

Supplementary Information (SI) for the paper submitted to
Microbial Ecology:

**Basal fungal clades are everywhere: what 18S
rRNA gene metabarcoding reveals about cross-
system distribution of fungi**

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Fig. S1. Reference phylogenetic tree of fungi and other Opisthokonta based on long 18S rRNA gene sequences. The tree was built using IQ-TREE with SYM+R10 model using 1031 Opisthokonta sequences and 12 outgroup sequences (clustered at 99% identity and 95% for Metazoa). Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

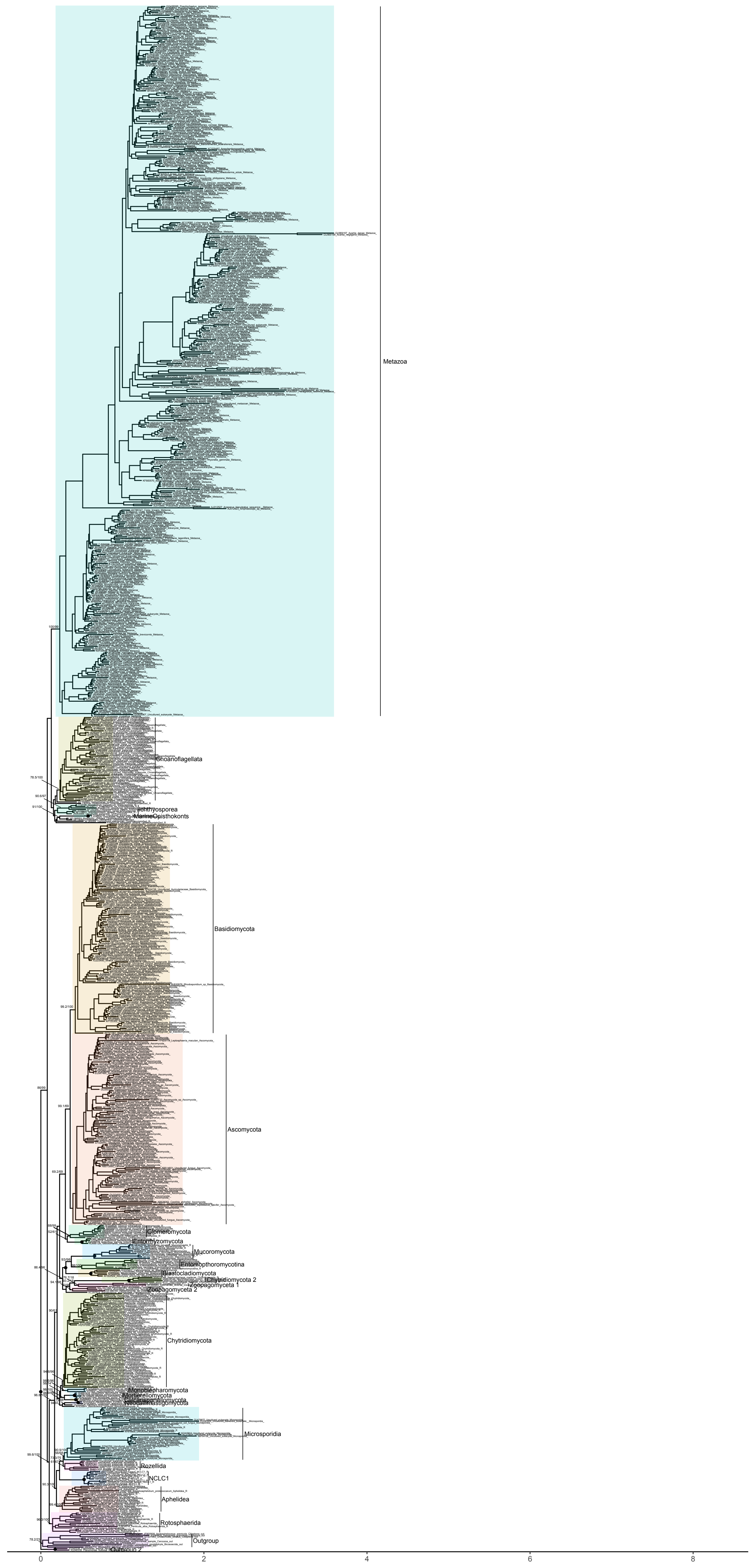
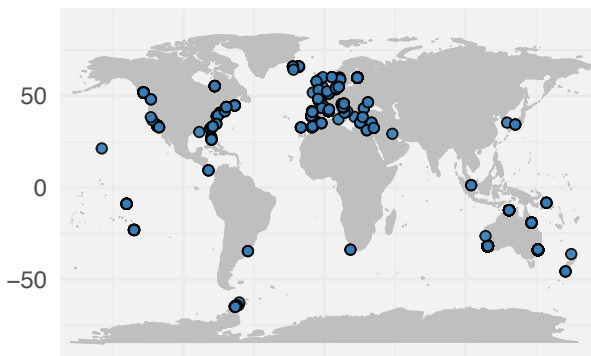


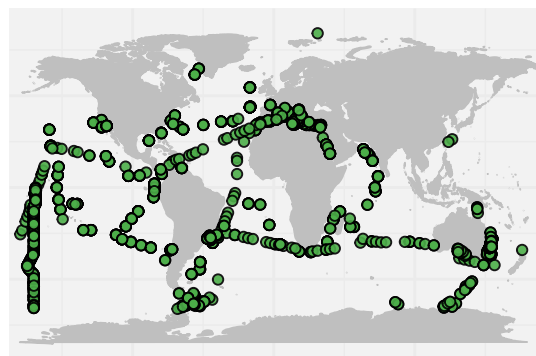
Fig. S2. World maps showing the geographic distribution of samples, grouped and displayed separately by habitat type.

Latitude (°)

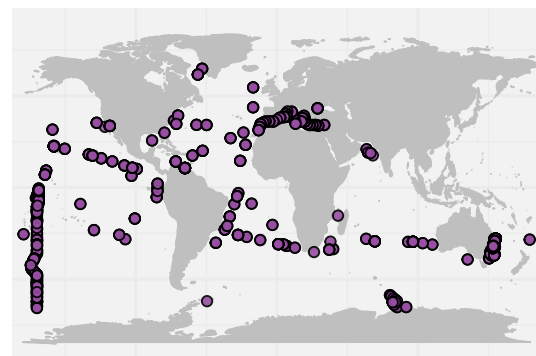
coastal marine water (n=1573)



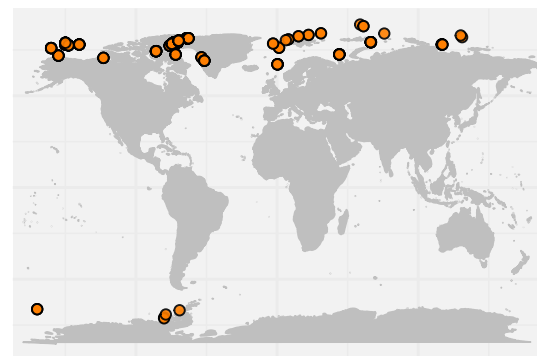
oceanic surface water (n=1562)



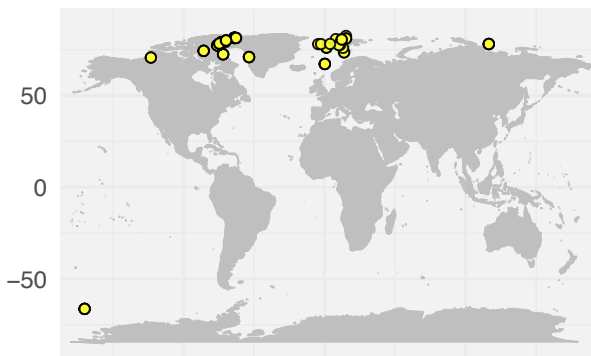
oceanic deep water (n=858)



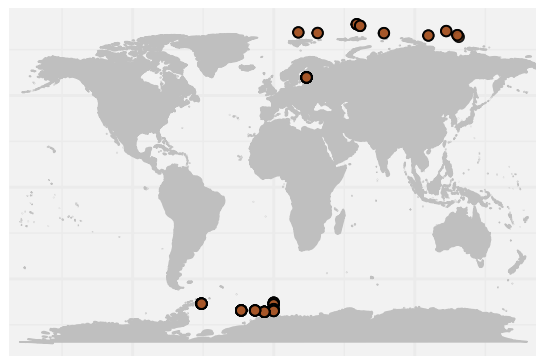
polar oceanic surface water (n=247)



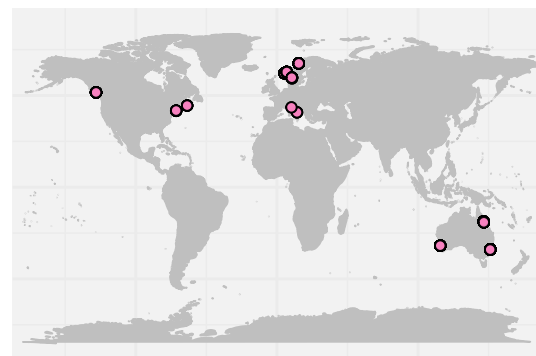
polar oceanic deep water (n=85)



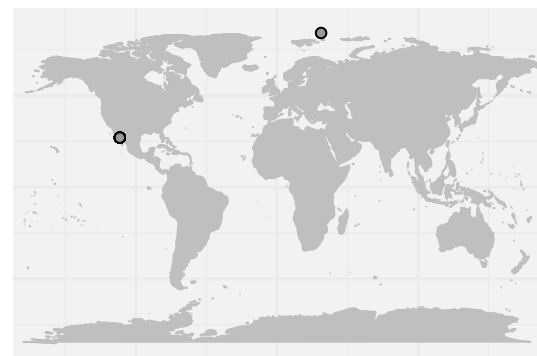
marine ice (n=88)



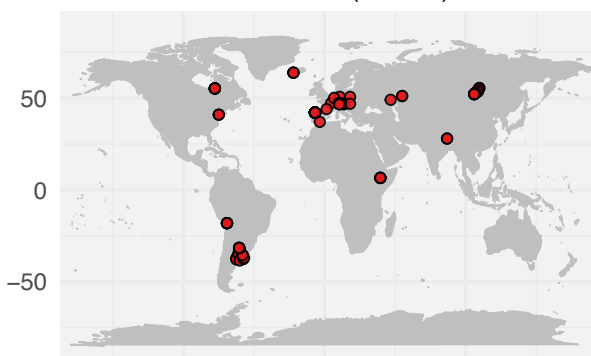
coastal marine sediment (n=504)



deep marine sediment (n=18)



freshwater (n=146)



polar freshwater (n=80)



brackish/saline water (n=59)



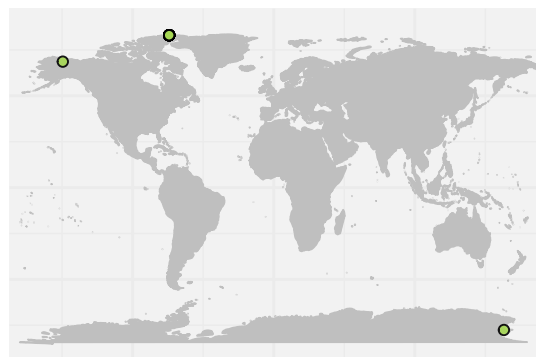
hypersaline water (n=39)



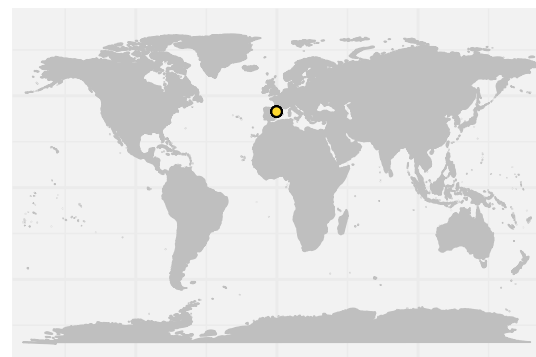
inland aquatic sediment (n=133)



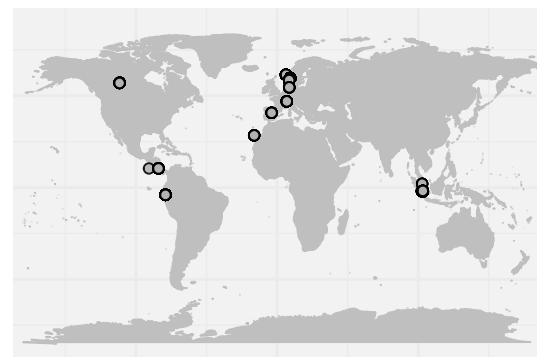
polar inland aquatic sediment (n=20)



hypersaline sediment (n=12)



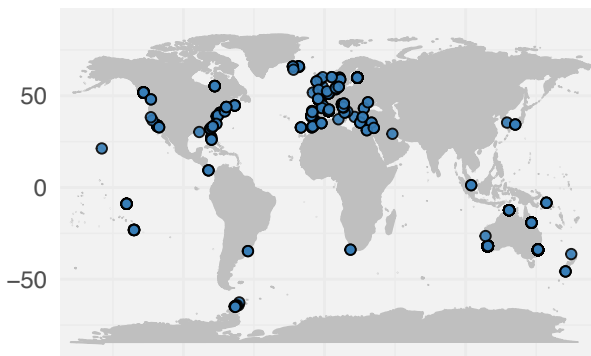
soil (n=730)



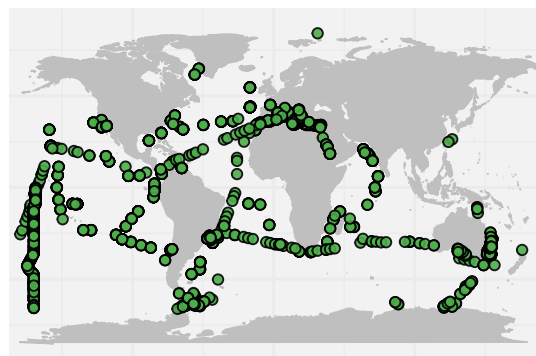
Longitude (°)

Latitude (°)

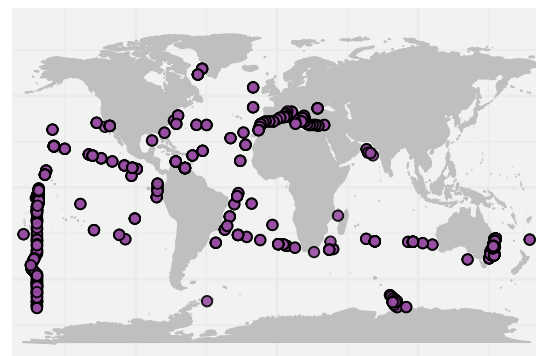
coastal marine water (n=1573)



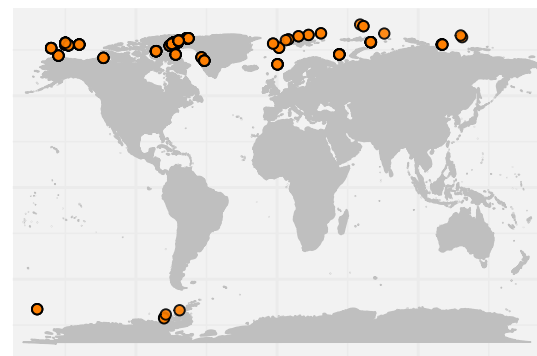
oceanic surface water (n=1562)



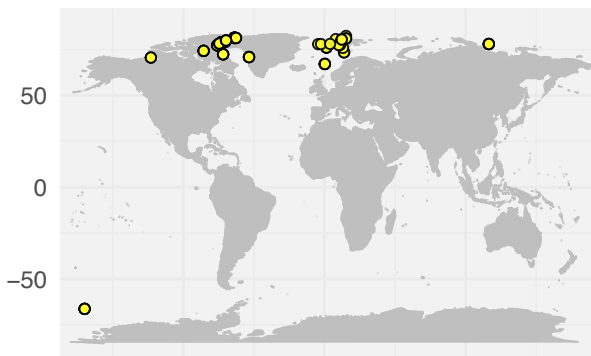
oceanic deep water (n=858)



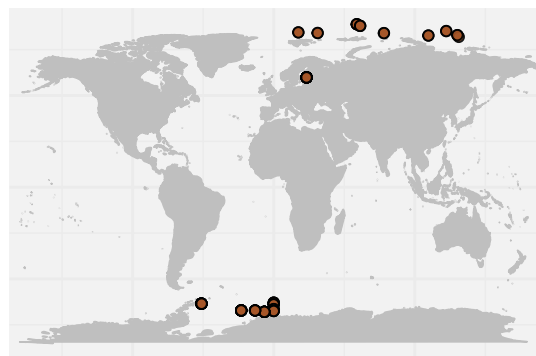
polar oceanic surface water (n=247)



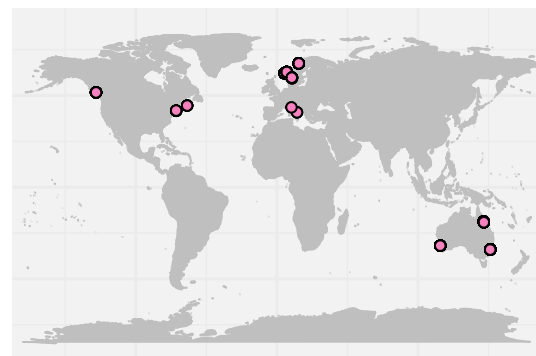
polar oceanic deep water (n=85)



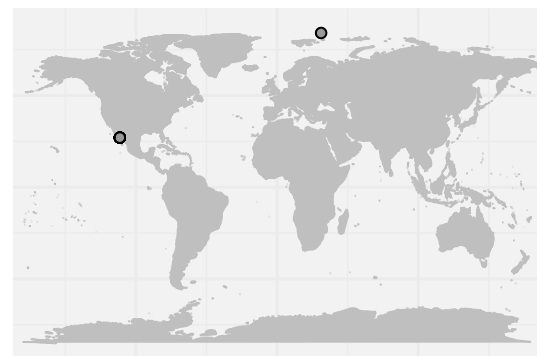
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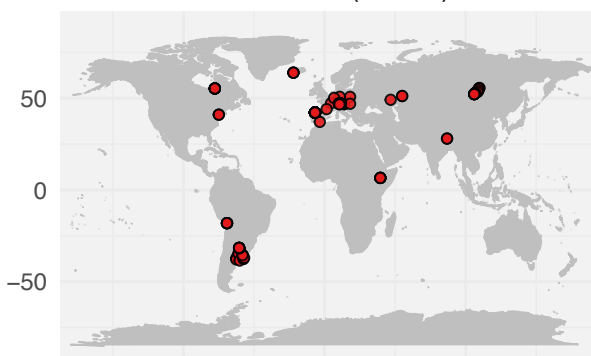
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polar freshwater (n=80)



brackish/saline water (n=59)



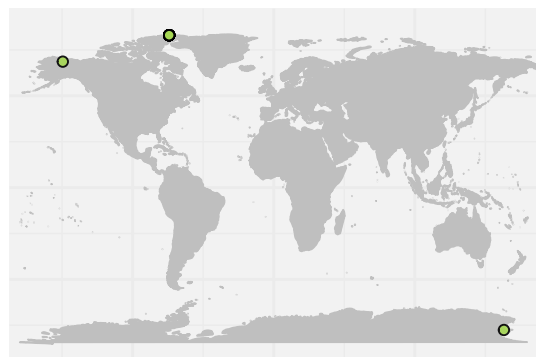
hypersaline water (n=39)



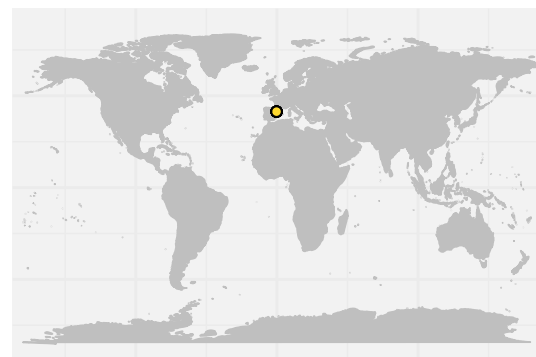
inland aquatic sediment (n=133)



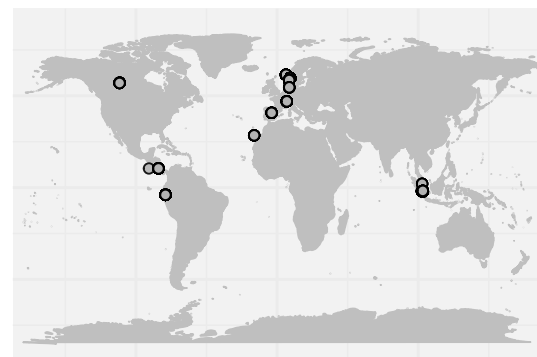
polar inland aquatic sediment (n=20)



hypersaline sediment (n=12)



soil (n=730)



Longitude (°)

Fig. S3. NMDS of samples based on fungal ASVs using Bray–Curtis dissimilarities for three main habitat categories. For this analysis, we considered only those samples that contained a minimum of 100 fungal ASV reads.

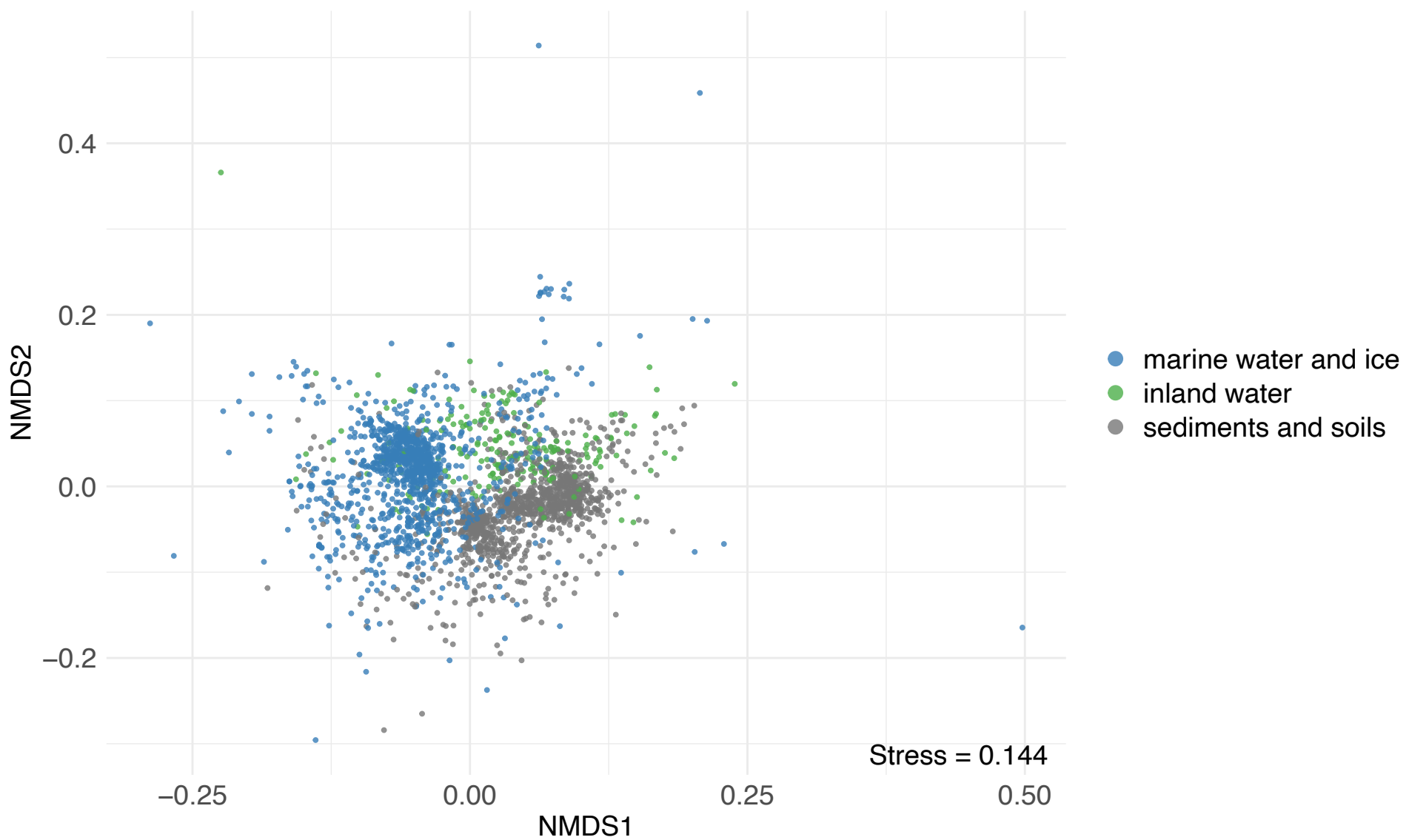


Fig. S4. Relative read abundance of the main fungal groups in various habitats. Each dot represents the pooled relative read abundance of all ASVs assigned to a given group within a sample. Values are shown on a logarithmic scale, with the lowest positive value in the dataset used as a pseudocount. Boxes in plots represent the interquartile range (IQR), with the median line inside. Whiskers extend 1.5 times the IQR and individual points beyond this range represent outliers.

Relative read abundance from all microeukaryotes (%)

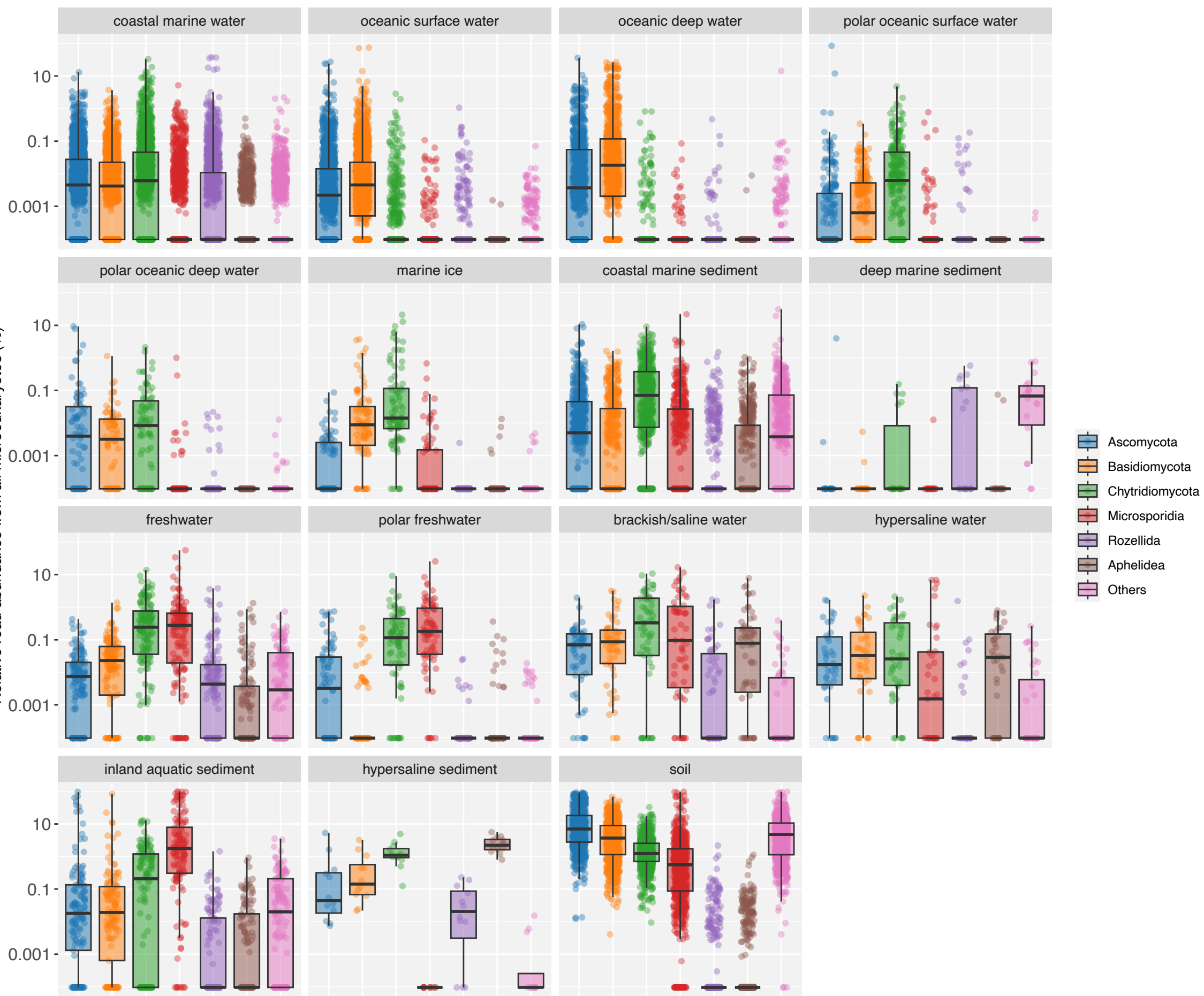
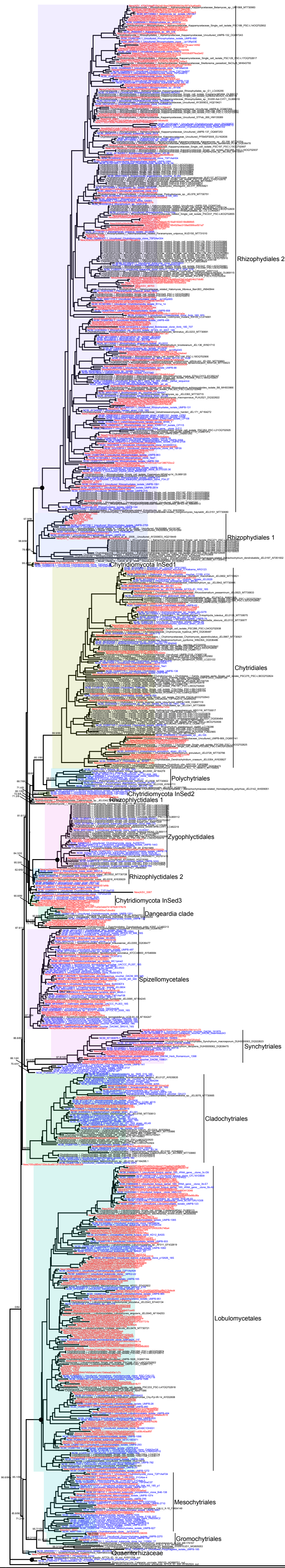


Fig. S5. Reference phylogenetic tree of Chytridiomycota based on the long reference 18S rRNA gene sequences. The tree was built using IQ-TREE with TIM2+F+R10 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

Fig. S6. Phylogenetic tree of Chytridiomycota based on the long and partial reference 18S rRNA gene sequences. In the tree, an alignment of complete reference sequences was first prepared and used to incorporate partial ASVs. ASVs present in more than 0.7% of samples and with a relative abundance greater than 0.1% were included. The tree was built using IQ-TREE with TIM2+F+R10 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.



Rhizophydiales 2

Rhizophydiales 1

Chytridiomycota InSed1

Chytridiales

Polychytriales

Chytridiomycota InSed2

Rhizophyctidiales 1

Zygochytridiales

Rhizophyctidiales 2

Chytridiomycota InSed3

Dangeardiaceae

Spizellomycetales

Synchronytriales

Cladochytriales

Lobulomycetales

Mesochytriales

Gromochytriales

Quarternizaceae

Fig. S7. Reference phylogenetic tree of Microsporidia plus Rozellida based on the long reference 18S rRNA gene sequences. The tree was built using IQ-TREE with GTR+F+R7 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

Fig S8. Phylogenetic tree of Microsporidia plus Rozellida based on the long and partial reference 18S rRNA gene sequences. In the tree, an alignment of complete reference sequences was first prepared and used to incorporate partial ASVs. ASVs present in more than 1% of samples and with a relative abundance greater than 0.1% were included. The tree was built using IQ-TREE with GTR+F+R7 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

Rozellida sensu lato

Fig. S9. Reference phylogenetic tree of Aphelidea based on the long reference 18S rRNA gene sequences. The tree was built using IQ-TREE with TIM2+F+R4 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

Fig. S10. Phylogenetic tree of Aphelidea based on the long and partial reference 18S rRNA gene sequences. In the tree, an alignment of complete reference sequences was first prepared and used to incorporate partial ASVs. All ASVs were included. The tree was built using IQ-TREE with SYM+R6 model. Support values were estimated using 1000 SH-aLRT and 1000 UFBoot replicates.

