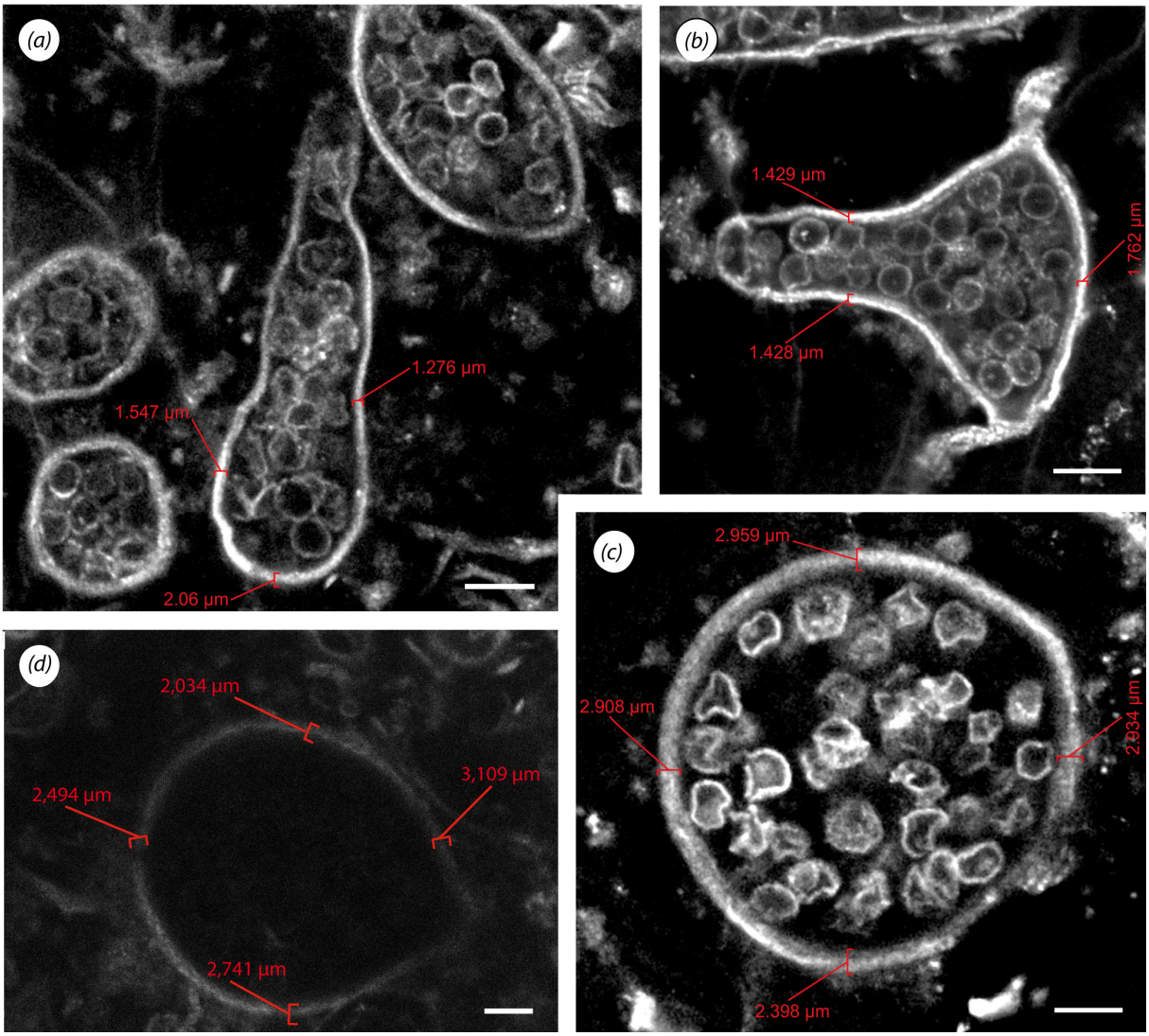
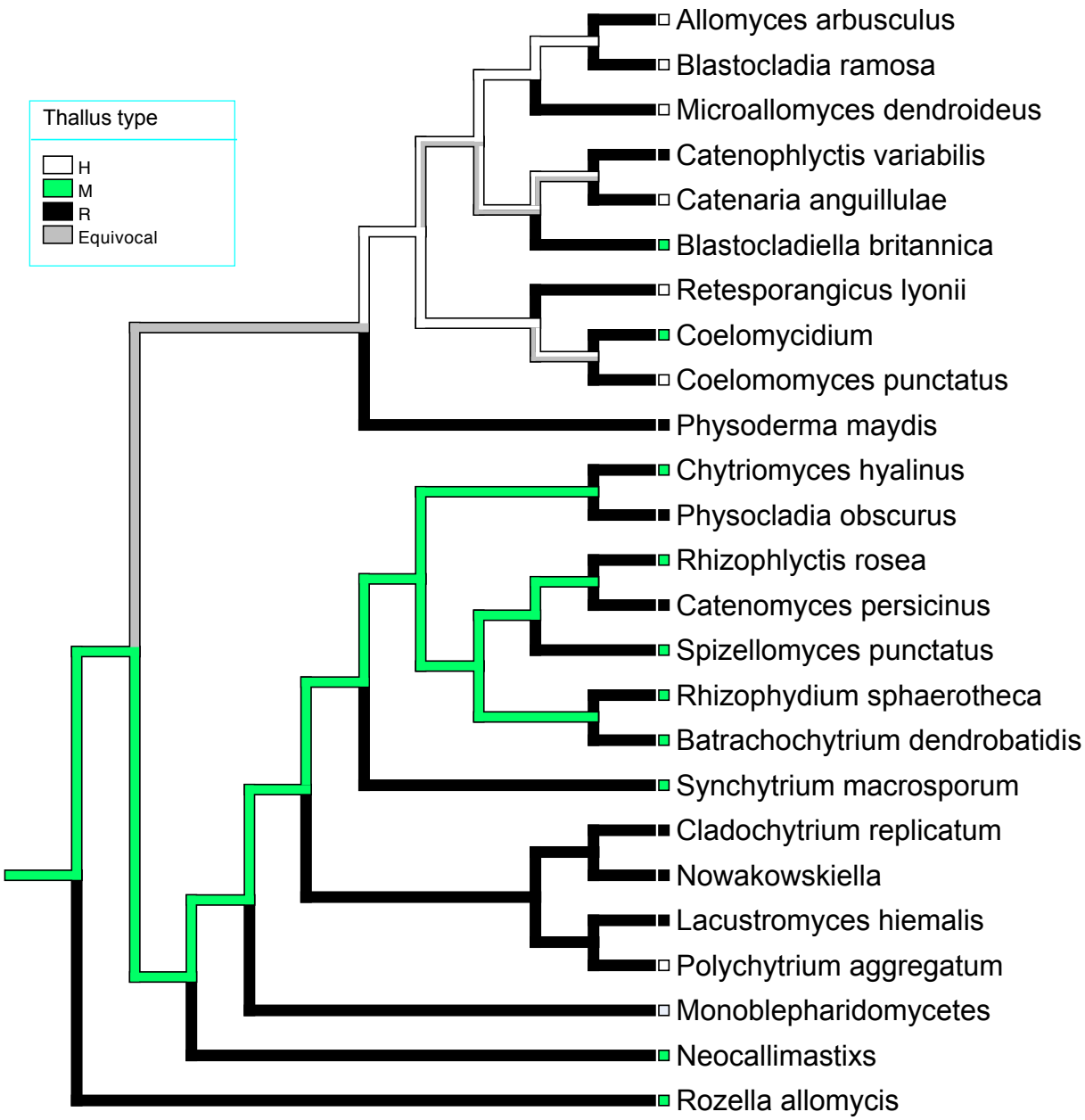
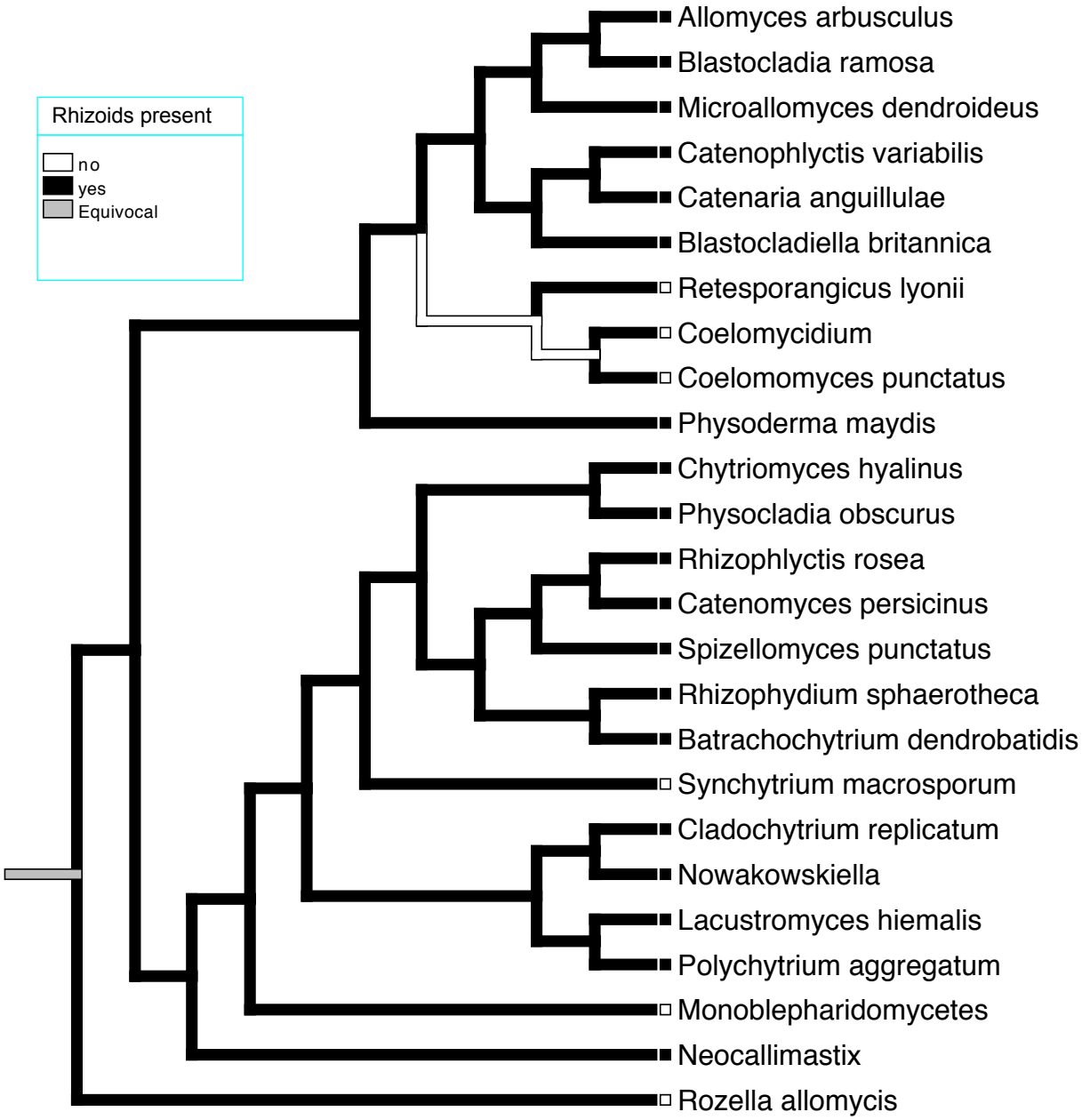


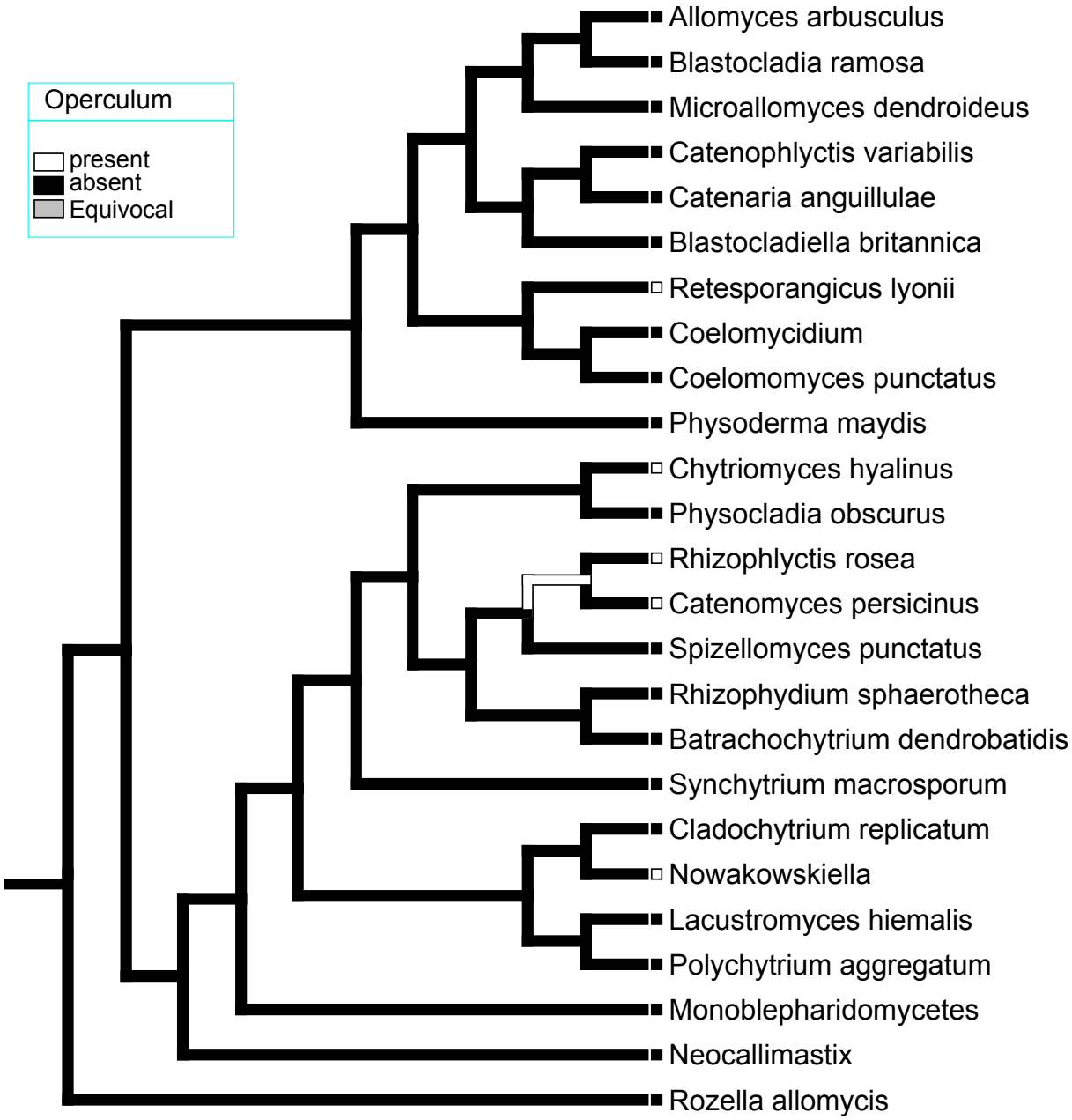

Supplementary figure S1. Comparison between thicknesses of the walls of the two main types of swellings in *Retesporangicus lyonii* (a, b, c: zoosporangia ; d : resting sporangia). Scale bars =10 µm.



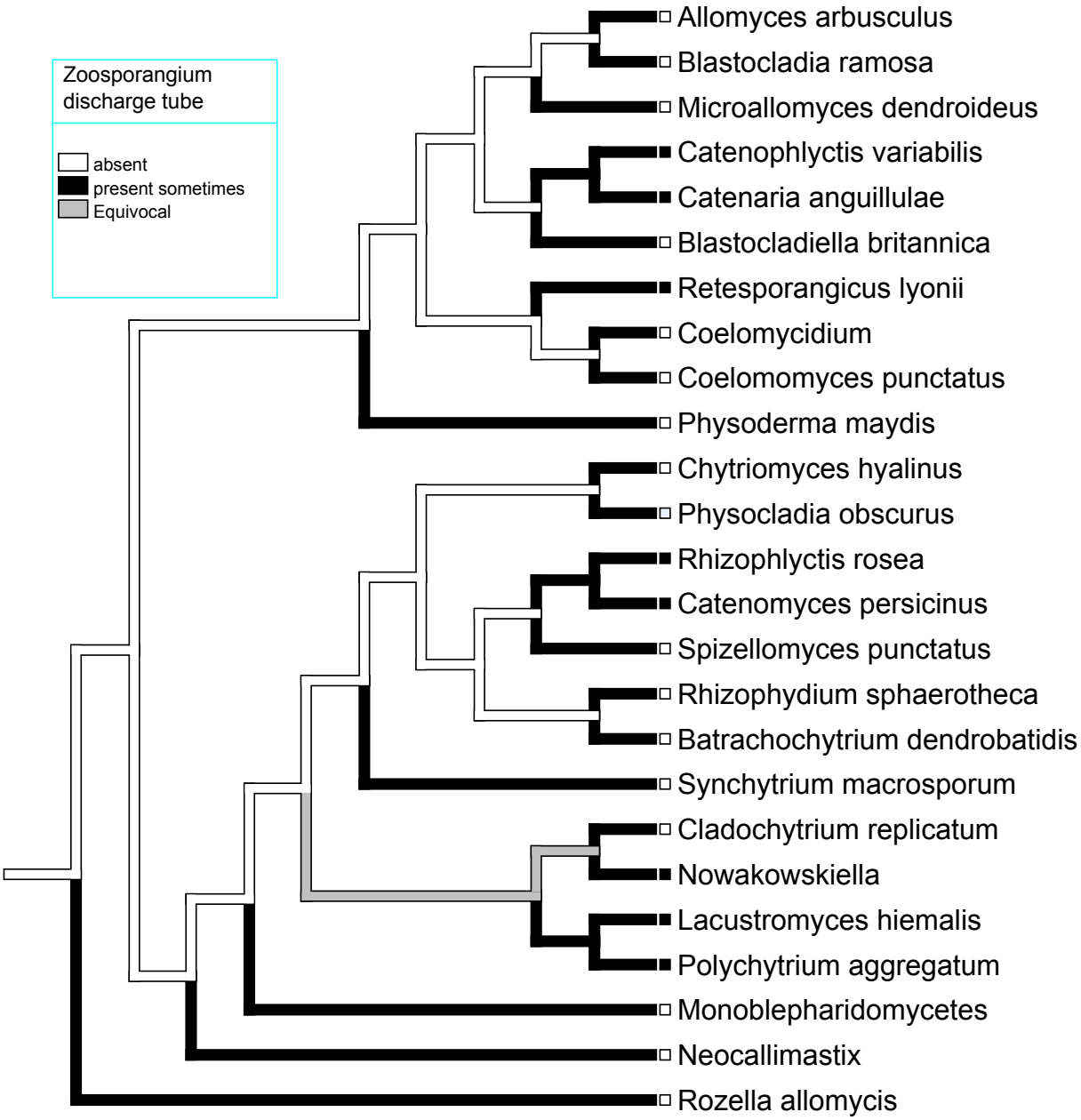

Supplementary figure S2. Ancestral state reconstruction suggests that monocentric thalli were ancestral but that hyphae evolved early in Blastocladiomycota. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. Thallus types are: (H) hyphal, defined as having cylindrical, branching filaments that make up at least part of the thallus; (M) monocentric, in which one thallus produces a single sporangium; (R) rhizomycelial, a thallus comprises swellings connected by narrow, branching filaments. Branch colours indicate ancestral states. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.



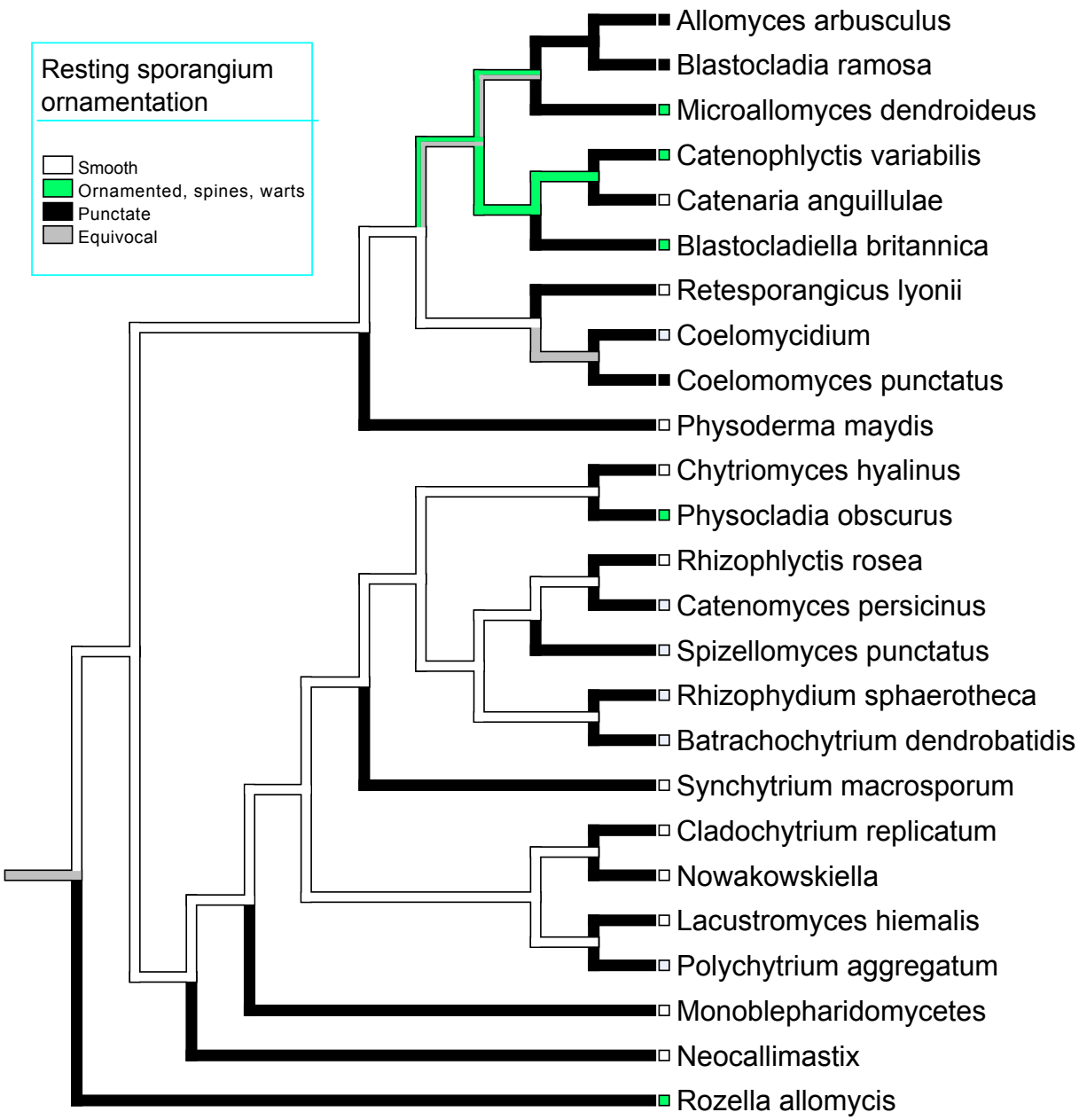

Supplementary figure S3. Ancestral state reconstruction suggests that rhizoids are ancestral in Chytridiomycota and Blastocladiomycota. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. Branch colours indicate ancestral states. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.



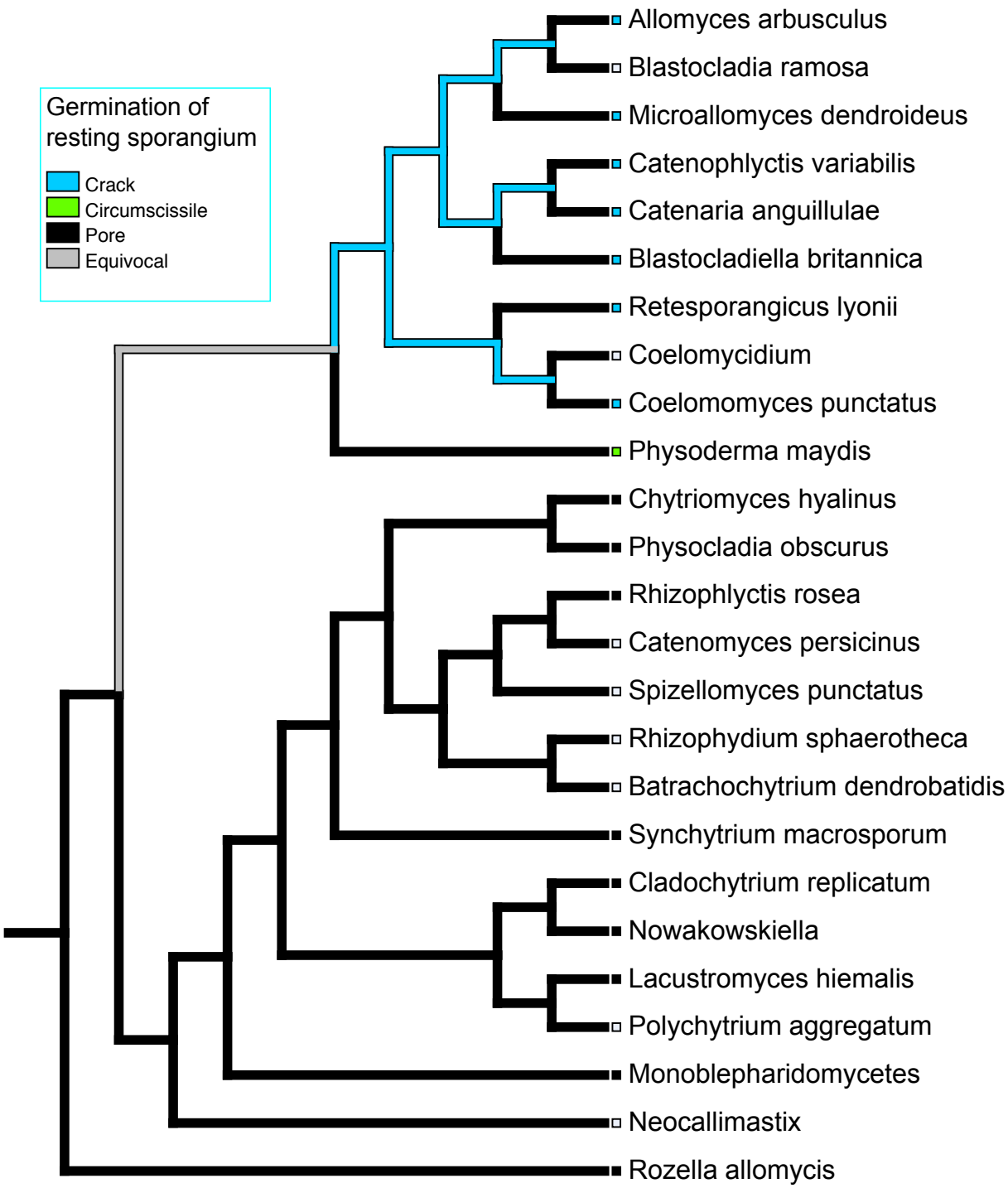

Supplementary figure S4. Ancestral state reconstruction showing the distribution of opercula, or lids, which block the exits of zoosporangia prior to zoospore release. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. *R. lyonii* is the only operculate member of phylum Blastocladiomycota but opercula evolved convergently three times among sampled Chytridiomycota. Branch colours indicate ancestral states. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.




Supplementary figure S5. Ancestral state reconstruction suggests that elongate discharge tubes in zoosporangia (which develop prior to zoospore release) evolved multiple times among Blastocladiomycota and Chytridiomycota. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. Branch colours indicate ancestral states. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.




Supplementary figure S6. Ancestral state reconstruction of the ornamentation on outer walls of resting sporangia of Blastocladiomycota and Chytridiomycota. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. Branch colours indicate ancestral states. Smooth walled resting sporangia appear ancestral in both Chytridiomycota and Blastocladiomycota. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.




Supplementary figure S7. Ancestral state reconstruction of the type of opening that characterizes germinating resting sporangia of Blastocladiomycota and Chytridiomycota. The tree shows one of four most parsimonious positions of the fossil *Retesporangicus lyonii* in a phylogeny of 24 extant taxa. In Blastocladiomycota as in the fossil, the sporangium walls usually open with an elongate crack. In Chytridiomycota, the wall usually opens with a pore. Branch colours indicate ancestral states. Squares to the left of names specify the character state present in each taxon. Branches to terminal taxa have ancestral character states to match the terminal taxa, although this is not indicated by their colours.