

Figure S1. Phylogenetic placement of soil-inhabiting fungi among identified taxa and other sequences from the environment based on a Maximum Likelihood phylogram of full concatenated 18S and 28S rRNA genes. Red, blue, and black fonts depict groups recovered here, in other environmental sequencing studies, and based on vouchers collections, respectively. Shaded clusters indicate prominent clades and branches discussed.

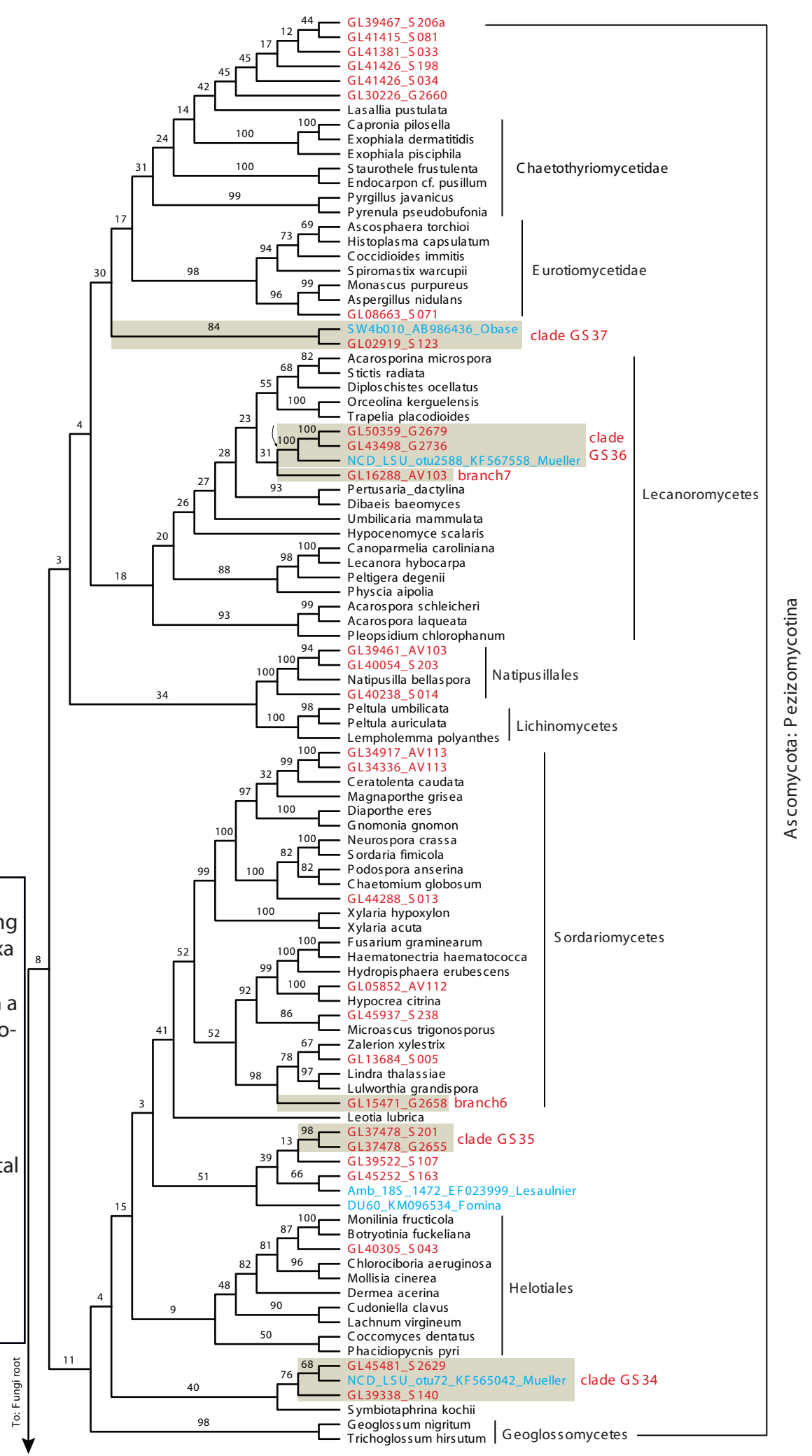


Figure S1.1

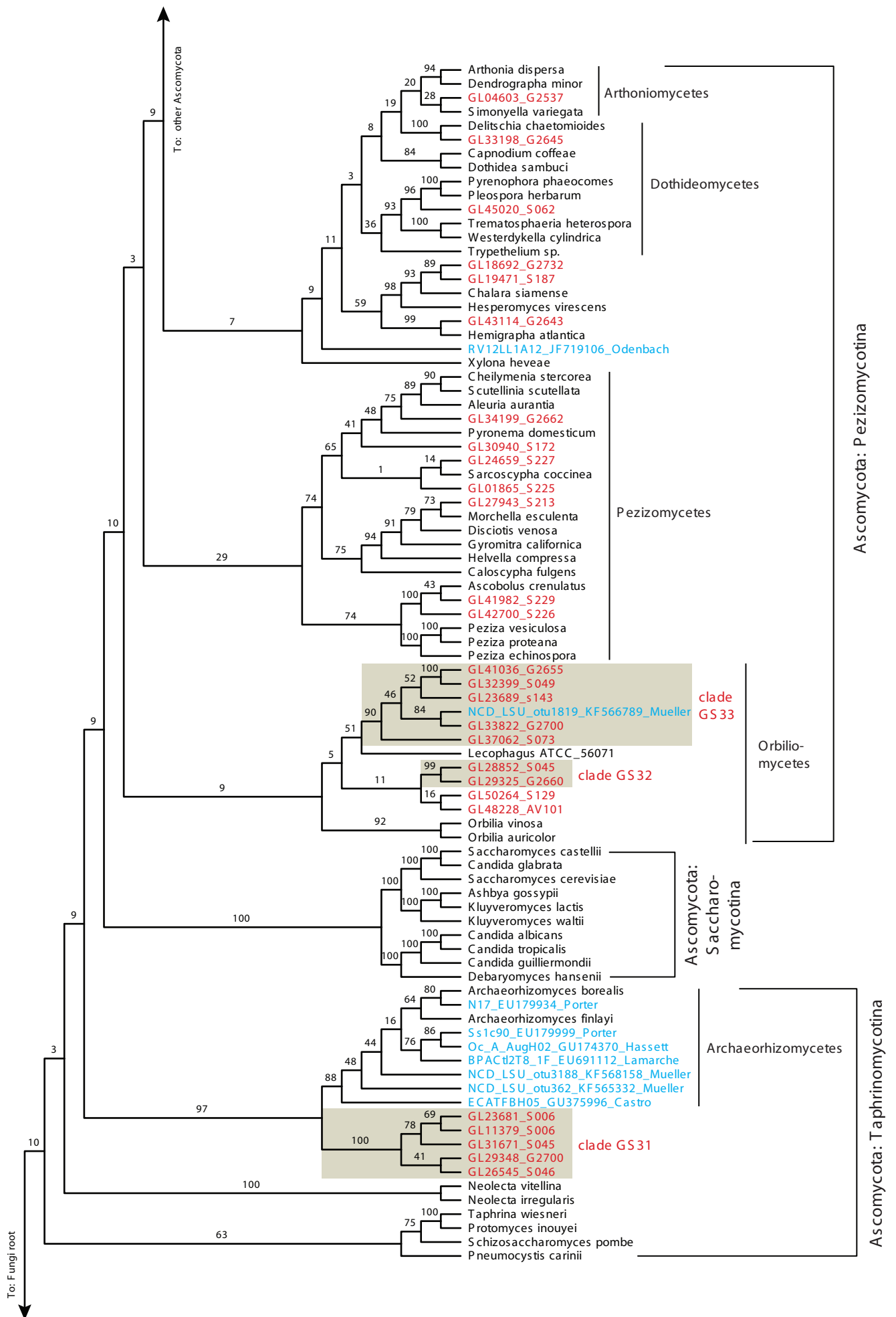


Figure S 1.2

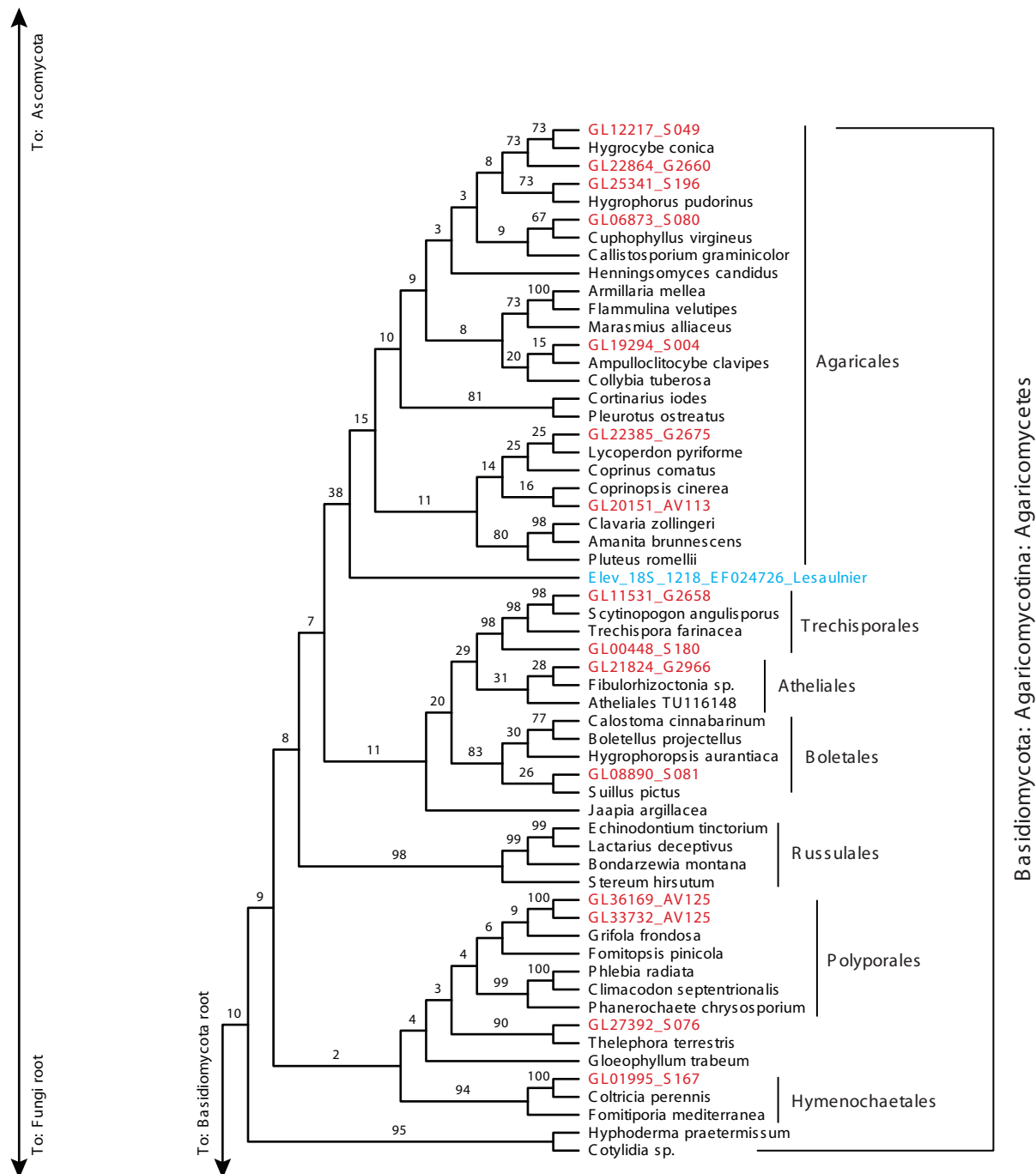


Figure S1.3

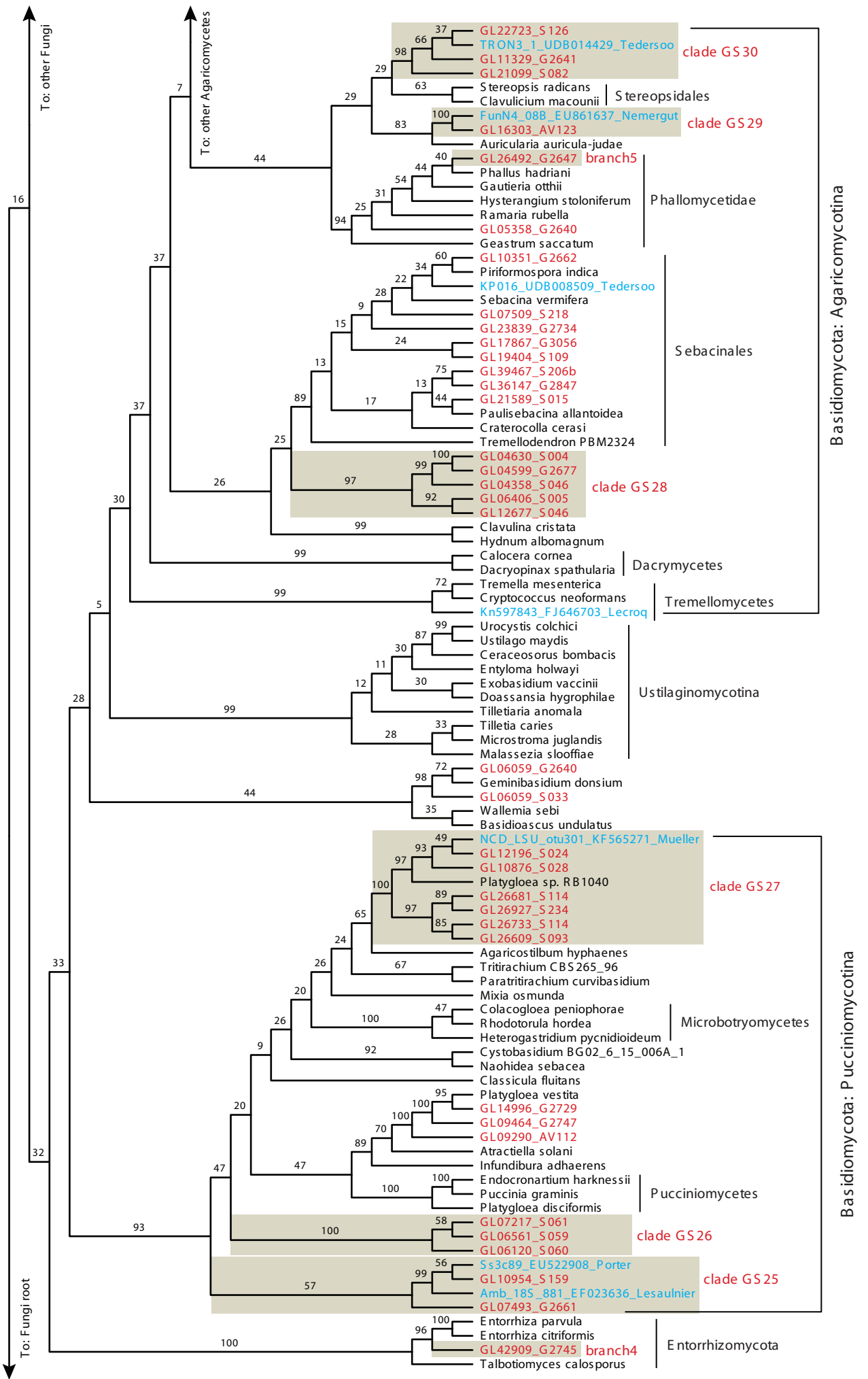


Figure S 1.4

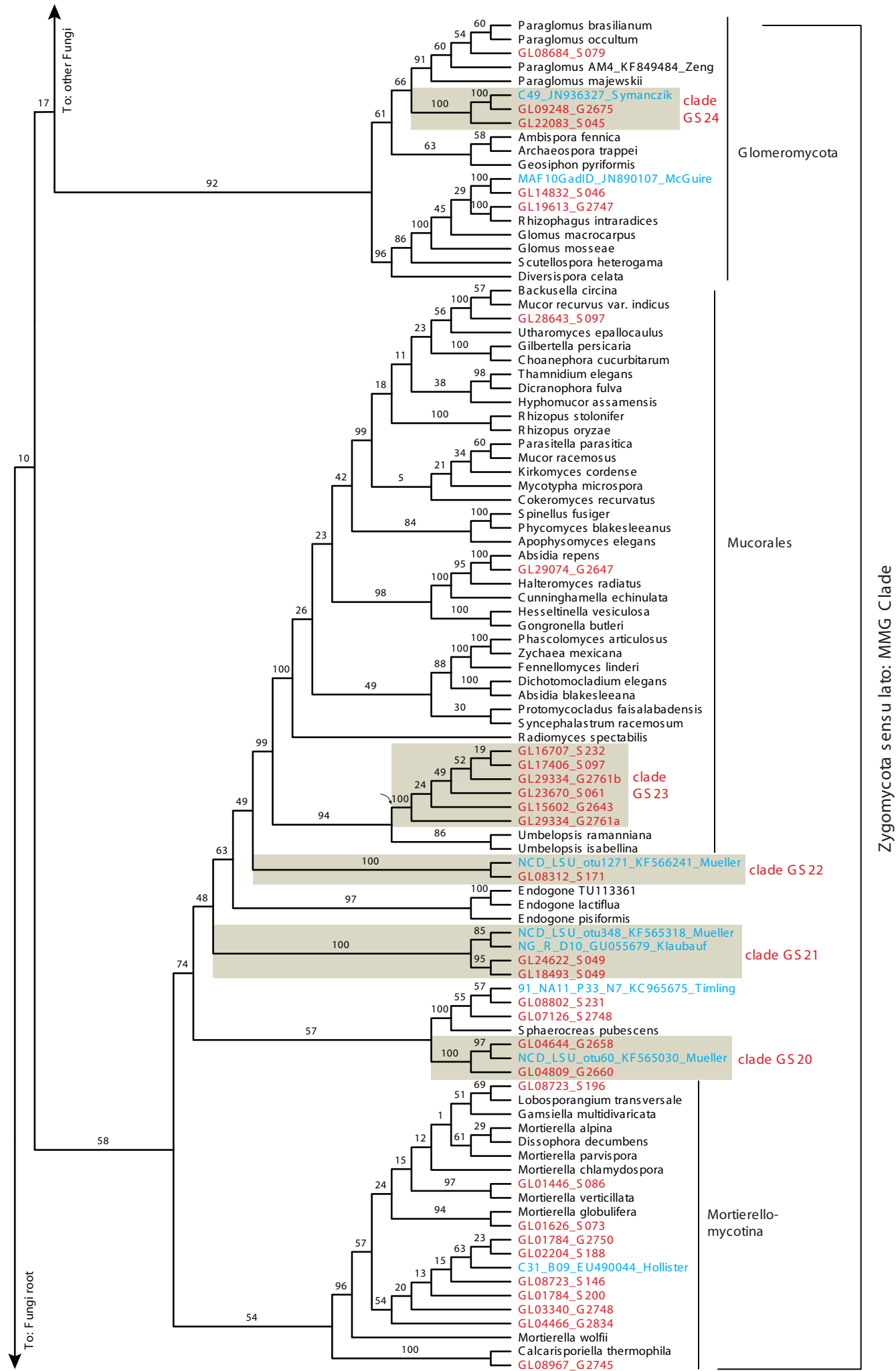


Figure S 1.5

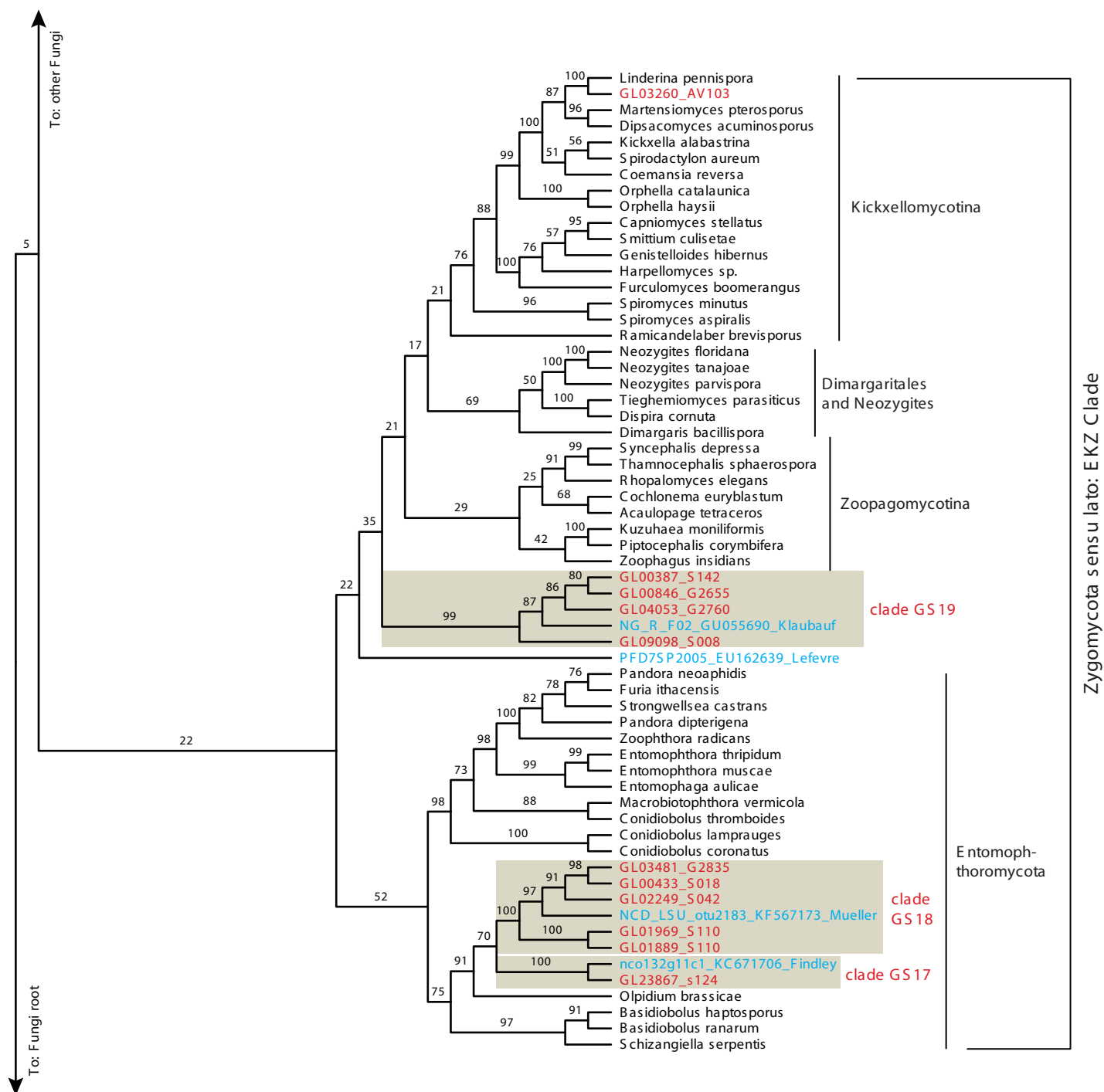


Figure S 1.6

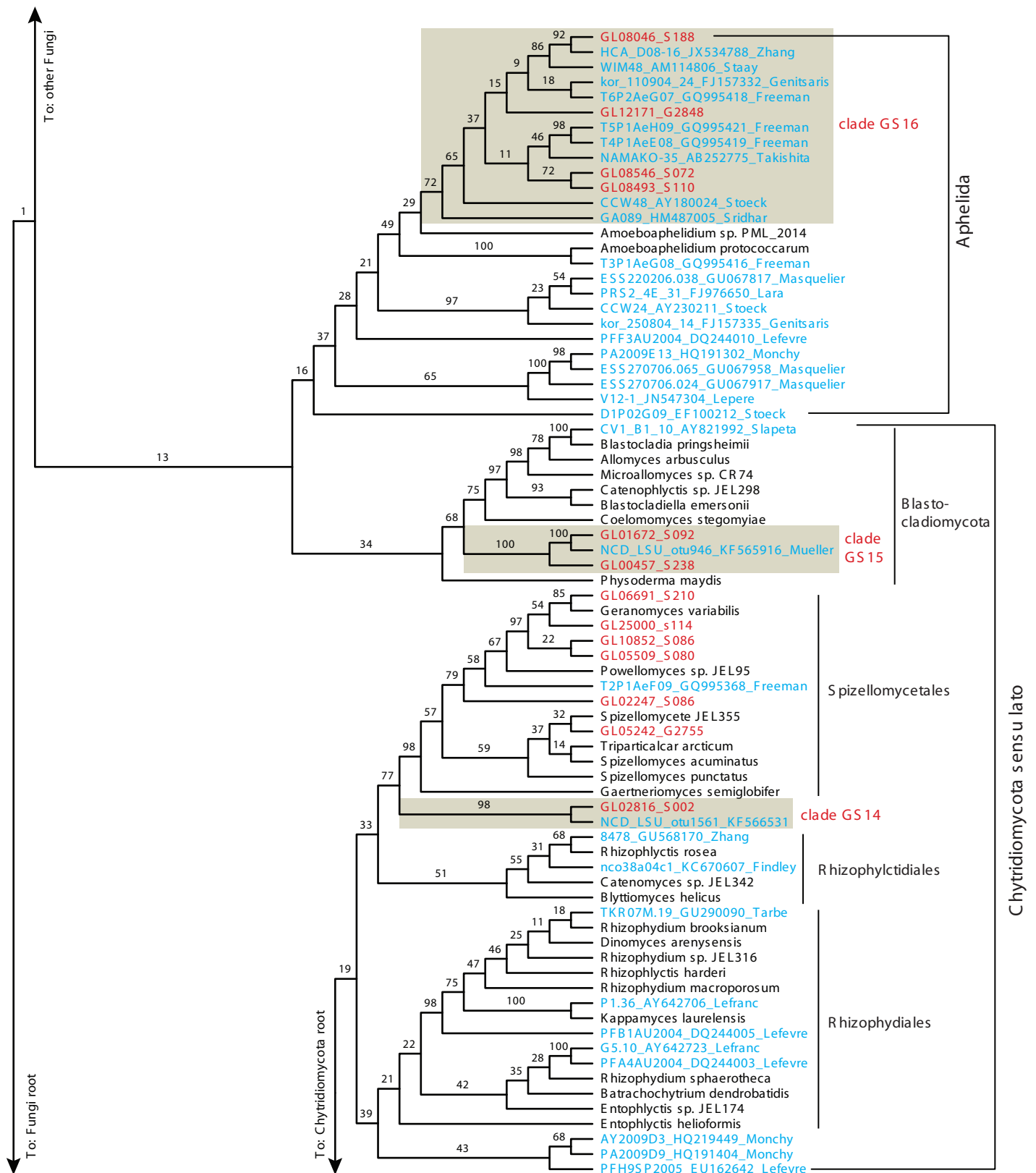
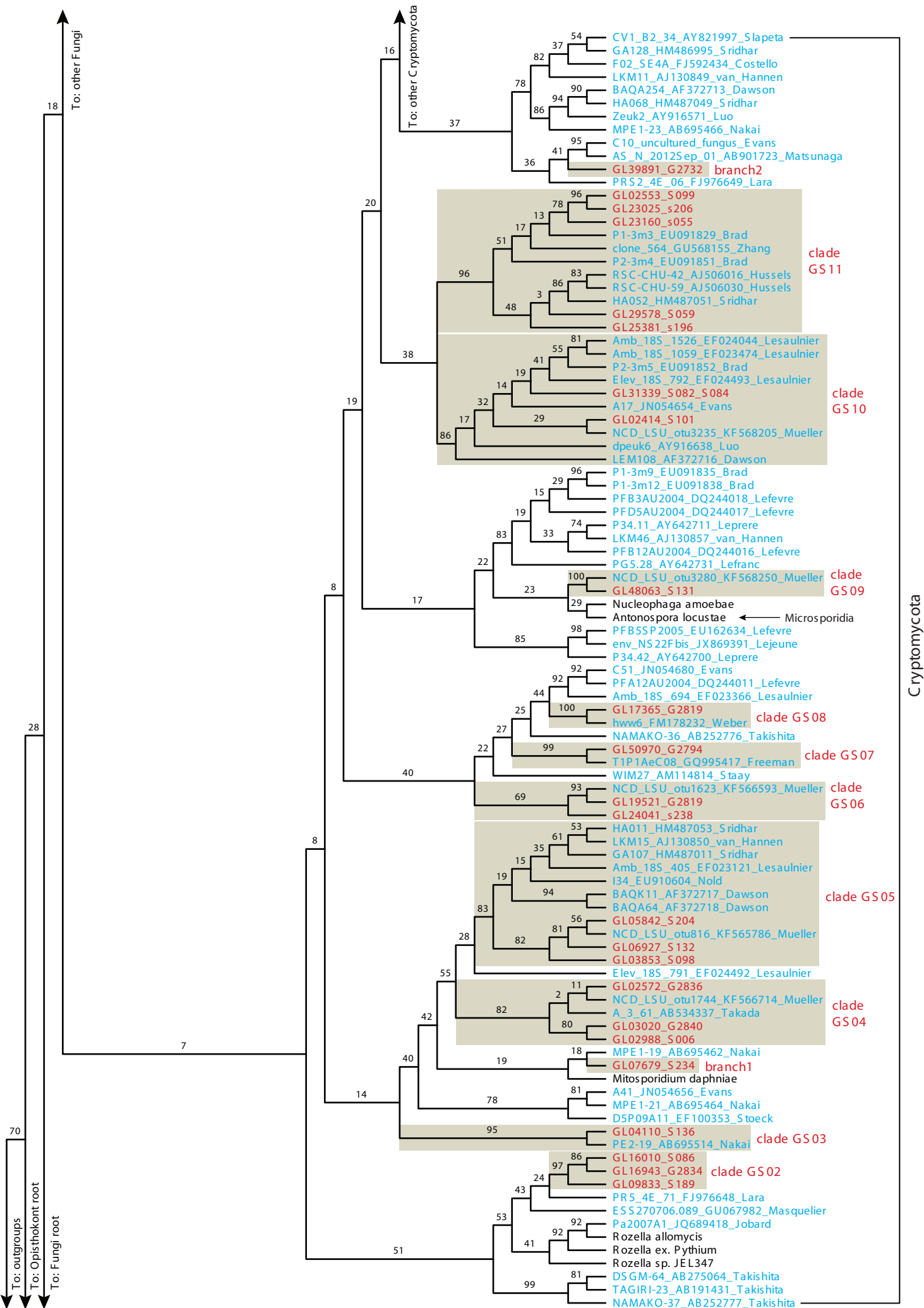


Figure S 1.7

Figure
S1.9



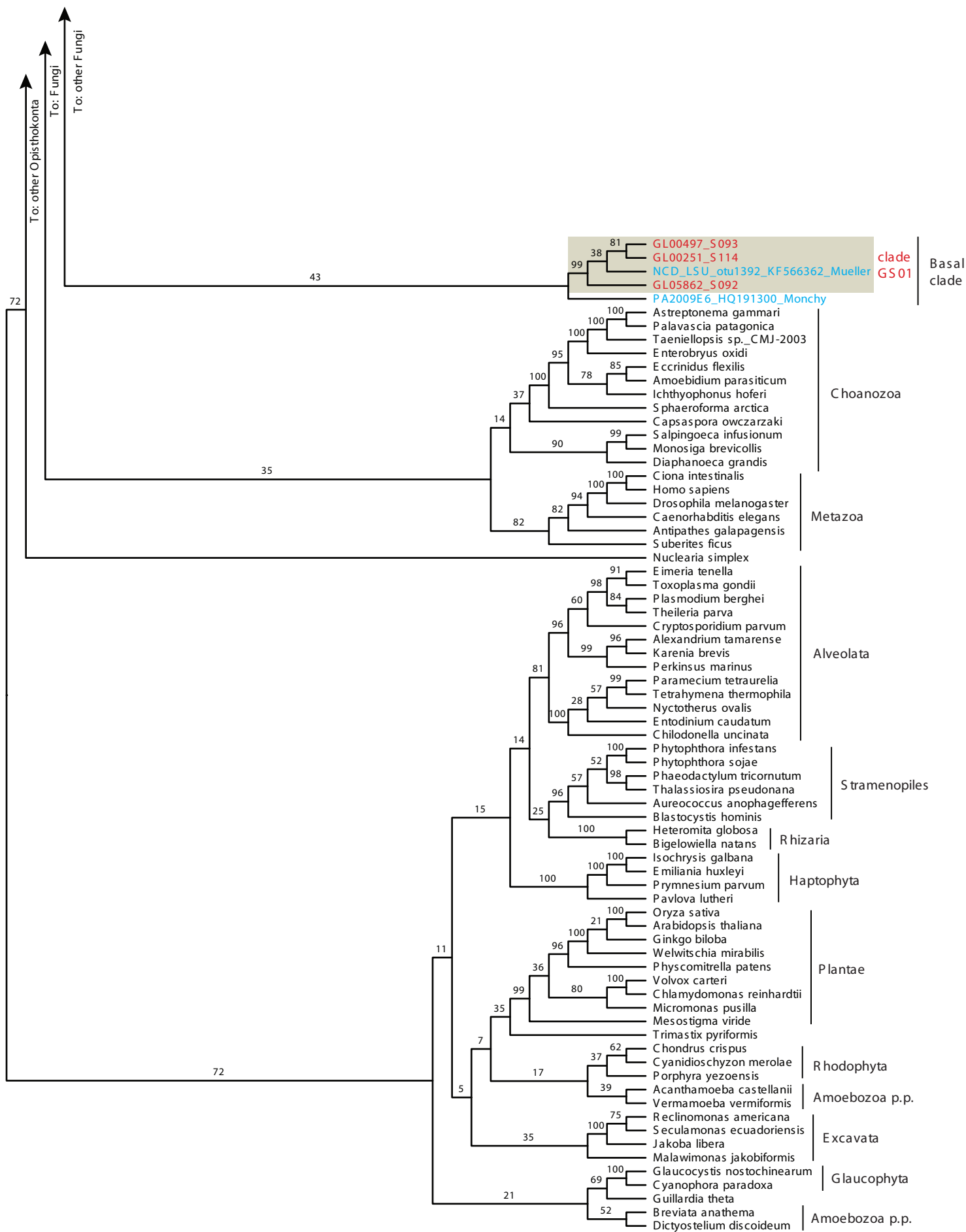


Figure S 1.10

Figure S2. Phylogenetic placement of soil-inhabiting fungi among identified taxa and other sequences from the environment based on a full 18S rRNA gene Maximum Likelihood phylogram. Red, blue, and black fonts depict groups recovered here, in other environmental sequencing studies and based on vouchered collections, respectively. Shaded clusters indicate prominent clades and branches discussed.

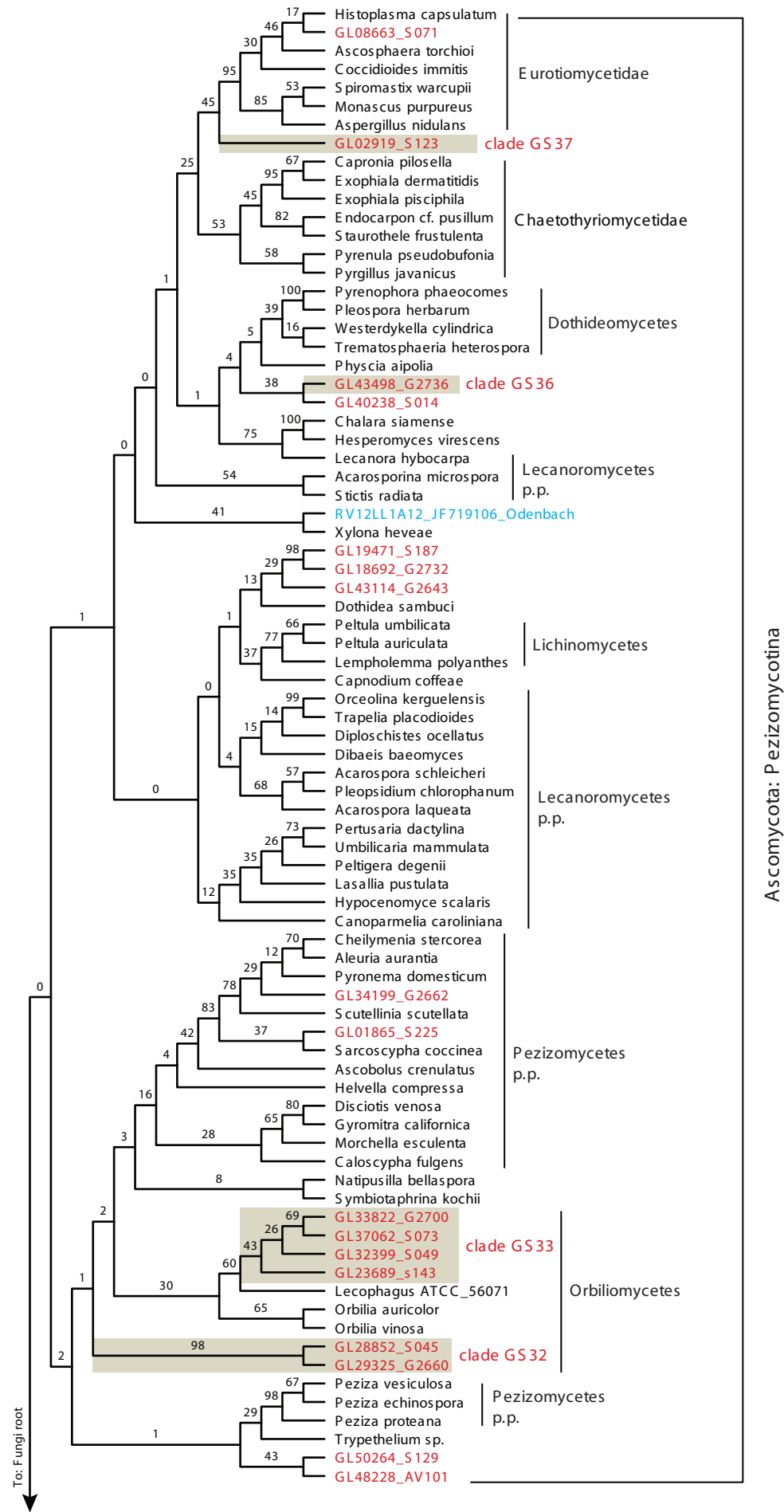


Figure S2.1

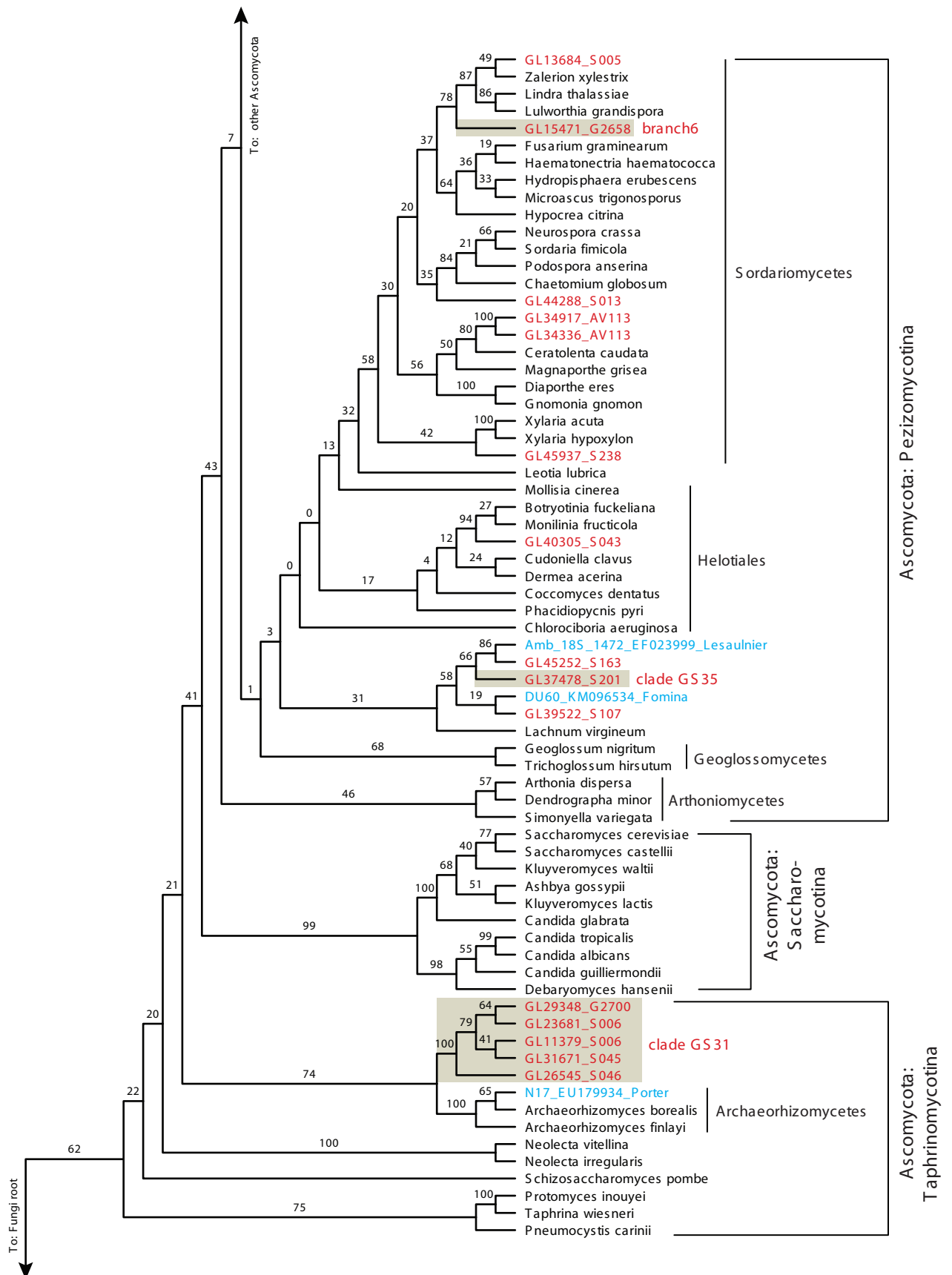


Figure S2.2

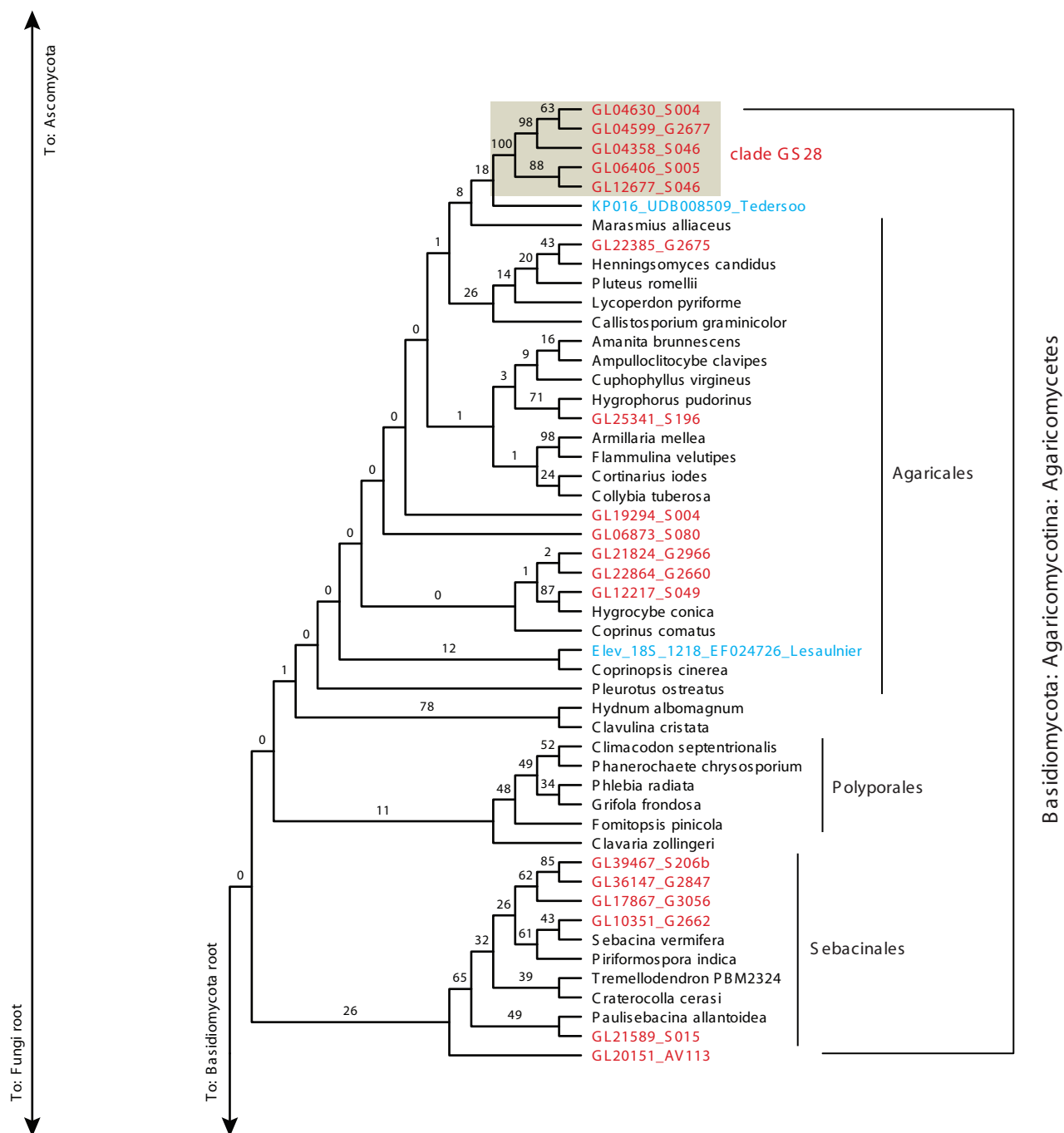


Figure S2.3

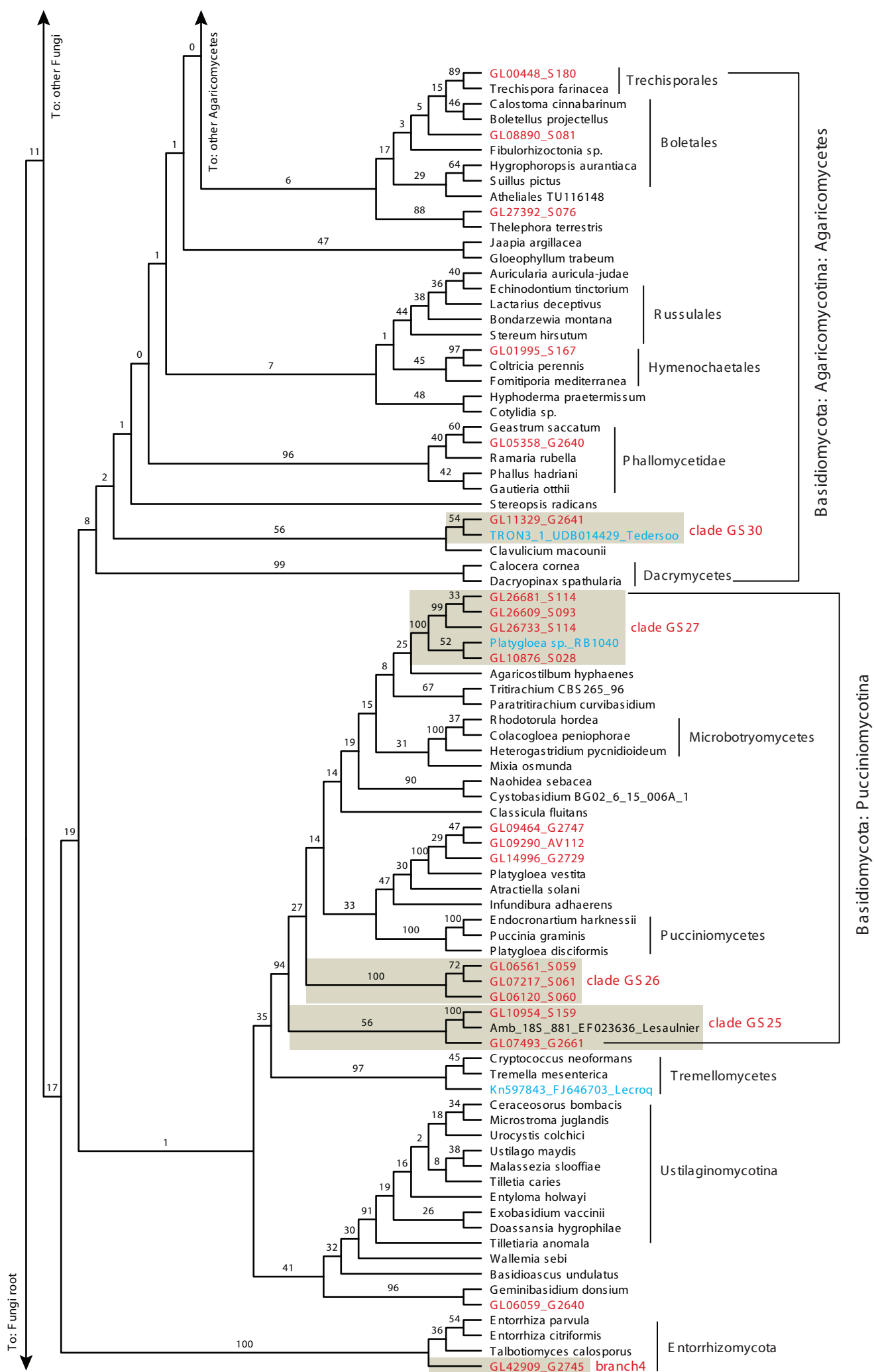


Figure S2.4

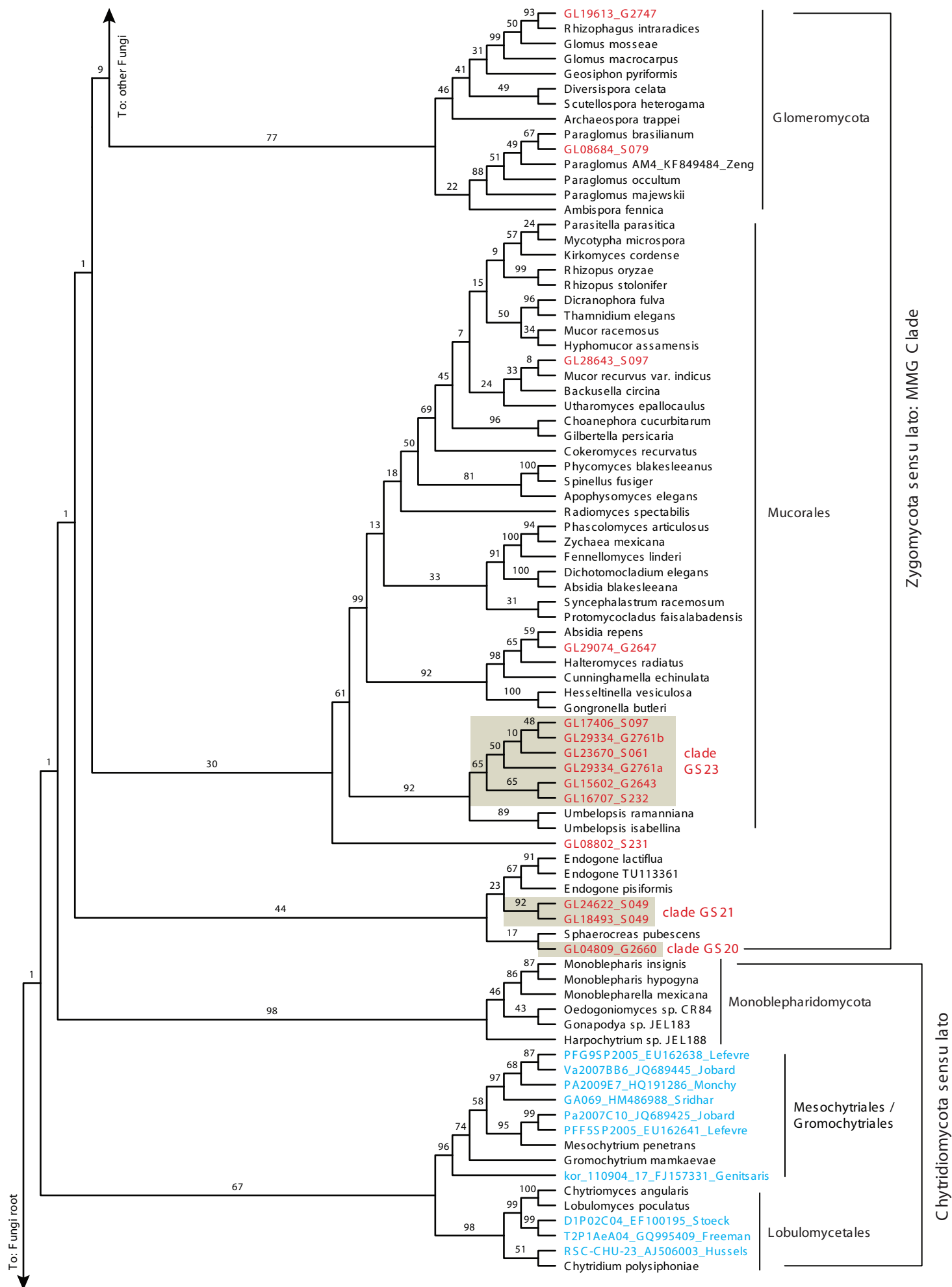


Figure S2.5

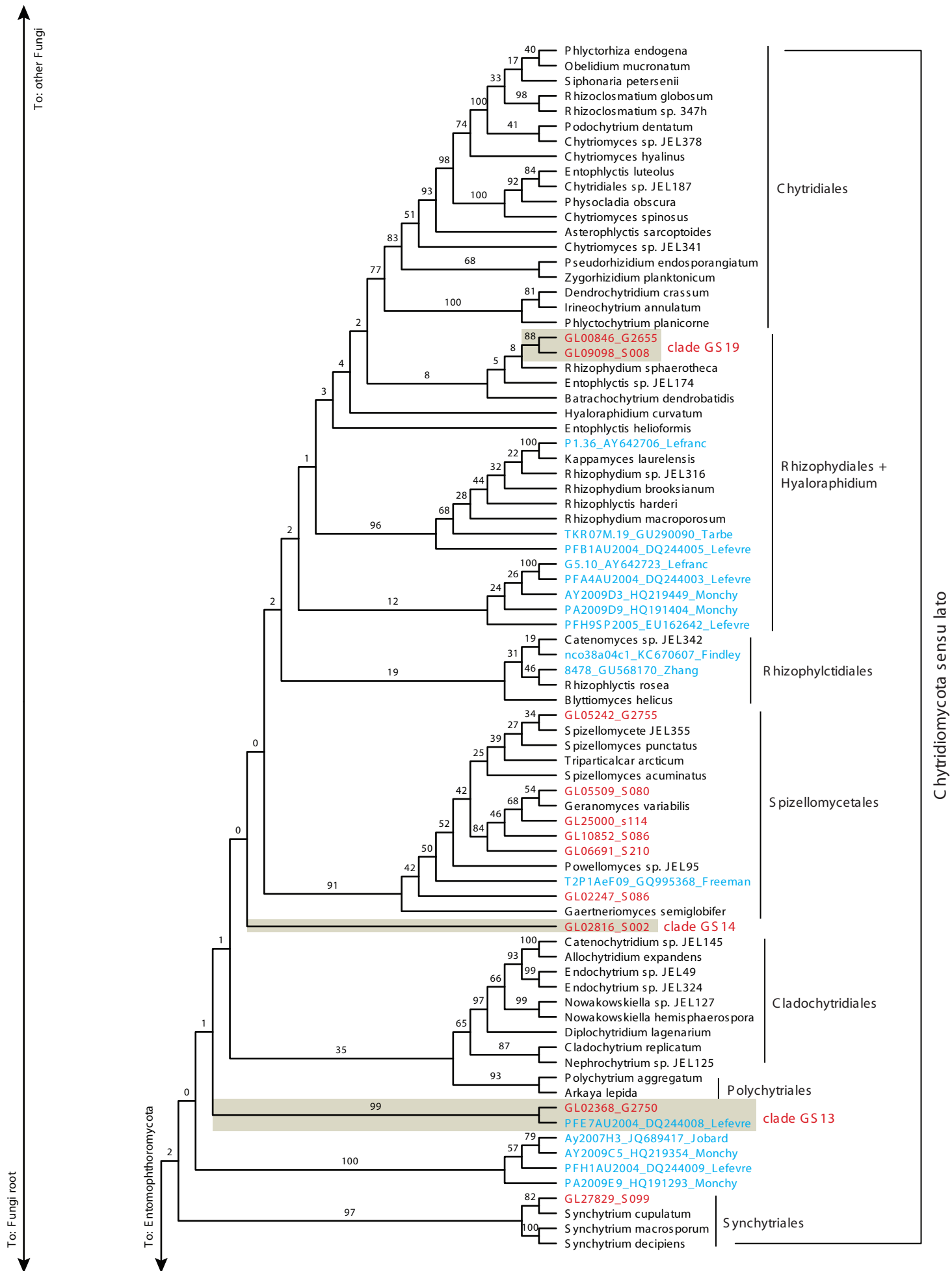


Figure S 2.6

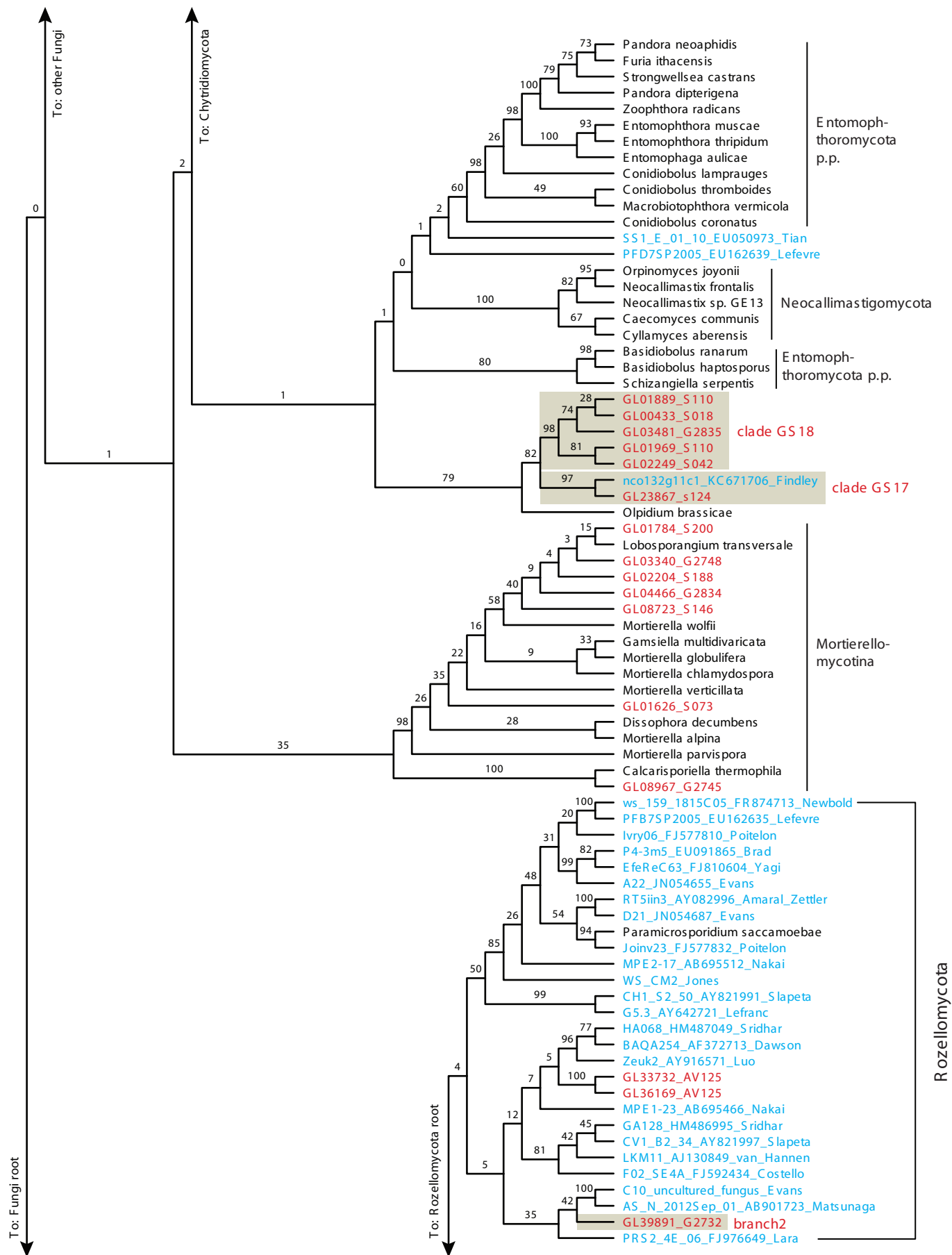


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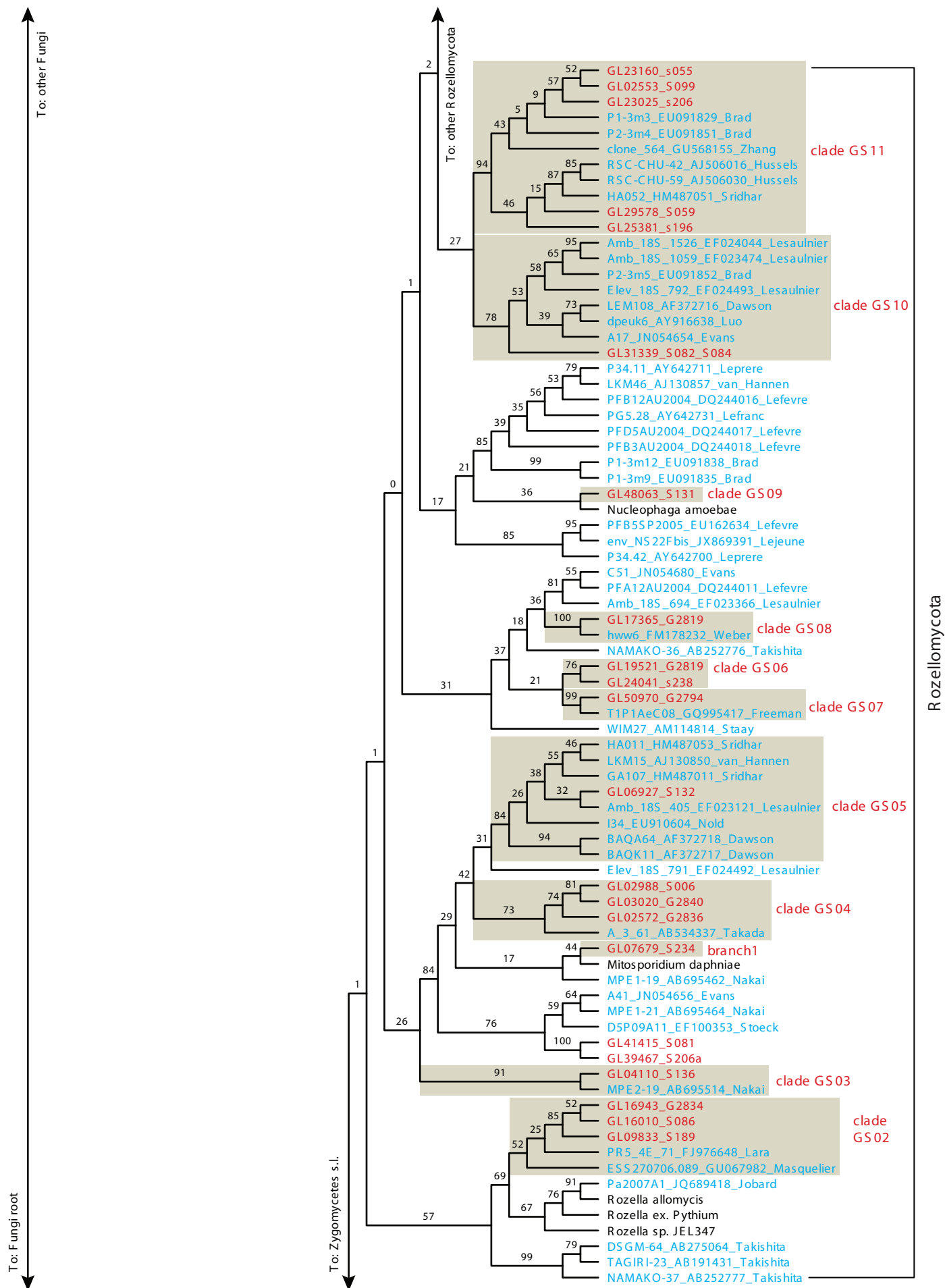


Figure S2.8

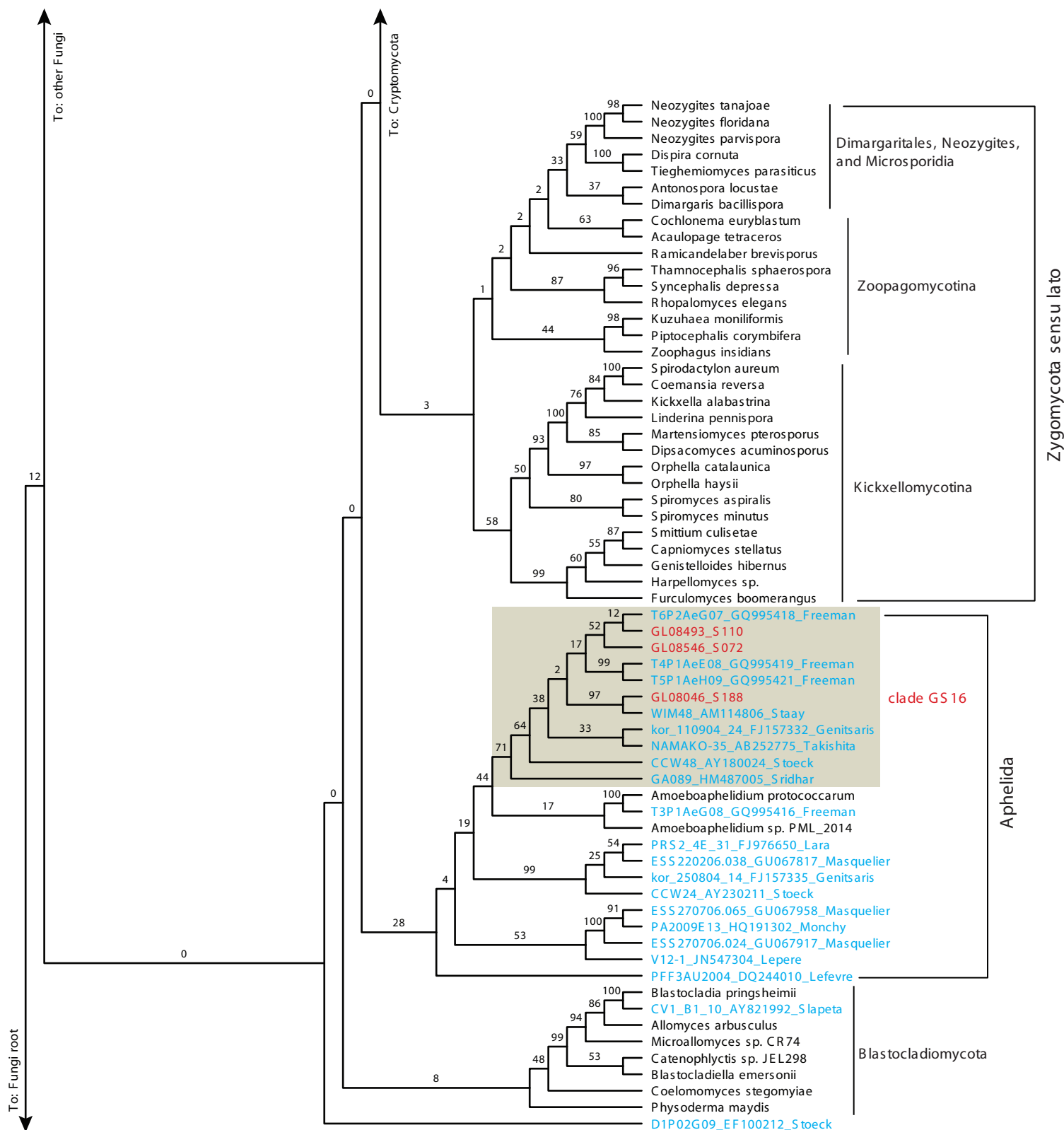


Figure S2.9

Figure S3. Phylogenetic placement of soil-inhabiting fungi among identified taxa and other sequences from the environment based on a full 28S rRNA gene Maximum Likelihood phylogram. Red, blue, and black fonts depict groups recovered here, in other environmental sequencing studies, and based on vouchered collections, respectively. Shaded clusters indicate prominent clades and branches discussed.

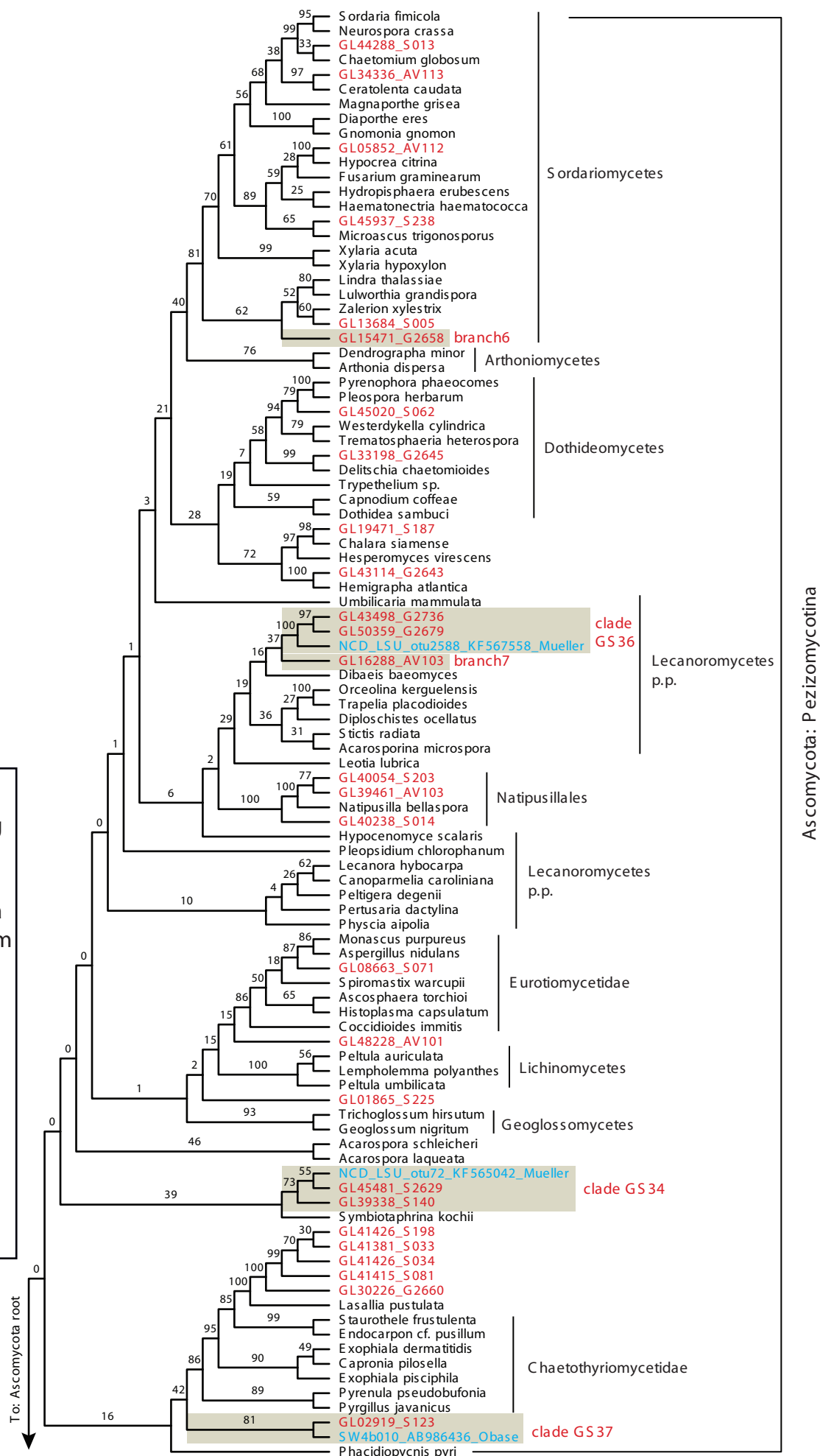


Figure S3.1

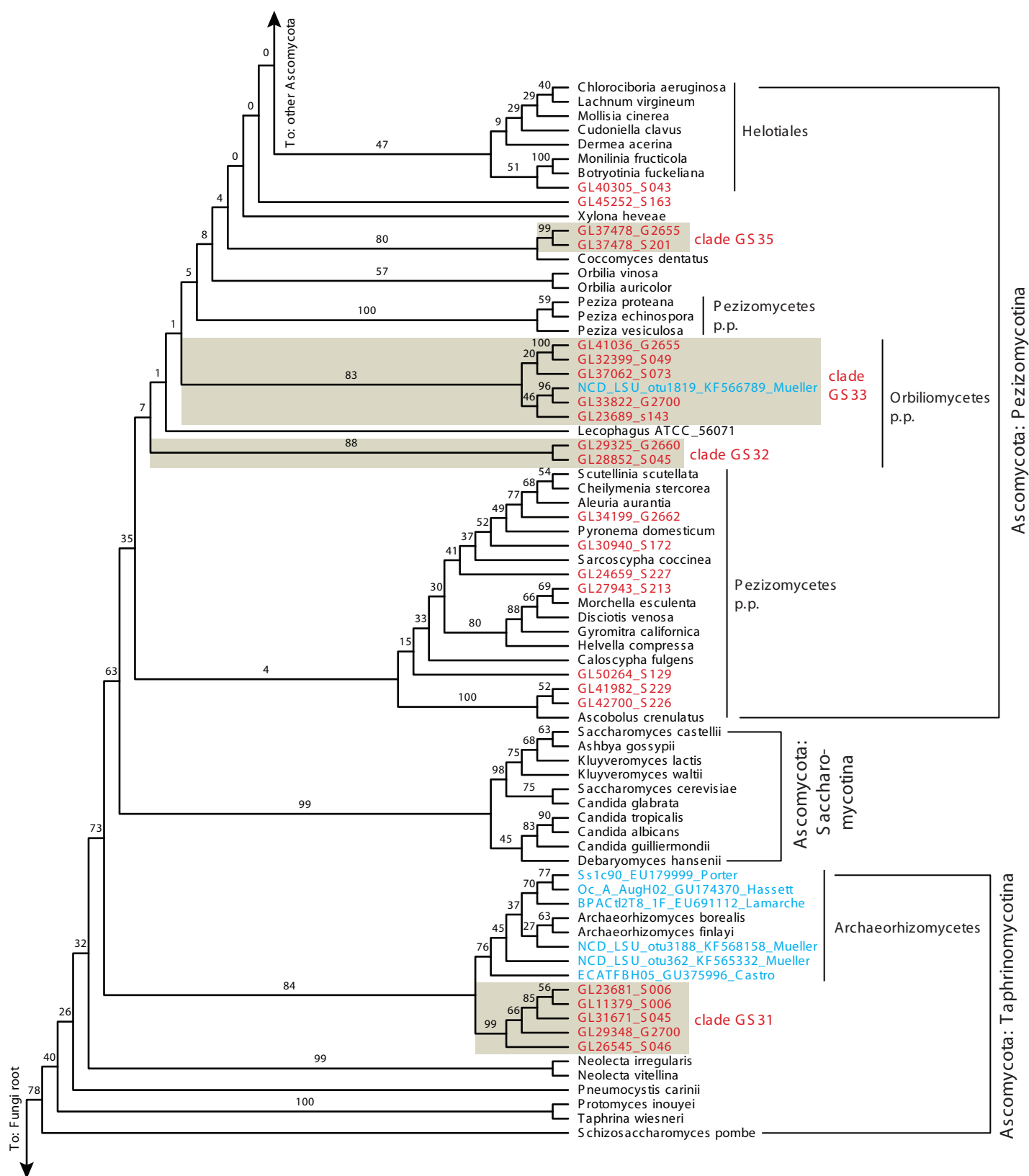


Figure S3.2

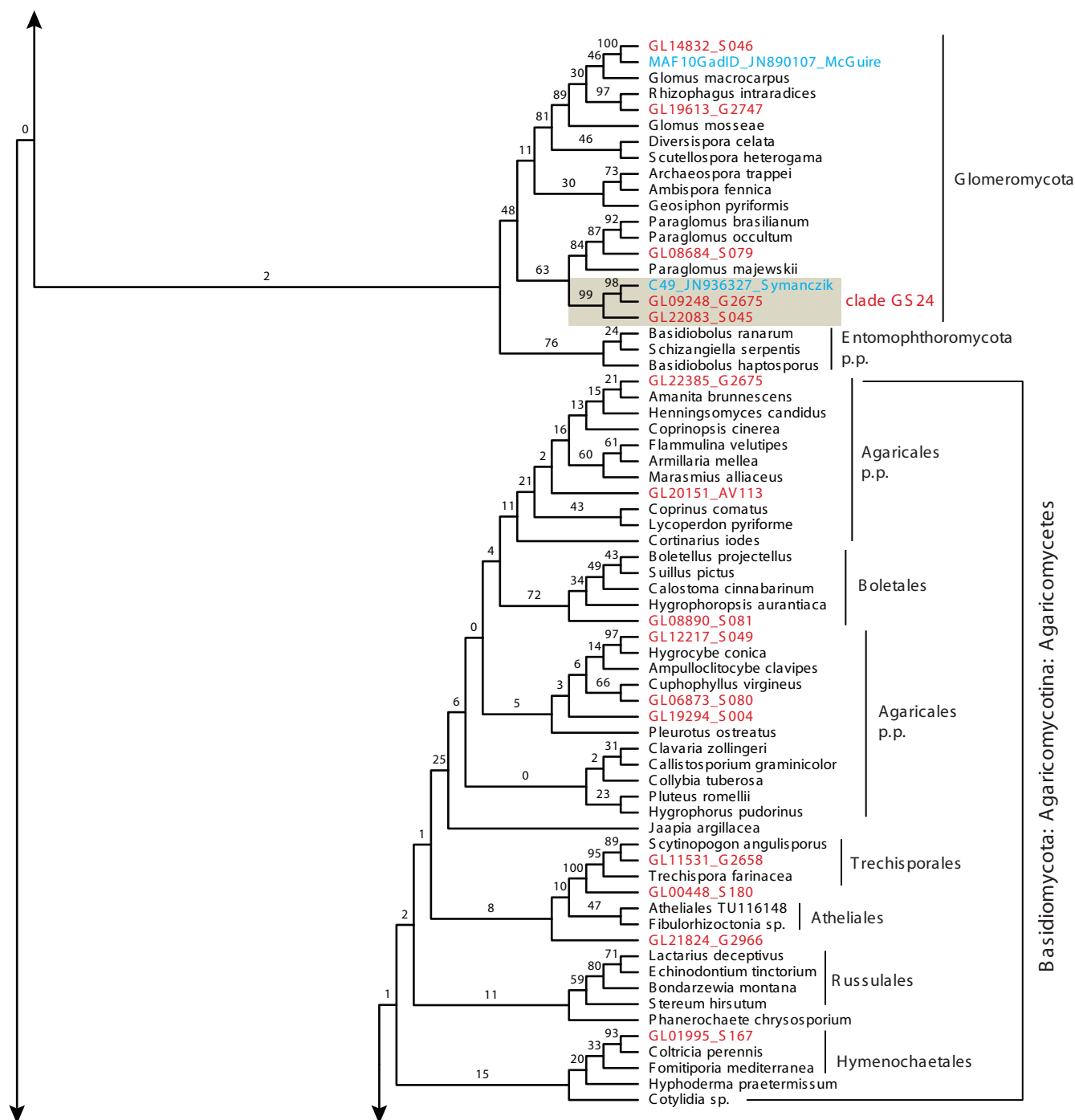


Figure S3.3



Figure S 3.4

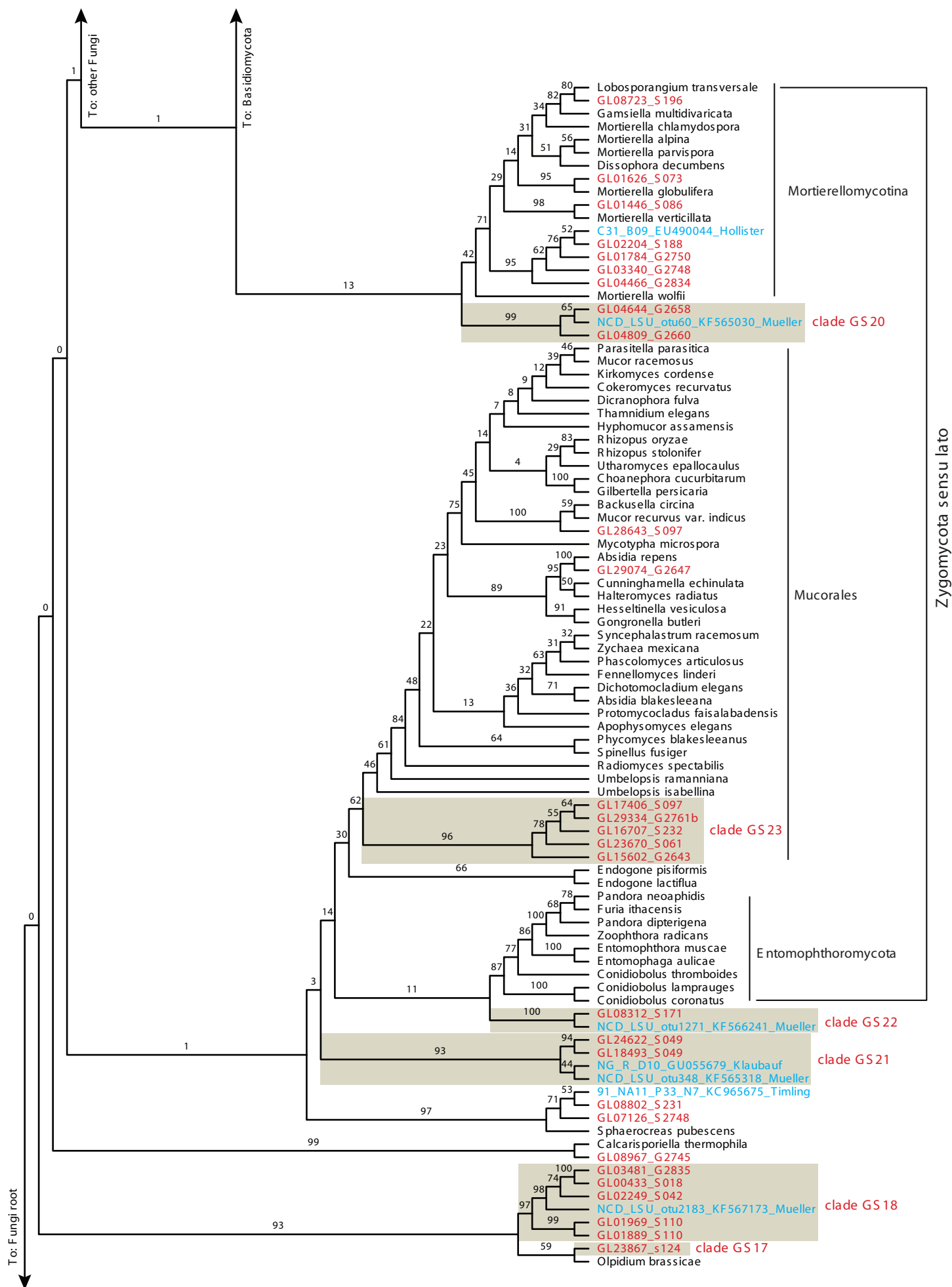
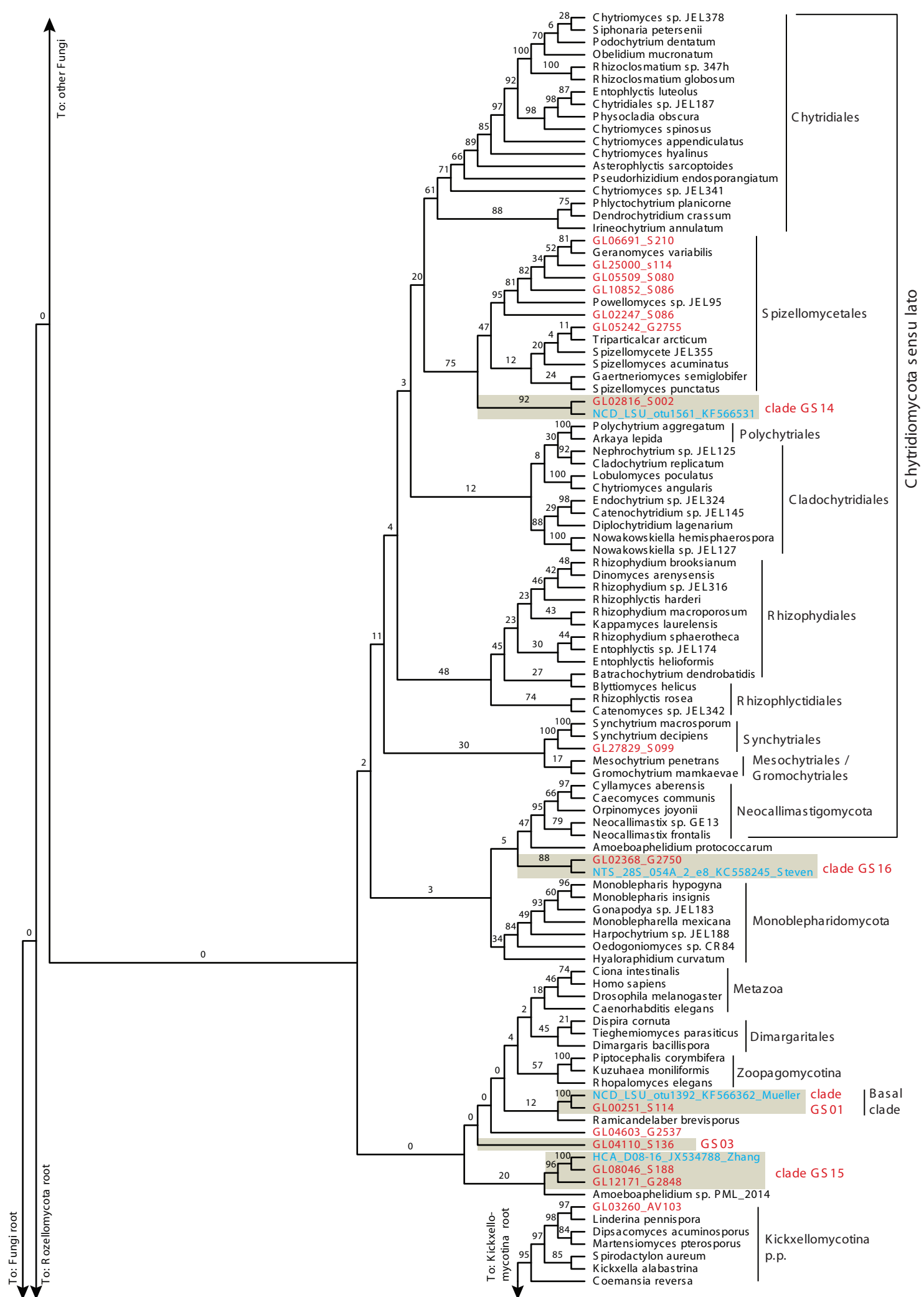


Figure S3.5



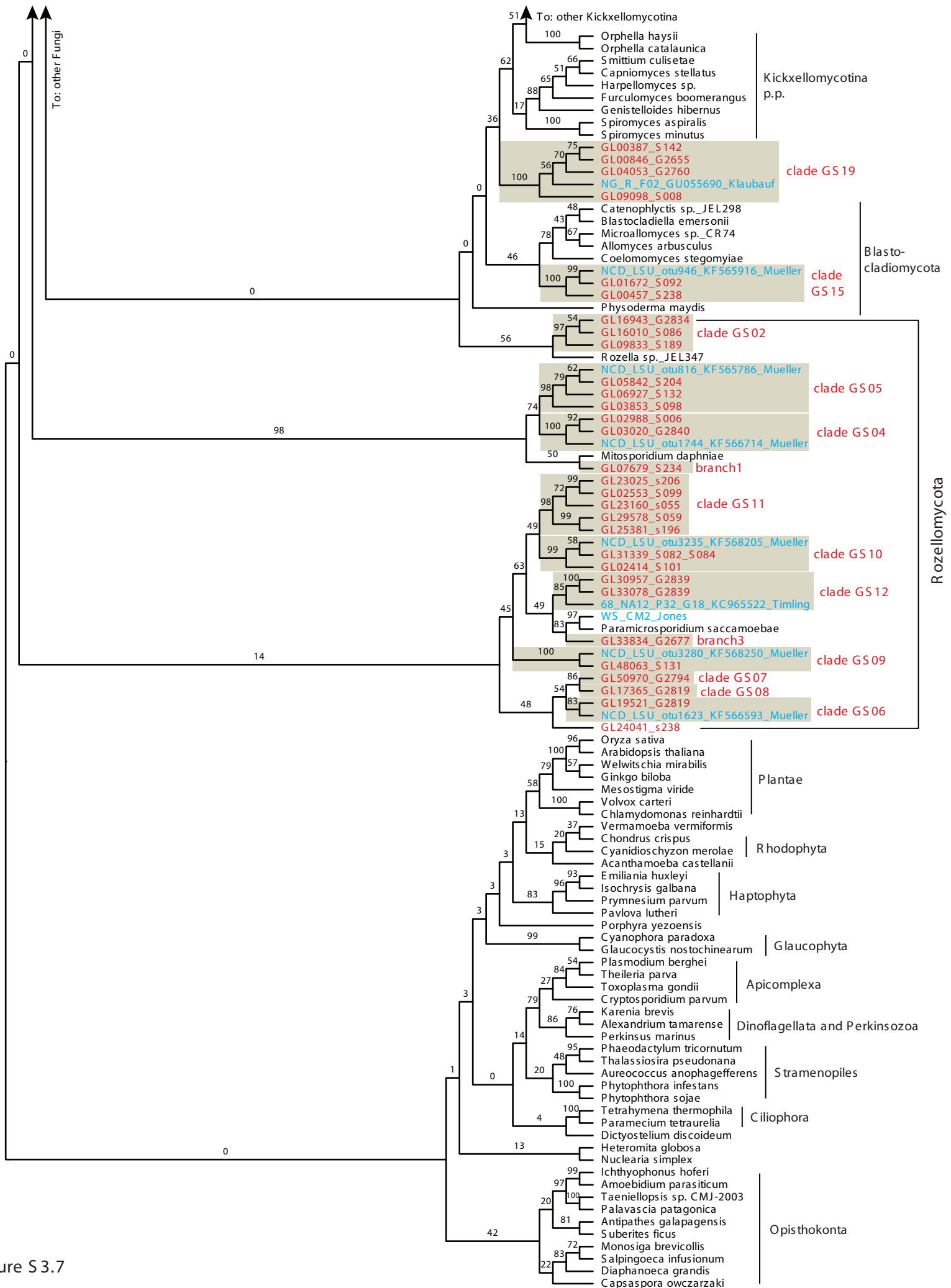


Figure S3.7

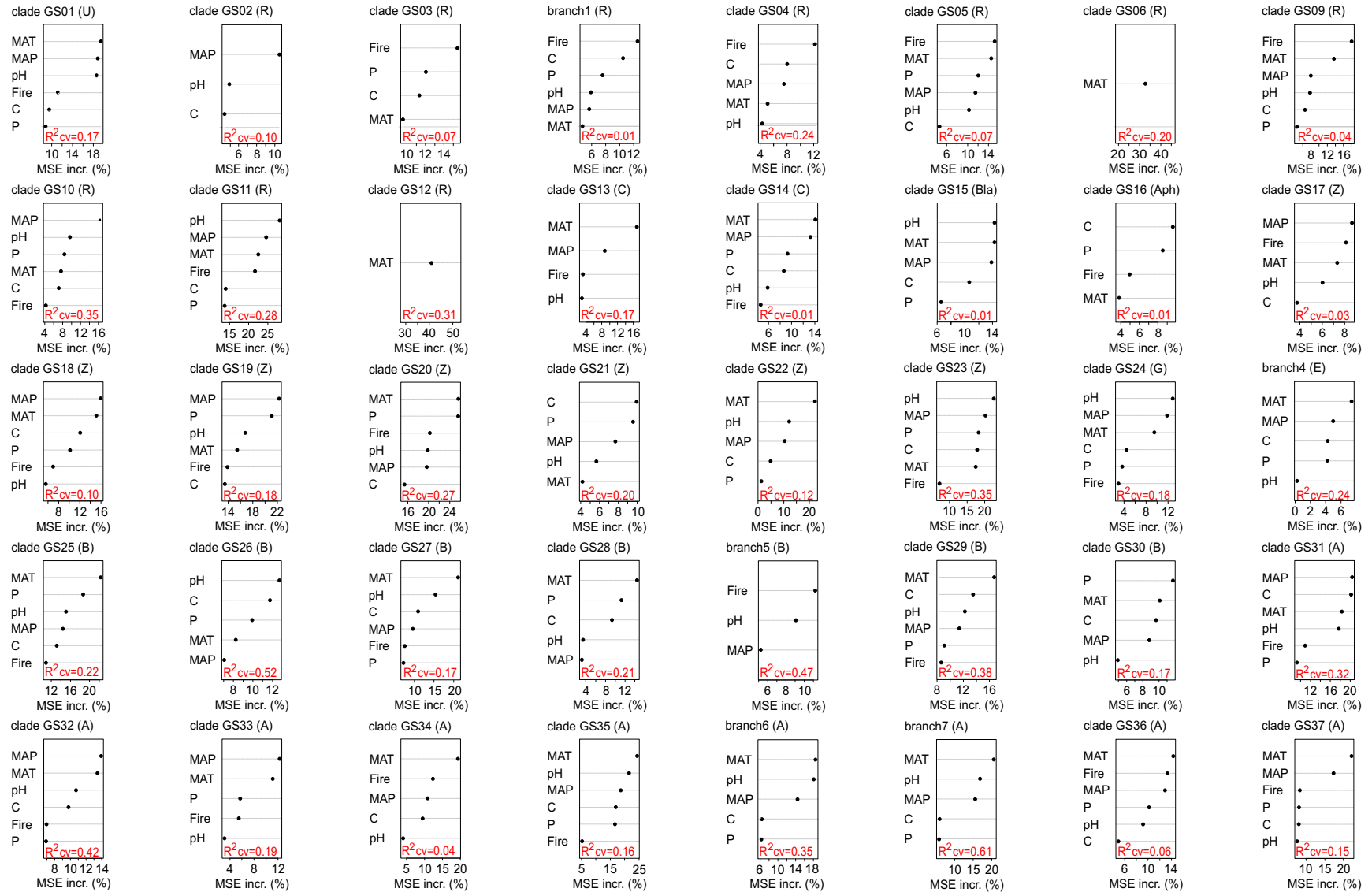


Figure S4. Best models of Random Forest machine learning-based niche analysis of fungal clades and prominent branches. The values on x-axis indicate increase in the mean square error (MSE, %). R^2_{cv} represents the cross-validation accuracy index. Clade GS08 is not shown, because none of the variables were included in the model. Clade GS07 and branches 2 and 3 were not tested, because these were represented by a single OTU. Names of phyla are abbreviated in parentheses: A, Ascomycota; Aph, Aphelidia; B, Basidiomycota; Bla, Blastocladiomycota; C, Chytridiomycota; E, Entorrhizomycota; G, Glomeromycota; R, Rozellomycota; Z, Zygomycota s.lat.; U, unassigned.

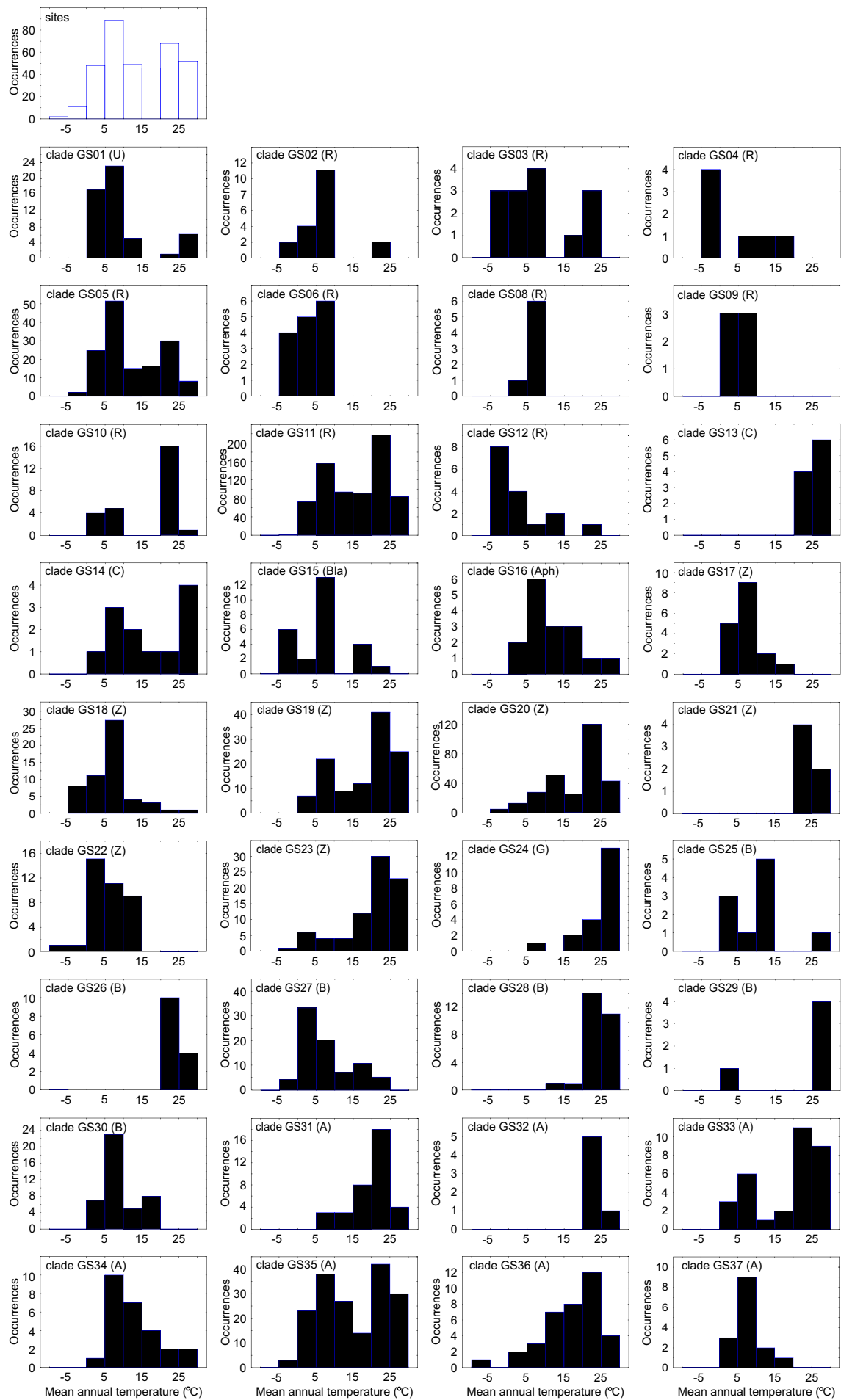


Figure S5. Histograms indicating the distribution of fungal clades (summed occurrences of OTUs) in sites with specified mean annual temperature. The upleft graph indicates the climatic coverage of study sites (null distribution). Names of phyla are abbreviated in parentheses: A, Ascomycota; Aph, Aphelida; B, Basidiomycota; Bla, Blastocladiomycota; C, Chytridiomycota; E, Entorrhizomycota; G, Glomeromycota; R, Rozellomycota; Z, Zygomycota s.lat.; U, unassigned.

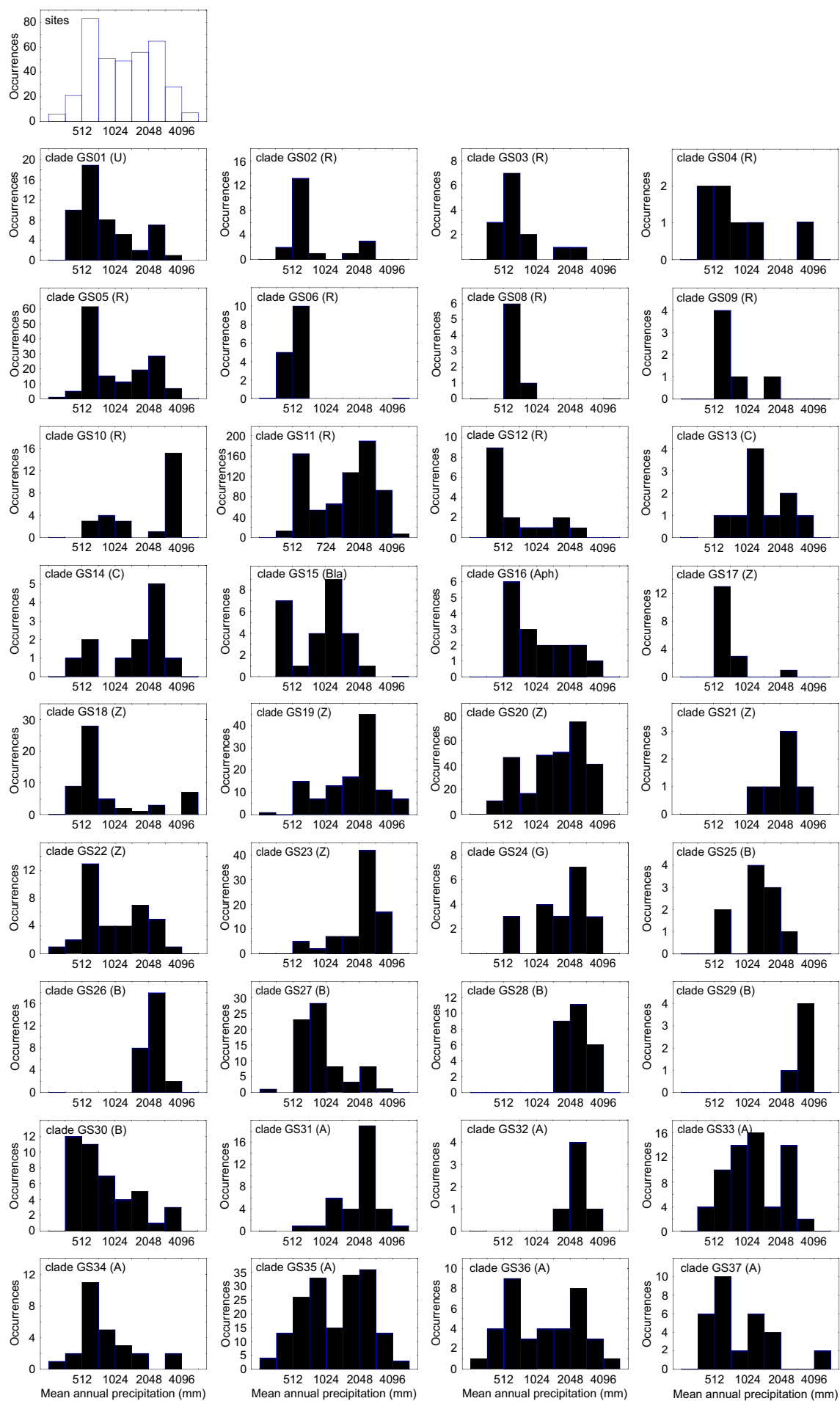


Figure S6. Histograms indicating the distribution of fungal clades (summed occurrences of OTUs) in sites with specified mean annual precipitation. The upleft graph indicates the climatic coverage of study sites (null distribution). Note the 2-base logarithmic scale. Names of phyla are abbreviated in parentheses: A, Ascomycota; Aph, Aphelida; B, Basidiomycota; Bla, Blastocladiomycota; C, Chytridiomycota; E, Entorrhizomycota; G, Glomeromycota; R, Rozellomycota; Z, Zygomycota s.lat.; U, unassigned.

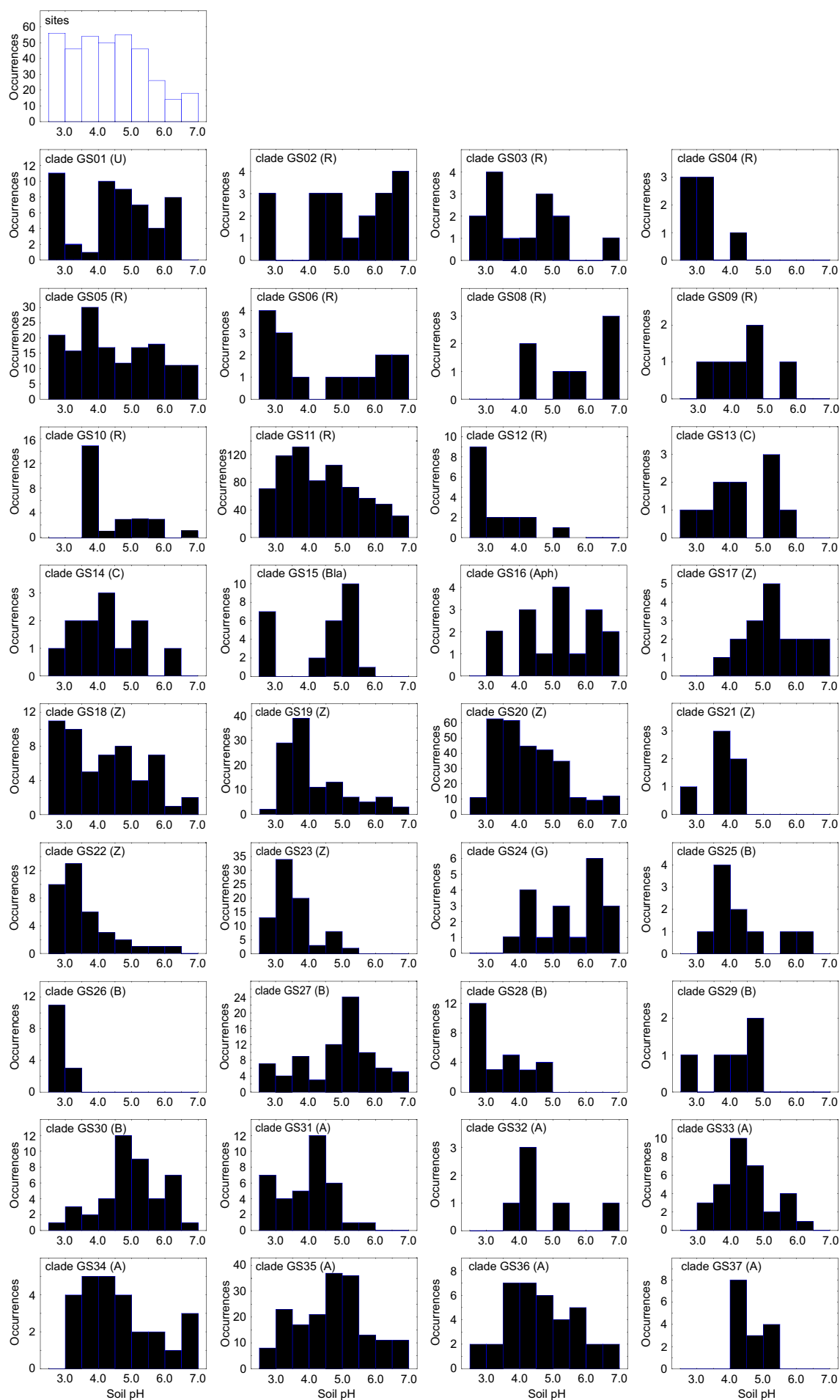


Figure S7. Histograms indicating the distribution of fungal clades (summed occurrences of OTUs) in sites with specified soil pH. The upleft graph indicates the pH coverage of study sites (null distribution). Names of phyla are abbreviated in parentheses: A, Ascomycota; Aph, Aphelida; B, Basidiomycota; Bla, Blastocladiomycota; C, Chytridiomycota; E, Entorrhizomycota; G, Glomeromycota; R, Rozellomycota; Z, Zygomycota s.lat.; U, unassigned.

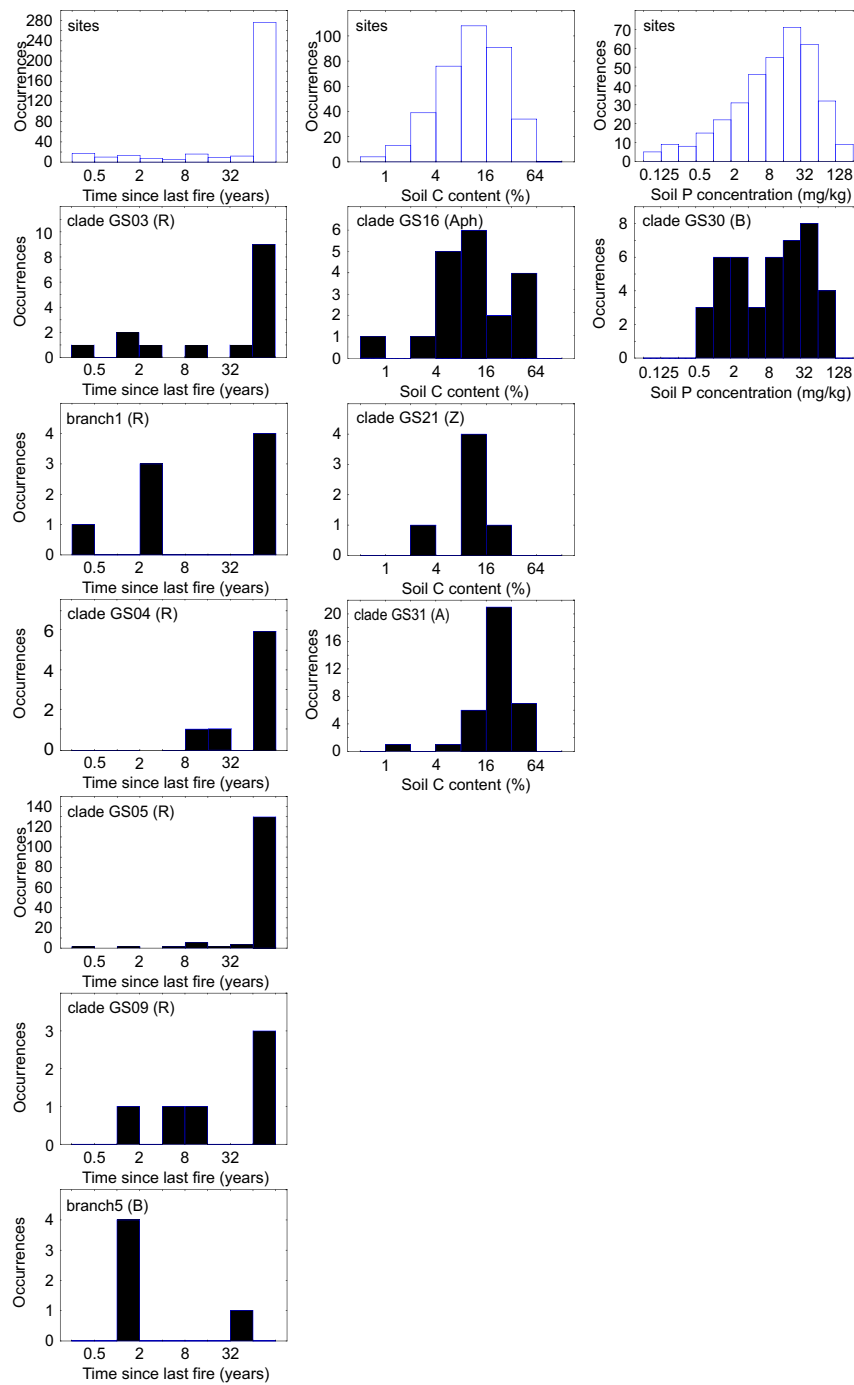


Figure S8. Histograms indicating the distribution of fungal clades (summed occurrences of OTUs) in sites with specified time since last fire (left panels), soil carbon content (central panels), and soil phosphorus concentration (right panels). The upmost diagrams indicates the distribution of these variables across all study sites (null distribution). Note the 2-base logarithmic scale. Names of phyla are abbreviated in parentheses: A, Ascomycota; Aph, Aphelida; B, Basidiomycota; Bla, Blastocladiomycota; C, Chytridiomycota; E, Entorrhizomycota; G, Glomeromycota; R, Rozellomycota; Z, Zygomycota s.lat.; U, unassigned.

Text S1. Profiles of undescribed clades and prominent branches of fungi.

Clade GS01

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014611 (habitat: site S114; Czech Republic; 49.0174 N/
13.4751 W; montane temperate coniferous forest dominated by *Picea abies*)
Contains other sequences: UDB014707, UDB014621, KF566362

Phylogenetic position: Along with an orphan sequence HQ191300 forms a sister group to the rest of the Fungi, albeit with no support. Group-specific 18S rRNA gene primers near the V9 subregion: fwd ACCGCCGTCGCTTTT; rev CTAAGCCATYCAATCGGAAA (specific positions underlined); several mismatches to ITS1F, ITS1, ITS2, and ITS3 primers

Ecological habitat: cool temperate climate over a wide pH range
Distribution: detected from most regions and biomes; strikingly more common in Europe and Southern South America

Other habitats: temperate forest soil in NC, USA (KF566362)

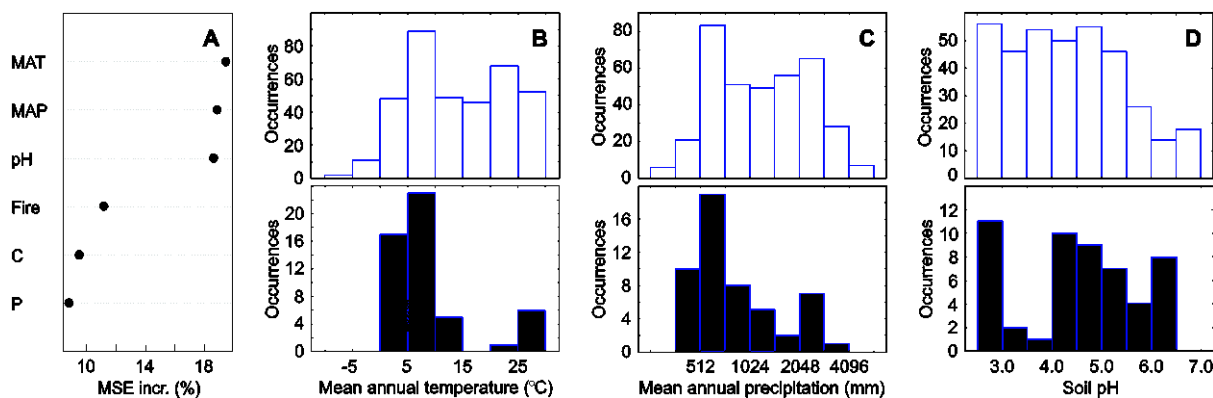


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS02

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_001709

Representative sequence: UDB014756 (habitat: site S189; BJ, China; 42.4292 N/128.1167 E); montane temperate coniferous forest dominated by *Pinus sylvestrisformis*)
Contains other sequences: UDB014795, UDB014794, GU067982, FJ976648

Phylogenetic position: a sister clade to the genus *Rozella* but with poor support. The sequences produced in this study form a well-supported monophyletic group.

Ecological habitat: prefers low to moderate rainfall and neutral and weakly acidic soils in temperate deciduous forests
Distribution: no significant trends but mostly found in Europe

Other habitats: freshwater lake (GU067982) and peat bog (FJ976648) in Europe

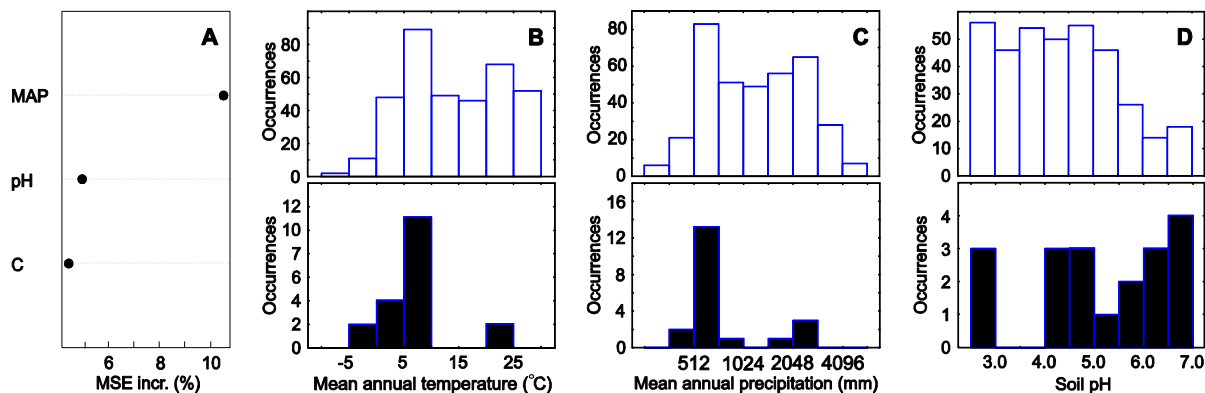


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS03

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014679 (habitat: site S136; Udmurtia, Russian Fed.; 57.1041 N/ 53.0757 E; boreal forest dominated by *Pinus sylvestris*)
Contains other sequences: AB695514

Phylogenetic position: one of the branches of Rozellomycota

Ecological habitat: relatively common in sites with recent fire. The clade tends to be more frequent in relatively cold habitats such as tundra and boreal forest biomes. Other studies suggest widespread distribution in saltwater, freshwater, and anoxic habitats. both in extremely cold and hot ecosystems.

Distribution: present in most regions

Other habitats: Antarctic freshwater lake (AB695514)

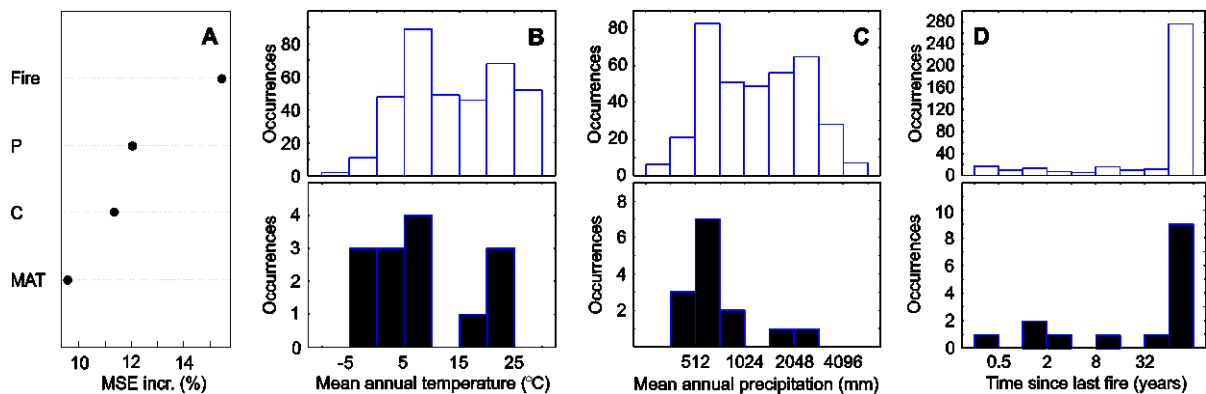


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average time since last fire relative to all studied soils (upper panels).

Branch1

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014728 (habitat: site S234; Finland; 69.1691 N/
26.9992 E; southern tundra dominated by dwarf *Betula pubescens*)
Contains other sequences: -

Phylogenetic position: A single deep branch within Rozellomycota

Ecological habitat: tolerates recent fire and cold; mostly found in tropical habitats.
Distribution: most frequent in Central America.

Other habitats: -

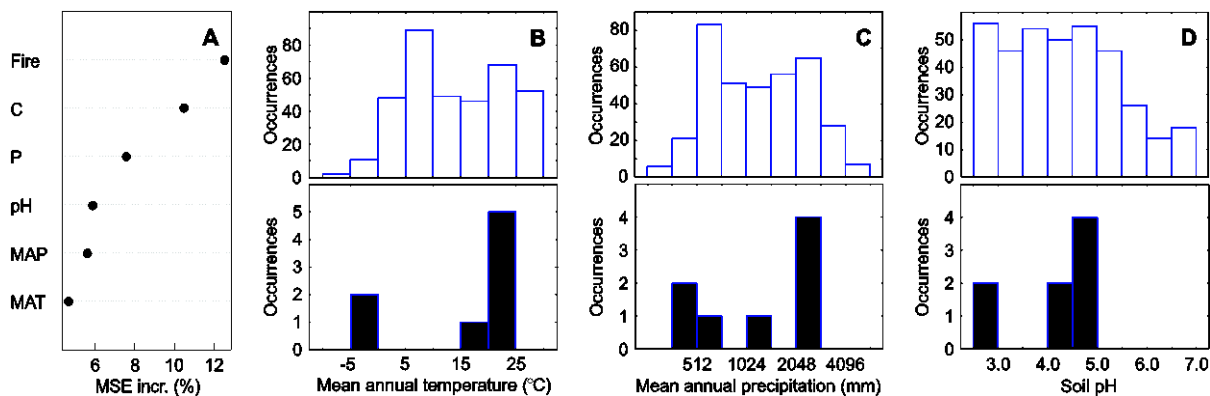


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS04

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014664 (habitat: site G2840; Finland; 68.0636 N/
24.0339 E; mountain tundra dominated by *Betula nana*)
Contains other sequences: UDB014656, UDB014663, AB534337, KF566714

Phylogenetic position: one of the groups related to Mitosporidium within Rozellomycota

Ecological habitat: tends to be most abundant in the tundra biome in high-carbon soils
Distribution: present in cold and temperate habitats of the Northern and Southern Hemisphere

Other habitats: agricultural soil in Japan (AB534337), temperate forest soil in NC, USA (KF566714)

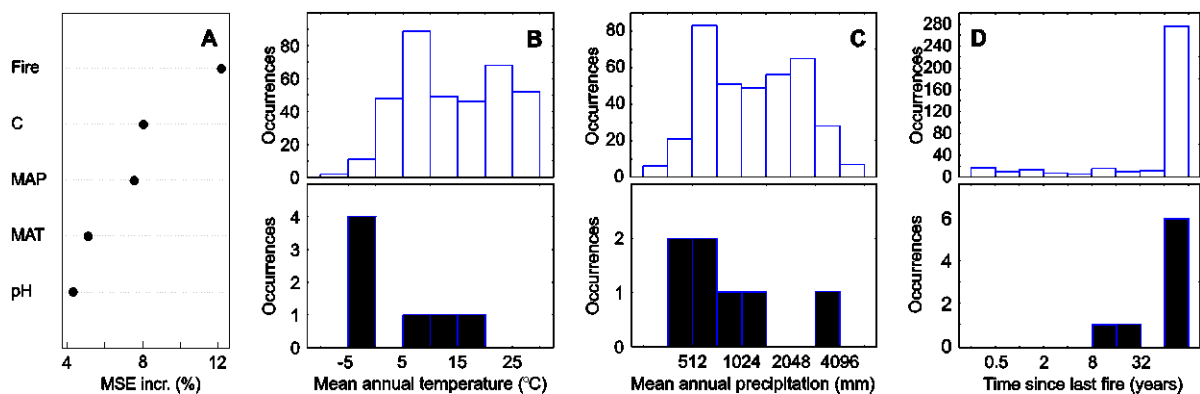


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil C content relative to all studied soils (upper panels).

Clade GS05

Previous names for the clade: LKM15 (van Hannen et al. 1999, Appl. Environ. Microbiol. 65: 2478; Panzer et al. 2015, PLoS ONE: e0134377)

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014721 (habitat: site S132; VO, Russia; 51.9557 N/ 39.4676; temperate coniferous forest dominated by *Pinus sylvestris*)

Contains other sequences: UDB014673, UDB014705; AF372718, AF372717, AJ130850, EF023121, EF023117, EU910604, HM487053, HM487011, KF565786

Phylogenetic position: one of the groups related to *Mitosporidium* within Rozellomycota

Ecological habitat: frequent in all biomes, especially temperate deciduous forests; not observed in tundra; wide pH tolerance; relatively more common in unburnt sites.

Distribution: frequent in all ecoregions, especially in Europe and West Asia, but relatively less common in the Southern Hemisphere. Other studies have recovered it from lake and marine sediments and water.

Other habitats: amphipod feces (HM487053, HM487011), soil in deciduous forests of USA (HM487..., KF565786), temperate marine sediments (AF372...), temperate lake sediments (EU910604), and freshwater mesocosms (AJ130850)

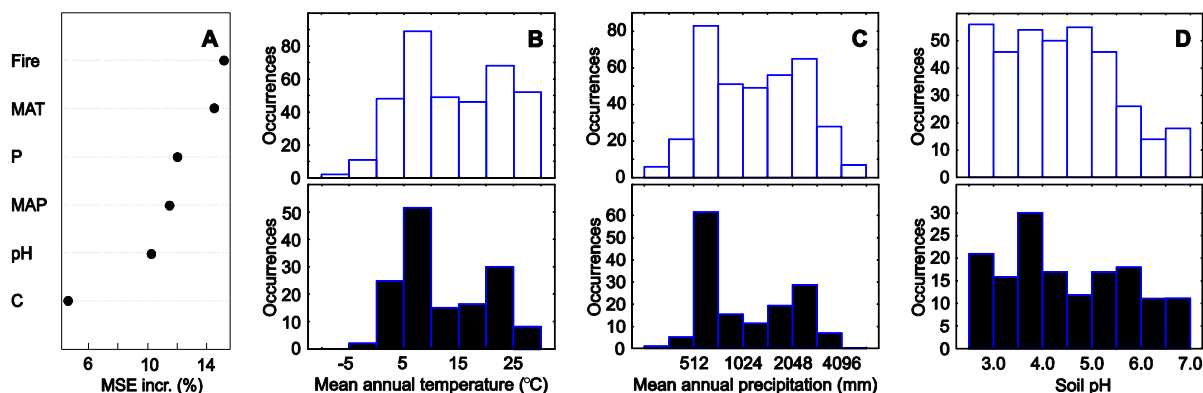


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS06

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

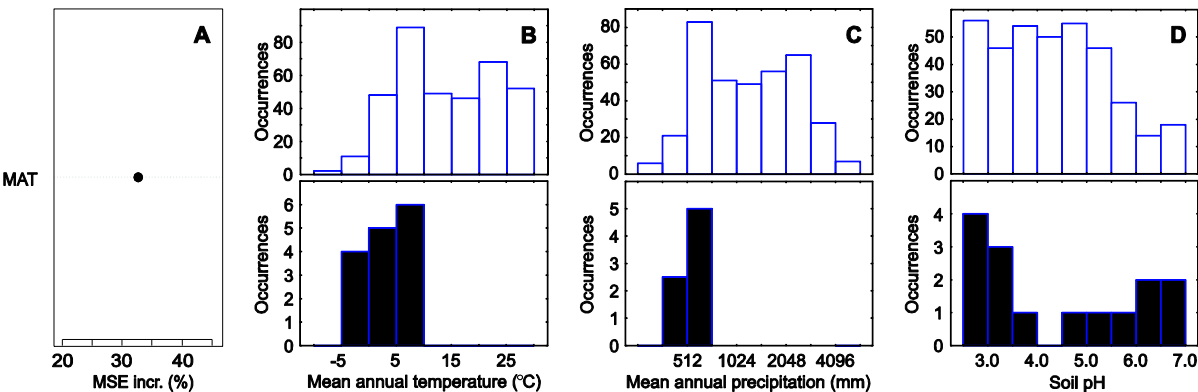
Representative sequence: UDB014815 (habitat: site G2819; Estonia; 58.2341 N/
22.4411 E; overgrown temperate woodland dominated by *Quercus robur*)
Contains other sequences: UDB014850, KF566593

Phylogenetic position: a clade within a large group of unidentified Rozellomycota

Ecological habitat: found mainly in boreal forest and tundra ecosystems across a wide range of soil pH.

Distribution: found only in Europe but also in North America based on another study.

Other habitats: temperate forest soil in NC, USA (KF566593)



Clade GS07

Previous names for the clade: -

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014956 (habitat: site G2794; Estonia; 58.4865 N/ 22.8318 E; moderately grazed woodland dominated by *Corylus avellana*)

Contains other sequences: GQ995417

Phylogenetic position: a clade within a large group of unidentified Rozellomycota

Ecological habitat: probably very broad but not tested, because this clade was represented by a single OTU in this study

Distribution: Represented by a single widespread OTU with distribution in Europe, Southern South America, and Central Africa

Other habitats: alpine tundra soil from CO, USA, or Nepal (not specified by the sequence authors; GQ995417)

Clade GS08

Previous names for the clade: -

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014958 (habitat: site G2819; Estonia; 58.2341 N/ 22.4411 E; overgrown temperate woodland dominated by *Quercus robur*)

Contains other sequences: FM178232

Phylogenetic position: a clade within a large group of unidentified Rozellomycota

Ecological habitat: no significant patterns; the clade is distributed in the cool temperate coniferous and deciduous forests.

Distribution: known only from Europe and East Asia.

Other habitats: aerobic sludge granules in Central Europe (FM178232)

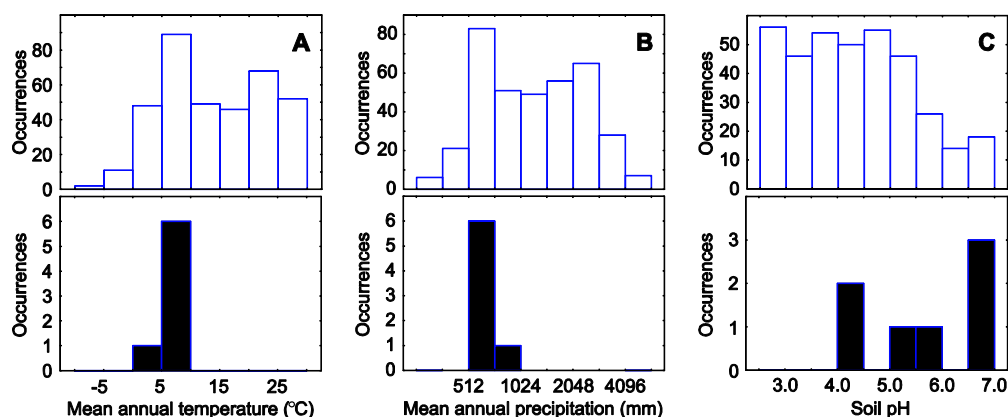


Figure. Niche analysis of the clade. A-C. Distribution of clade members (lower panels) in sites with (A) different mean annual temperature, (B) mean annual precipitation, and (C) average soil pH relative to all studied soils (upper panels).

Clade GS09

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014949 (habitat: site S131; VO, Russia; 51.9107 N/39.4572; temperate coniferous forest dominated by *Pinus sylvestris*)
Contains other sequences: KF568250

Phylogenetic position: A deeply branching clade within Rozellomycota

Ecological habitat: occurs both in fire-disturbed habitats and unburnt sites; narrow temperature range in cool temperate habitats.
Distribution: all continents of the Northern Hemisphere

Other habitats: temperate forest soil in NC, USA (KF568250)

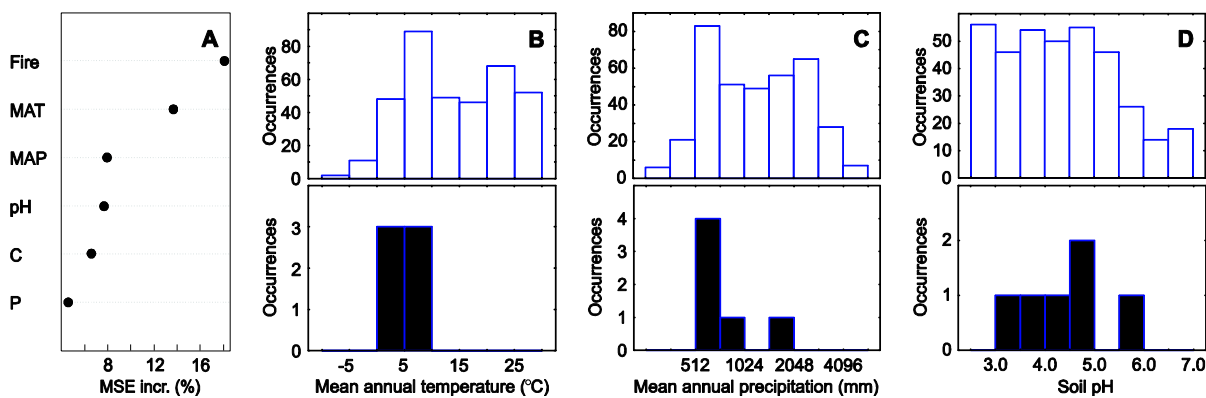


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS10

Previous names for the clade: -

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014882 (habitat: site S084; Argentina; 40.1411 S/ 71.4692 W; montane temperate deciduous forest dominated by *Nothofagus obliqua*)
Contains other sequences: UDB014651, KF568205, AF372716, AY916638, AY916644, JN054654, EF024044, EF023474, EU091852

Phylogenetic position: One of the lineages of Rozellomycota

Ecological habitat: the frequency of taxa related to UDB014882 peaks in cool temperate climate and near-neutral soils, whereas OTUs related to UDB014651 are distinctly more common in acidic soils in tropical climate. Other studies suggest frequent occurrence in freshwater. Probably very wide ecological amplitude.

Distribution: both tropical and cool temperate habitats in both hemispheres

Other habitats: temperate forest soil in USA (KF568205, EF024...), temperate lake sediments in USA and the Netherlands, (AF372716, EU091852), sulphide-rich spring in USA (AY916...), and aerated activated sludge in Australia (JN054654)

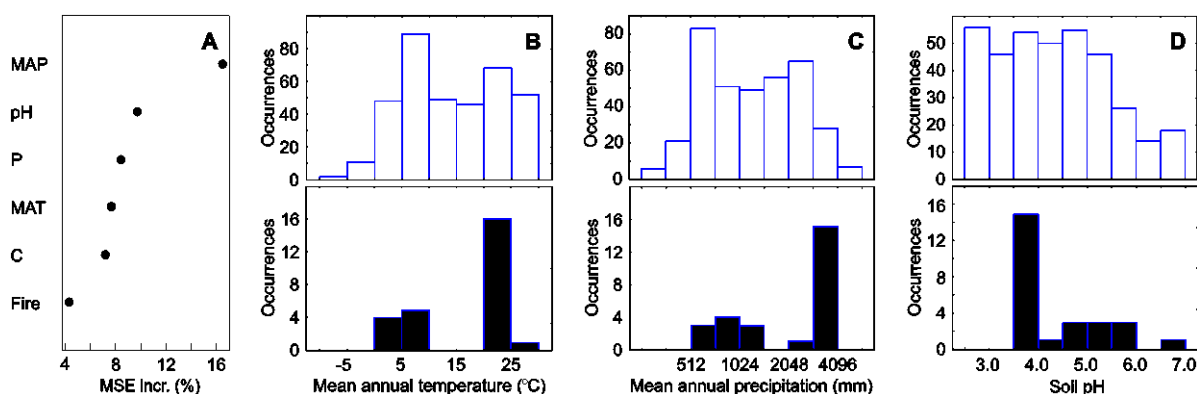


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS11

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_003716, UCL7_007517

Representative sequence: UDB014836 (habitat: site S206; Q, Australia; 28.2733 S/
153.1724 E; warm temperate forest dominated by *Nothofagus moorei*)
Contains other sequences: UDB014654, UDB014838, UDB014856, UDB014876,
AJ506016, AJ506030, EU091829, EU091851, GU568155, HM487051

Phylogenetic position: a compact lineage within Rozellomycota with no long branches

Ecological habitat: widely distributed in all biomes except tundra; especially common in
tropical lowland and montane rain forests and temperate deciduous forests; a wide pH
range with an optimum at low and medium-low values, but tends to avoid pH<3.
Distribution: world-wide distribution but strikingly less common in southern South
America.

Other habitats: amphipod feces (HM487051), temperate agricultural soil (GU568155,
AJ506016, AJ506030), and lake sediments (EU091829, EU091851)

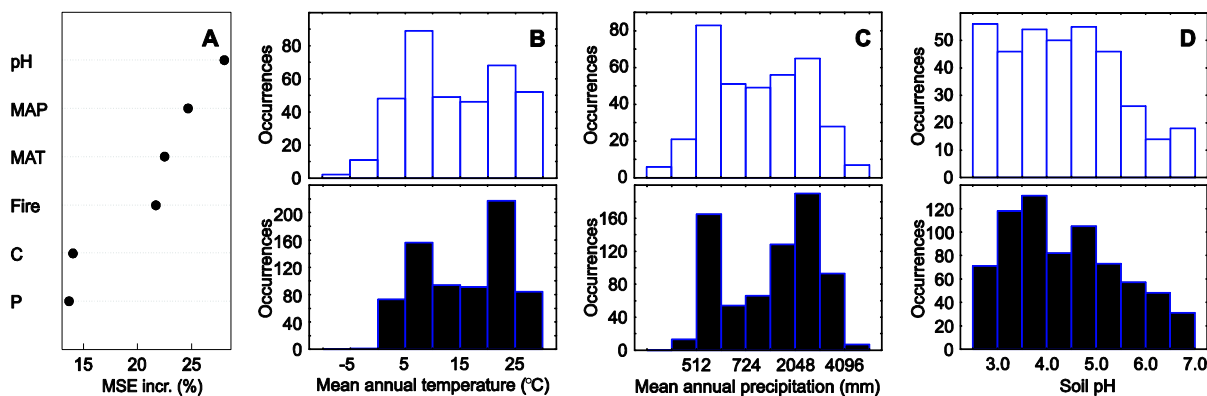


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch2

Previous names for the clade: -

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014923 (habitat: site G2732; Papua New Guinea; 5.9305 S/ 145.0333 W; tropical montane forest dominated by *Lithocarpus* spp.)

Contains other sequences: -

Phylogenetic position: a single long branch within Rozellomycota

Ecological habitat: too rare to evaluate

Distribution: A single rare OTU distributed in Estonia and Papua New Guinea

Other habitats: -

Clade GS12

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014881 (habitat: site G2839; Norway; 70.1473 N/ 24.7869 E; the northernmost natural *Pinus sylvestris*-dominated boreal forest)
Contains other sequences: UDB014889, KC965522

Phylogenetic position: One of the lineages of Rozellomycota

Ecological habitat: mostly boreal forest and tundra ecosystems with relatively cool climate and acidic soils
Distribution: mostly northern parts of Europe, Asia, and North America; almost missing in lowland tropical habitats

Other habitats: North American tundra (KC965522)

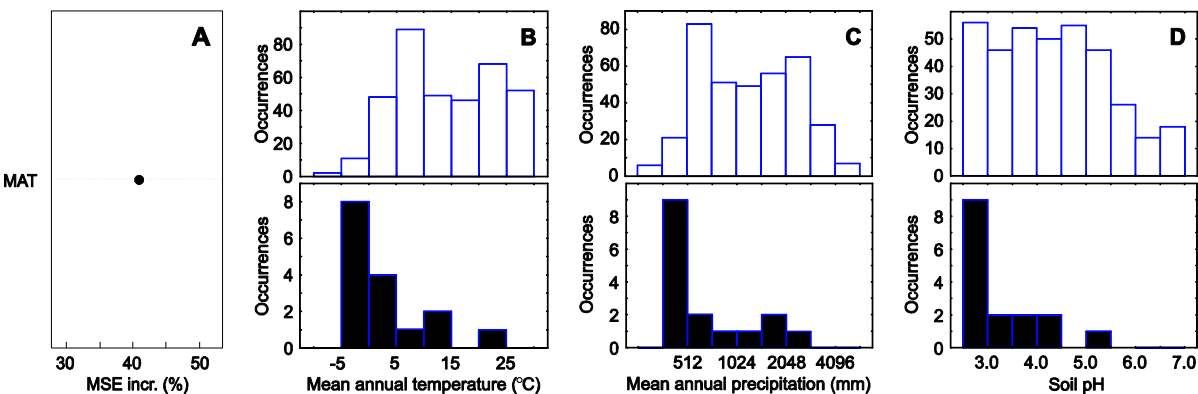


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch3

Previous names for the clade: -

Corresponding PlutoF compound cluster: -

Representative sequence: UDB014895 (habitat: site G2677; Papua New Guinea; 6.0173 S; 145.4160 E; tropical montane forest dominated by Lauraceae)

Contains other sequences: -

Phylogenetic position: a single long branch within Rozellomycota

Ecological habitat: too rare to evaluate

Distribution: a single OTU found twice in tropical montane forests of New Guinea

Other habitats: -

Clade GS13

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014895 (habitat: site G2750; NT, Australia; 13.7655 S/
131.4395 E; alluvial dry tropical forest dominated by *Melaleuca* sp.)
Contains other sequences: DQ244008, KC558245

Phylogenetic position: one of the lineages within Chytridiomycota *s. lat.*

Ecological habitat: narrow niche for high-temperature over wide pH and precipitation ranges
Distribution: most common in Australian dry tropical forests and savannas

Other habitats: lake water in France (DQ244008); desert soil in ID, USA (KC558245)

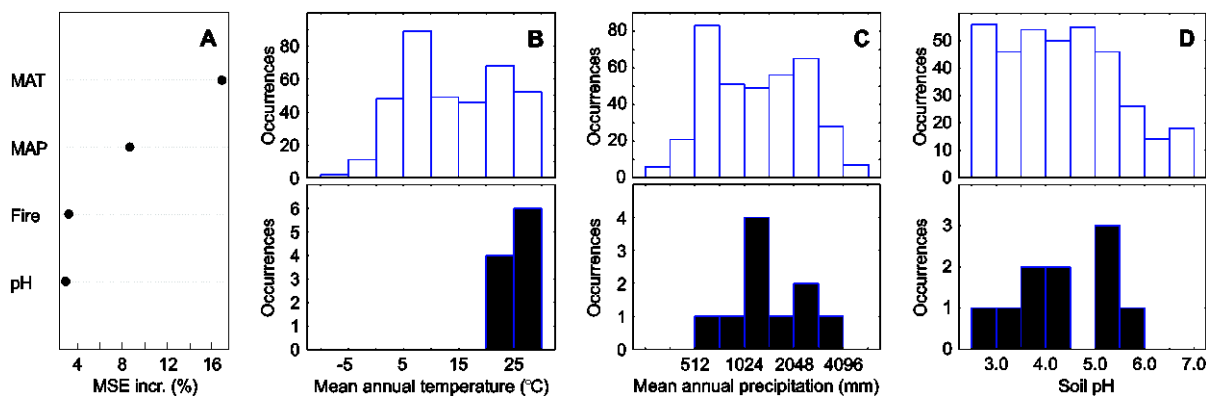


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS14

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_005854

Representative sequence: UDB014658 (habitat: site S002; Madagascar; 24.9514 S/
47.0001 E; dry tropical forest dominated by *Sarcolaena* spp.)
Contains other sequences: KF566531

Phylogenetic position: A well-supported sister group of Spizellomycetales within
Chytridiomycota *s.str.*

Ecological habitat: tends to be more common in relatively warm and wet climate,
moderately acid soil; found in all biomes except boreal forests and tundra
Distribution: present in most regions; tends to be more common in Southern Hemisphere

Other habitats: temperate forest soil in NC, USA (KF566531)

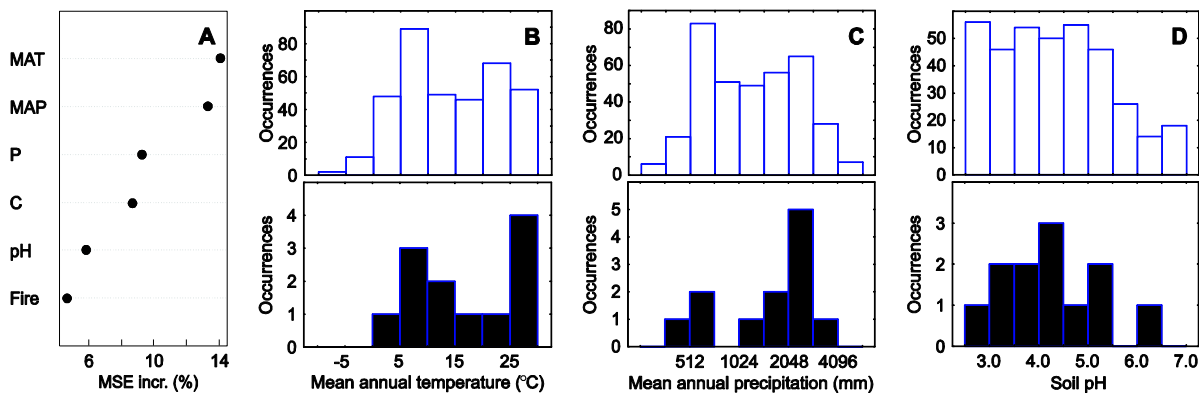


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS15

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014619 (habitat: site S238; Finland; 68.9678 N/
20.9432 E; mountain tundra dominated by dwarf *Betula pubescens*)
Contains other sequences: UDB014635, UDB014631, KF565916

Phylogenetic position: a sister group to Blastocladales

Ecological habitat: non-tropical biomes; two distinct pH optima at low pH and nearly neutral soils
Distribution: mostly Southern South America but present in Australia, Europe, and Central America

Other habitats: temperate forest soil of NC, USA (KF565916)

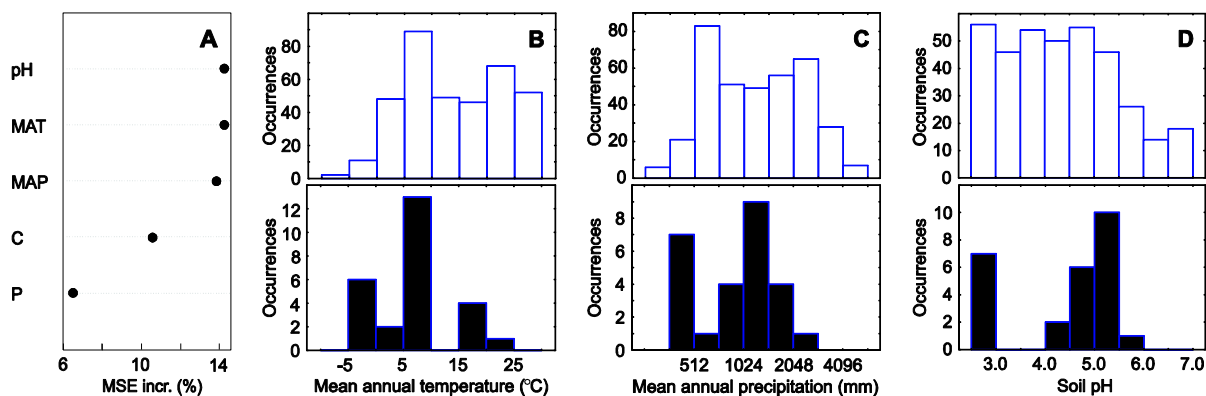


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS16

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014729 (habitat: site S188; BJ, China; 42.3841 N/128.0935 E; montane temperate deciduous forest dominated by *Quercus mongolica*)
Contains other sequences: UDB014777, UDB014731, UDB014732, HM487005, AY180024, AB252775, GQ995421, GQ995419, GQ995418, FJ157332, AM114806, JX534788

Phylogenetic position: nested within Aphelidea forming a monophyletic group including multiple sequences of uncultured fungi

Ecological habitat: mostly temperate soils with high C content; wide pH amplitude
Distribution: present in most ecoregions with no trends; very wide ecological amplitude based on other studies

Other habitats: amphipod feces (HM487005), freshwater (FJ157332), marine sediments (AY180024), salt lake sediments (AB252775), tundra soil of Co, USA and/or Nepal (GQ995...), temperate agricultural soil in the Netherlands and China (AM114806, JX534788)

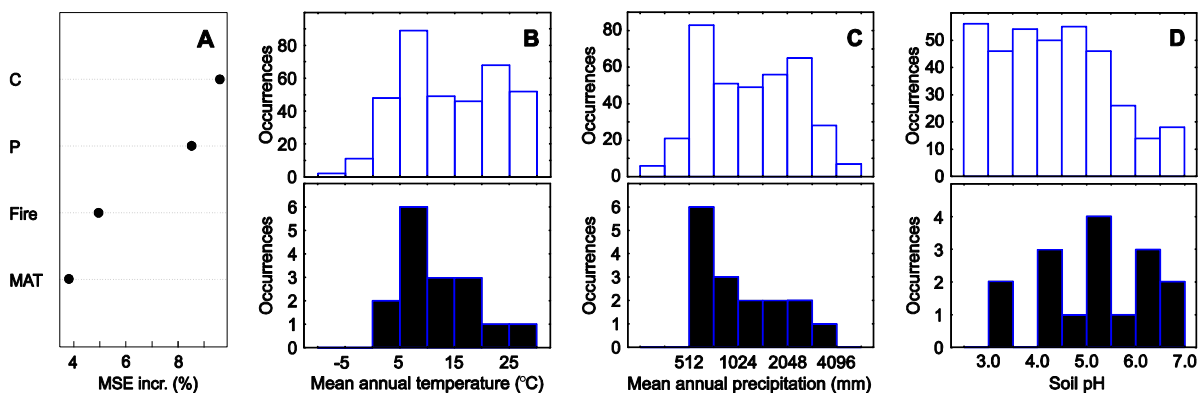


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS17

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014847 (habitat: site S124; Italy; 37.8747 N/ 14.0158 E; montane temperate deciduous forest dominated by *Fagus sylvatica*)
Contains other sequences: KC671706

Phylogenetic position: one of the two well-supported sister lineages to Olpidiales

Ecological habitat: temperate forest soils with moderate precipitation and weakly acidic pH
Distribution: known only from the Northern Hemisphere

Other habitats: human skin (KC671706)

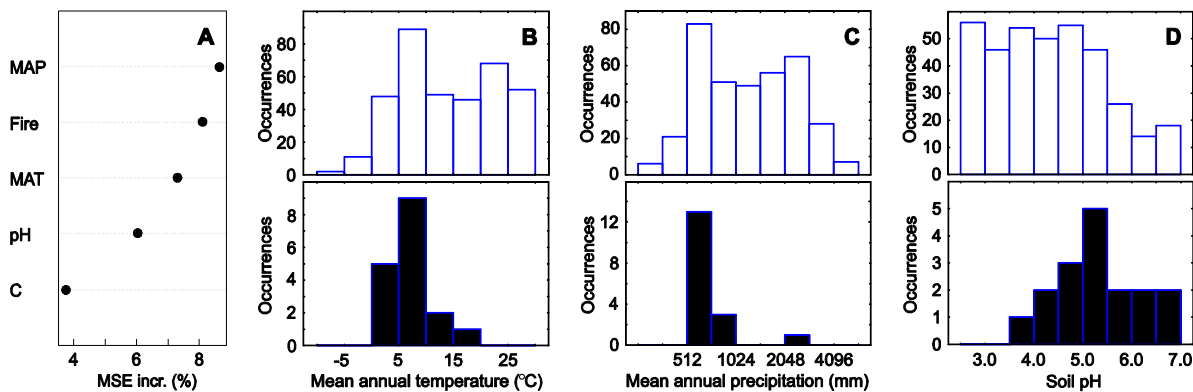


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS18

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_008108

Representative sequence: UDB014671 (habitat: site G2835; Sweden; 68.2259 N/ 21.9452 E; northern boreal forest dominated by *Pinus sylvestris*)
Contains other sequences: UDB014615, UDB014640, UDB014641, UDB014647, UDB014671, KF567173

Phylogenetic position: one of the two well-supported sister lineages to Olpidiales

Ecological habitat: prefers boreal and temperate coniferous forests with moderate precipitation and strongly to moderately acidic pH
Distribution: by far most common in temperate Eurasia

Other habitats: temperate forest soils in NC, USA (KF567173)

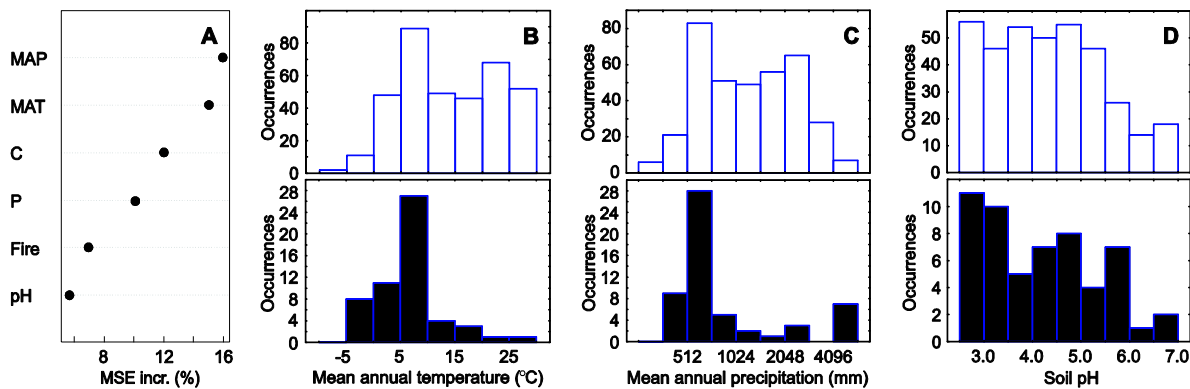


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS19

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_009149

Representative sequence: UDB014747 (habitat: site S008; Madagascar; 22.5615 S/
45.3810 E; dry subtropical savanna dominated by *Sarcolaena* spp.)
Contains other sequences: UDB014614, UDB014678, GU055690

Phylogenetic position: An isolated lineage among zygomycetes *s.lat.*

Ecological habitat: preferential occurrence in humid tropical climate (especially tropical
rain forests and dry forests) at low soil pH
Distribution: found in nearly all ecoregions; particularly common in SE Asia.

Other habitats: agricultural soil in Austria (GU055690)

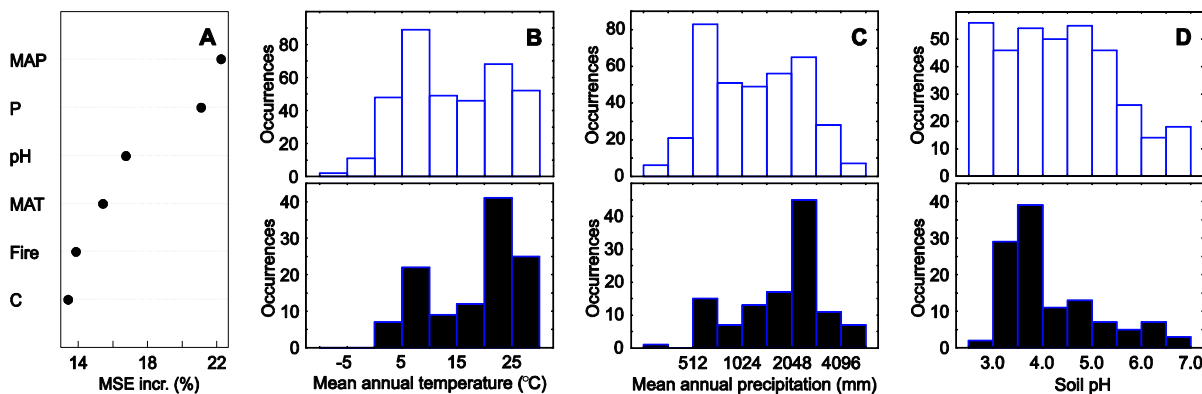


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS20

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_006587

Representative sequence: UDB014697 (habitat: site G2660; Papua New Guinea; 9.4218 S/ 147.3692 E; tropical lowland rain forest with no dominant trees)
Contains other sequences: UDB014694, KF565030
Phylogenetic position: one of the basal lineages of Mucoromycotina, with unsupported relationship to Endogonales

Ecological habitat: widely distributed especially in tropical climate (rain forest and savanna habitats) in strongly to moderately acidic soils with relatively low P concentration.
Distribution: found in all regions, except New Zealand

Other habitats: temperate forest soil in NC, USA (KF565030)

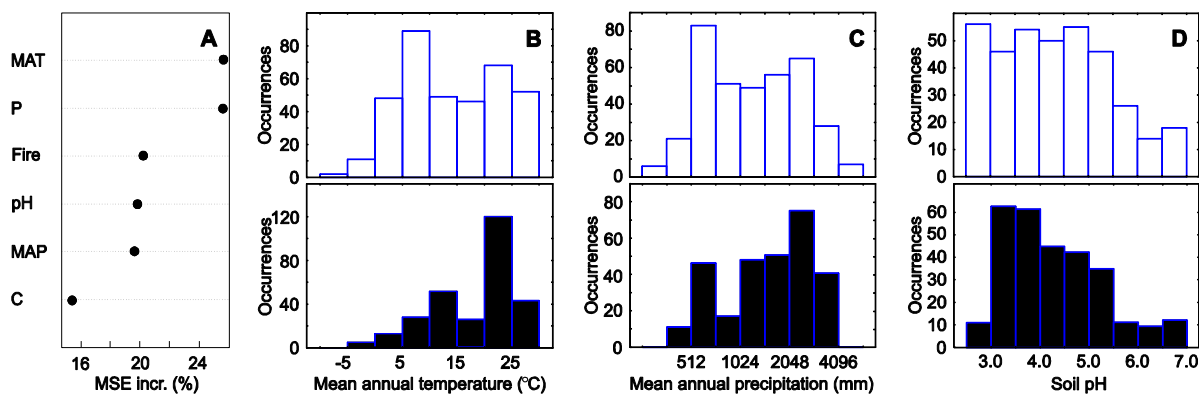


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS21

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014852 (habitat: site S049; Puerto Rico; 18.3210 N/
65.8197 W; tropical lowland rain forest dominated by *Coccoloba swartzii*)
Contains other sequences: UDB014810, GU055679, KF565318

Phylogenetic position: one of the basal lineages of Mucoromycotina, with unsupported
relationship to Endogonales

Ecological habitat: only in tropical rain forest and savanna habitats in soils with medium P
and C concentrations and low pH

Distribution: present in tropical ecosystems of all continents. Other studies suggest
wider distribution in temperate soils.

Other habitats: temperate forest soil in NC, USA (KF565318), agricultural soil in Austria
(GU055679)

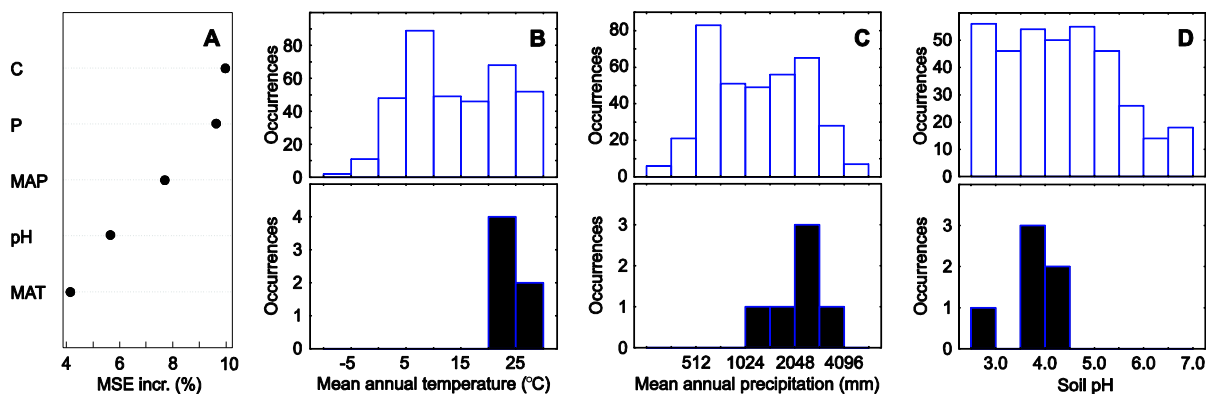


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS22

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014740 (habitat: site S171; New Zealand; 42.3024 S/
172.1041 E; montane temperate deciduous forest dominated by *Nothofagus menziesii*)
Contains other sequences: KF566241

Phylogenetic position: one of the basal lineages of Mucoromycotina, with unsupported
relationship to Endogonales

Ecological habitat: especially common in boreal forests of Eurasia in highly acidic soils.
Distribution: widespread in non-tropical habitats, especially New Zealand; also relatively
common in Eurasia.

Other habitats: temperate forest soil in NC, USA (KF566241)

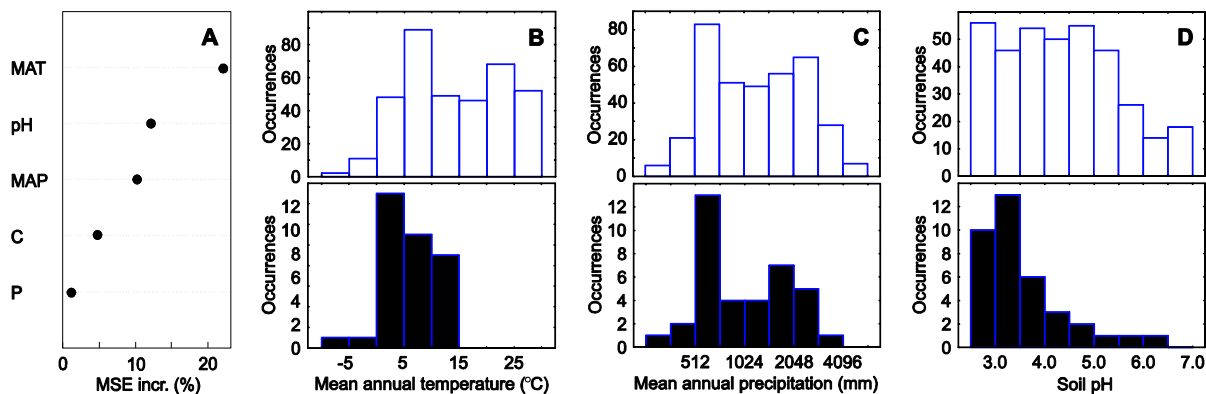


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS23

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014792 (habitat: site G2643; WA, Australia; 34.9522 S/
116.7588 E; Mediterranean woodland dominated by *Eucalyptus jacksonii*)
Contains other sequences: UDB014874, UDB014840, UDB014805, UDB014806

Phylogenetic position: well-supported sister group to the Umbelopsidaceae

Ecological habitat: tropical and subtropical with high humidity; in soils with low pH
Distribution: present in all continents but especially common in SE Asia

Other habitats: -

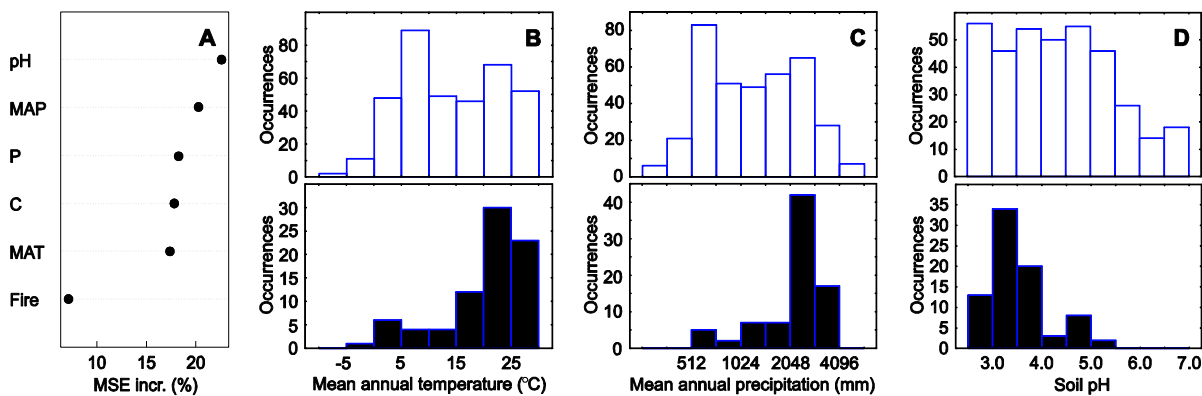


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS24

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014833 (habitat: site S045; Puerto Rico; 18.3167 N/
65.8167 W; tropical lowland rain forest with no clear dominant trees)
Contains other sequences: UDB014749, JN936327

Phylogenetic position: a group with a sister position to Paraglomeromales within Glomeromycota

Ecological habitat: mostly tropical soils with moderately acidic to neutral pH; most common in the dry tropical forests biome.
Distribution: several tropical ecoregions; particularly common in Central America and New Guinea.

Other habitats: desert soil in Oman (JN936327)

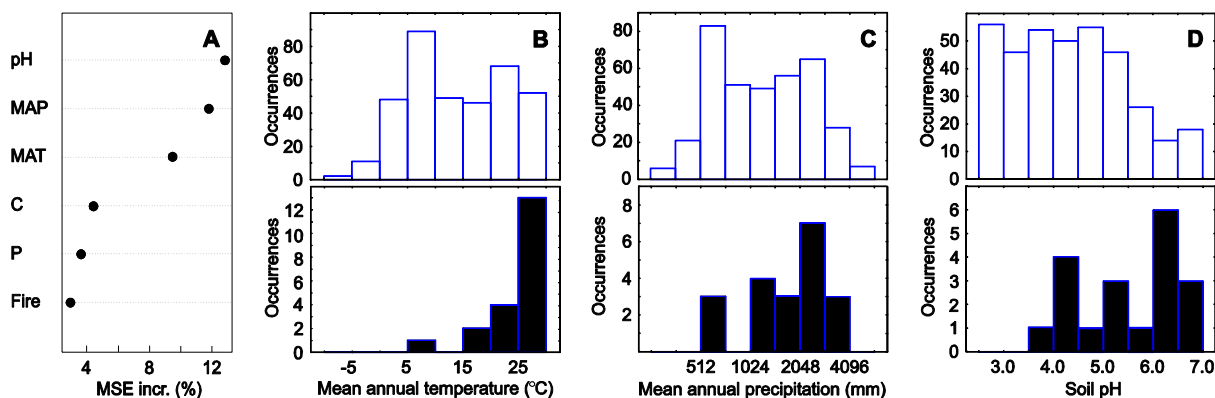


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch4

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014934 (habitat: site G2745; NT, Australia; 12.7188 S/
131.7455 E; dense savanna dominated by *Eucalyptus* spp.)
Contains other sequences: -

Phylogenetic position: a single lineage with a strongly supported position between
Entorrhizomycetes and Talbotiomyces within the Entorrhizomycota

Ecological habitat: tends to be more common in tropical habitats; found in moderately
acidic soils

Distribution: most often found in *Eucalyptus* woodlands of the Northern Territory,
Australia, with single occurrences in New Guinea, Southern South America, and Europe

Other habitats: -

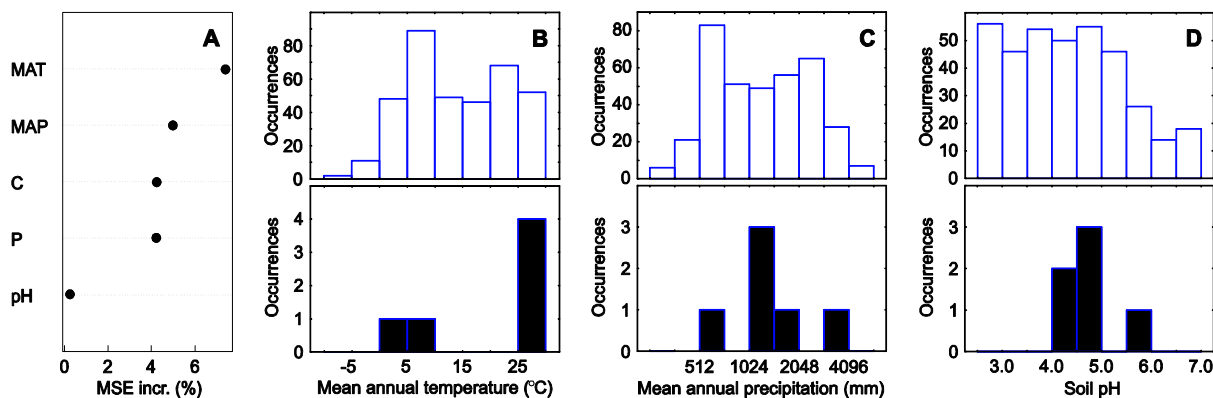


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS25

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014764 (habitat: site S159; NF, Canada; 48.9895 N/
57.7870 W; temperate deciduous forest dominated by *Betula alleghanensis*)
Contains other sequences: UDB014726, EU522908, EF023636

Phylogenetic position: one of the early branching lineages of Pucciniomycotina within
Basidiomycota

Ecological habitat: most common in temperate habitats and moderately acidic soils
Distribution: found in most continents with no evident biogeographic patterns

Other habitats: temperate forest soil in ON, Canada (EU522908) and WI, USA (EF023636)

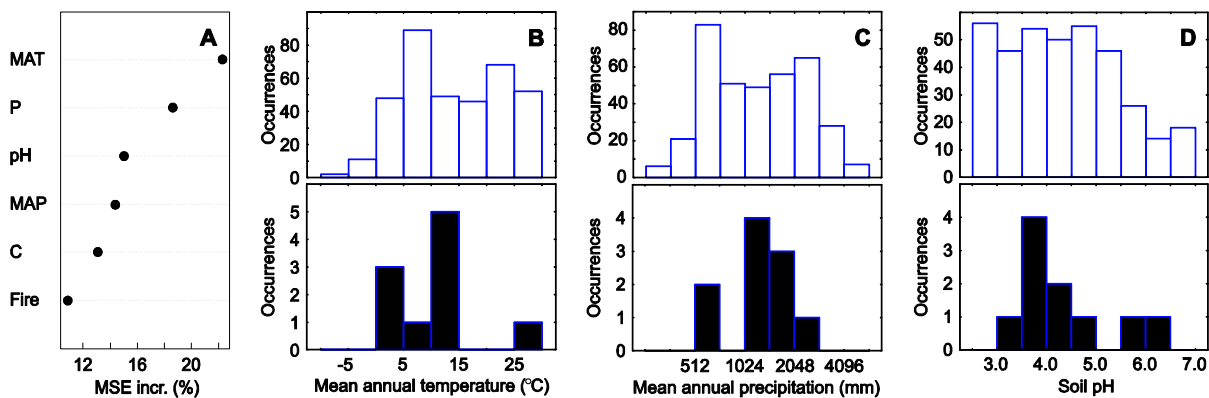


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS26

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014723 (habitat: site S060; Guyana; 5.2795 N/-59.9159; tropical lowland rain forest dominated by *Dicymbe corymbosa*)
Contains other sequences: UDB014713, UDB014717

Phylogenetic position: one of the early branching lineages of Pucciniomycotina within Basidiomycota

Ecological habitat: extremely acidic tropical rain forest soils
Distribution: found only in the Roraima massif of Guyana

Other habitats: -

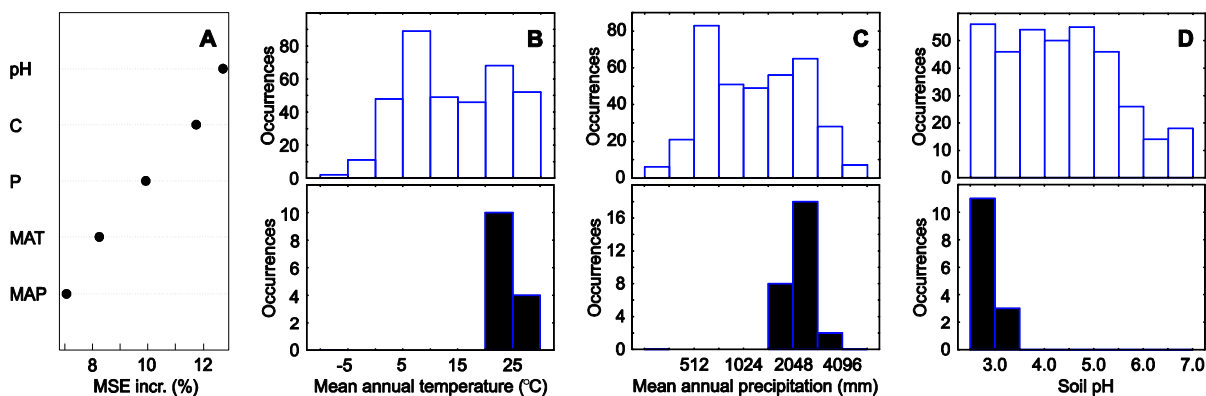


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS27

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014864 (habitat: site S114; Czech Republic; 49.0174 N/13.4751 W; montane temperate coniferous forest dominated by *Picea abies*)
Contains other sequences: UDB014861, UDB014624, UDB014761, UDB014779, DQ198784, KF565271

Phylogenetic position: related to Agaricostilbomycetes and Tritirachiomycetes within Pucciniomycotina (Basidiomycota); contains two coherent lineages, one of which is represented by a voucher specimen RB1040 and tentatively (mis)named as *Platyglea*

Ecological habitat: prefers cool temperate climate (especially boreal forests and temperate deciduous forests) and weakly acidic soils; wide tolerance to extreme values of soil pH
Distribution: present in all continents; common in the Northern and Southern Hemisphere

Other habitats: Other habitats: temperate forest soil in NC, USA; source of the culture RB1040 is unknown

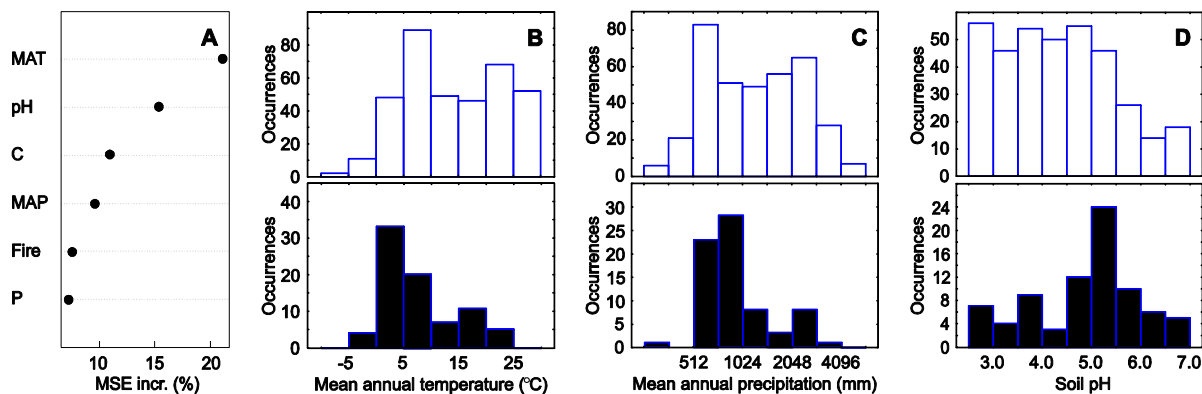


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS28

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014693 (habitat: site S004; Madagascar; 47.0020 S/
24.9520 E; dry deciduous forest dominated by *Uapaca* spp.)
Contains other sequences: UDB014783, UDB014691, UDB014682, UDB014716

Phylogenetic position: a long but well-supported branch related to Sebaciniales and
Cantharellales at the base of Agaricomycetes (Basidiomycota)

Ecological habitat: wet tropical climate (rain forest and dry forest biomes); tends to prefer
highly acidic soils
Distribution: pantropical distribution but particularly common in northern South America
and Madagascar

Other habitats: -

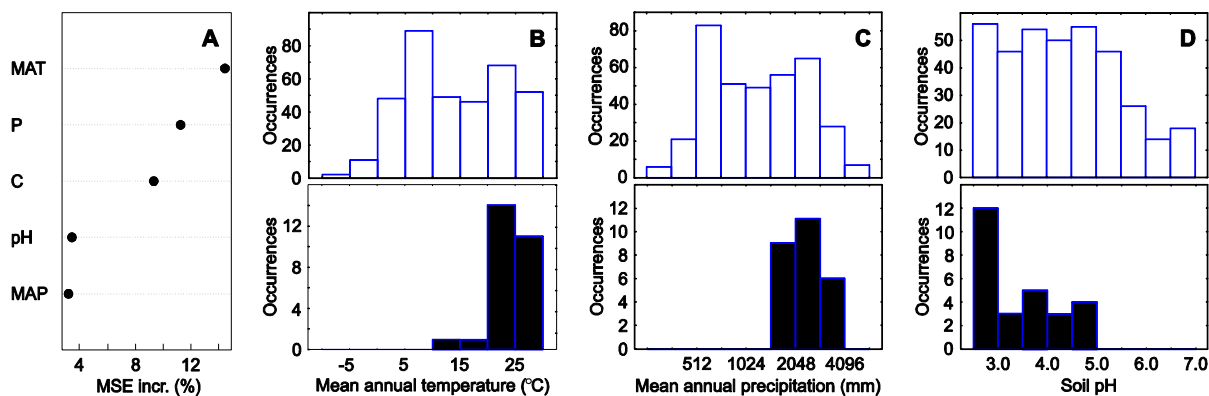


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch5

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014858 (habitat: site G2647; WA, Australia; 34.9543 S/
116.8395 E; Mediterranean sclerophyll forest dominated by *Eucalyptus jacksonii*)
Contains other sequences: -

Phylogenetic position: unsettled position in the Phallomycetidae within Basidiomycota; it
may represent an early diverging group of Hysterangiales

Ecological habitat: moist tropical forests and savannas of Queensland and West Australia;
Relatively more common in sites with recent fire (1-2 years prior to sampling)
Distribution: only known from Queensland and West Australia

Other habitats: -

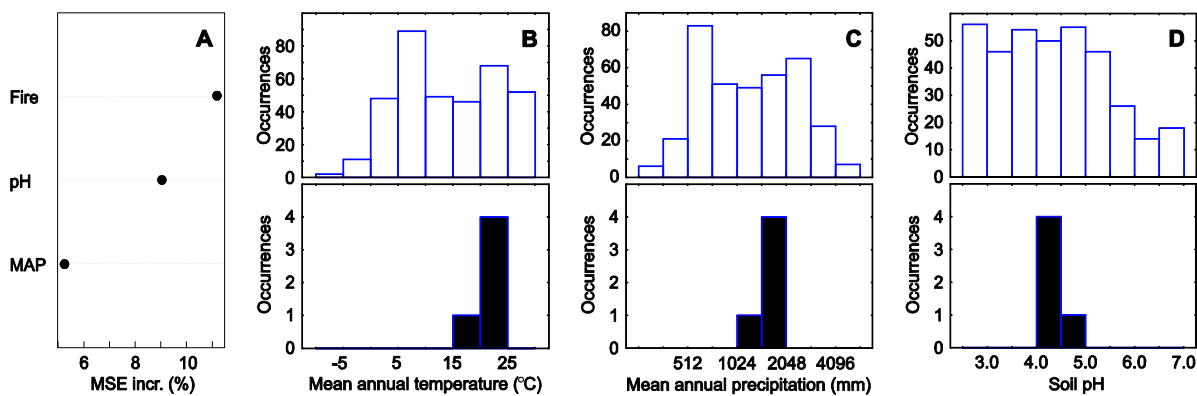


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS29

Previous names for the clade: -
Corresponding PlutoF compound cluster: UCL7_006369

Representative sequence: UDB014802 (habitat: site AV123; Colombia; 4.8670 N/
75.2500 W; paramo montane grassland)
Contains other sequences: EU861637

Phylogenetic position: sister group of Auriculariales within Basidiomycota

Ecological habitat: prefers wet tropical climate and low pH
Distribution: found only in the Southern Hemisphere (New Guinea and northern South
America), but other studies indicate much broader distribution and climate tolerance

Other habitats: grassland soil in CO, USA (EU861637)

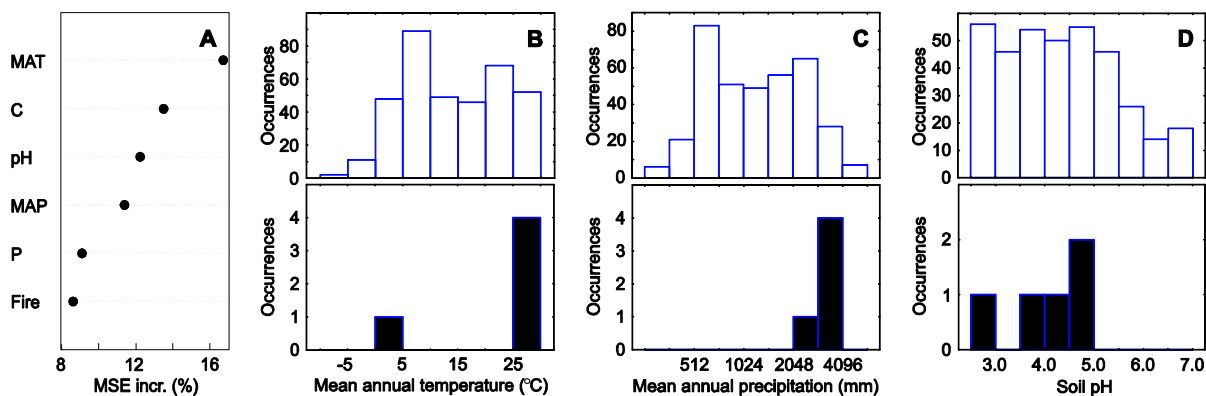


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS30

Previous names for the clade: covers the ectomycorrhizal lineage /agaricomycetes1 and its potentially non-mycorrhizal sister group (Tedersoo & Smith 2013; Fung. Biol. Rev. 27: 83-99.)

Corresponding PlutoF compound cluster: UCL7_008472

Representative sequence: UDB014766, (habitat: site G2641; WA, Australia; 34.3629 S/ 116.2800 E; Mediterranean forest dominated by *Eucalyptus patens*)

Contains other sequences: UDB014827, UDB014829, UDB014429

Phylogenetic position: related to Phallomycetidae within Basidiomycota

Ecological habitat: includes both the ectomycorrhizal and non-mycorrhizal members; temperate habitats in the southern and northern temperate deciduous forests and Mediterranean biome

Distribution: strikingly most common in the temperate habitats in southern South America, New Zealand, and Australia; less common in temperate habitats in North America and Europe

Other habitats: ectomycorrhizal root tips of *Nothofagus* in Argentina (UDB014429)

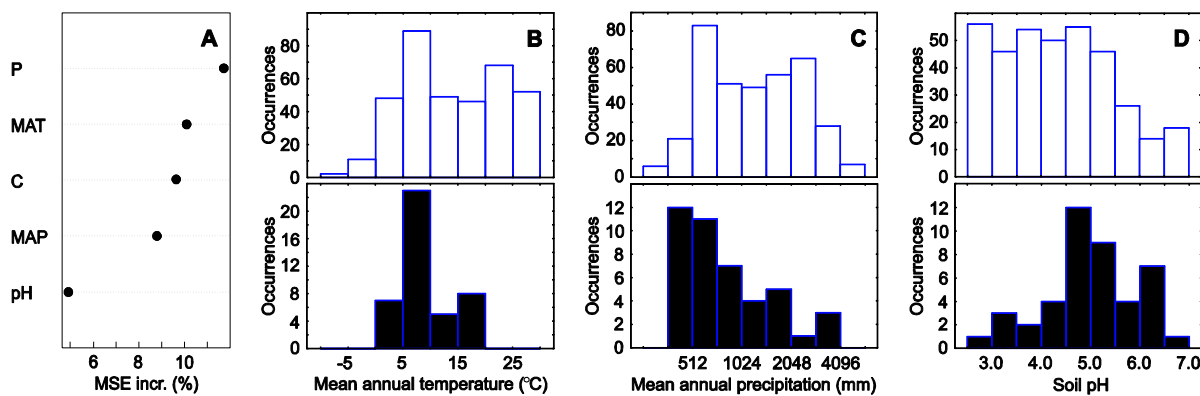


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS31

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014859 (habitat: site S046; Puerto Rico; 18.3167 N/
65.8167 W; tropical lowland rain forest with no clear dominants)
Contains other sequences: UDB014768, UDB014843, UDB014875, UDB014884

Phylogenetic position: well-supported sister group of the Archaeorhizomycetales of
Taphrinomycotina (Ascomycota)

Ecological habitat: particularly common in humid tropical climate, especially rain forest and
dry forest biomes; prefers soil with low pH
Distribution: found in nearly all ecoregions but strikingly more common in Central America

Other habitats: -

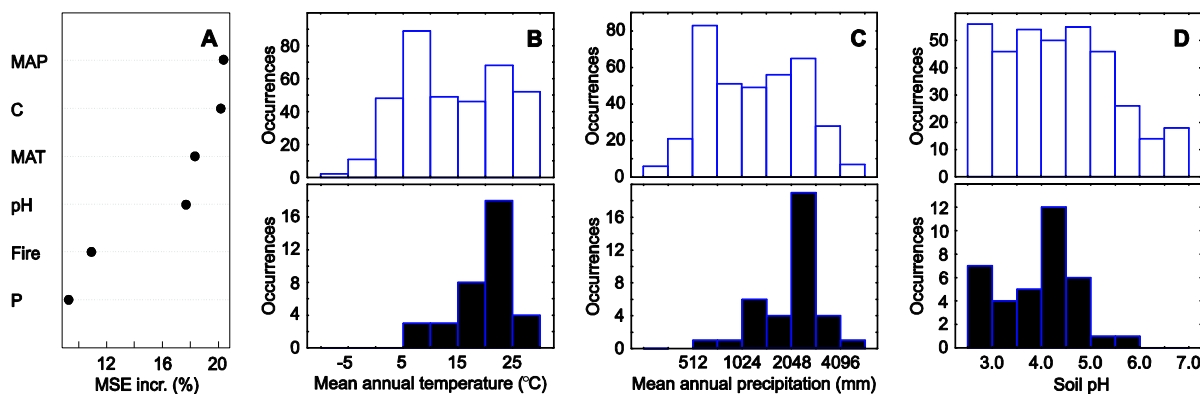


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS32

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014870 (habitat: site G2660; Papua New Guinea; 9.4218 S/ 147.3692 E; moderately disturbed tropical savanna dominated by *Eucalyptus papuana*)
Contains other sequences: UDB014869

Phylogenetic position: one of the deep order-level lineages of Orbiliomycetes at the base of Pezizomycotina within Ascomycota

Ecological habitat: humid tropical climate (lowland rain forest) over a wide pH range
Distribution: Central America, with a single locality in New Guinea

Other habitats: -

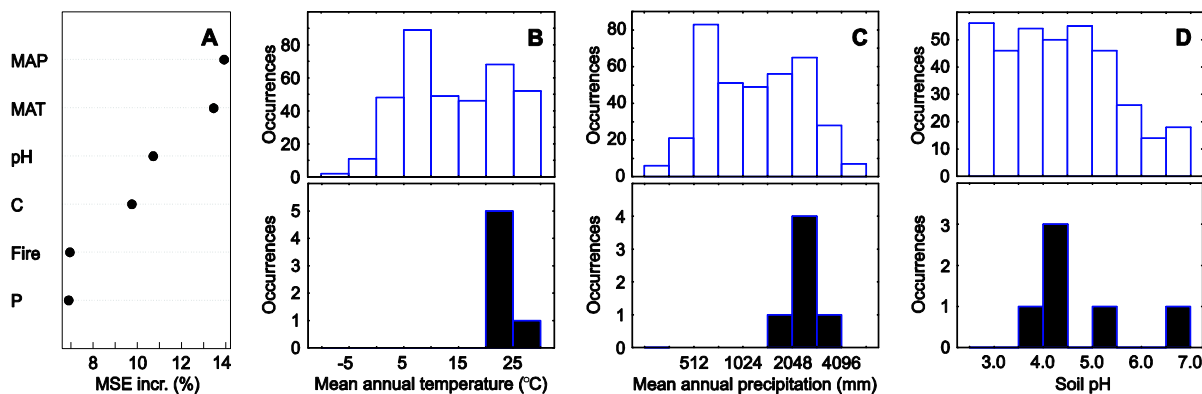


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS33

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014886 (habitat: site S049; Puerto Rico; 18.3210 N/
65.8197 W; tropical lowland rain forest dominated by *Coccoloba swartzii*)
Contains other sequences: UDB014844, UDB014906, UDB014896, UDB014888, KF566789

Phylogenetic position: one of the deep order-level lineages of Orbiliomycetes within Ascomycota

Ecological habitat: more common in tropical moderately acidic soils; most common in the savanna biome
Distribution: found in most ecoregions but most common in Australia, Central America, and Madagascar

Other habitats: temperate forest soil in NC, USA (KF566789)

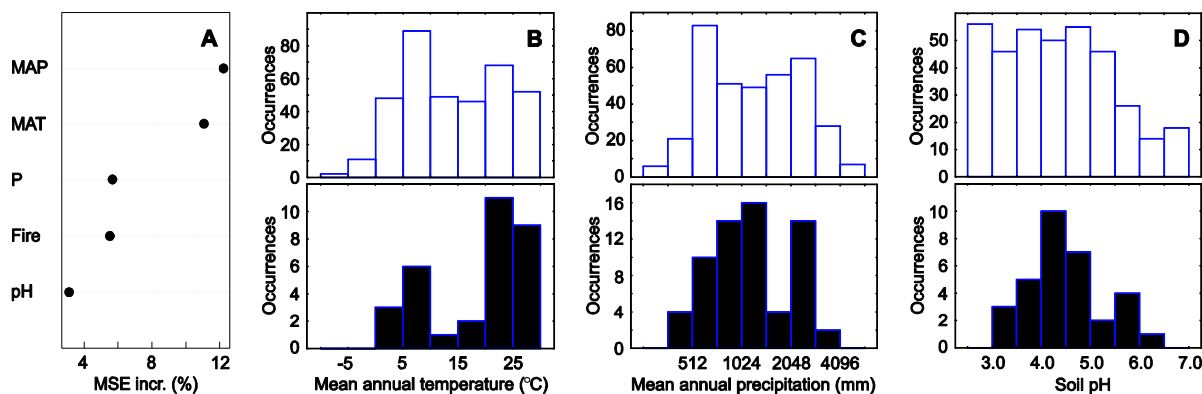


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS34

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014912 (habitat: site G2629; Estonia; 58.0458 N/
24.7119 E; old-growth temperate coniferous forest dominated by *Picea abies*)
Contains other sequences: UDB014911, KF565042

Phylogenetic position: related to Symbiotaphrinales within Ascomycota, albeit with low support

Ecological habitat: particularly common in temperate habitats, especially grasslands and shrublands

Distribution: found in all continents but most common in North America

Other habitats: temperate forest soil in NC, USA (KF566789)

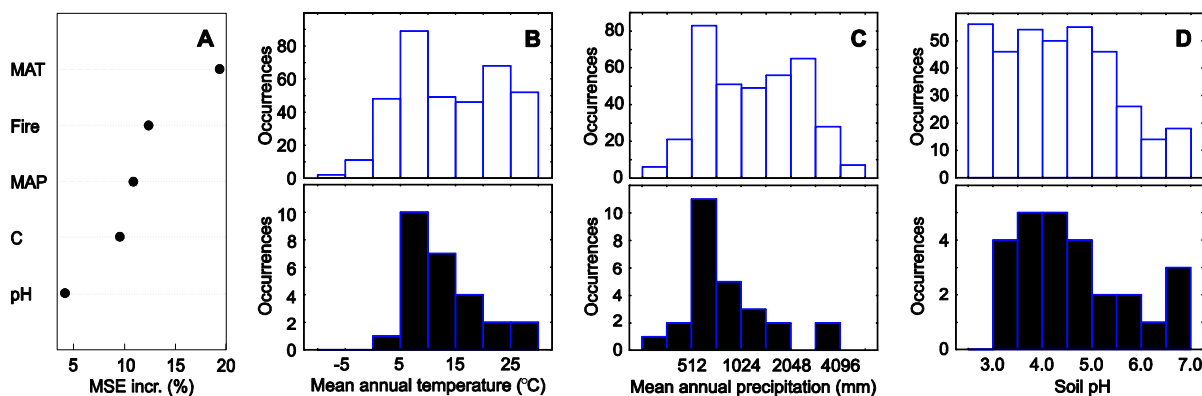


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS35

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014945 (habitat: site S163; Mexico; 19.1697 N/
97.3000 W; montane subalpine coniferous forest dominated by *Pseudotsuga menziesii*)
Contains other sequences: UDB014907, UDB014919, UDB014898, EF023999, KM096534

Phylogenetic position: a clade related to Leotiomycetes and Sordariomycetes, albeit with low support

Ecological habitat: very broad ecological amplitude regarding climate and soil pH; most common in grasslands and shrublands
Distribution: present in all continents and ecoregions without obvious differences.

Other habitats: temperate forest soils in WI, USA (EF023999), and uranium mine in Scotland (KM096534)

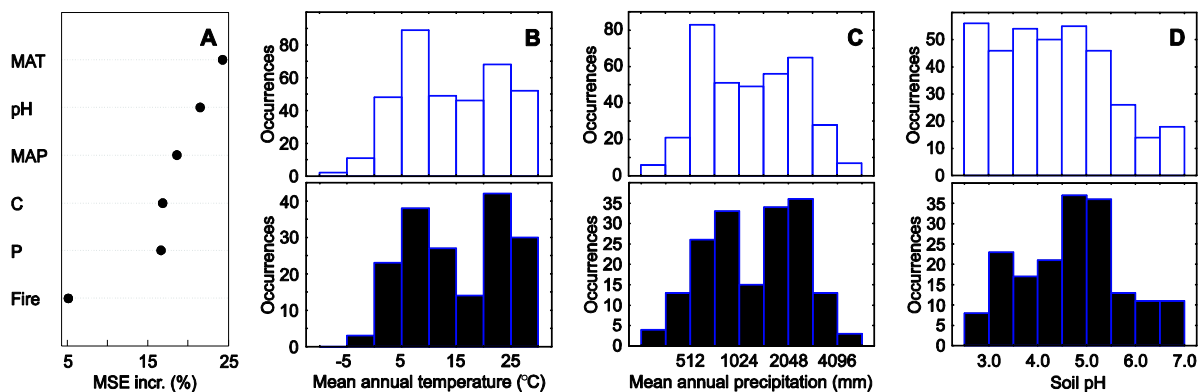


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch6

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014790 (habitat: site G2658; Papua New Guinea; 9.4350 S; 147.3755 E; burnt tropical savanna dominated by *Eucalyptus tereticornis*)
Contains other sequences: -

Phylogenetic position: a sister group to the rest of Lulworthiales within Sordariomycetes, Ascomycota

Ecological habitat: tropical dry forests but also savannas and lowland rain forests in soils of moderately high pH

Distribution: most common in Central America, Africa, Papua New Guinea, and India

Other habitats: -

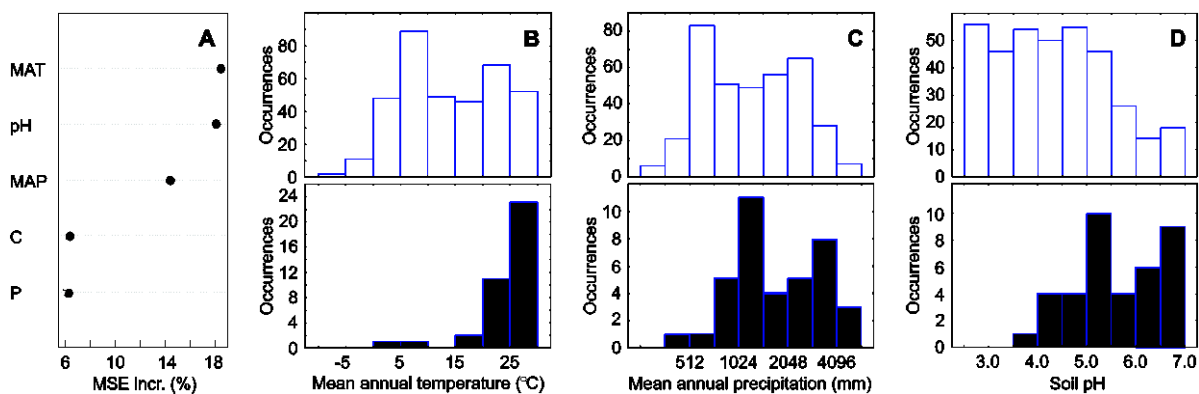


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Branch7

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014800 (habitat: site AV103; Colombia; 0.3919 S/
72.0461 W; tropical lowland rain forest with no clearly dominant trees)
Contains other sequences: -

Phylogenetic position: a single divergent branch within Lecanoromycetes, Ascomycota

Ecological habitat: tropical lowland rain forests at extremely low pH
Distribution: almost exclusive to northern South America, except a single finding from India

Other habitats: -

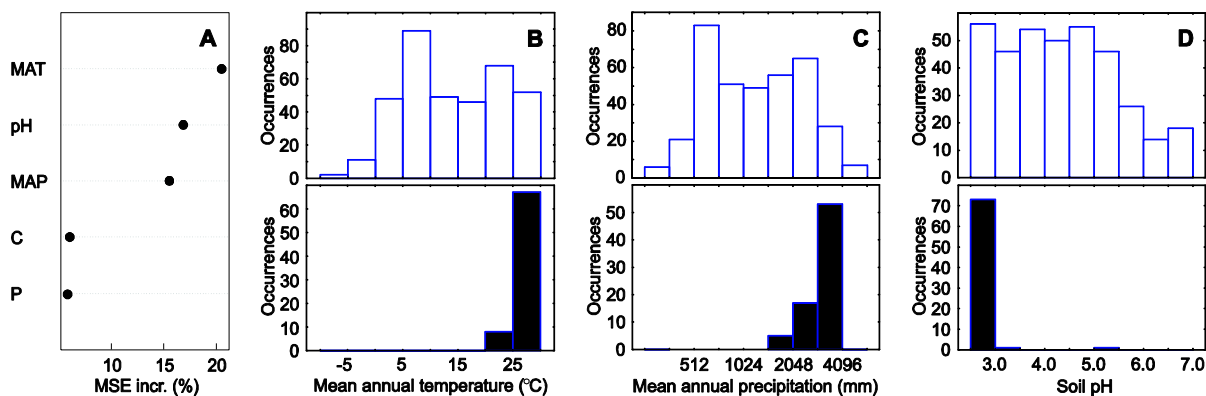


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS36

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014939 (habitat: site G2736; Papua New Guinea; 6.3755 S/ 145.2558 E; tropical montane rain forest dominated by *Castanopsis acuminatissima*)
Contains other sequences: UDB014955, KF567558

Phylogenetic position: a clade within Lecanoromycetes, Ascomycota

Ecological habitat: most common in various tropical biomes and Mediterranean habitats; very wide pH tolerance
Distribution: most common in Africa and Madagascar but present in all continents

Other habitats: temperate forest soil in NC, USA (KF567558)

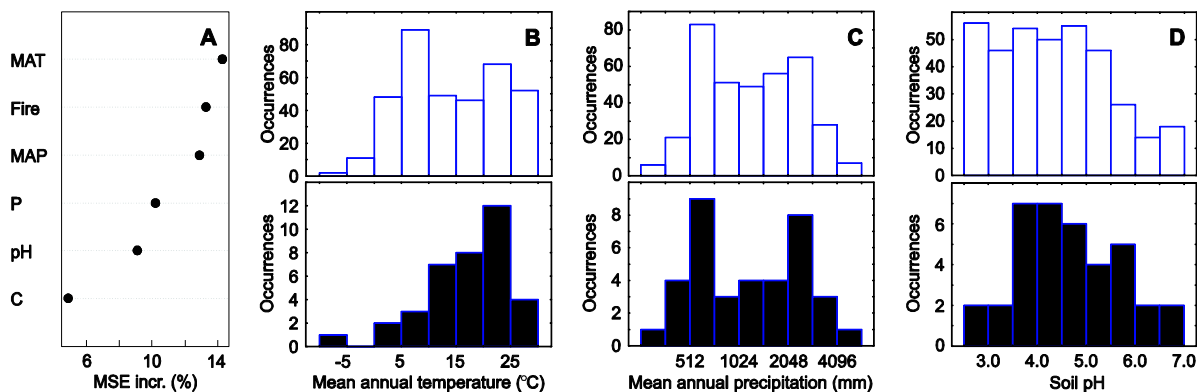


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).

Clade GS37

Previous names for the clade: -
Corresponding PlutoF compound cluster: -

Representative sequence: UDB014659 (habitat: site S123; Italy; 37.9017 N/
14.0000 E; montane temperate deciduous forest dominated by *Fagus sylvatica*)
Contains other sequences: AB986436

Phylogenetic position: one of the early diverging lineages of Eurotiomycetes, Ascomycota

Ecological habitat: cool temperate climate, narrow preference for moderately acidic soils
Distribution: most common in southern South America but present in temperate Eurasia
and tropical Africa

Other habitats: subtropical forest in FL, USA (AB986436)

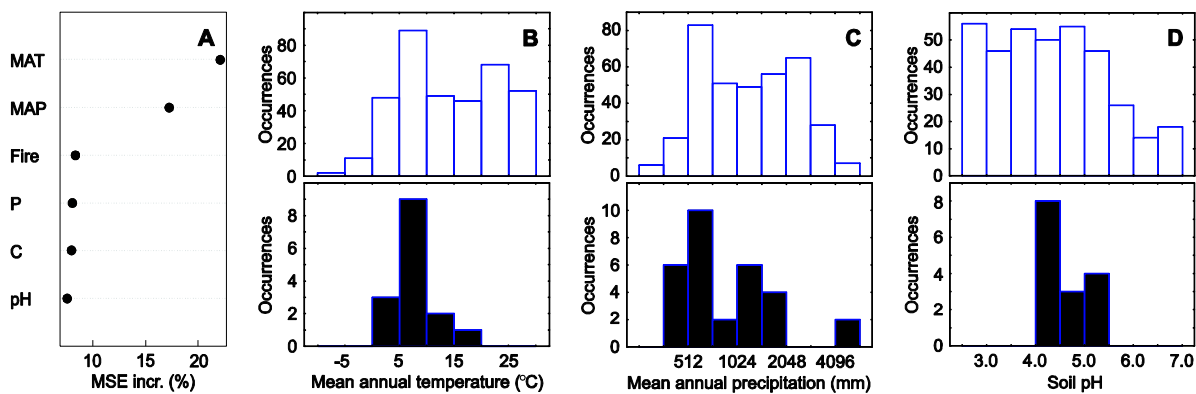


Figure. Niche analysis of the clade. A. Strongest predictors for the occurrence of clade members based on random forest analysis. B-D. Distribution of clade members (lower panels) in sites with (B) different mean annual temperature, (C) mean annual precipitation, and (D) average soil pH relative to all studied soils (upper panels).