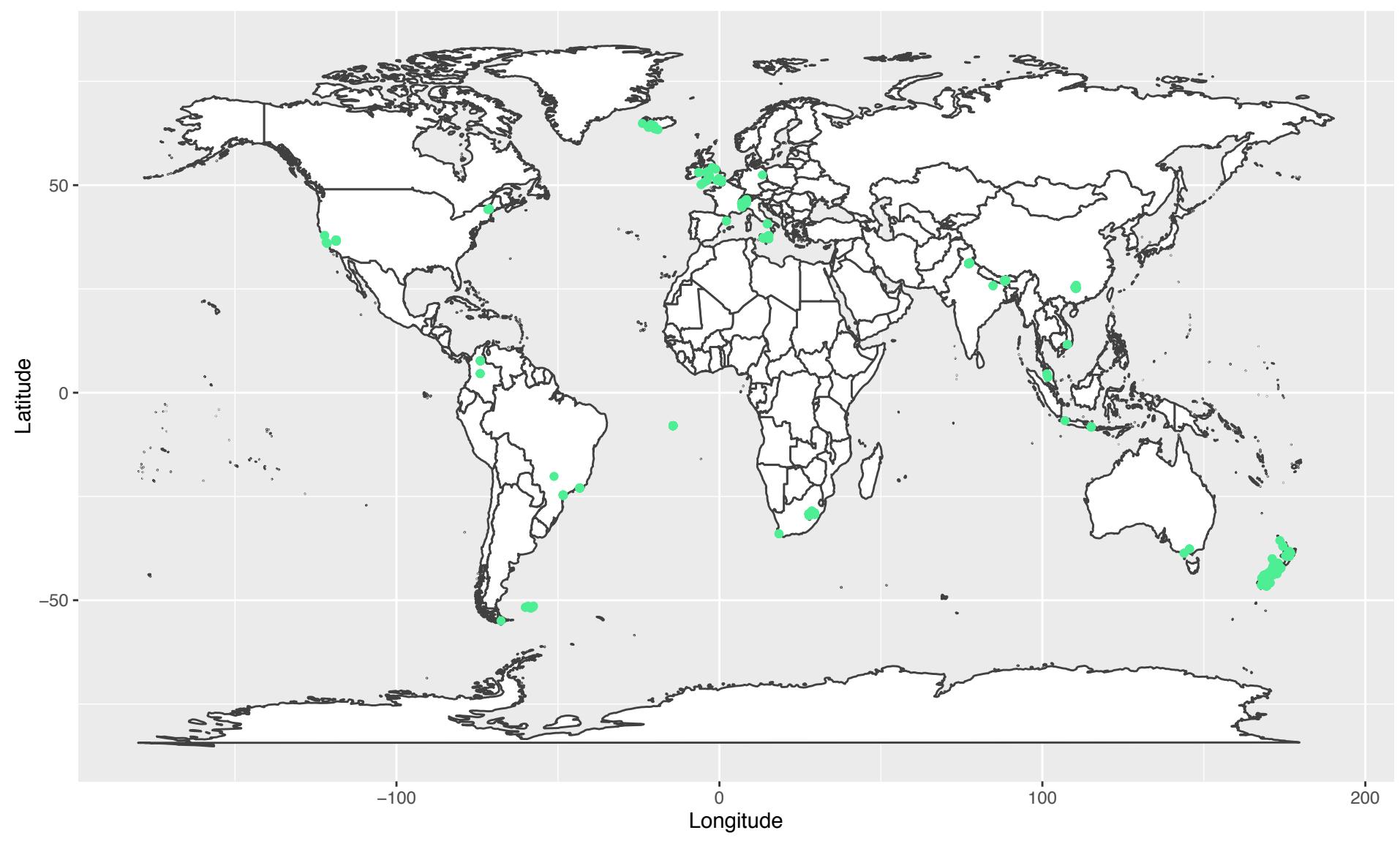


## **Supplementary material**

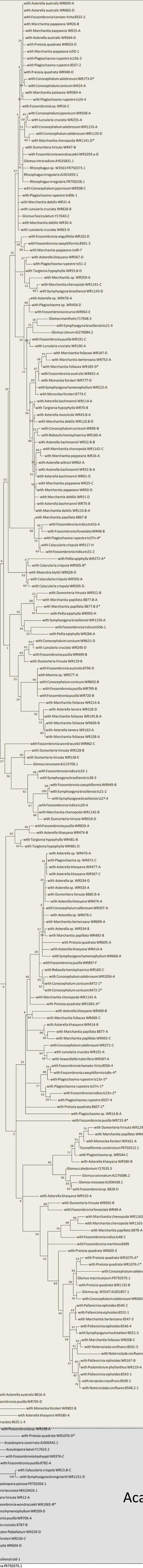
### **Figures S1 to S10**

**Figure S1. Global map showing liverwort collection sites.** Collection sites are highlighted in green. Map produced in RStudio using the 'ggmap' package.

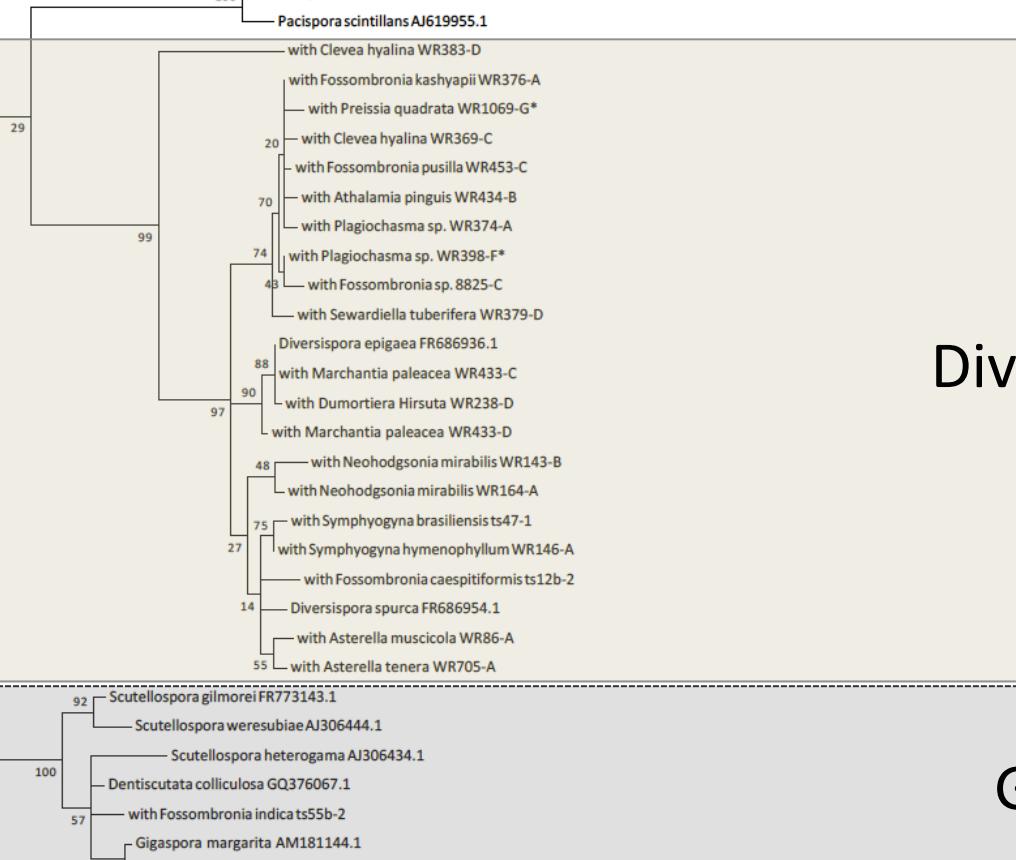


**Figure S2. Maximum likelihood analysis of Glomeromycotina sequences.** All 326 new sequences produced in this study are included in this phylogeny with reference sequences from Glomeromycotina spores. Maximum likelihood was run with 1,000 bootstrap replicates and a generalised time reversible model with invariant gamma rates. An asterisk indicates the DNA sequence is not the full-length 18S.

## Glomeraceae



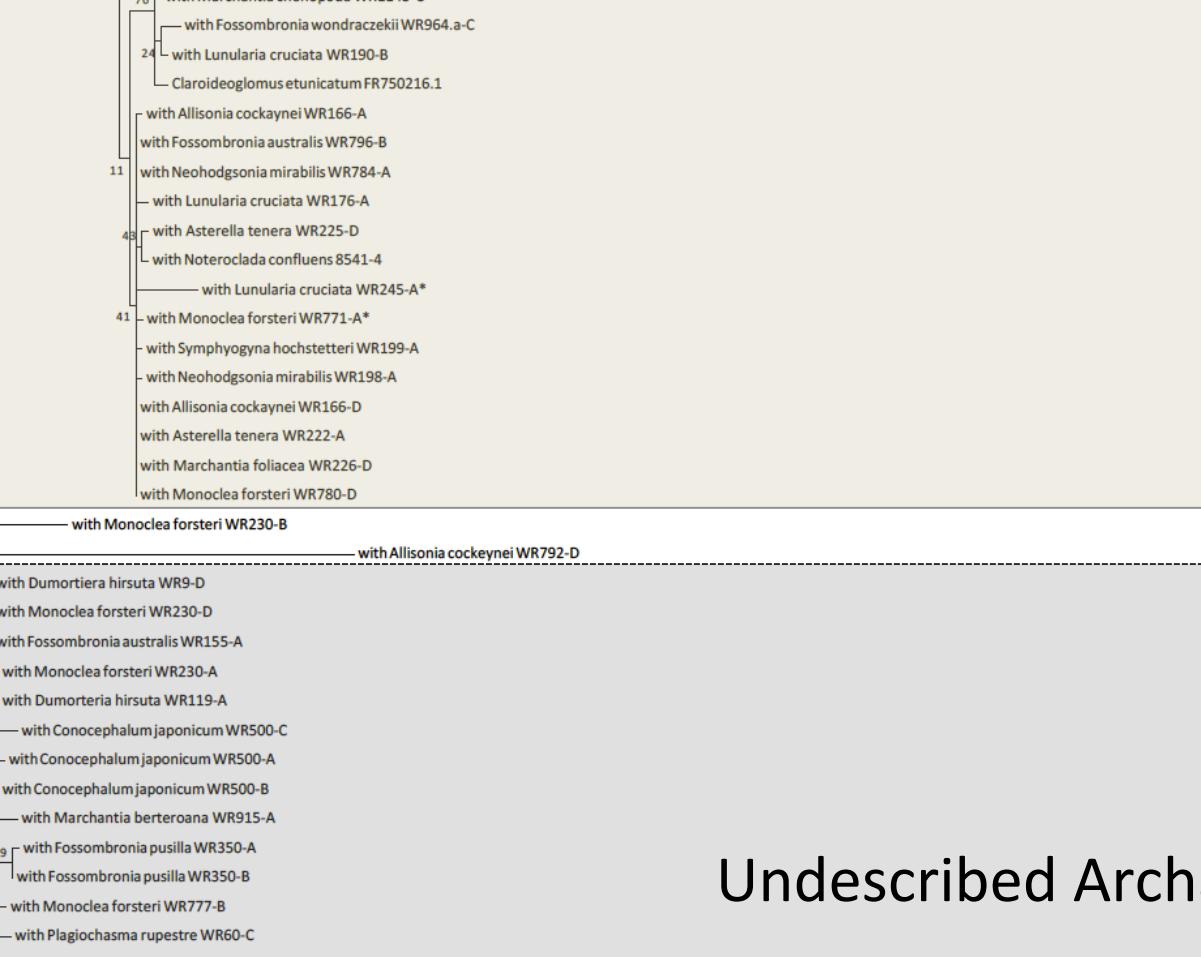
## Acaulosporaceae



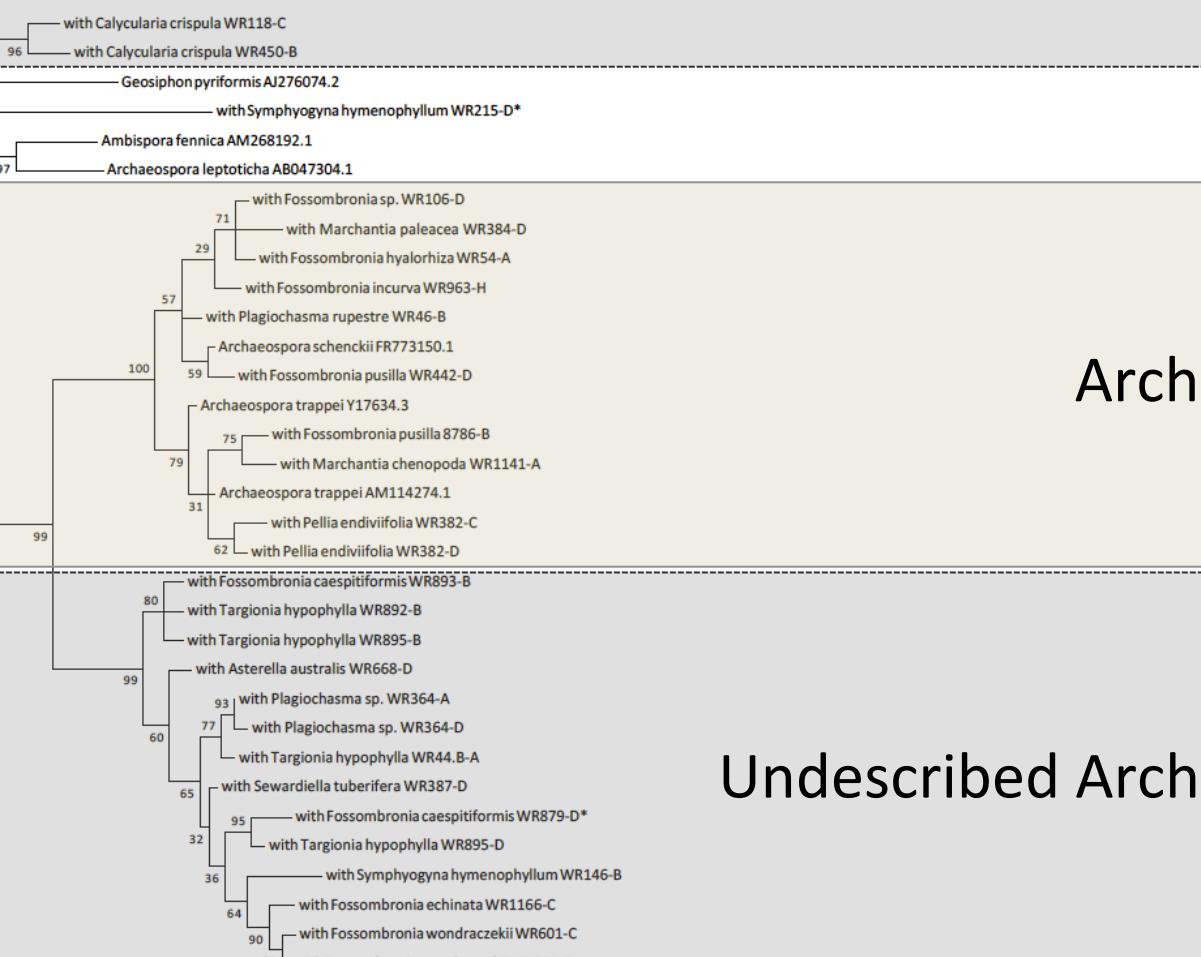
## Diversisporaceae



## Gigasporaceae



## Claroideoglomeraceae



## Undescribed Archaeosporales A



## Archaeosporaceae



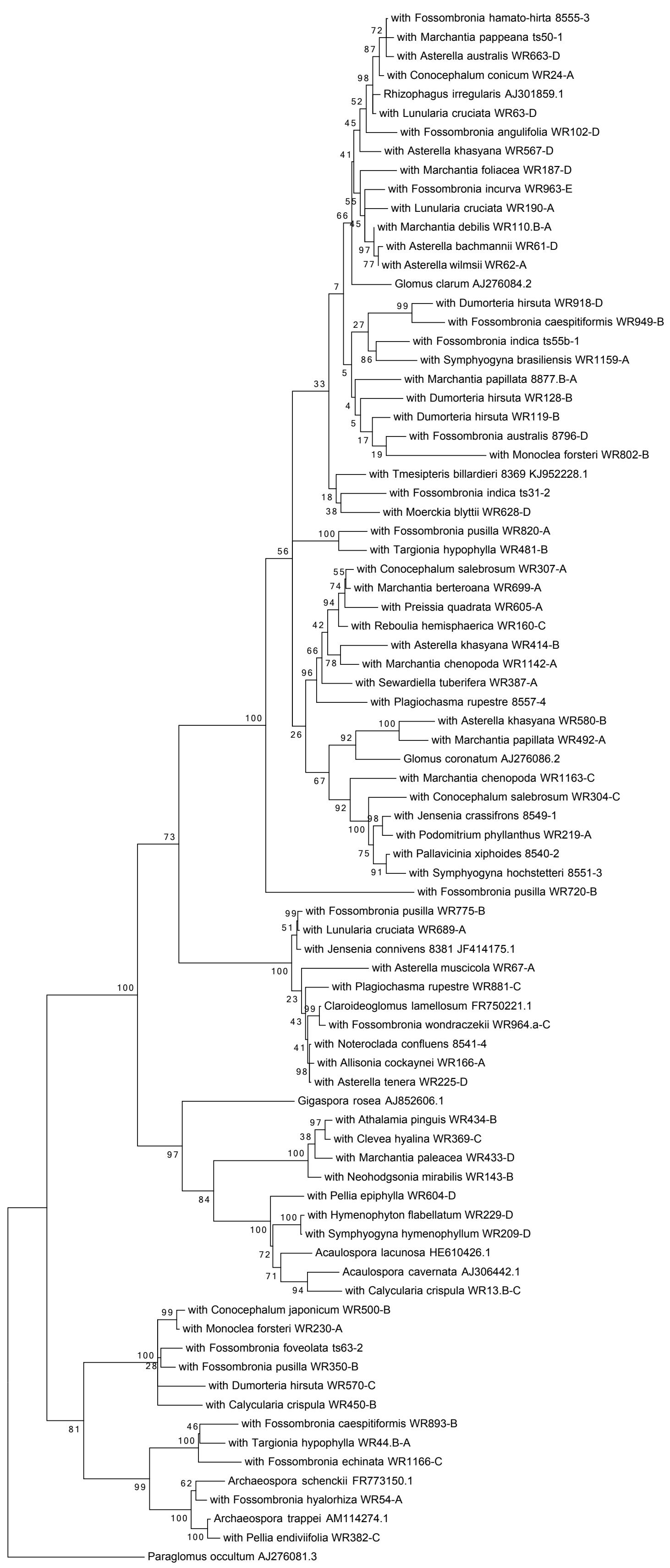
## Undescribed Archaeosporales B



## Paraglomeraceae

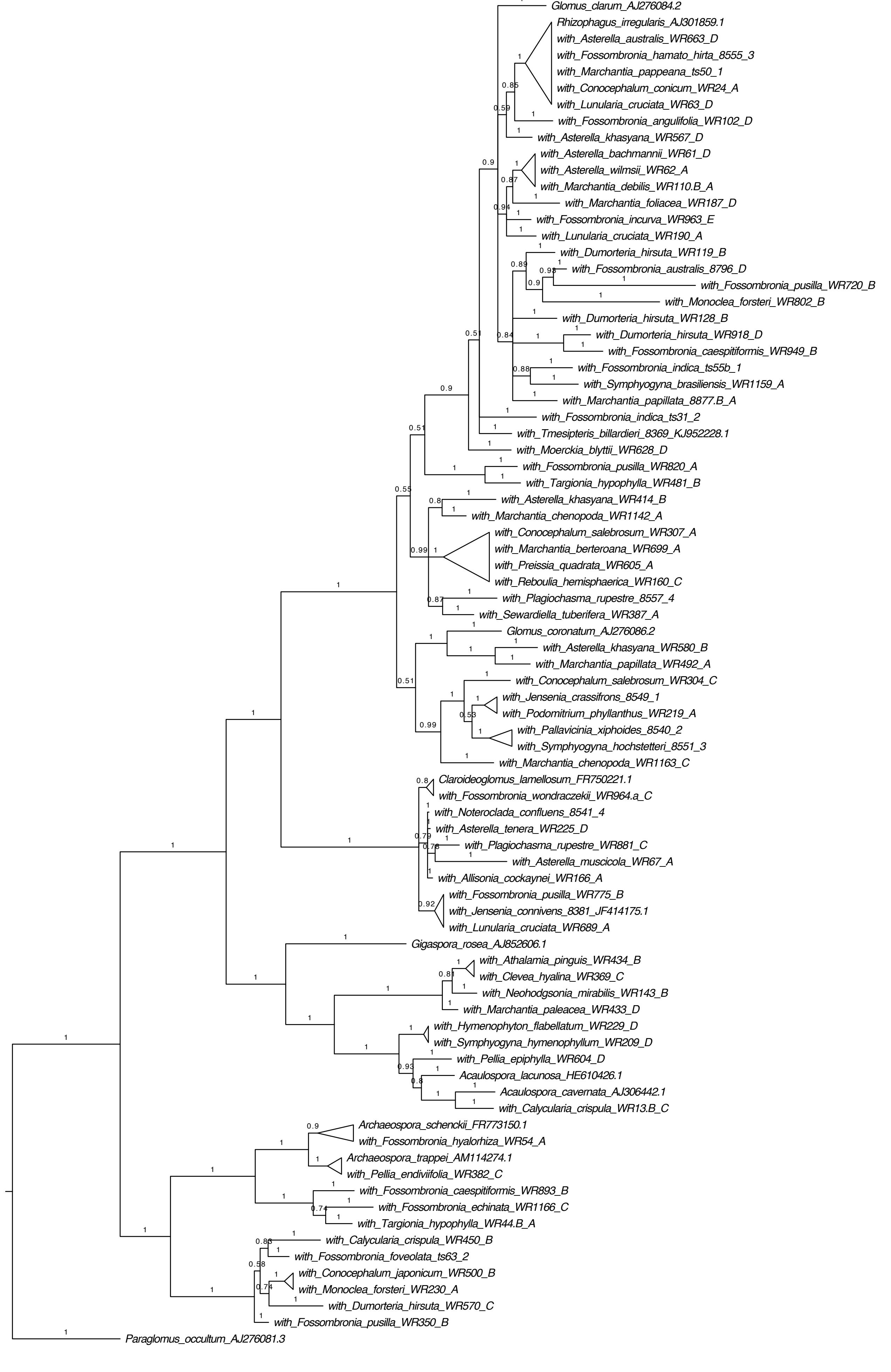
**Figure S3. Summary maximum likelihood phylogeny of Glomeromycotina fungi.**

This phylogenetic tree was used to produce figure 1. The analysis used a generalised time reversible model with invariant gamma rates and 1,000 bootstrap replicates.

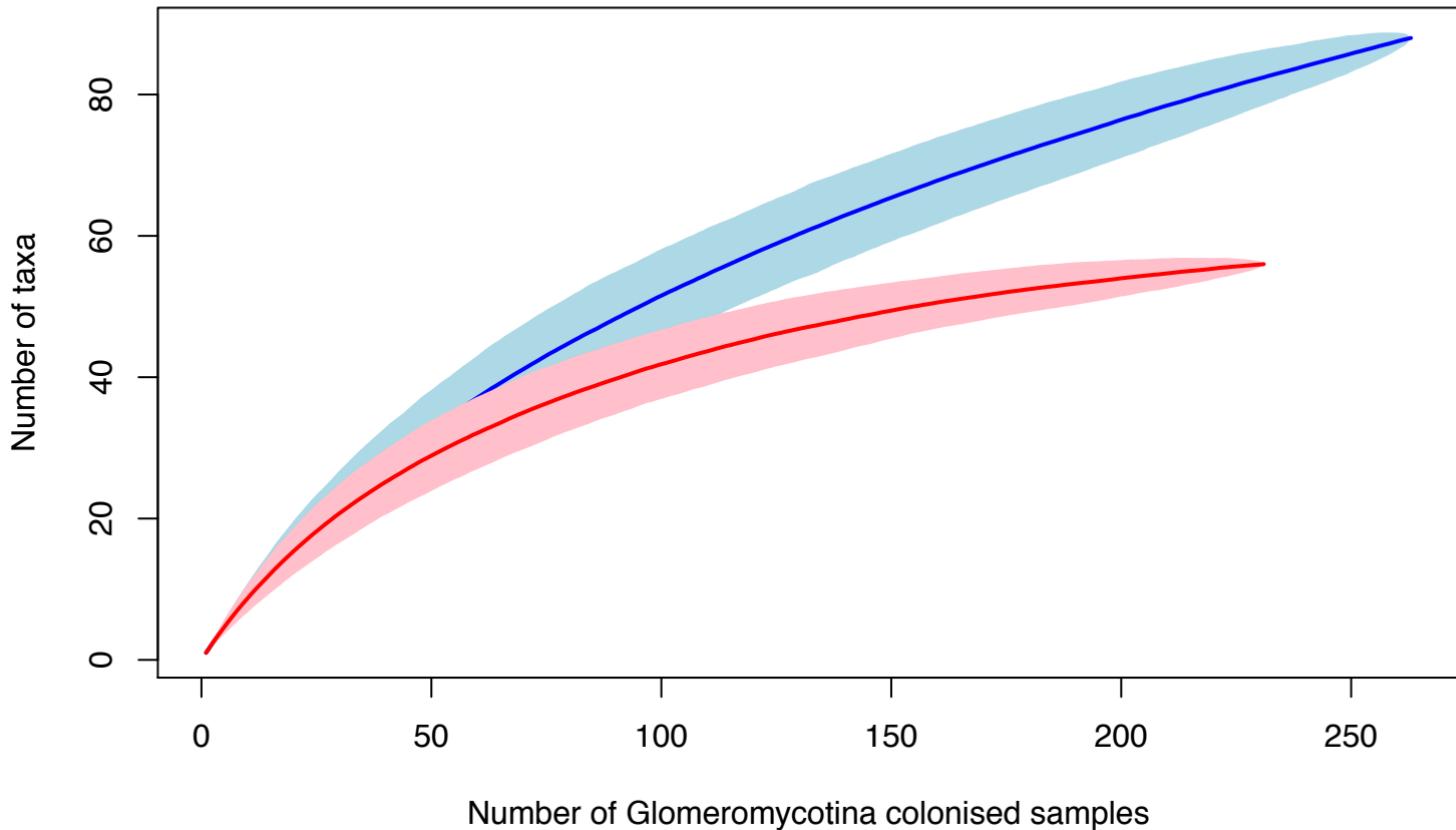


**Figure S4. Summary Bayesian inference phylogeny of Glomeromycotina fungi.**

This phylogenetic tree was used to provide support values for Figure 1. The MrBayes analysis was run for 10,000,000 million generations with the nst=6 model and invgamma rates.

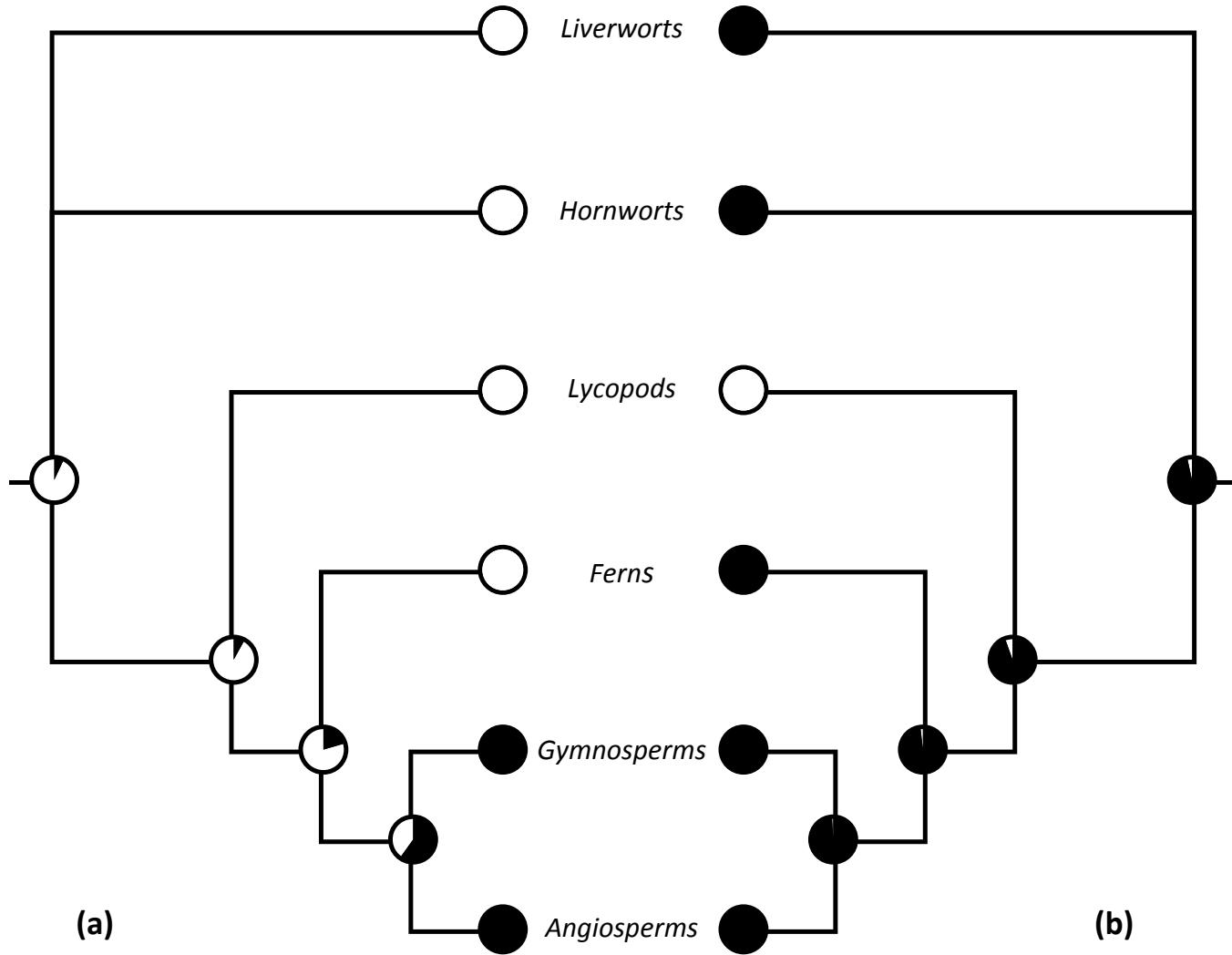


**Figure S5. Species accumulation curve of Glomeromycotina that colonise liverworts.** In blue are the results of using epGT and singletons and in red is the curve of only using epGT. The confidence intervals from 1,000 random permutations can be seen in the highlighted areas.



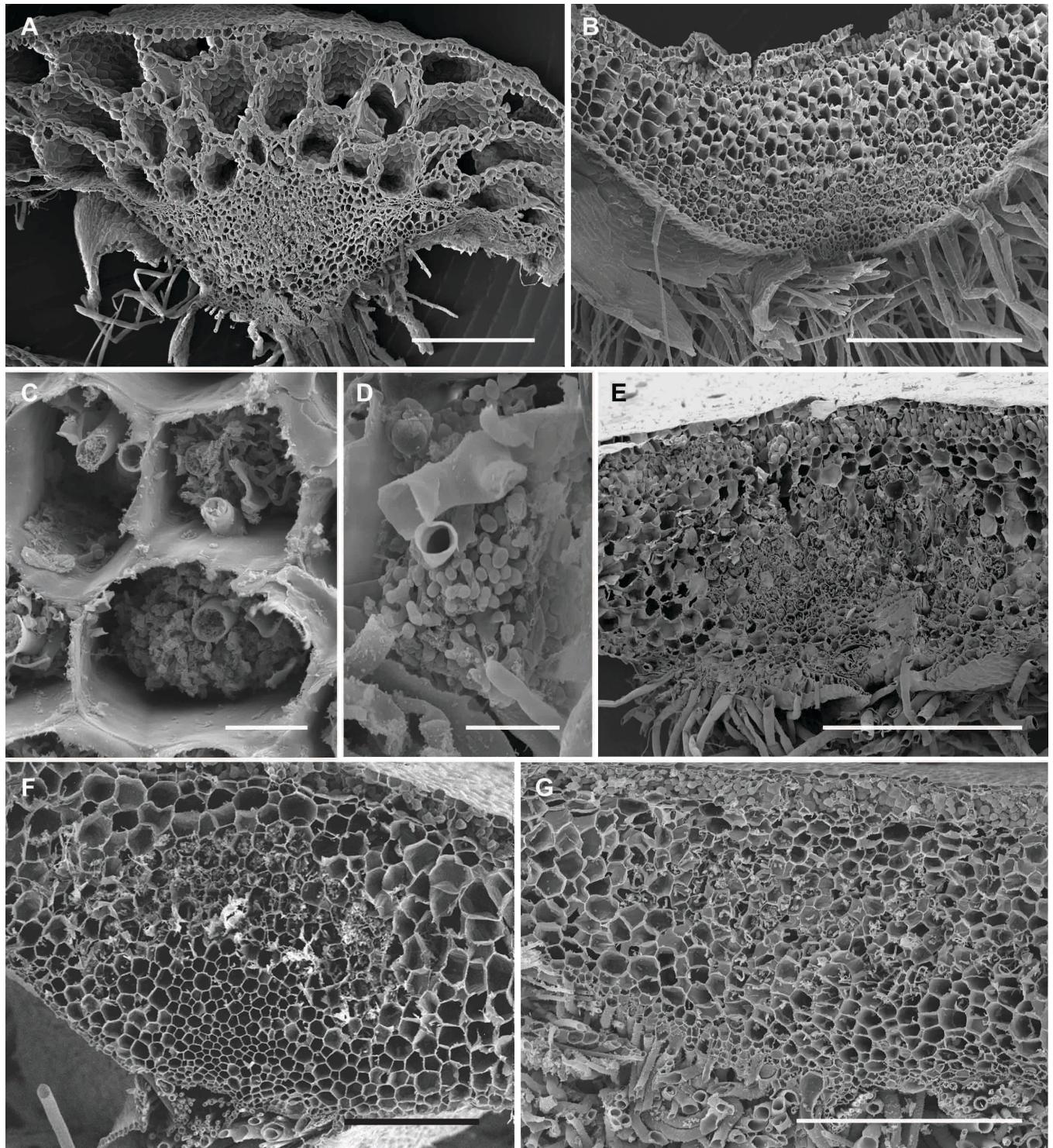
**Figure S6. Ancestral reconstruction of early-diverging Glomeromycotina lineages**

**in plants.** Black circles indicate the plant group has been shown, using molecular methods, to contain Glomeromycotina fungi that originated before the plant while white indicates they have not. (a) Our state of knowledge before this study and (b) our knowledge now.

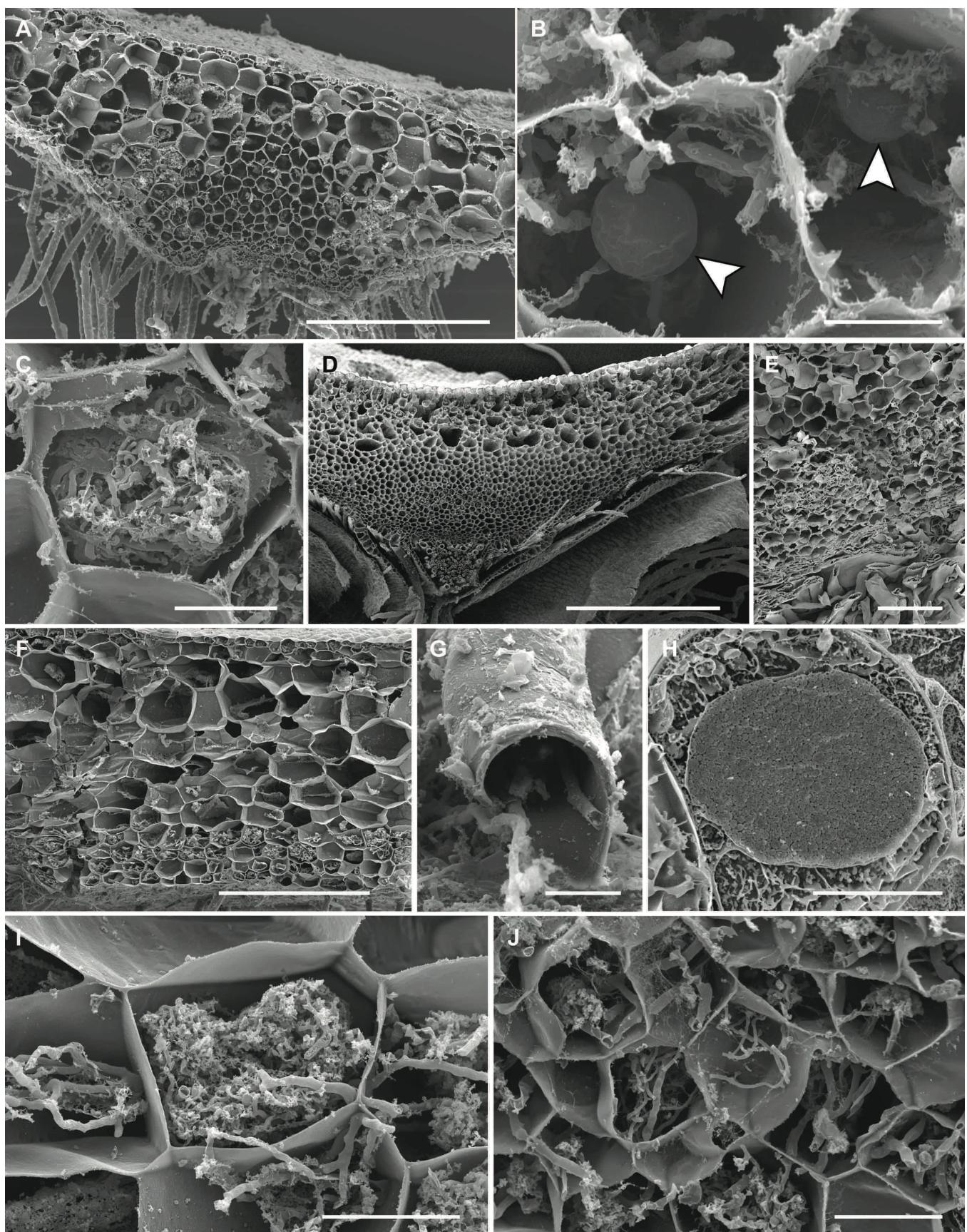


**Figure S7. Cytology of Glomeromycotina associations in Marchantiopsida**

**(complex thalloid) liverworts.** Scanning electron micrographs of cross sections through thalli of (A) *Neohodgsonia mirabilis*; (B, C) *Lunularia cruciata*; (D, E) *Marchantia pappeana*; (F) *M. foliacea*; (G) *M. paleacea*. Fungal colonisation usually occupies the thallus central midrib (A, E, F, G) and is sometimes confined to a region overarching the midrib hyaline strand (F). In some taxa, e.g. *L. cruciata* (B), fungal colonisation is restricted to the thallus ventral cell layers. (C, D) ‘Typical’ arbuscules terminal on trunk hyphae in *L. cruciata* (C) and *M. pappeana* (D). Scale bars: (A, B, E, G) 500 µm; (F) 250 µm; (C, D) 10 µm.

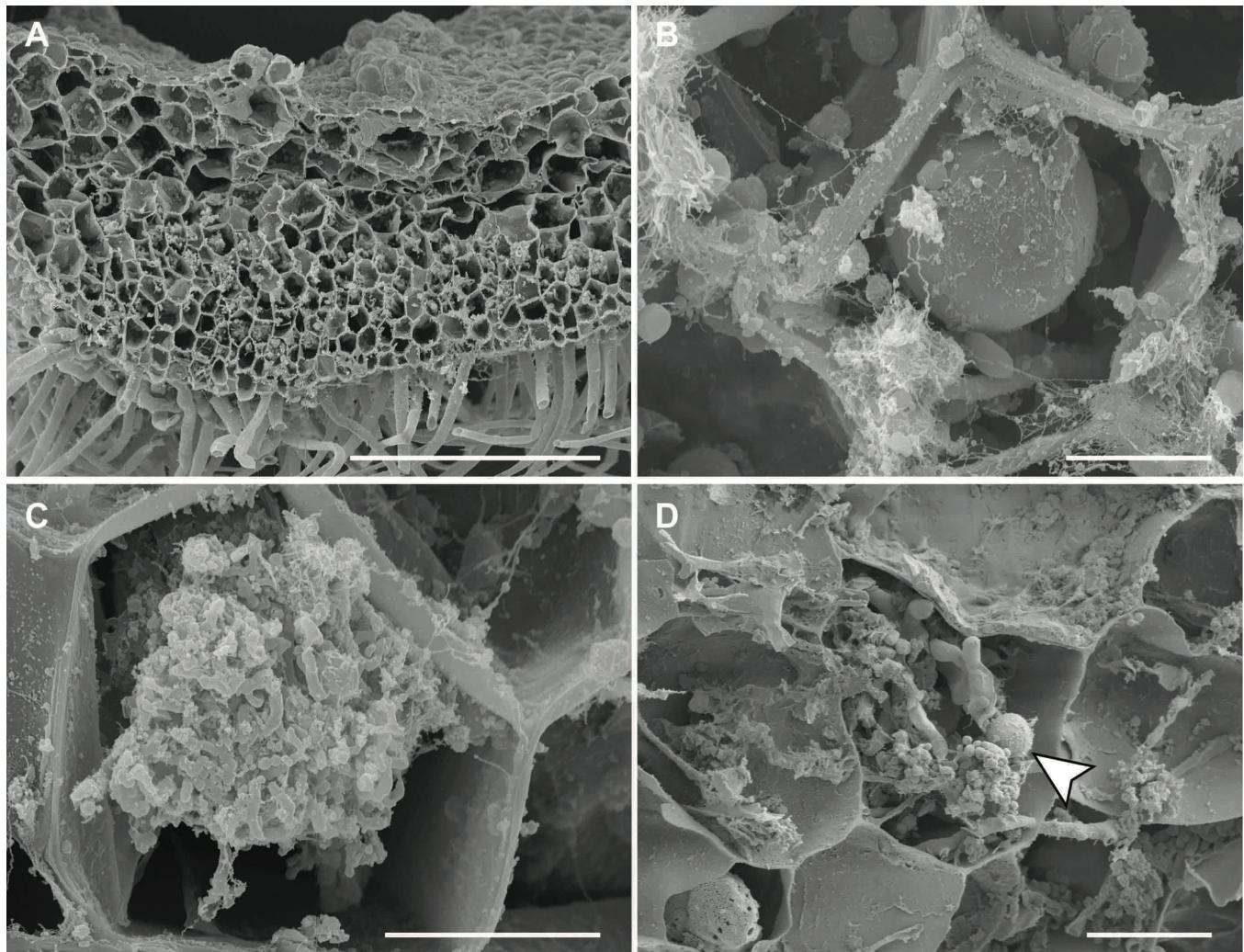


**Figure S8. Cytology of Glomeromycotina associations in Marchantiopsida (complex thalloid) liverworts, cont.** All scanning electron micrographs (except (H)) cryo-scanning electron micrograph) of cross sections through thalli (except (G) rhizoid) of (A-C) *Dumortiera hirsuta*; (D) *Asterella australis*; (E) *Plagiochasma rupestris*; (F-I) *Monoclea forsteri*; (J) *Conocephalum conicum*. Fungal colonisation in the region overarching the midrib hyaline strand in *D. hirsuta* (A), the central midrib in *A. australis* (D) and the ventral cell layers in *P. rupestris* (E) and *M. forsteri* (F). In *M. forsteri* the fungal zone extends right across the midribless thallus (F). Fungal structures include vesicles (B, arrowed), coils (C), arbusculated coils (I) and hyphae of varying diameters (J). Fungal entry is invariably via rhizoids (G) while oil bodies idioblasts are always free of fungal structures, shown here in an idioblast in *M. forsteri* (H). Scale bars: (A, D, F) 500 µm; (E) 100 µm; (I, J) 50 µm; (B, C, G) 20 µm; (H) 10 µm.



**Figure S9. Cytology of Glomeromycotina associations in Pelliidae (simple thalloid**

**I) liverworts.** Scanning electron micrographs of cross sections through thalli of (A-C) *Pellia epiphylla*; (D) *Sewardiella tuberifera*. Fungal colonisation in Pelliidae liverworts generally occupies the thallus midrib (A) and produces the same range of structures as in Marchantiopsida liverworts, including vesicles of varying sizes, with the largest observed in *P. epiphylla* (B) and the smallest in *S. tuberifera* (D, arrowed), and arbusculated coils (C). Scale bars: (A) 500 µm; (B-D) 20 µm.



**Figure S10. Cytology of Glomeromycotina associations in Pelliidae (simple thalloid I) liverworts, cont.** Scanning electron micrographs of cross sections through thalli of (A, C-F) *Fossombronia foveolata*; (B) *F. husnotii*; (G) *Allisonia cockaynei*; (H, I) *Pallavicinia xiphoides*; (J) *Symphyogyna brasiliensis*. Fungal structures are randomly distributed in the thallus midrib (A, G) and in *Fossombronia* consist of arbuscules with terminal ramification that are either fine (B) or resembling miniature cauliflowers (C, arrowed) and hyphae of varying dimensions (D), sometimes forming tightly wound coils (E) or with small terminal swellings (F, arrowed). In members of the Pallaviciniaceae fungal colonisation is restricted to the one hemisphere of the subterranean radial axes from which the rhizoids develop (H) and consists of both coils (I) and arbuscules (J). Scale bars: (G) 500 µm; (H) 250 µm; (A, I) 100 µm; (B, D-F, J) 20 µm; (C) 10 µm.

