST
Cercospora_nicotianae	188	dbEST
Cercospora_zeae-maydis	6.885	dbEST
Chaetomium_cupreum	2.238	dbEST
Claviceps_purpurea	4.753	dbEST
Cochliobolus_lunatus	937	dbEST
Colletotrichum_acutatum	461	dbEST
Colletotrichum_higginsianum	708	dbEST
Colletotrichum_trifolii	627	dbEST
Conidiobolus_coronatus	4.771	dbEST
Cordyceps_bassiana	5.156	dbEST
Cordyceps_militaris	1.792	dbEST
Corynascus_heterothallicus	4.576	dbEST
Cronartium_quercuum_f_sp_fusifforme	349	dbEST
Cryptococcus_laurentii	3.366	dbEST
Cunninghamella_elegans	5.029	dbEST
Edhazardia_aedis	143	dbEST
Emericella_nidulans	7.492	dbEST
Epichloe_festucaae	8.165	dbEST
Fusarium_oxysporum_f_sp_cucumerinum	3.840	dbEST
Fusarium_oxysporum_f_sp_melonis	1.192	dbEST
Fusarium_sporotrichioides	3.675	dbEST
Ganoderma_lucidum	617	dbEST
Geomyces_pannorum	4.532	dbEST
Gibberella_fujikuroi	97	dbEST
Gigaspora_margarita	260	dbEST
Gigaspora_rosea	347	dbEST
Gloeophyllum_trabeum	4.574	dbEST
Glomerella_cingulata	825	dbEST
Glomus_intraradices	2.340	dbEST
Glomus_versiforme	331	dbEST
Hebeloma_cylindrosporum	2.709	dbEST
Hortaea_werneckii	146	dbEST
Hypocrea_lixii	6.074	dbEST
Isaria_tenuipes	298	dbEST
Lactarius_quietus	415	dbEST
Lentinula_edodes	4.092	dbEST
Leptosphaeria_maculans	723	dbEST
Leucosporidium_scottii	4.151	dbEST
Metarhizium_anisopliae	1.701	dbEST
Metarhizium_anisopliae_var_acridum	1.523	dbEST
Microbotryum_violaceum	7.878	dbEST
Monacrosporium_haptotylum	1.157	dbEST
Mortierella_verticillata	2.307	TBestDB
Mycosphaerella_populorum	202	dbEST
Neocallimastix_patriciarum	624	dbEST
Neotyphodium_lolii	3.856	dbEST

Nuclearia_simplex_strain_2	675	TBestDB
Nuclearia_simplex_strain_4	720	TBestDB
Oidiodendron_maius	216	dbEST
Ophiostoma_novo-ulmi_subsp._novo-ulmi	447	dbEST
Ophiostoma_piliferum	3.779	dbEST
Passalora_fulva	531	dbEST
Paxillus_involutus	3.412	dbEST
Phaeosphaeria_nodorum_SN15	6.474	dbEST
Phakopsora_pachyrhizi	6.453	dbEST
Phlebiopsis_gigantea	181	dbEST
Phomopsis_sp._G2-919	131	dbEST
Piromyces	4.770	dbEST
Pisolithus_microcarpus	572	dbEST
Pisolithus_tinctorius	395	dbEST
Pneumocystis_carinii	1.803	dbEST
Roccella_montagnei	620	dbEST
Saitoella_complicata	1.116	dbEST
Sporobolomyces_roseus_IAM_13481	5.240	dbEST
Suillus_luteus	429	dbEST
Taphrina_deformans	1.422	dbEST
Thermomyces_lanuginosus	3.832	dbEST
Thielavia_terrestris	9.700	dbEST
Trametes_versicolor	3.037	dbEST
Trichoderma_aggressivum	577	dbEST
Trichoderma_asperellum	2.585	dbEST
Trichoderma_longibrachiatum	1.008	dbEST
Trichoderma_stromaticum	814	dbEST
Trichoderma_viride	1.005	dbEST
Trichophyton_rubrum_CBS_118892	424	dbEST
Tuber_borchii	2.091	dbEST
Uromyces_appendiculatus	4.885	dbEST
Uromyces_viciae-fabae	577	dbEST
Wolfiporia_cocos	180	dbEST
Zoophthora_radicans	582	dbEST

¹Number of annotated genes in the genome sequences or, alternatively number of non-redundant EST contigs.

Supplementary Table S3.

Chytridiomycota: *Spizellomyces punctatus*

<http://biomesfifth10.wikispaces.com/Coral+Reef+Facts>

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Neocallimastigomycotina: *Neocallimastix frontalis*

Copyright: Kerstin Voigt

Nuclearia: *Nuclearia termophila*

http://en.wikipedia.org/wiki/File:Nuclearia_sp_Nikko.jpg

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Microsporidia: *Fibrillanosema crangonycis*

http://en.wikipedia.org/wiki/File:Fibrillanosema_spore.jpg

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Glomeromycota: *Gigaspora margarita*

http://en.wikipedia.org/wiki/File:Gigaspora_margarita.JPG

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Mucoromycotina: *Rhizopus nigricans*

Copyright: Kerstin Voigt

Basidiomycota: *Chroogomphus rutilus*

http://de.wikipedia.org/w/index.php?title=Datei:Kupferroter_Gelbfu%C3%9F.jpg&filetimestamp=20040907220848

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Taphrinomycotina: *Taphrina crataegi*

<http://de.wikipedia.org/wiki/Datei:Taphrina.crataegi.-.lindsey.jpg>

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Saccharomycotina: *Saccharomyces cerevisiae*

http://en.wikipedia.org/wiki/File:S_cerevisiae_under_DIC_microscopy.jpg

public domain

Pepizomycetes: *Morchella esculenta*

http://de.wikipedia.org/w/index.php?title=Datei:Morchella_esculenta_84915.jpg&filetimestamp=20110511151318

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Eurotiomycetes: *Aspergillus fumigatus*

<http://de.wikipedia.org/w/index.php?title=Datei:Aspergillus.gif&filetimestamp=20060111215647>

public domain

Dothideomycetes: *Venturia inaequalis*

http://en.wikipedia.org/wiki/File:Apple_scab_SEM.jpg

public domain

Sordariomycetes: *Camarops polysperma*

http://de.wikipedia.org/w/index.php?title=Datei:Camarops_polysperma.jpg

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Leotiomycetes: *Uncinula tulasnei*

<http://de.wikipedia.org/w/index.php?title=Datei:UncinulaTulasneiDetail.jpg>

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Orbiliomycetes: *Orbilina sp.*

http://pt.wikipedia.org/wiki/Ficheiro:Orbilina_spp.jpg

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Entomophthorales: *Entomophthora muscae*

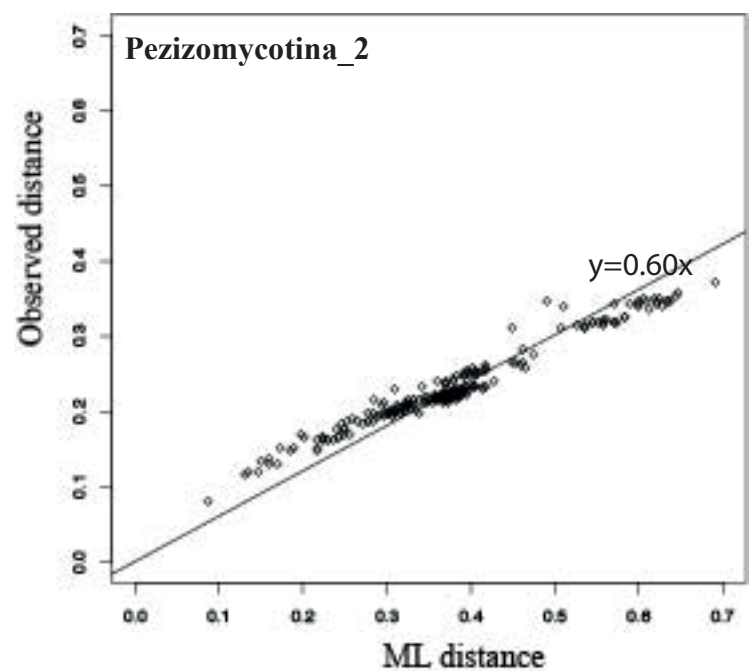
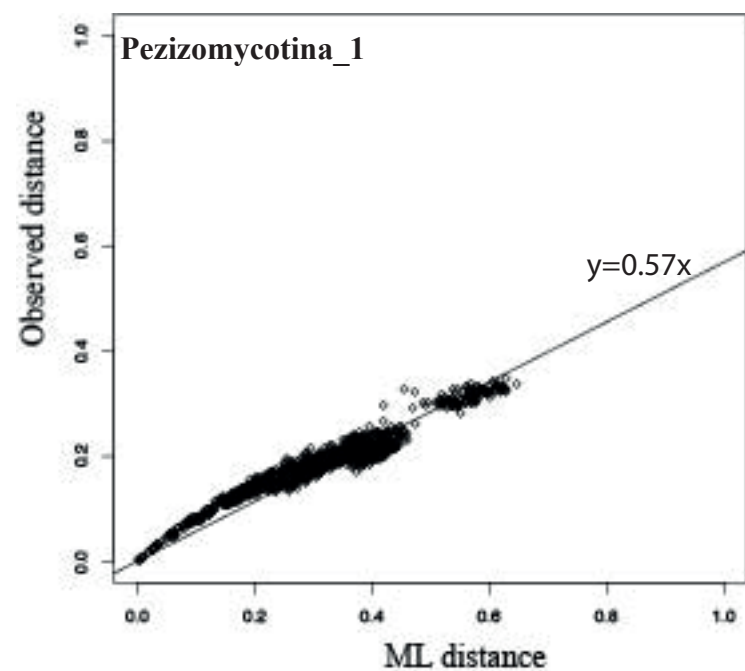
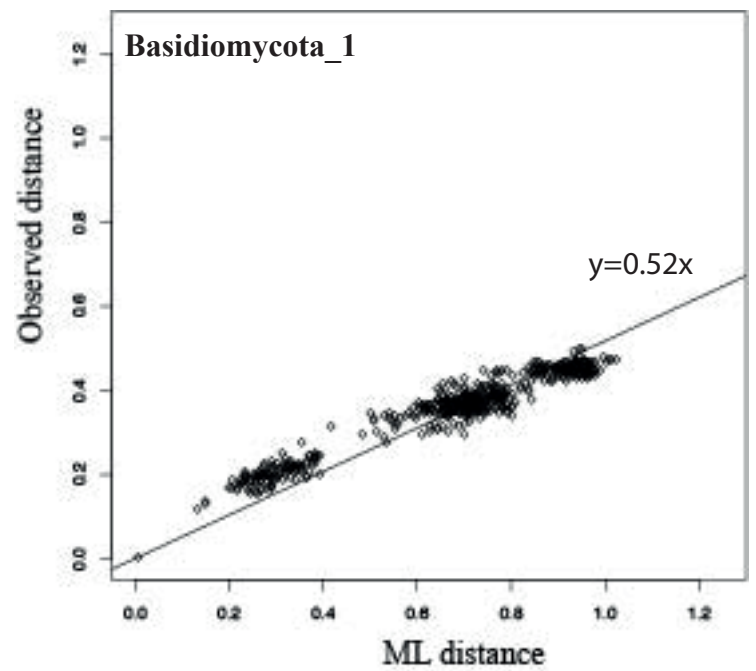
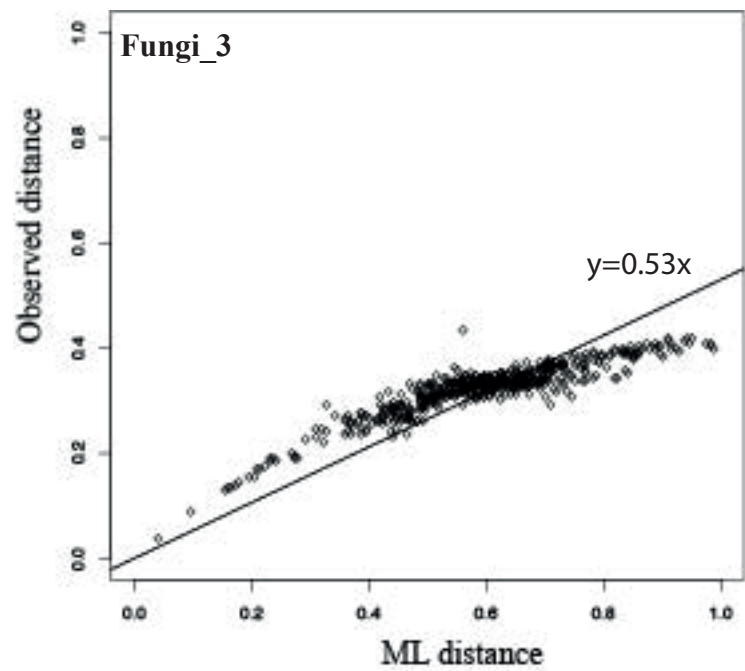
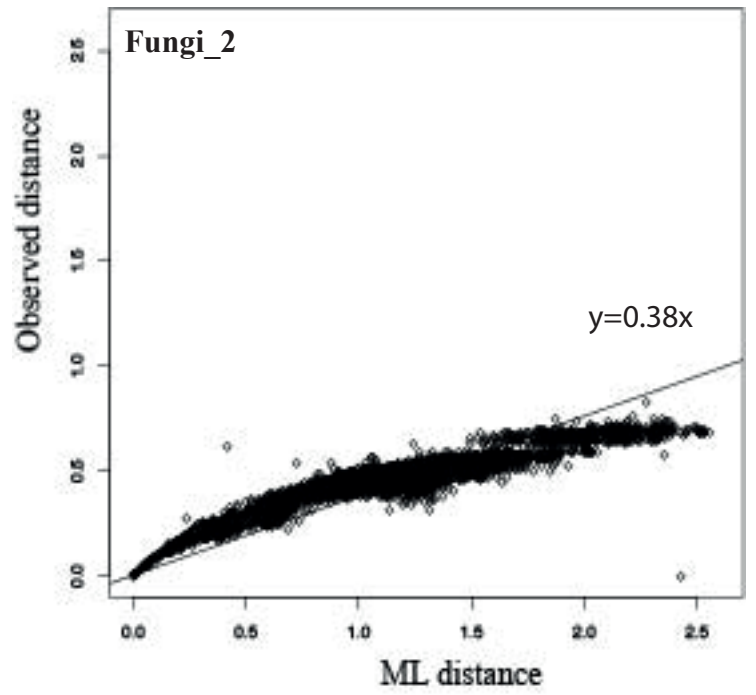
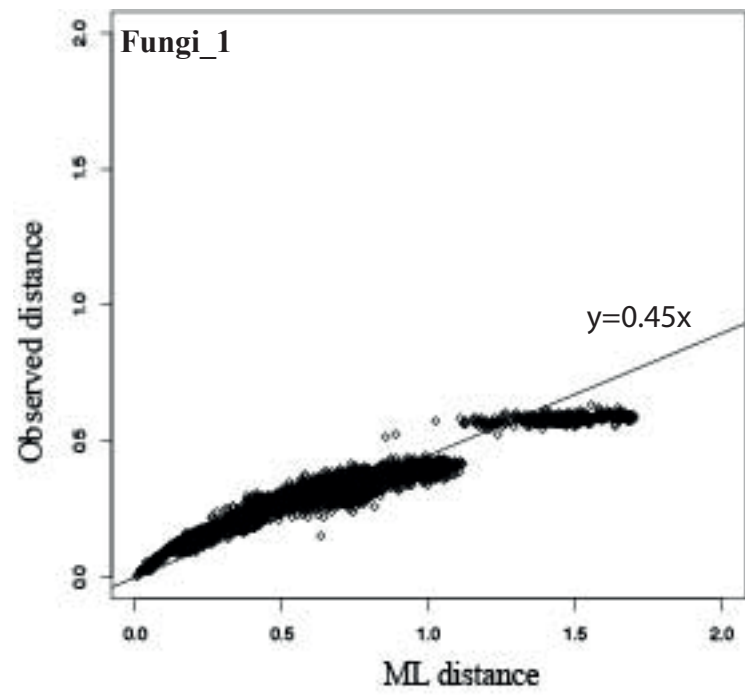
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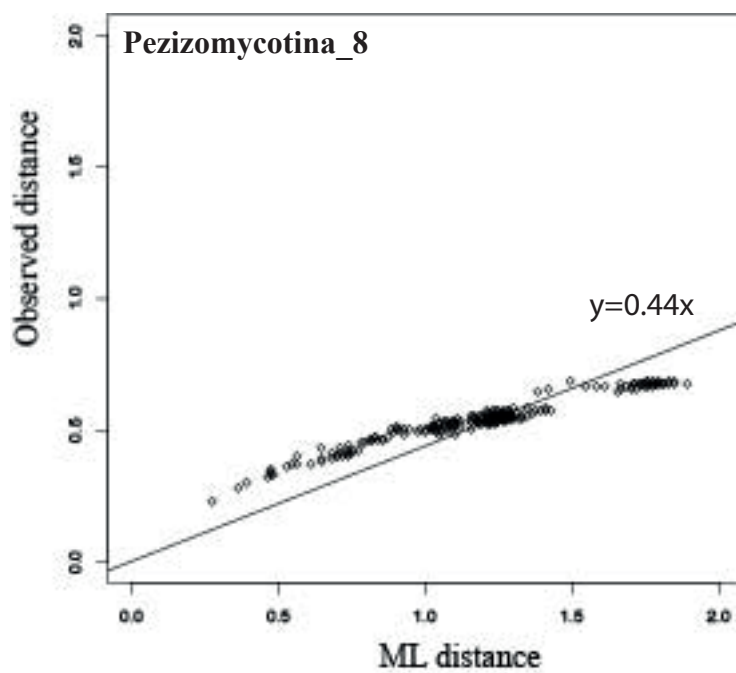
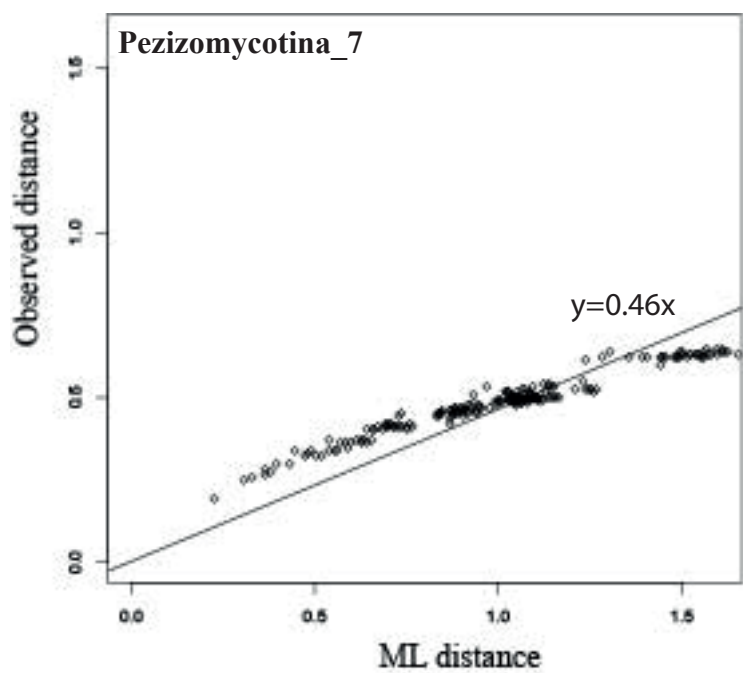
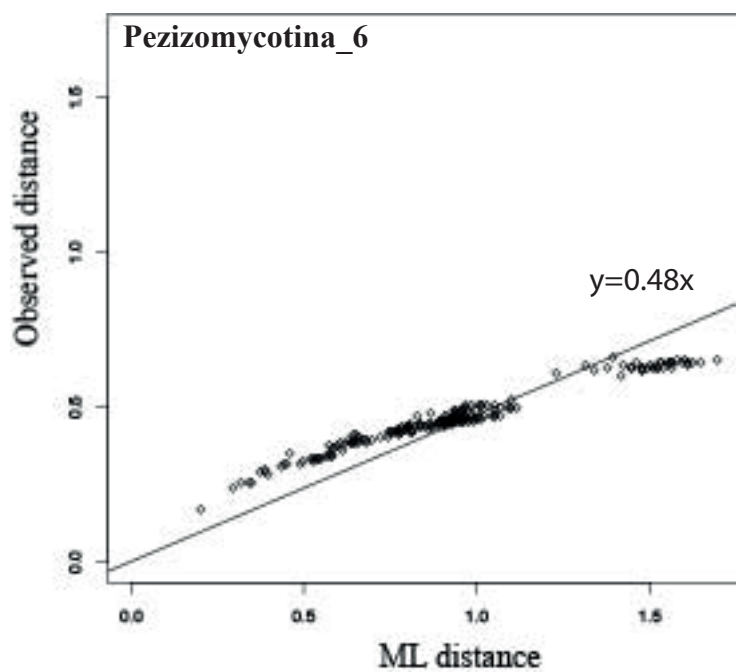
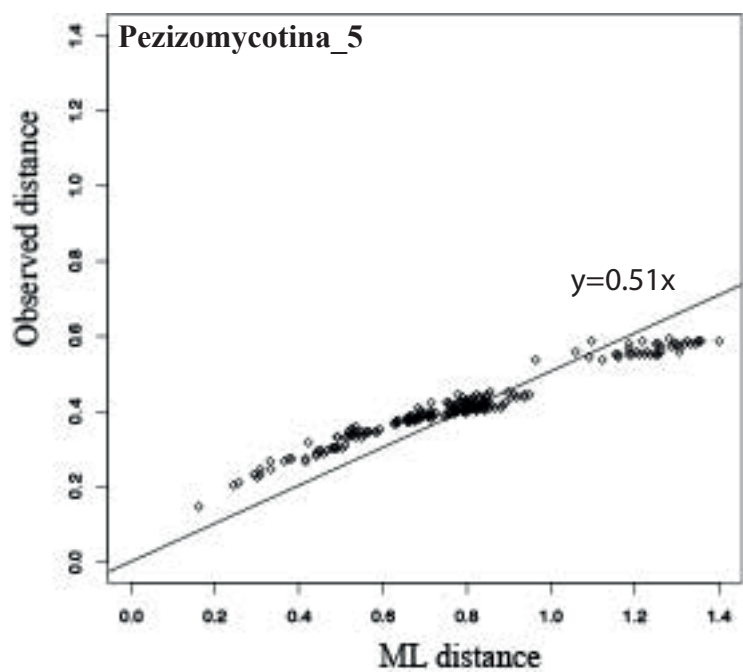
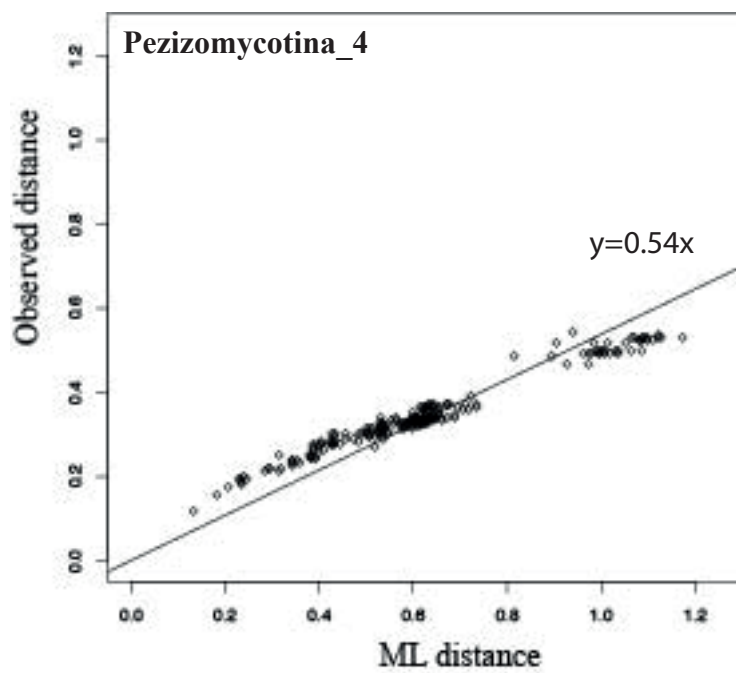
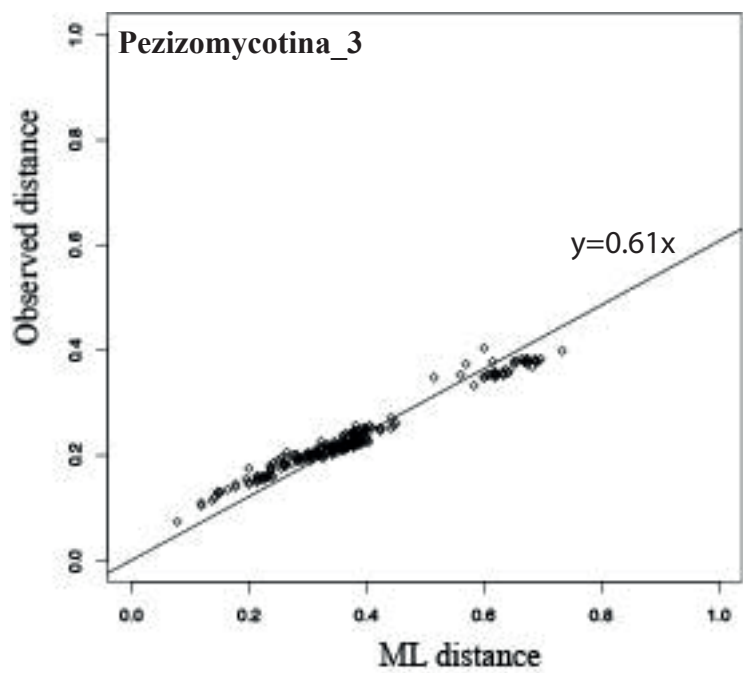
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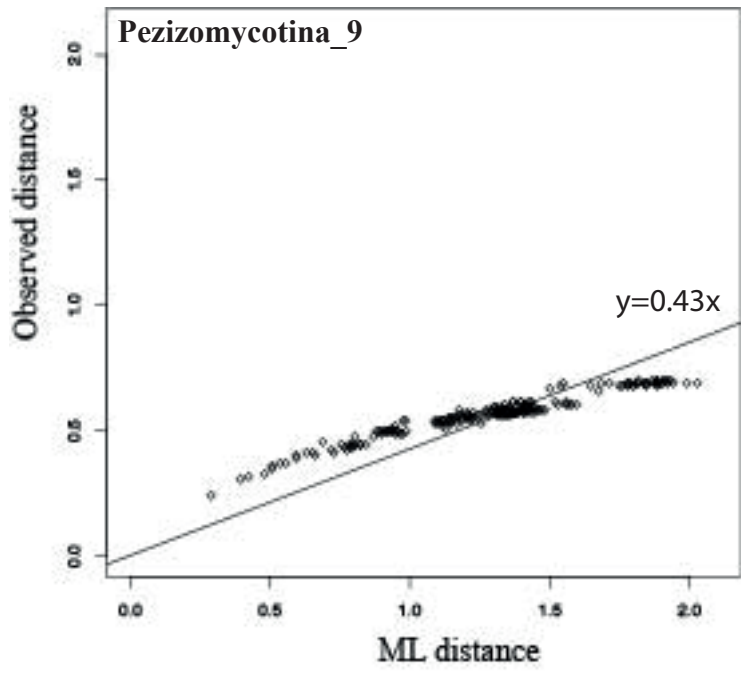
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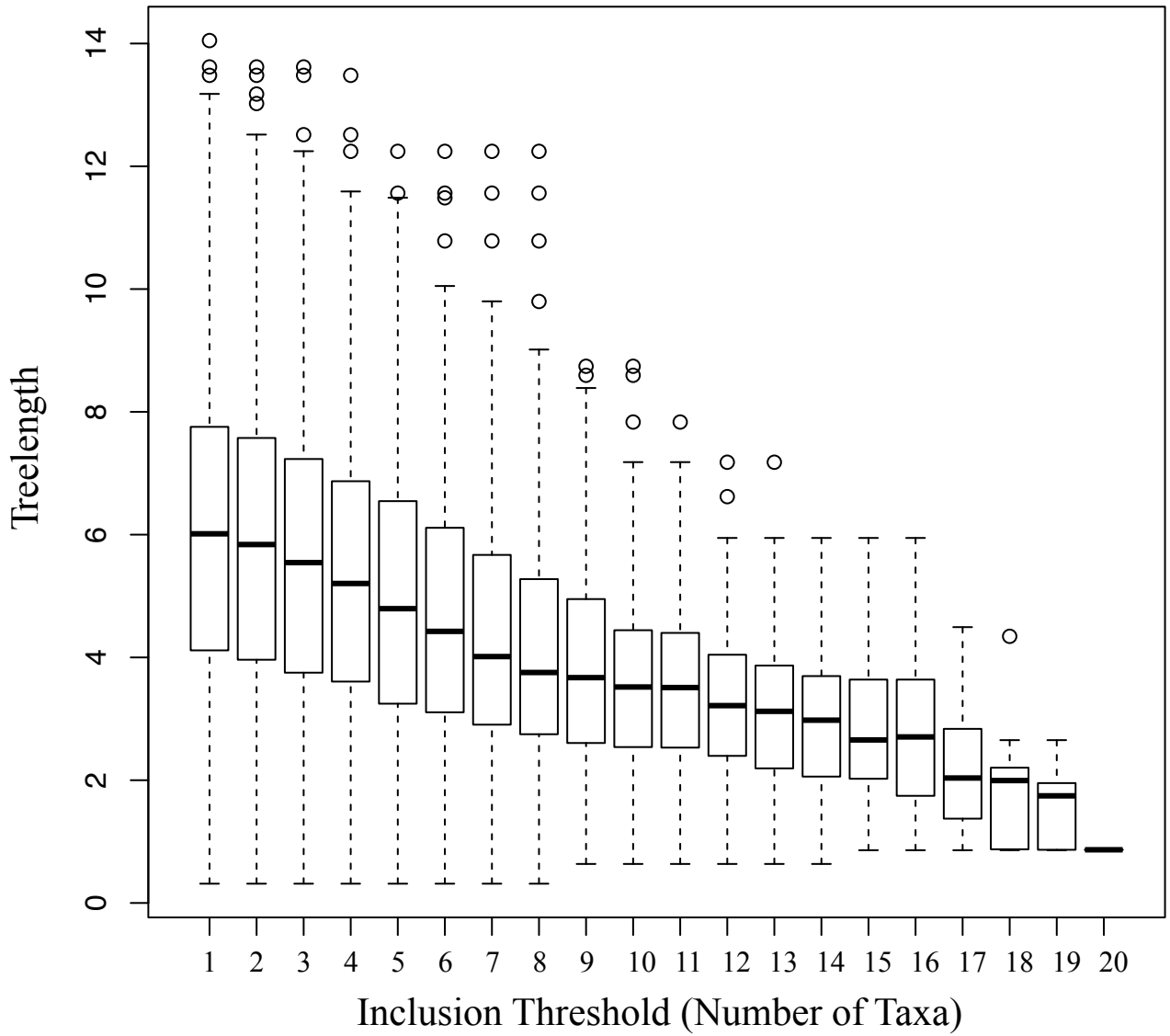
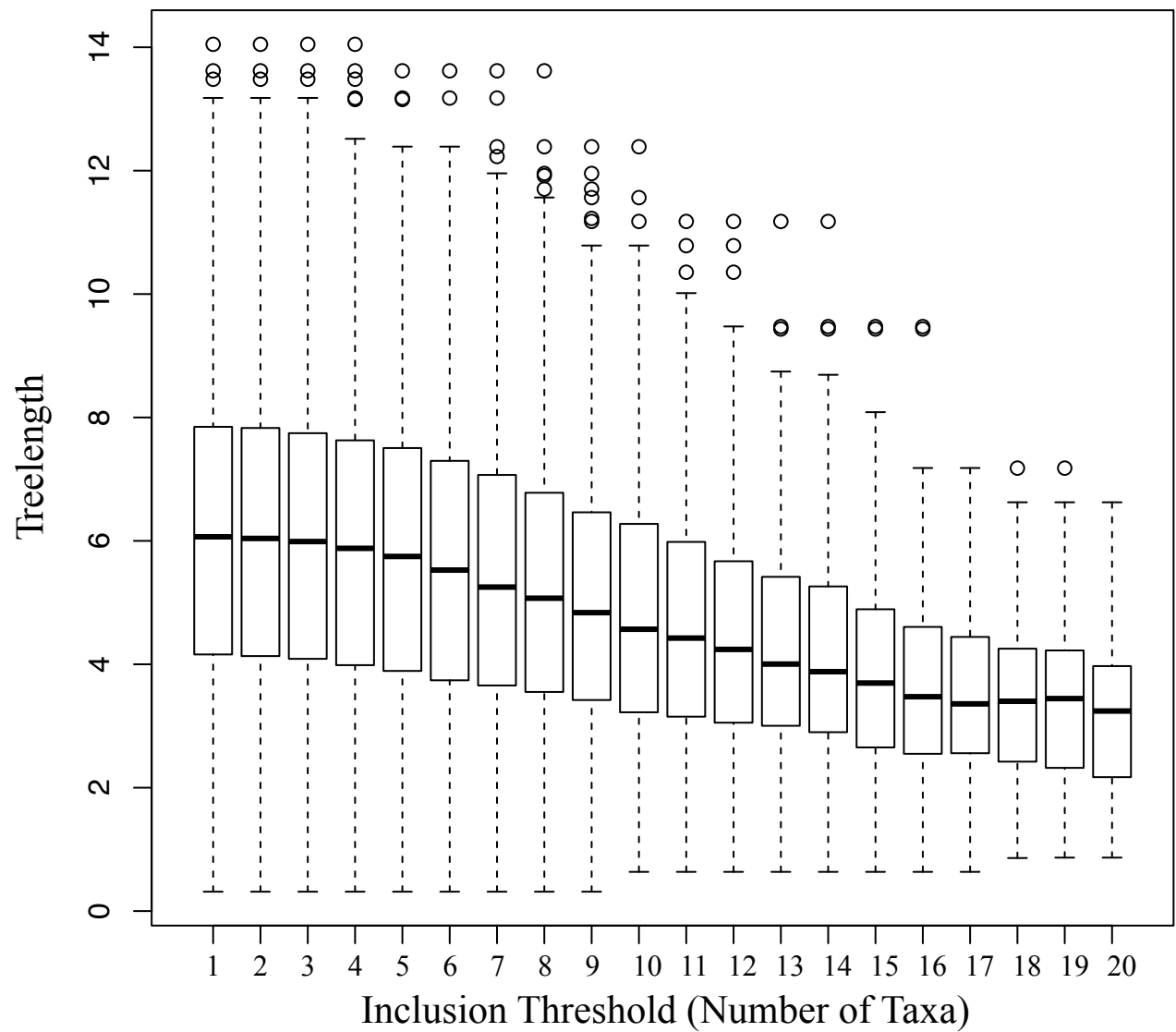
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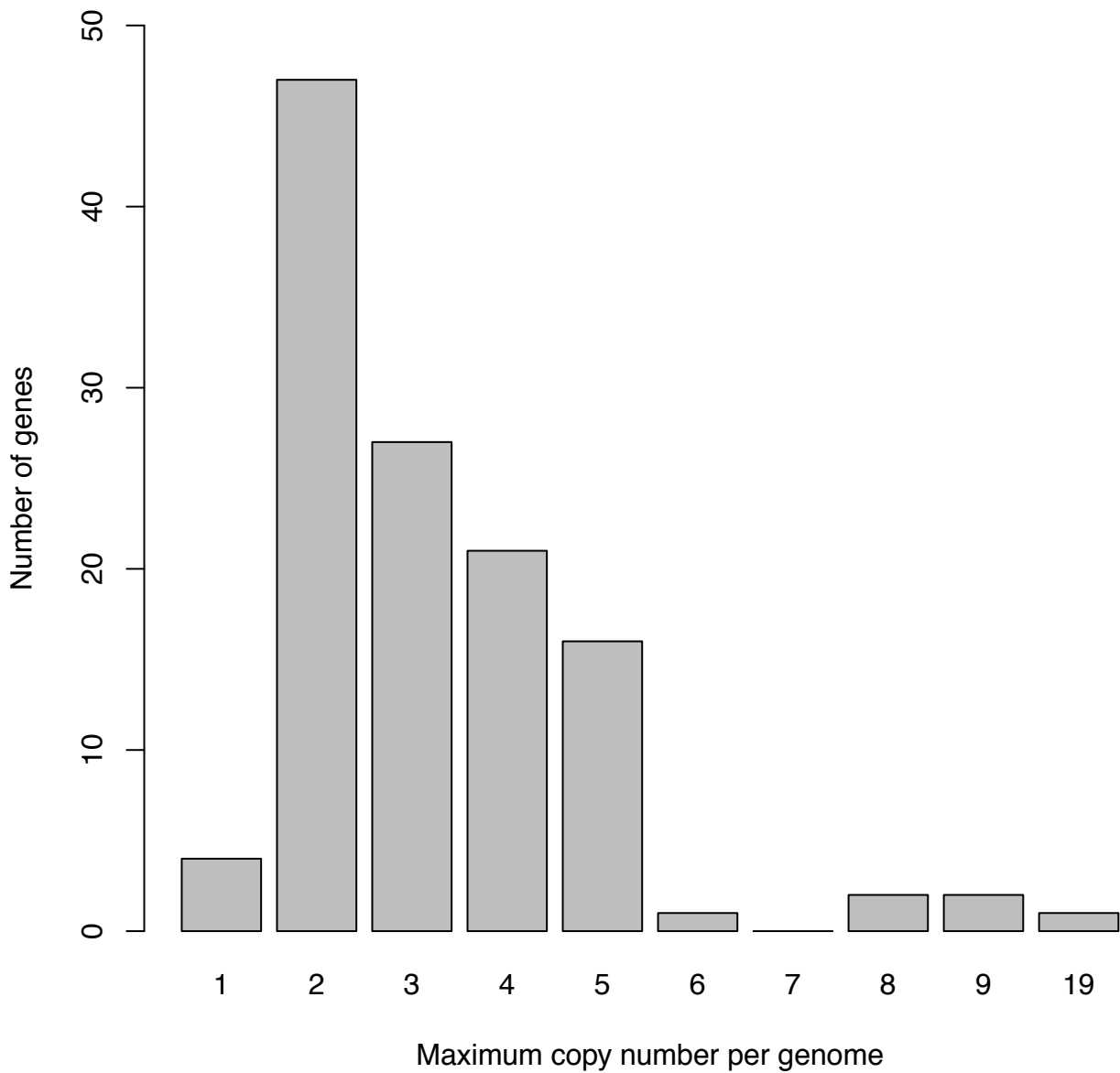




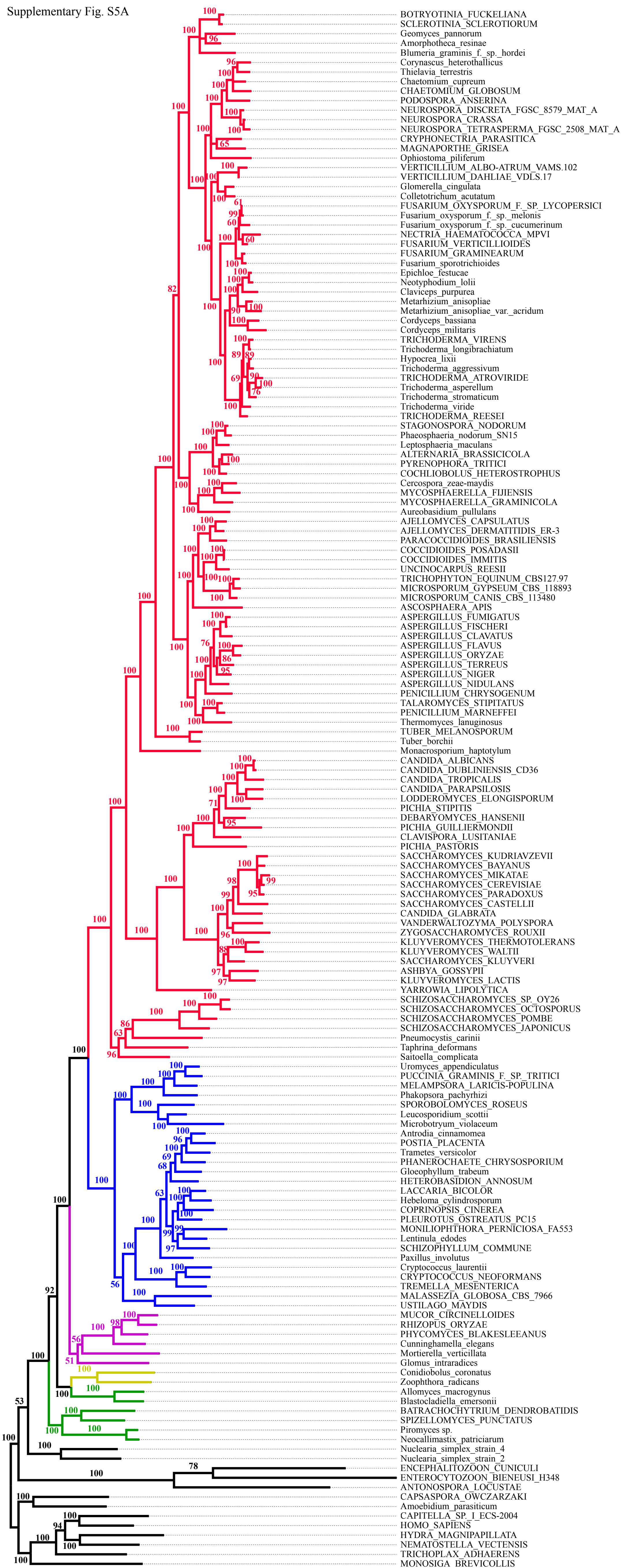


A**B**

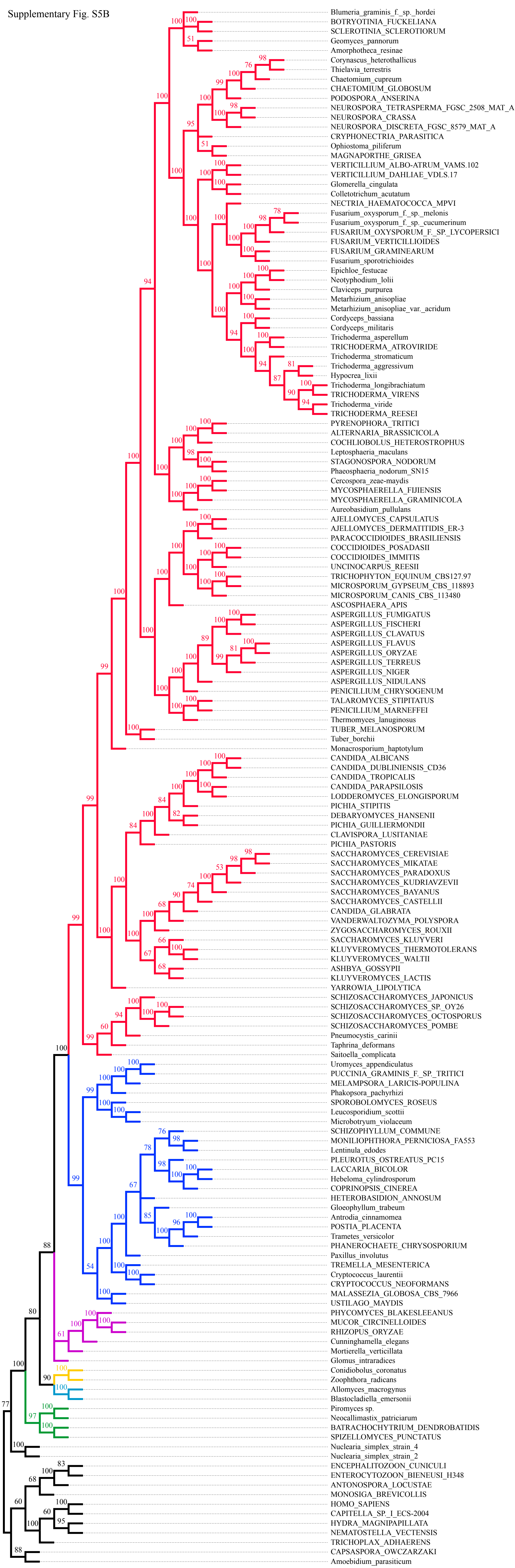
Supplementary Fig. S3



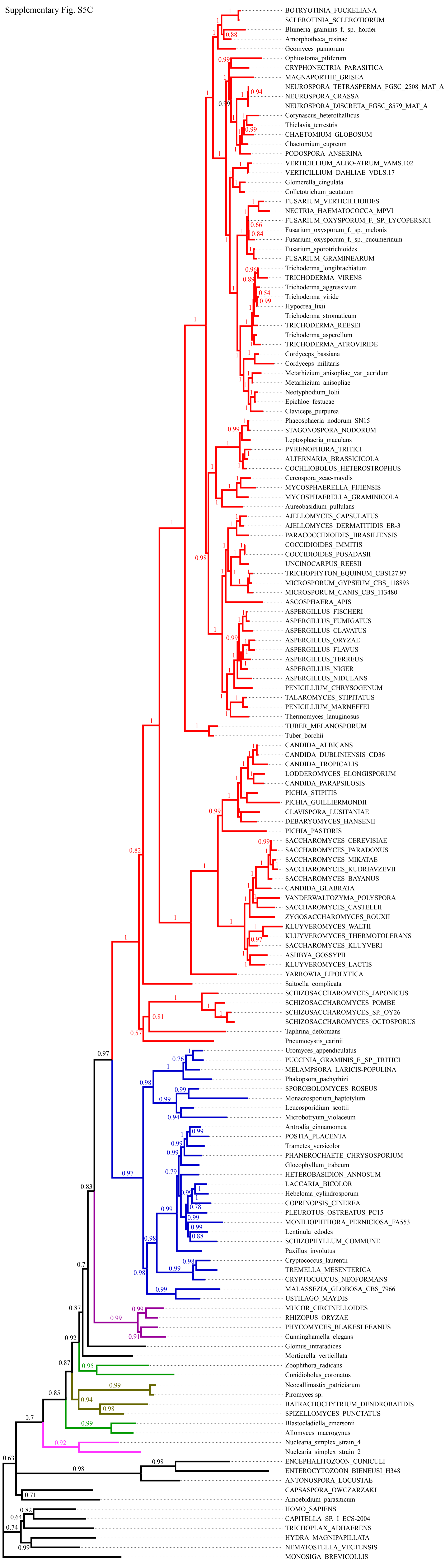
Supplementary Fig. S5A



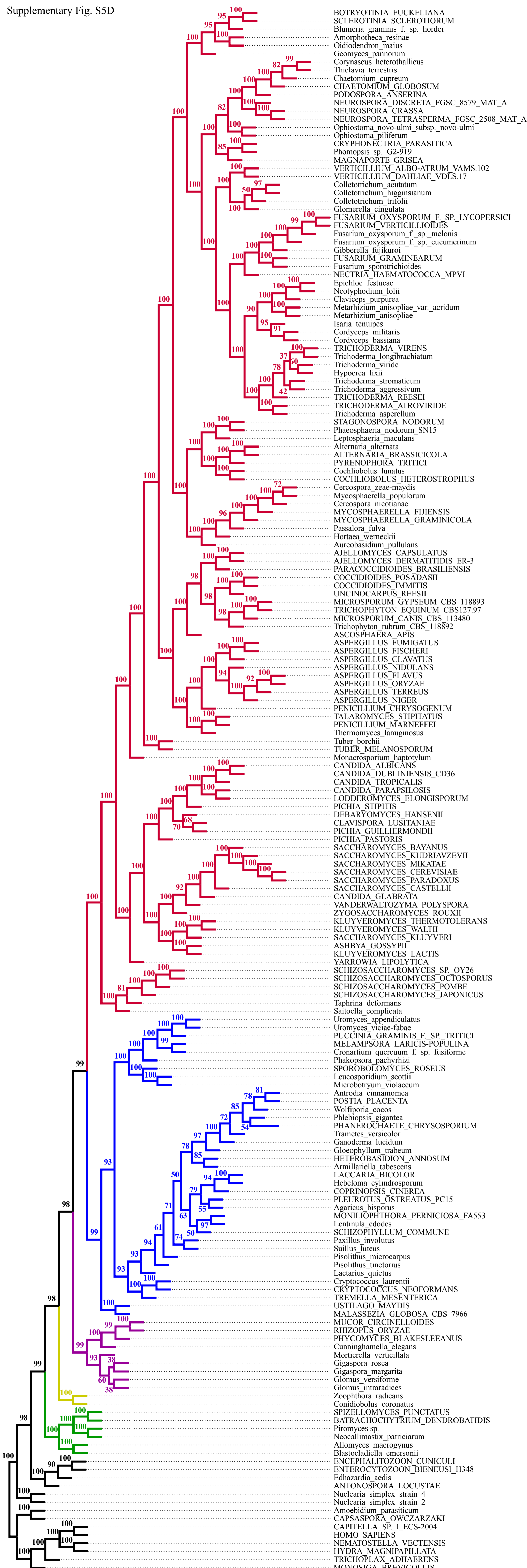
Supplementary Fig. S5B



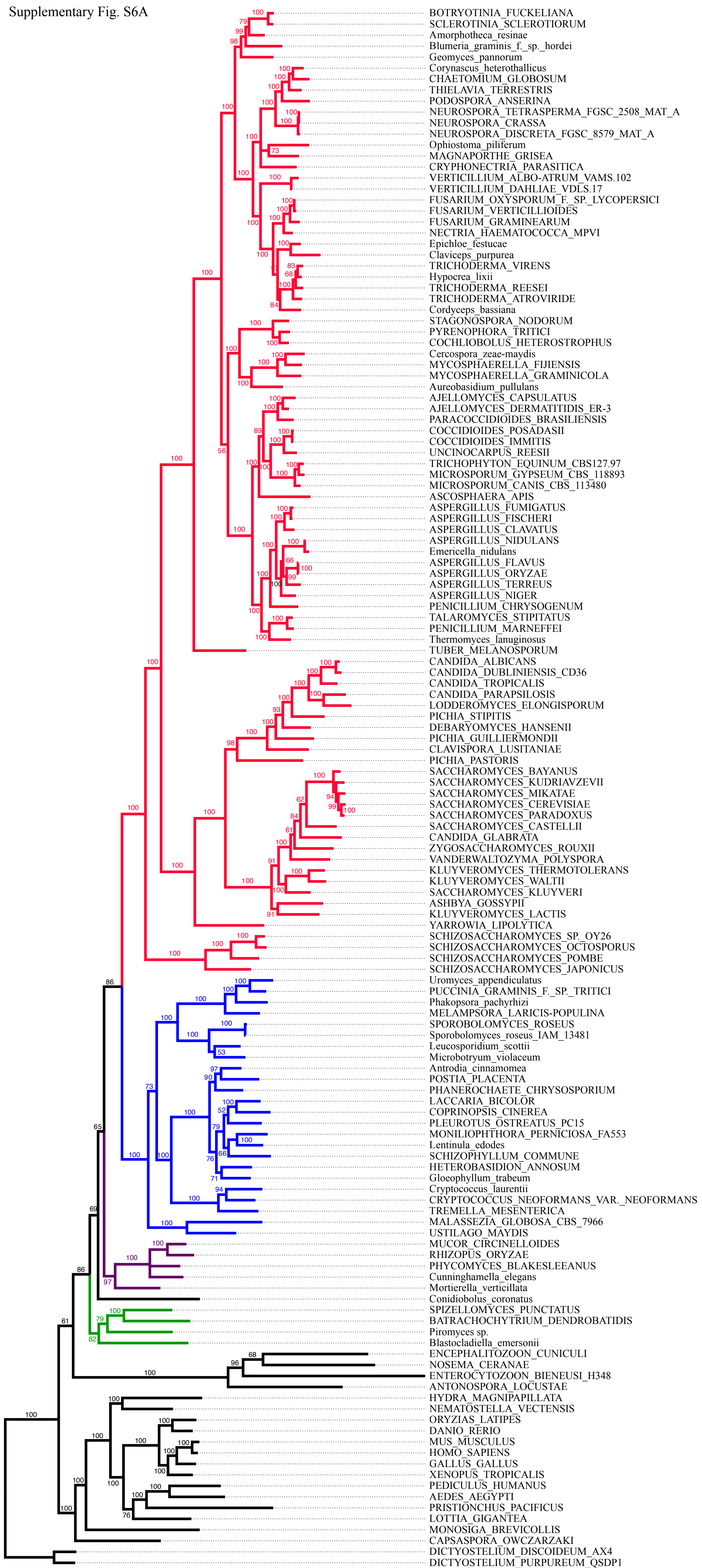
Supplementary Fig. S5C



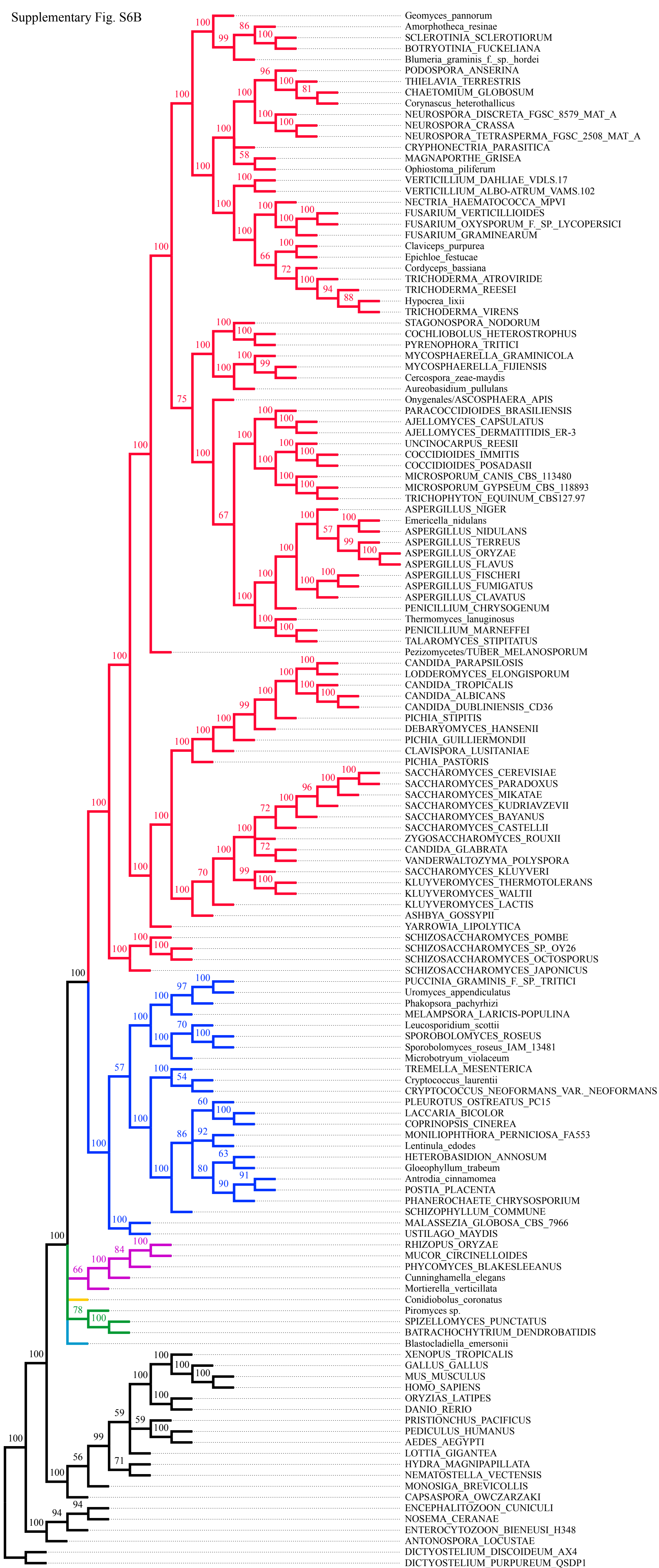
Supplementary Fig. S5D

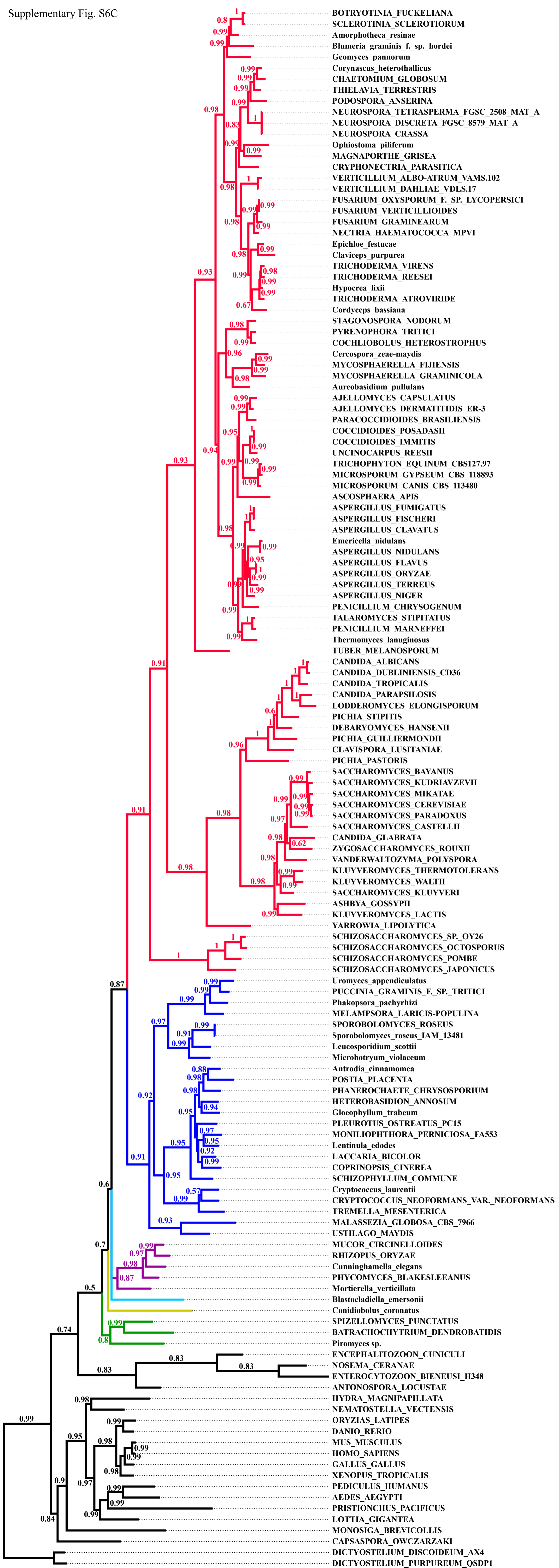


Supplementary Fig. S6A

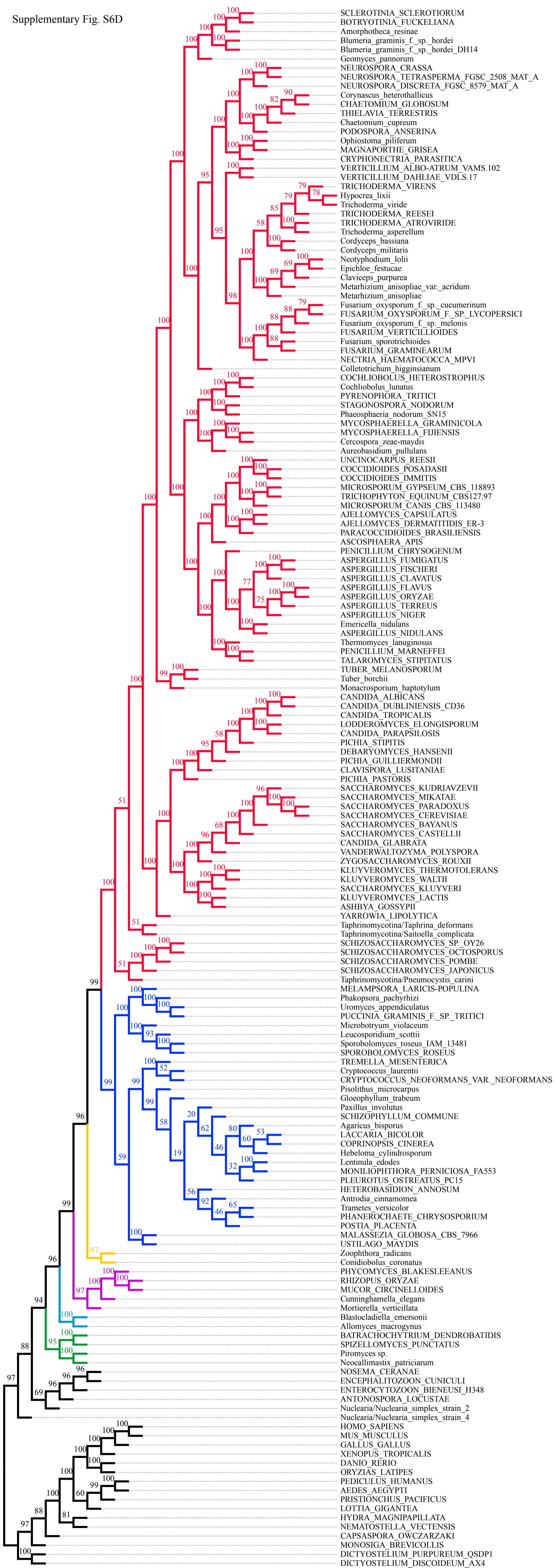


Supplementary Fig. S6B

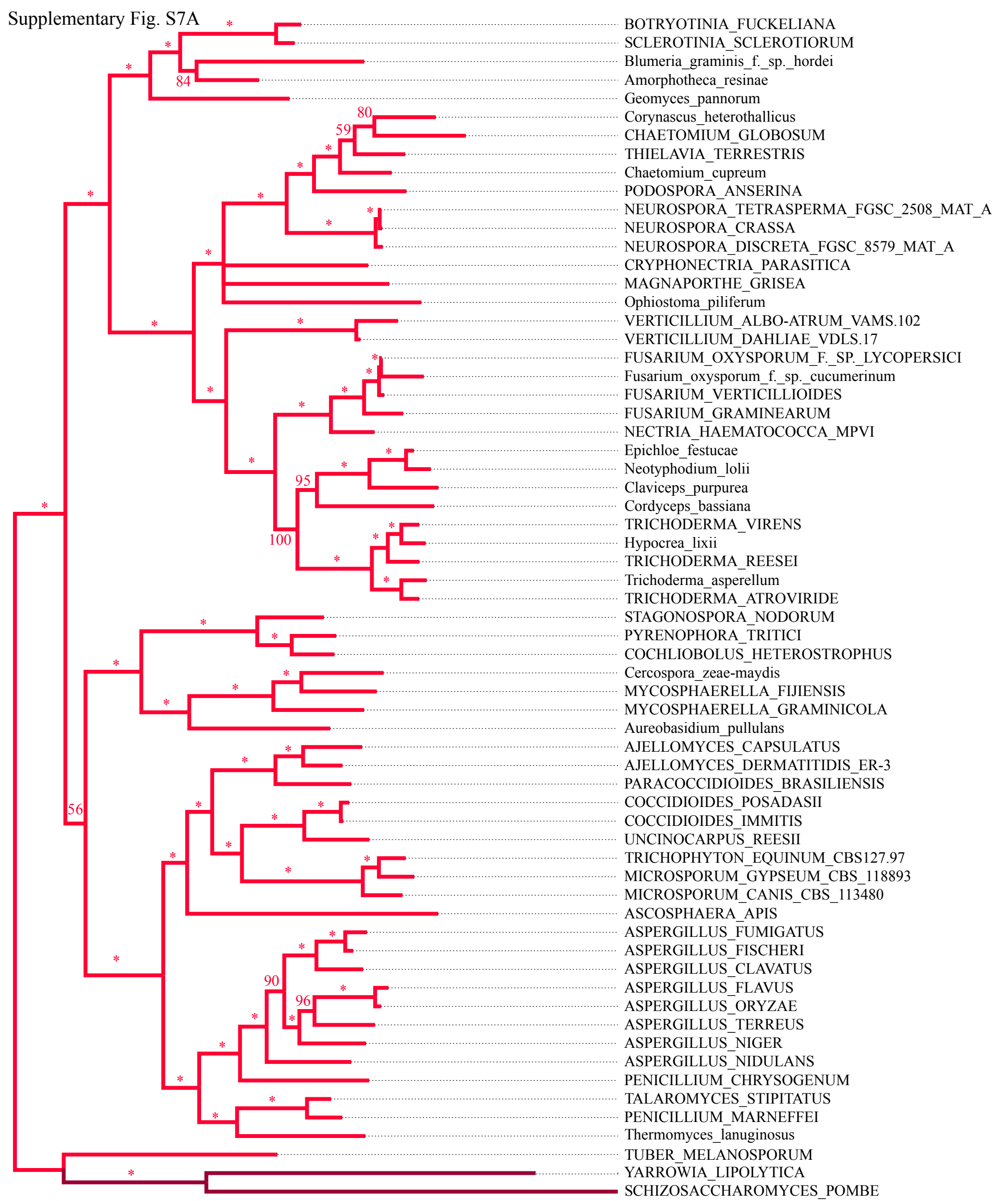




Supplementary Fig. S6D

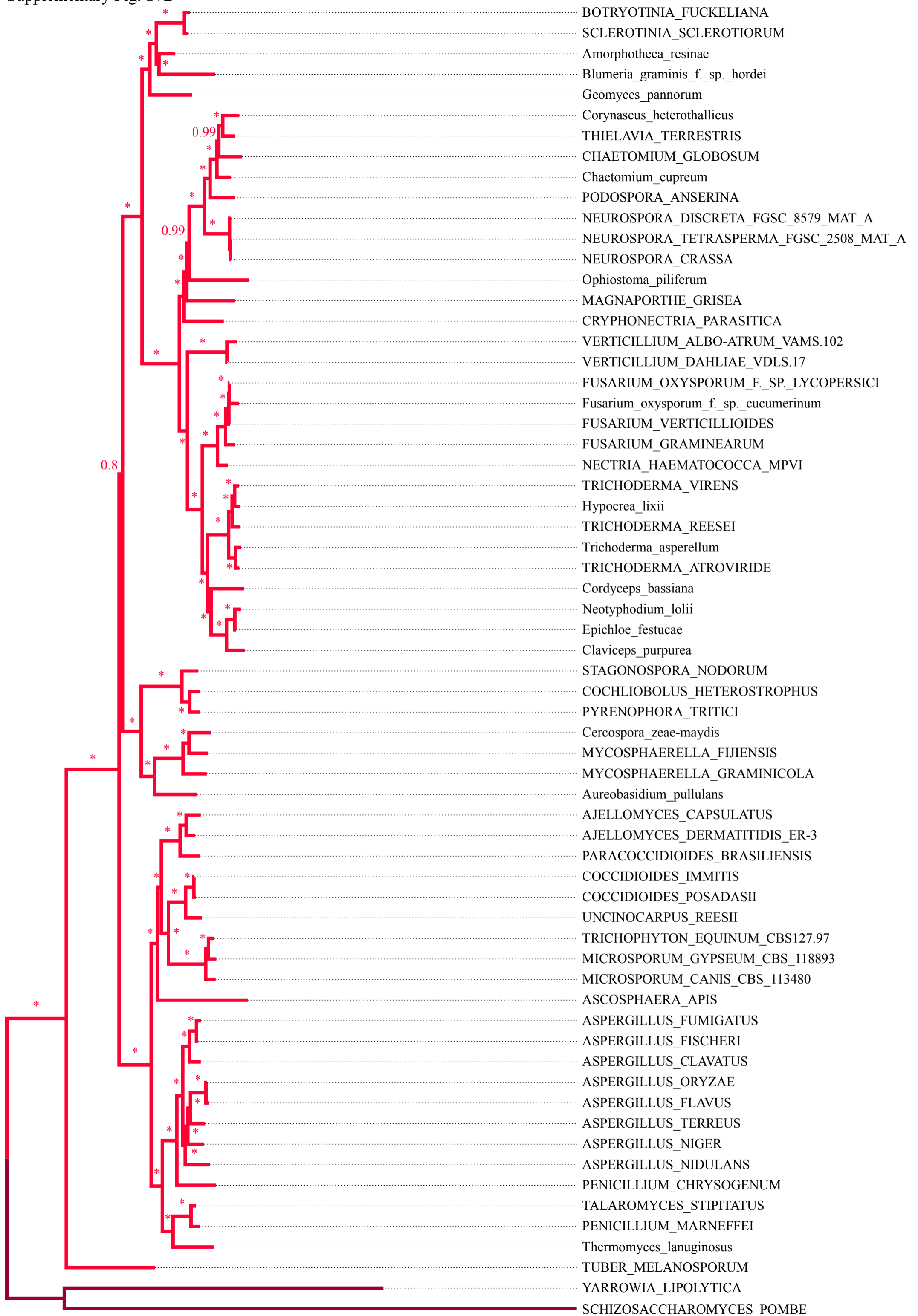


Supplementary Fig. S7A



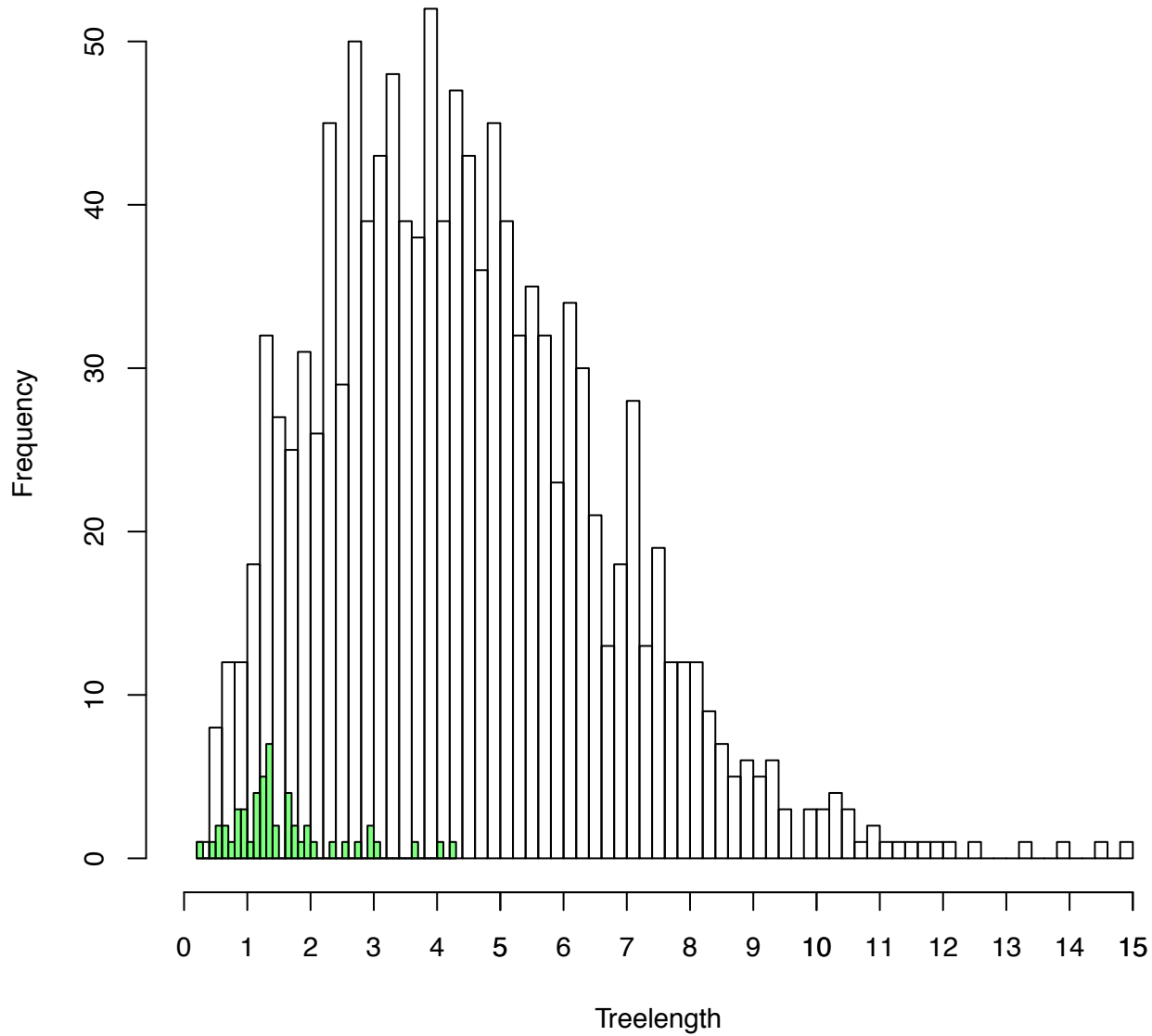
0.04

Supplementary Fig. S7B



0.2

Supplementary Fig. S8



Supplementary Fig. S9

