

Supplementary Figure S1: Maximum Likelihood tree of fungal 18S rRNA gene sequences. The tree was rooted with sequences of eight species of the *Choanoflagellates*. Branch support was estimated with bootstrap method. Only support values $\geq 50\%$ are indicated. Sequences derived from the KSMP-Kiel culture collection are printed in bold. Color code, contextual data: colored background of fungal taxa, habitat occurrence of fungal taxa; colored lines beside sequence full name, geographical origin of fungal taxa. Subcategories of the geographical origin displayed as letter to the right of the colored stripe. *, wrong full name annotation of sequence.

Figure 1: Subsection of *Tremellomycetes*

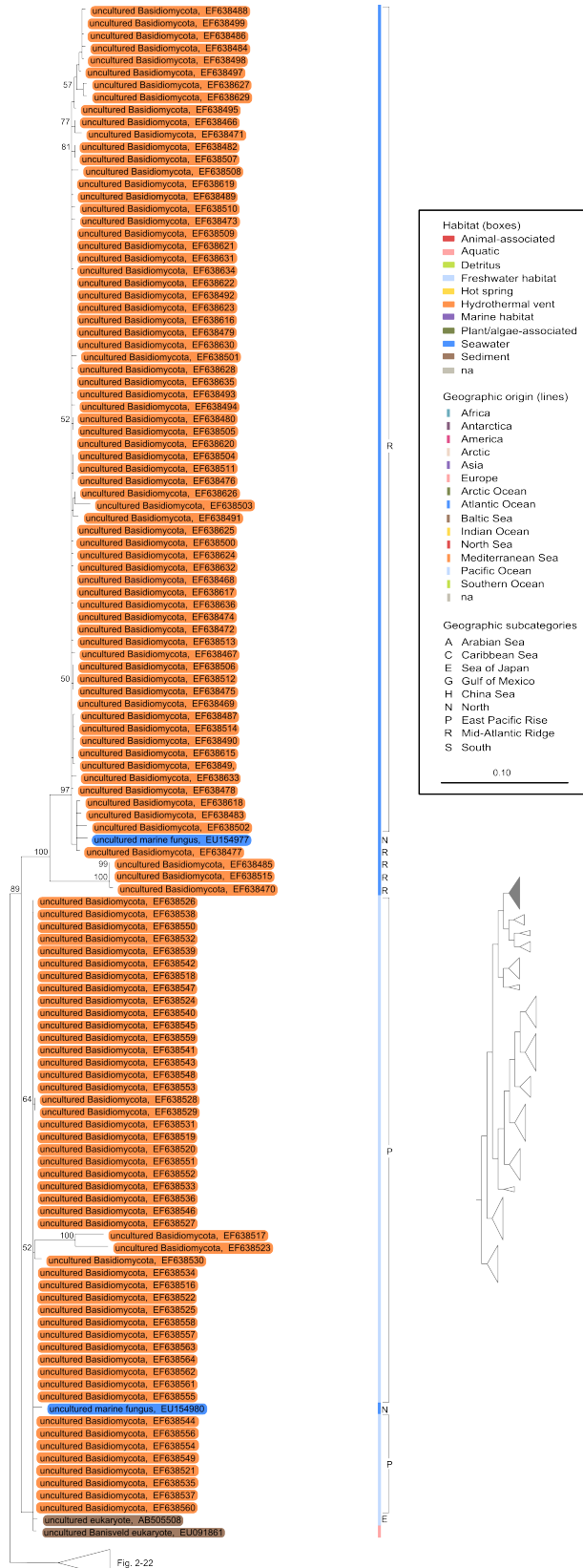


Figure 2: Subsection of *Agaricomycotina*

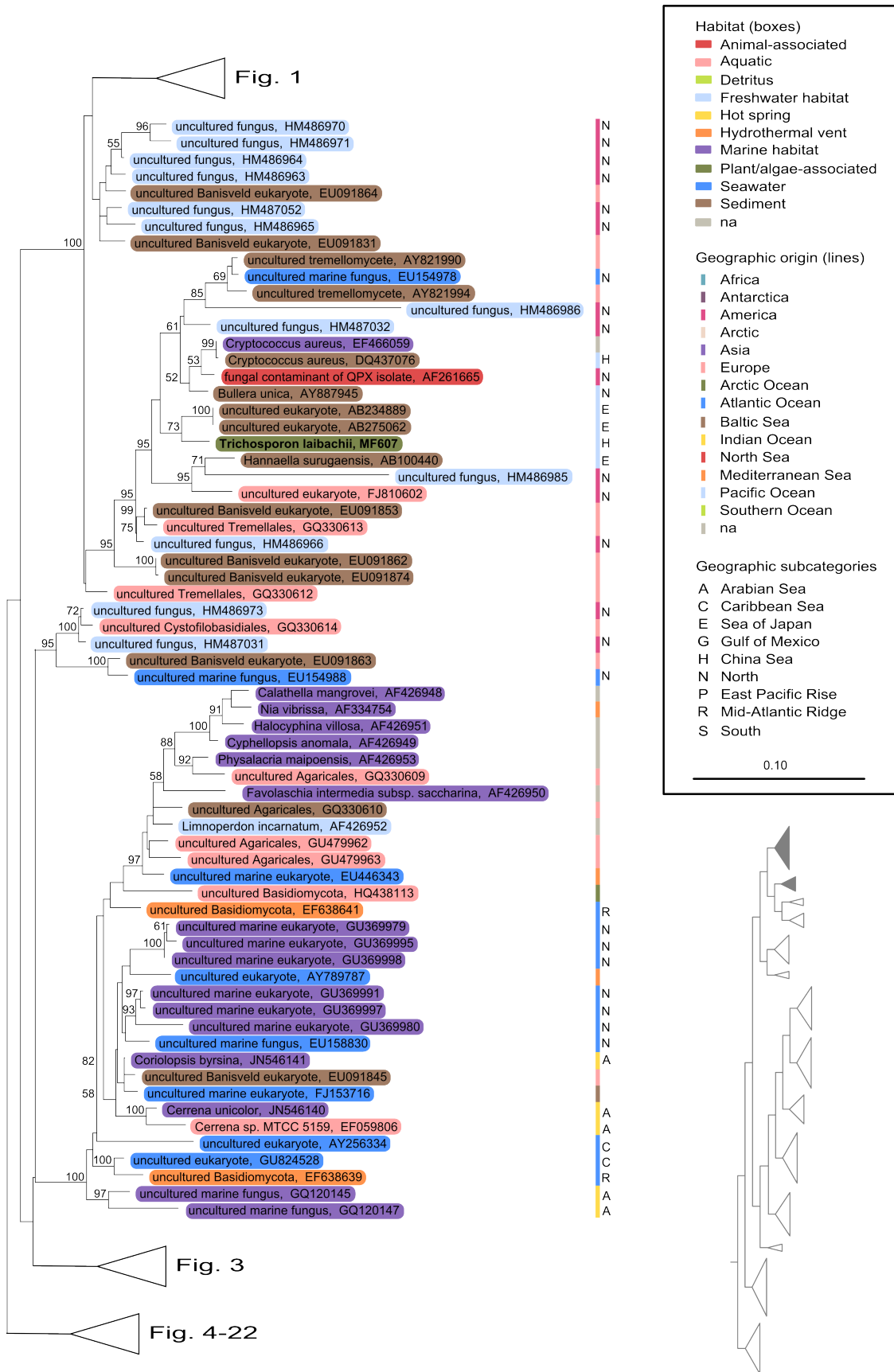


Figure 3: Subsection of *Pucciniomycotina*

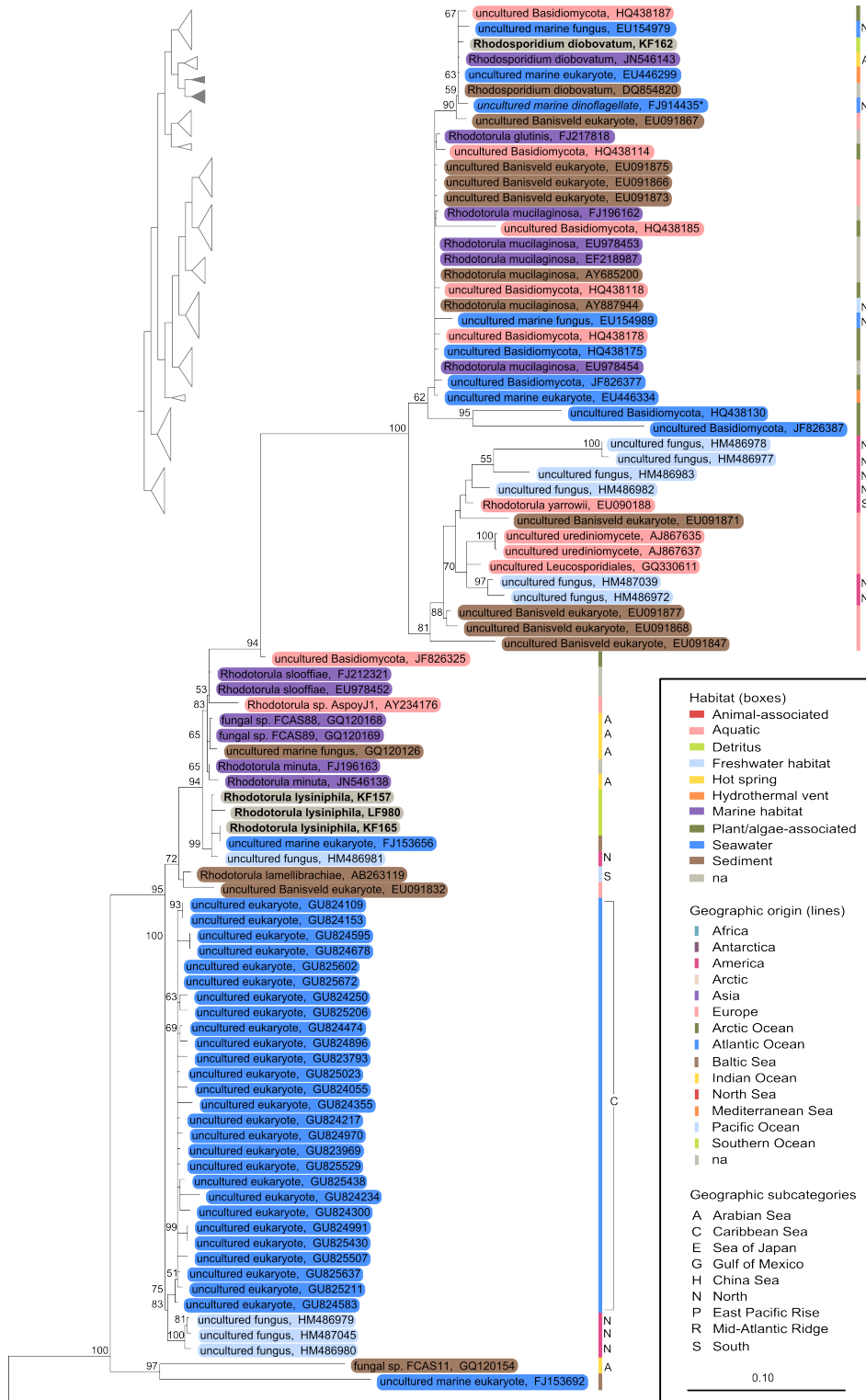


Fig. 1,2,4-22

Figure 4: Subsection of *Exobasidiomycetes*

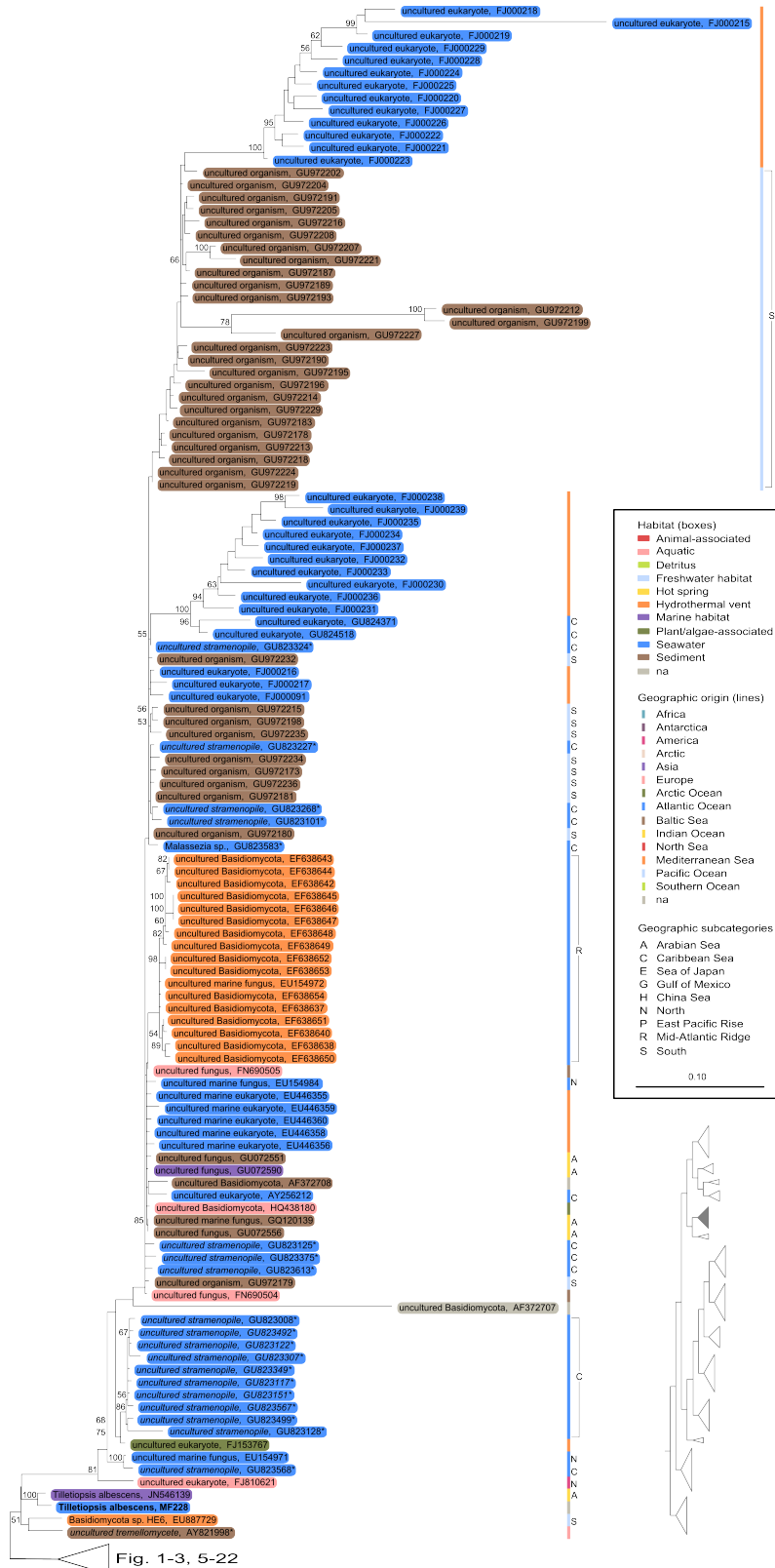


Figure 5: Subsection of *Ustilaginomycetes*

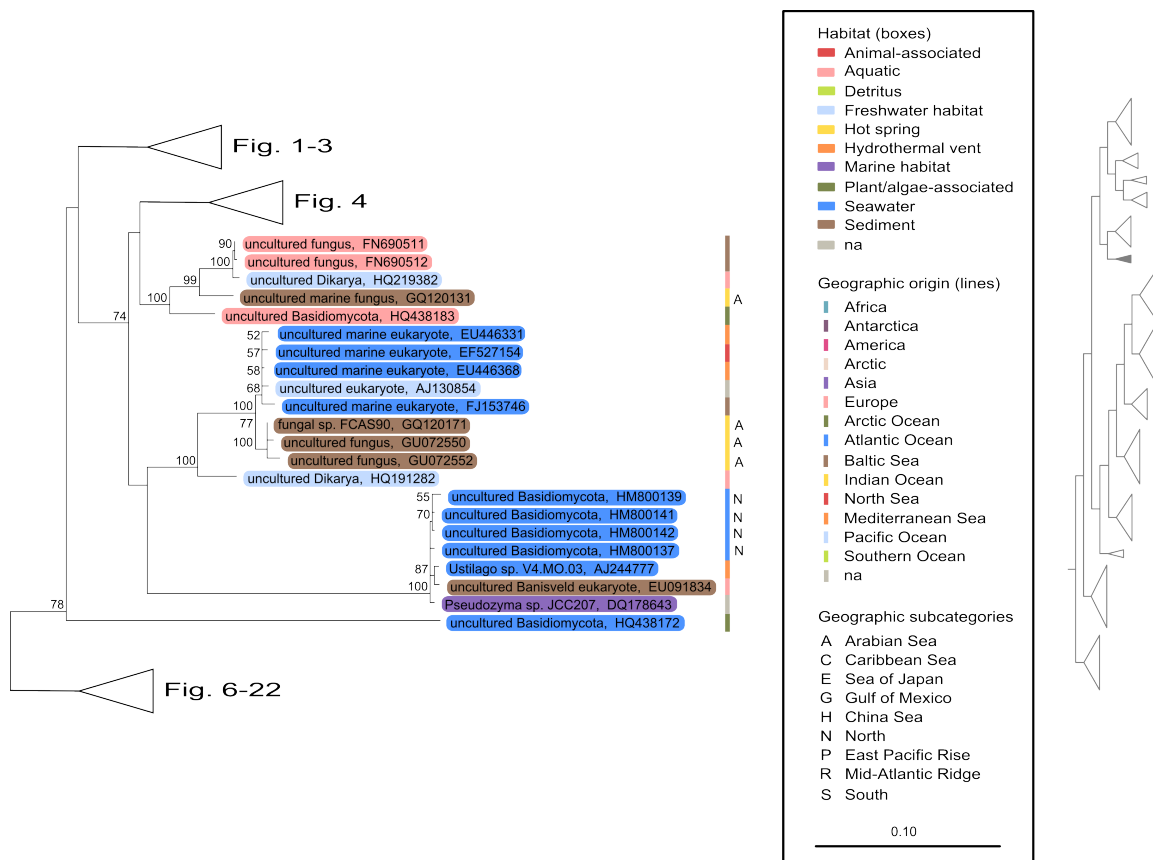


Figure 6: Subsection of *Eurotiomycetes*

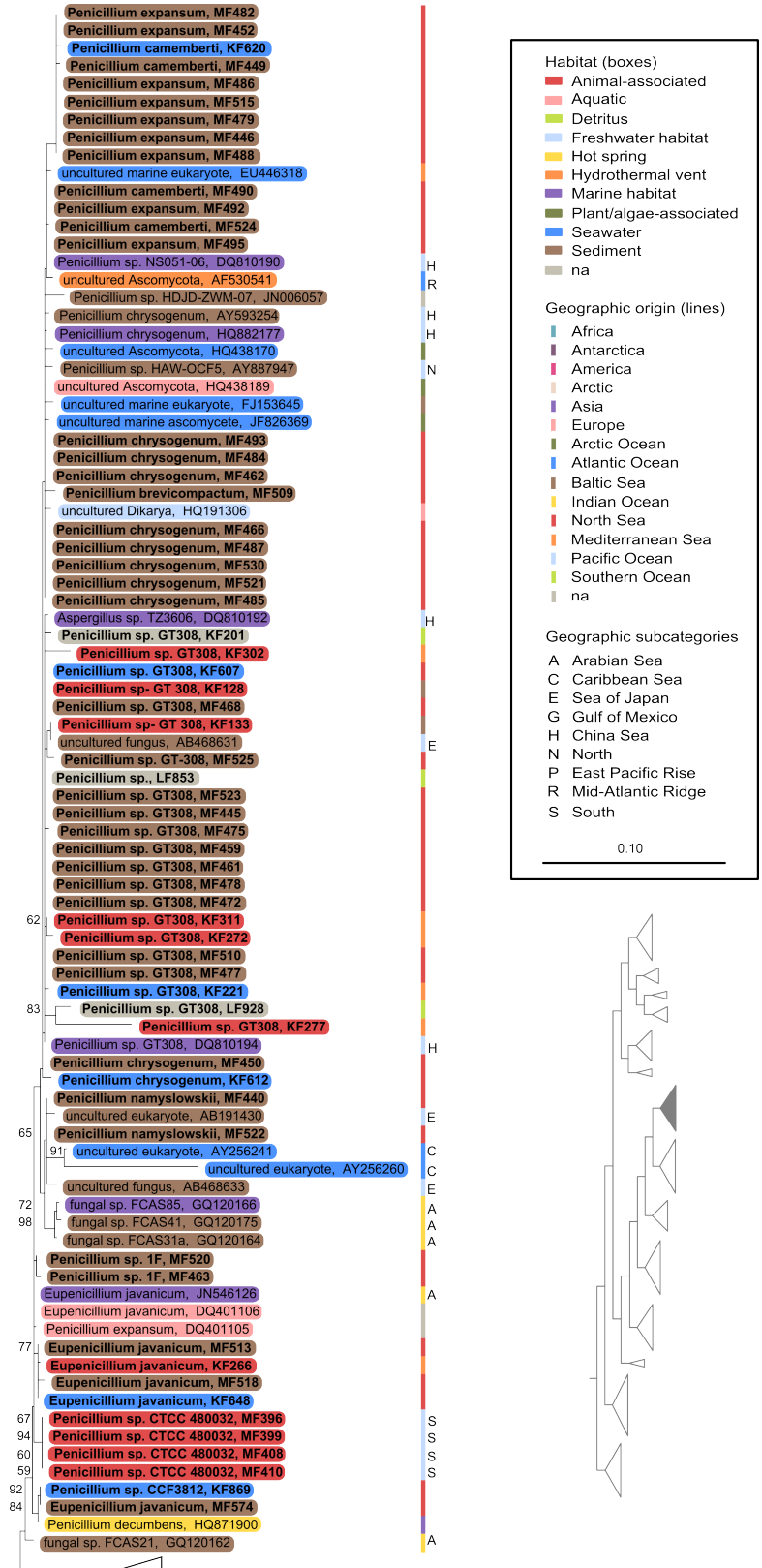


Figure 7: Subsection of *Eurotiomycetes*

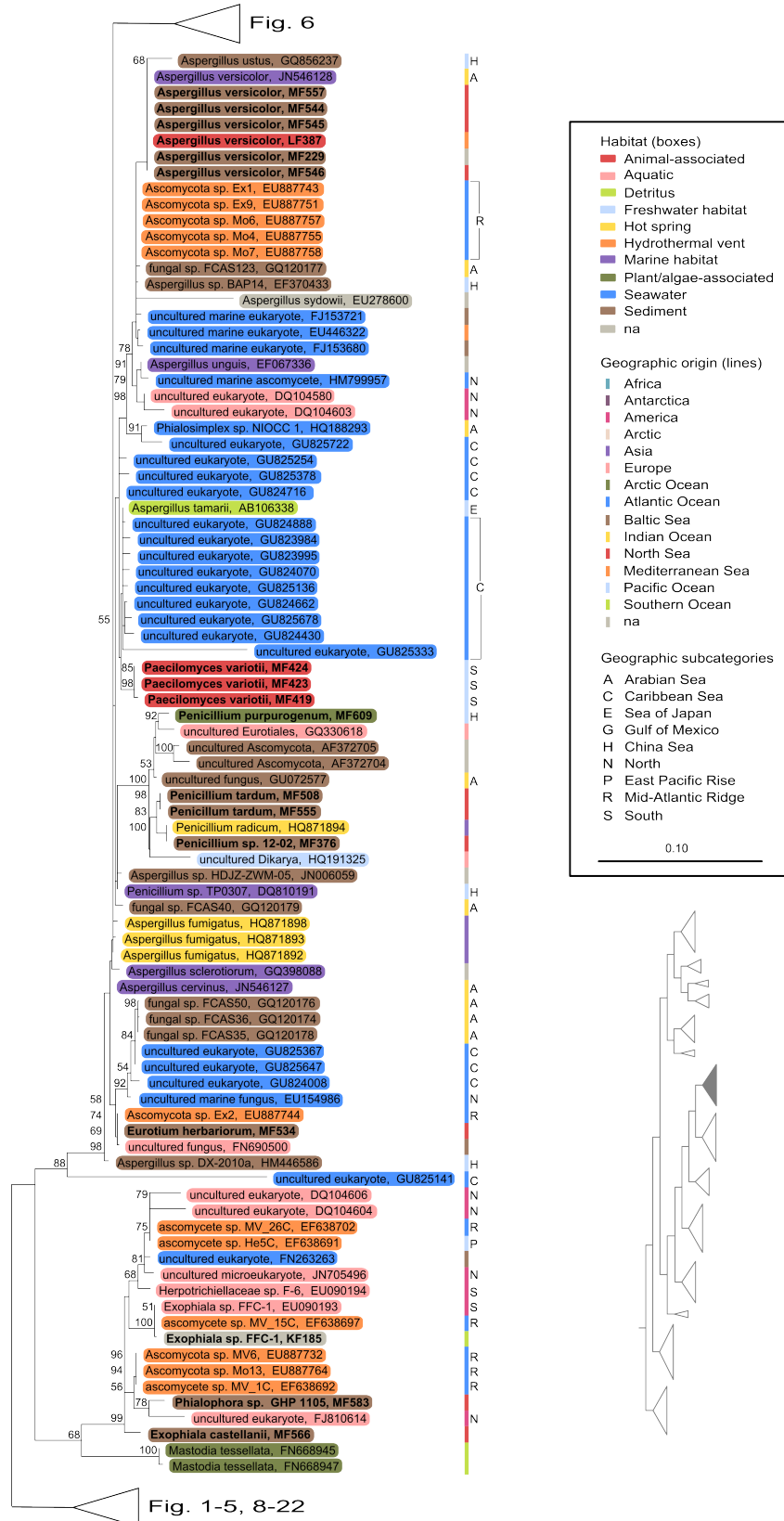


Figure 8: Subsection of *Dothideomycetes*

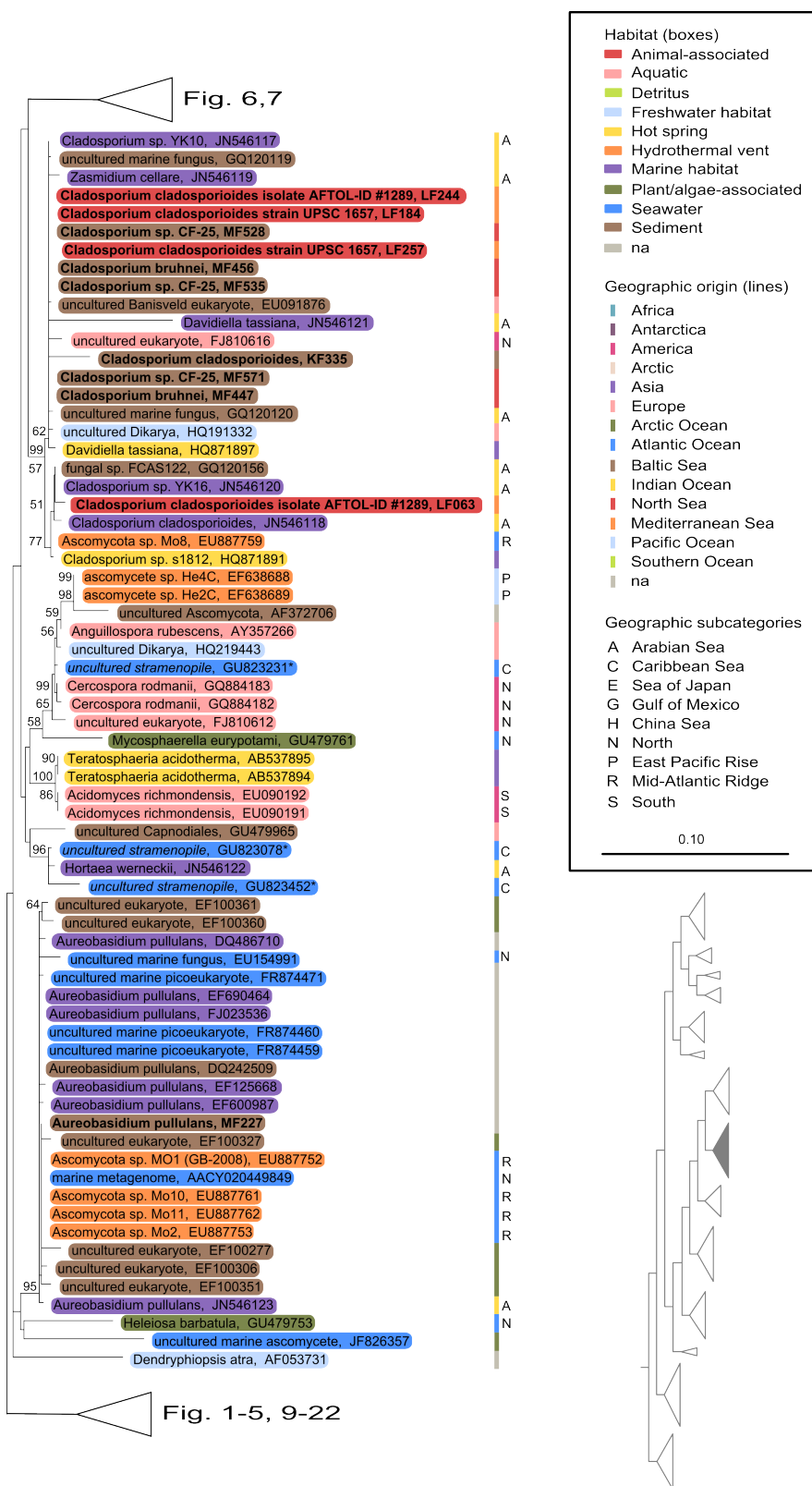


Figure 9: Subsection of *Dothideomycetes*

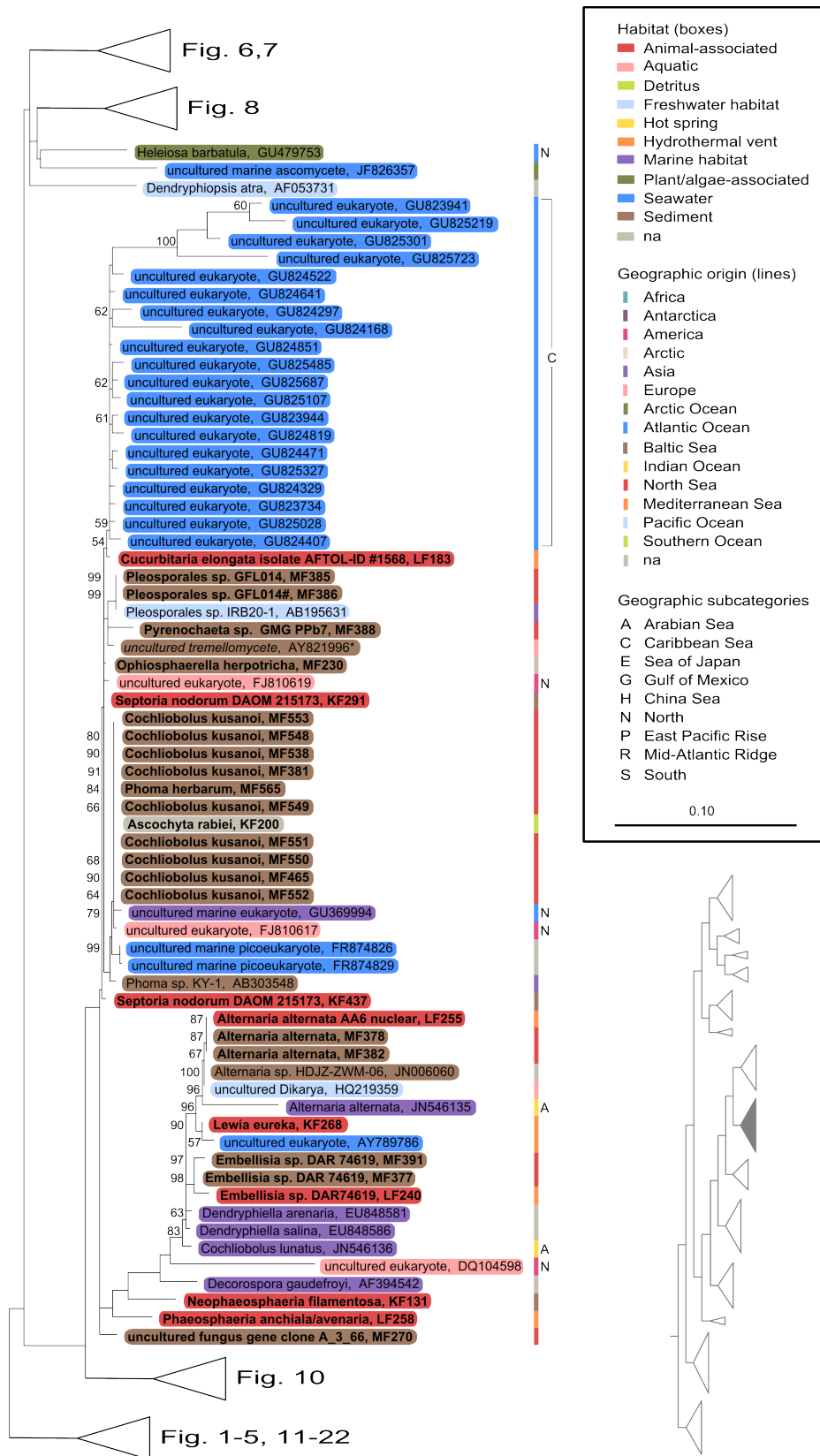


Figure 10: Subsection of *Dothideomycetes*

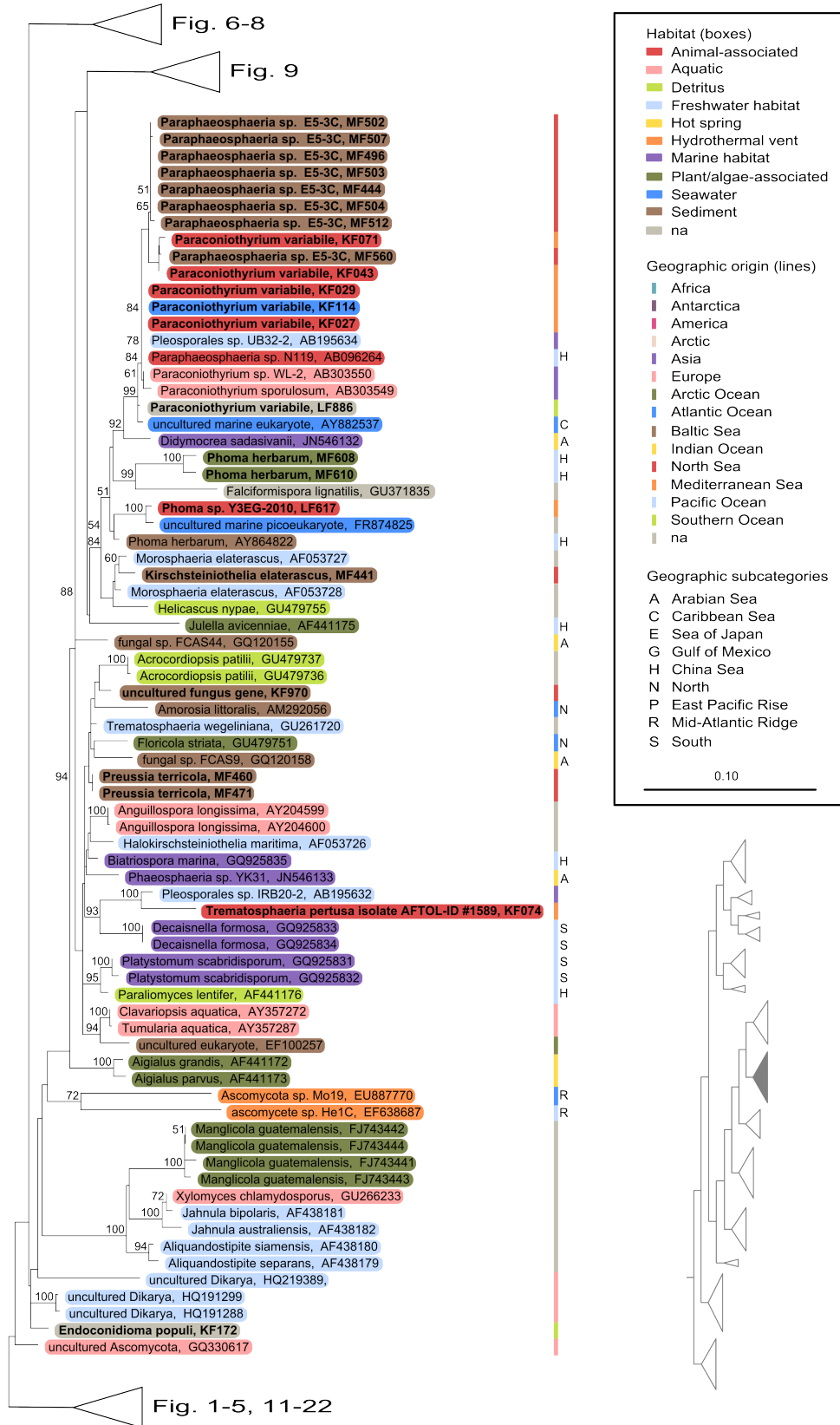


Figure 11: Subsection of *Leotiomyces*

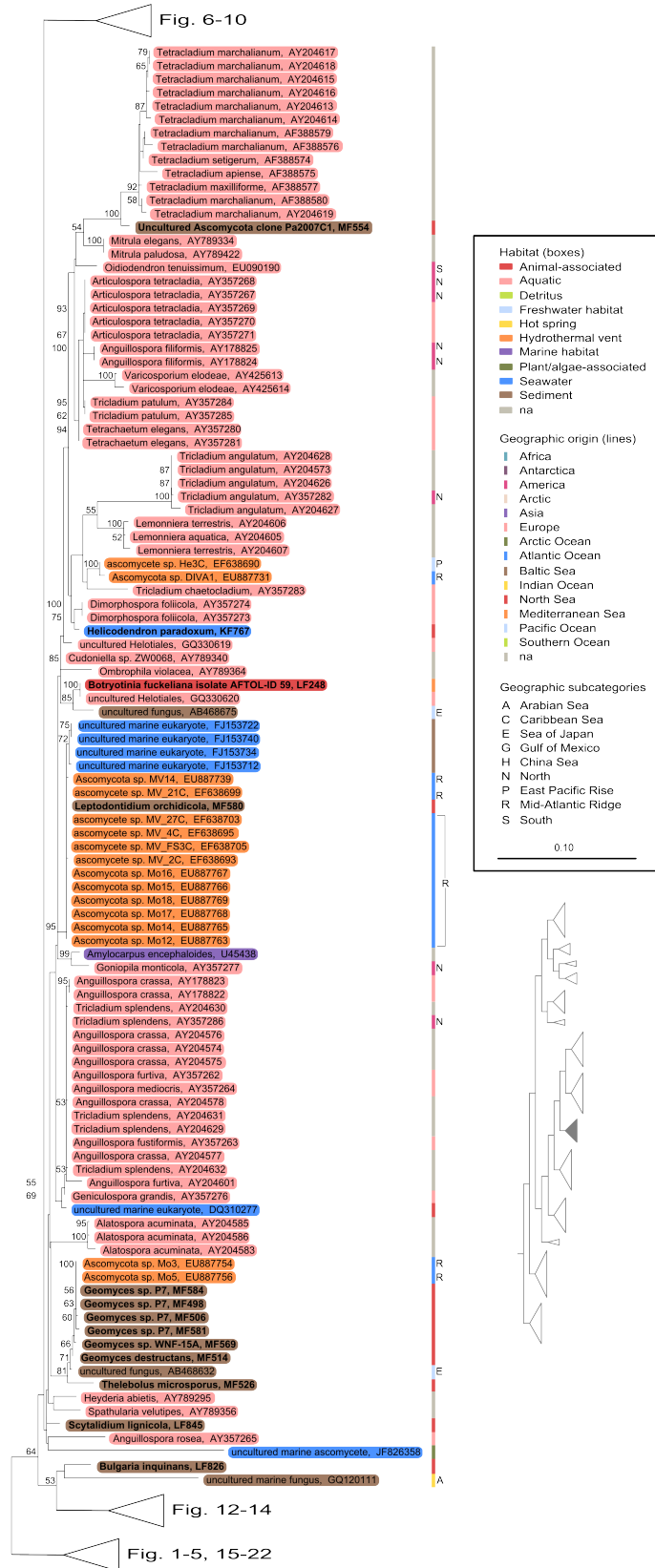


Figure 12: Subsection of *Sordariomycetes*

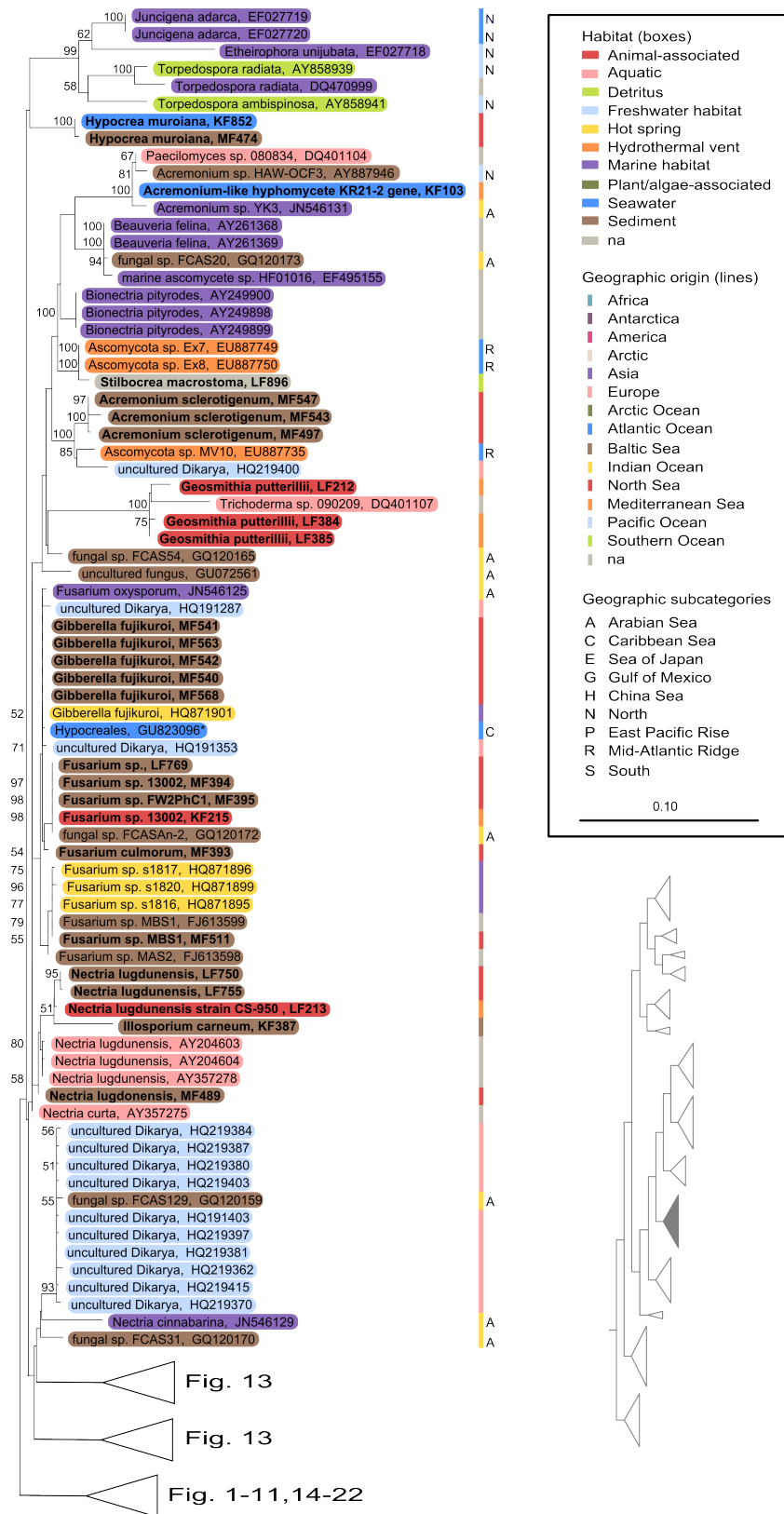


Figure 13: Subsection of *Sordariomycetes*

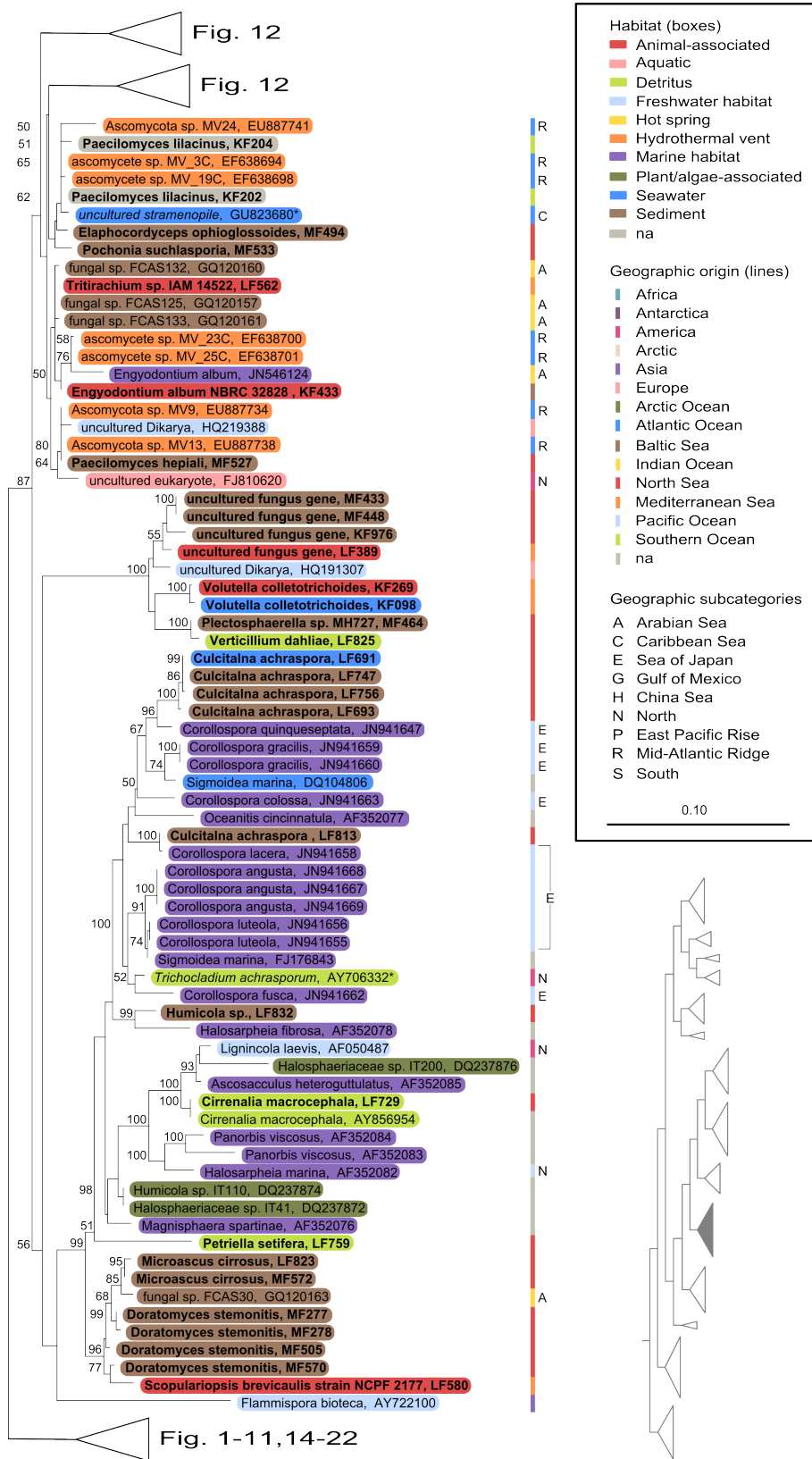


Figure 14: Subsection of *Sordariomycetes*

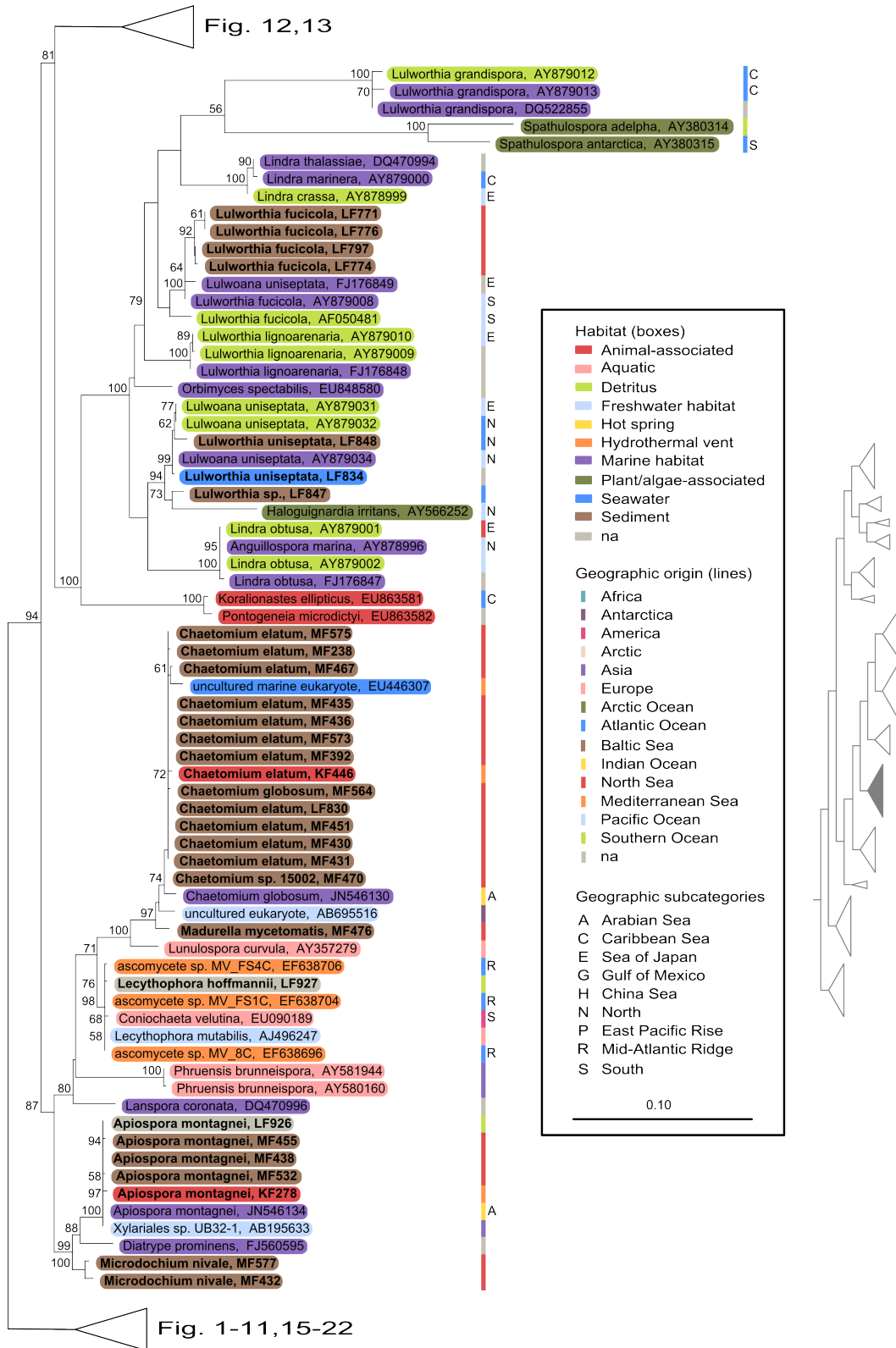


Figure 15: Subsection of *Saccharomyces*



Figure 16: Subsection of *Saccharomyces*

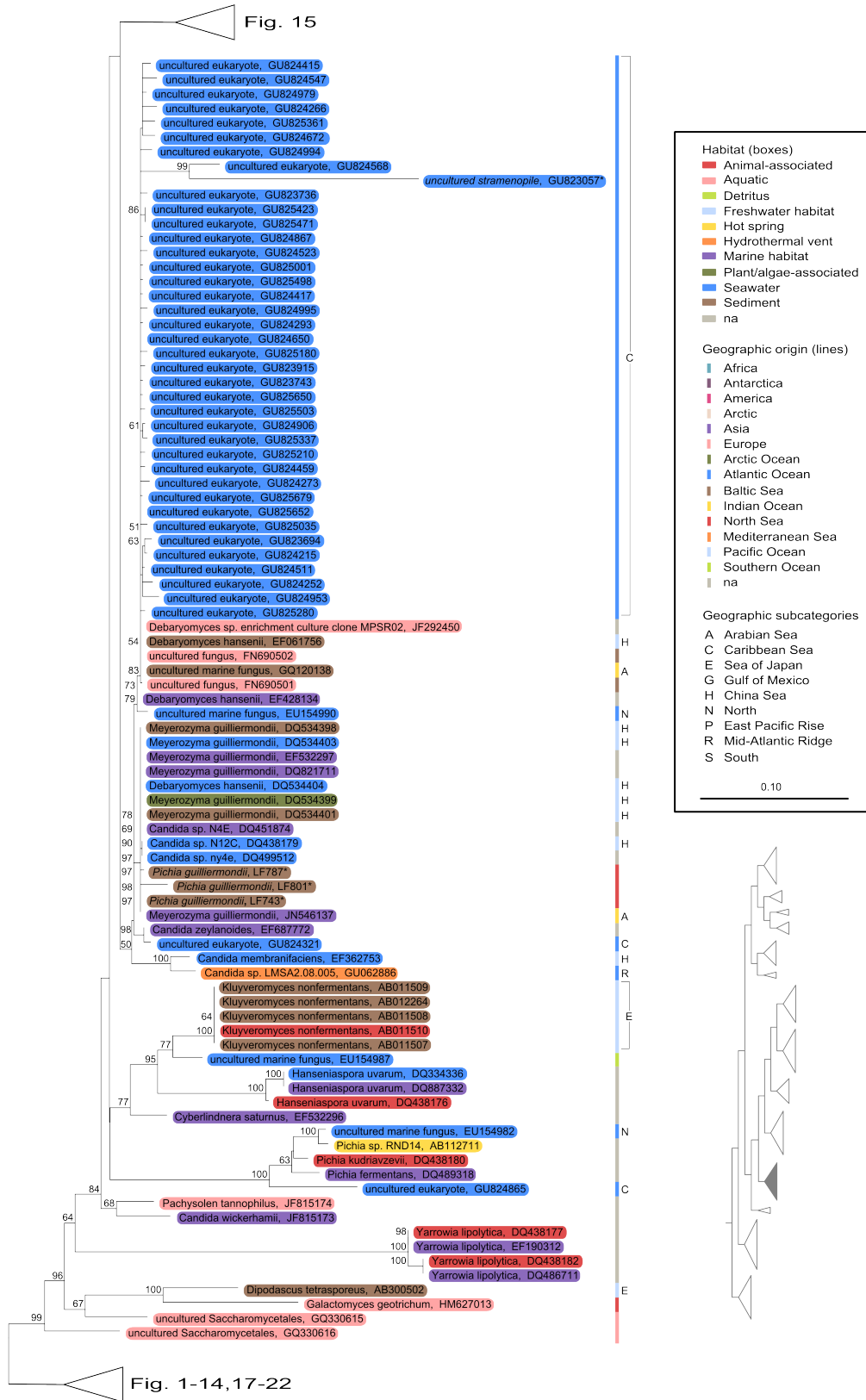


Figure 17: Subsection of *Taphrinomycotina*

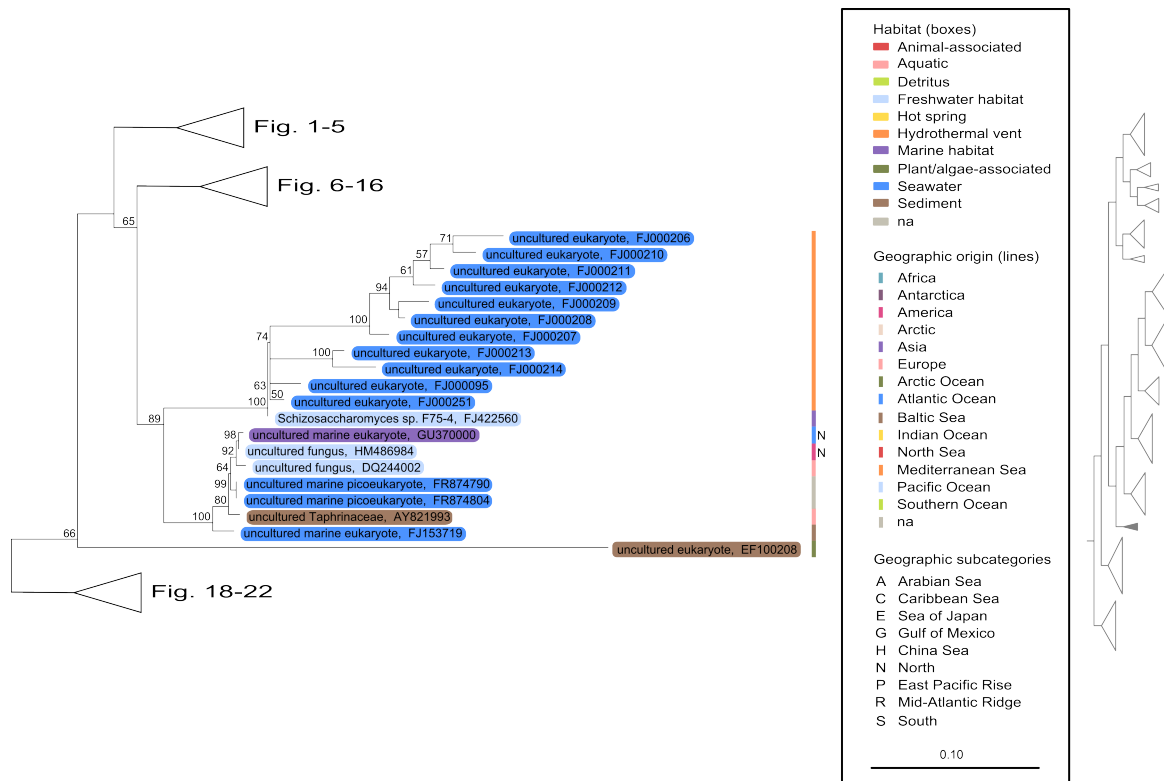


Figure 18: Subsection of *Chytridiomycota*

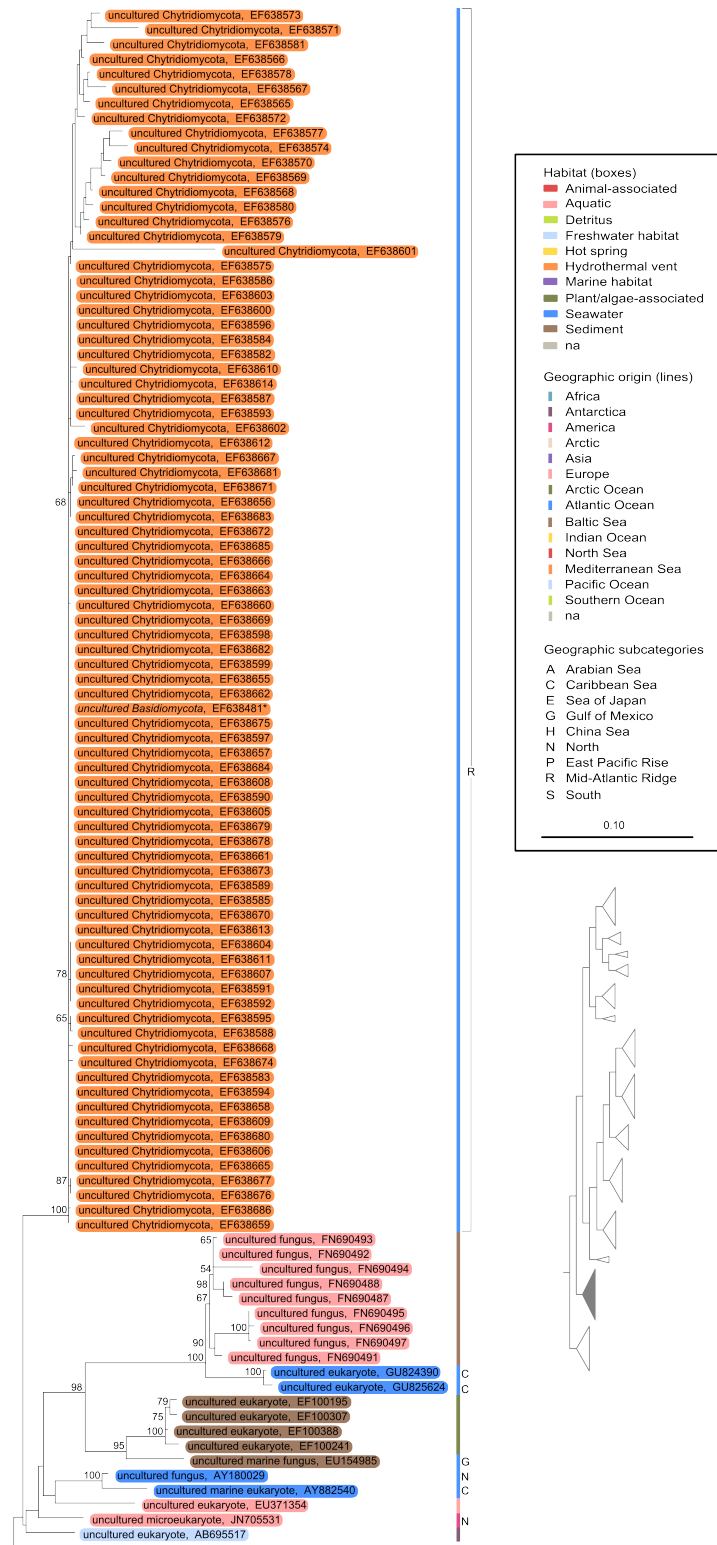


Figure 19: Subsection of *Chytridiomycota*

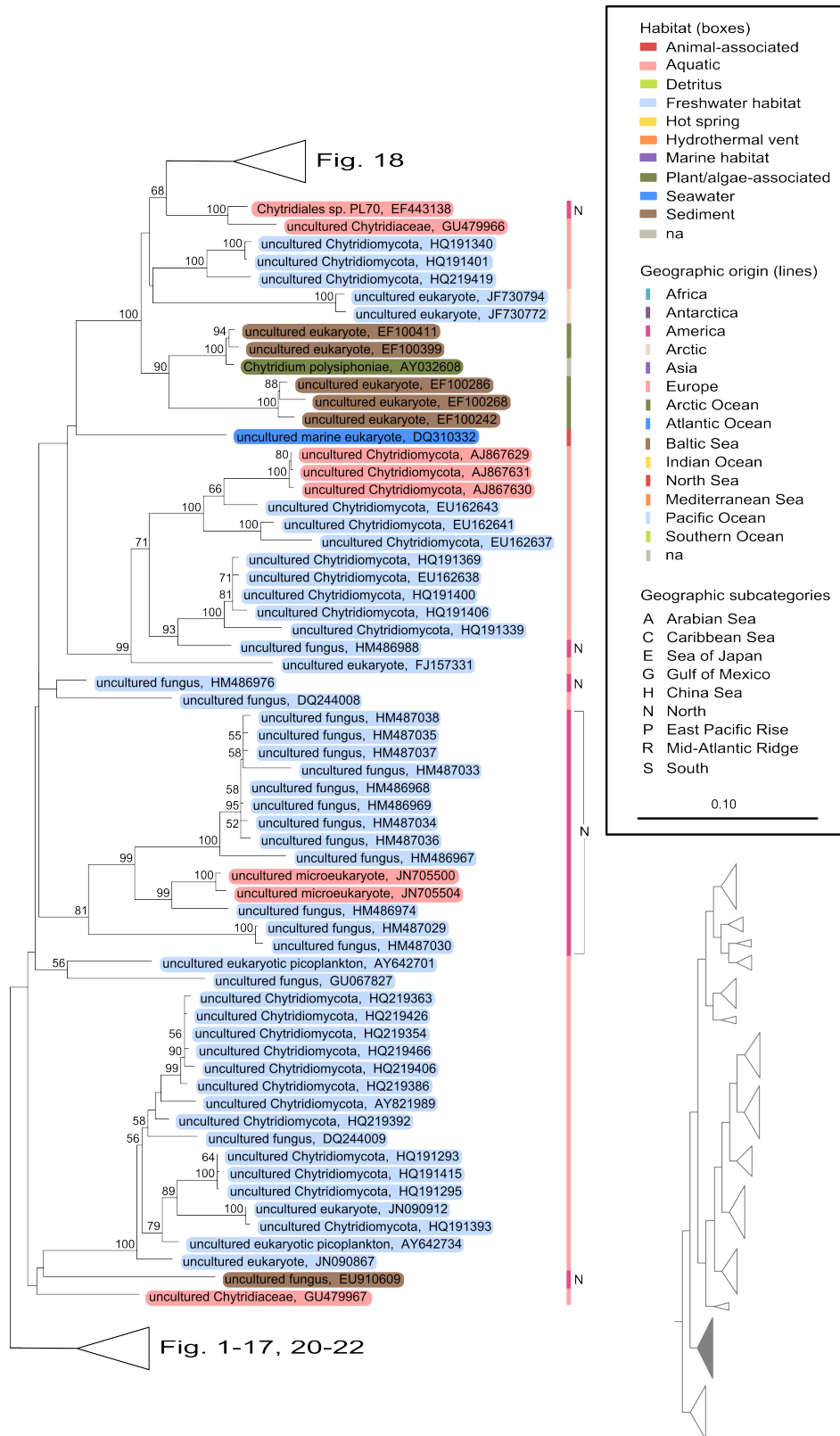


Figure 20: Subsection of *Chytridiomycota*

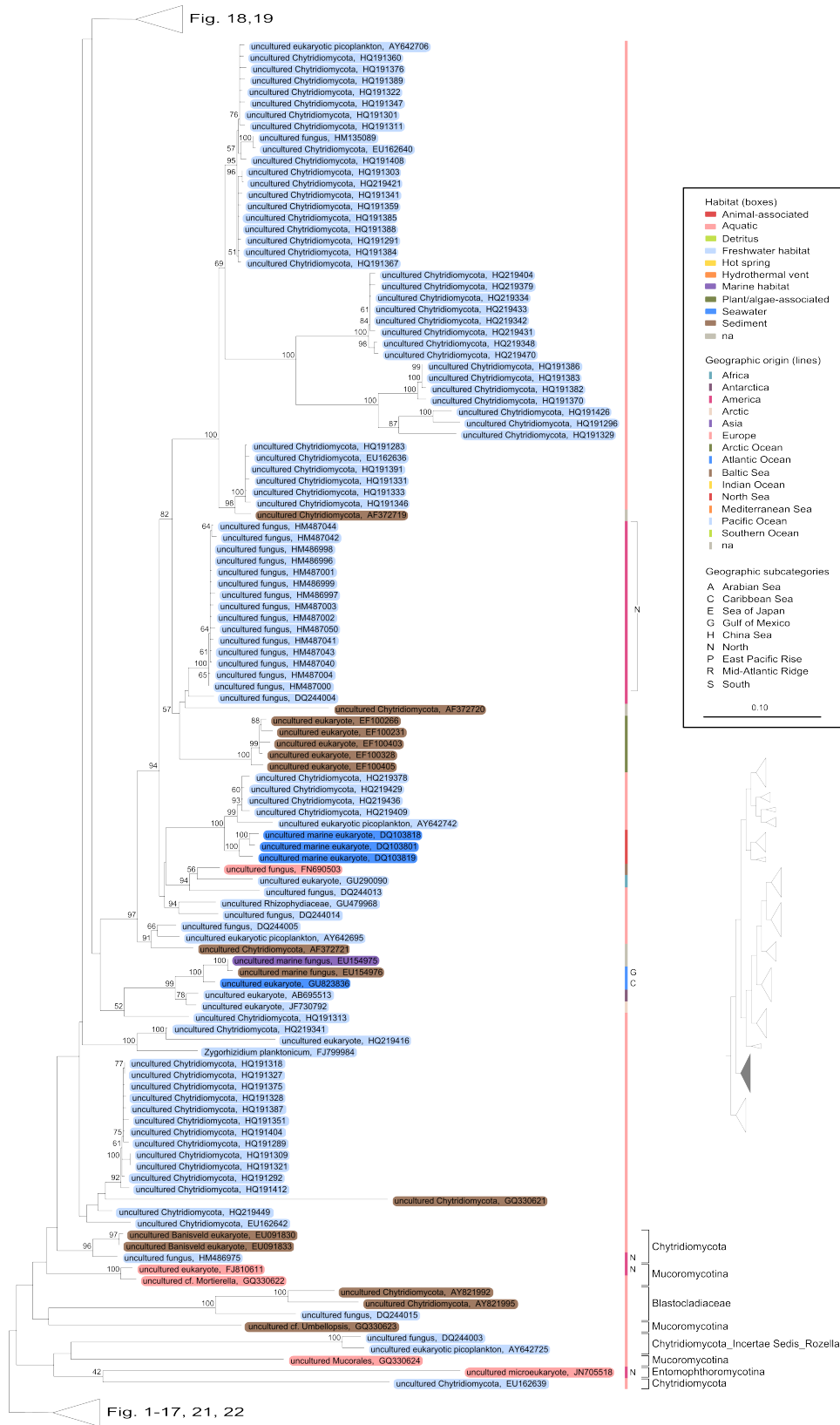


Figure 21: Subsection of basal fungal lineages

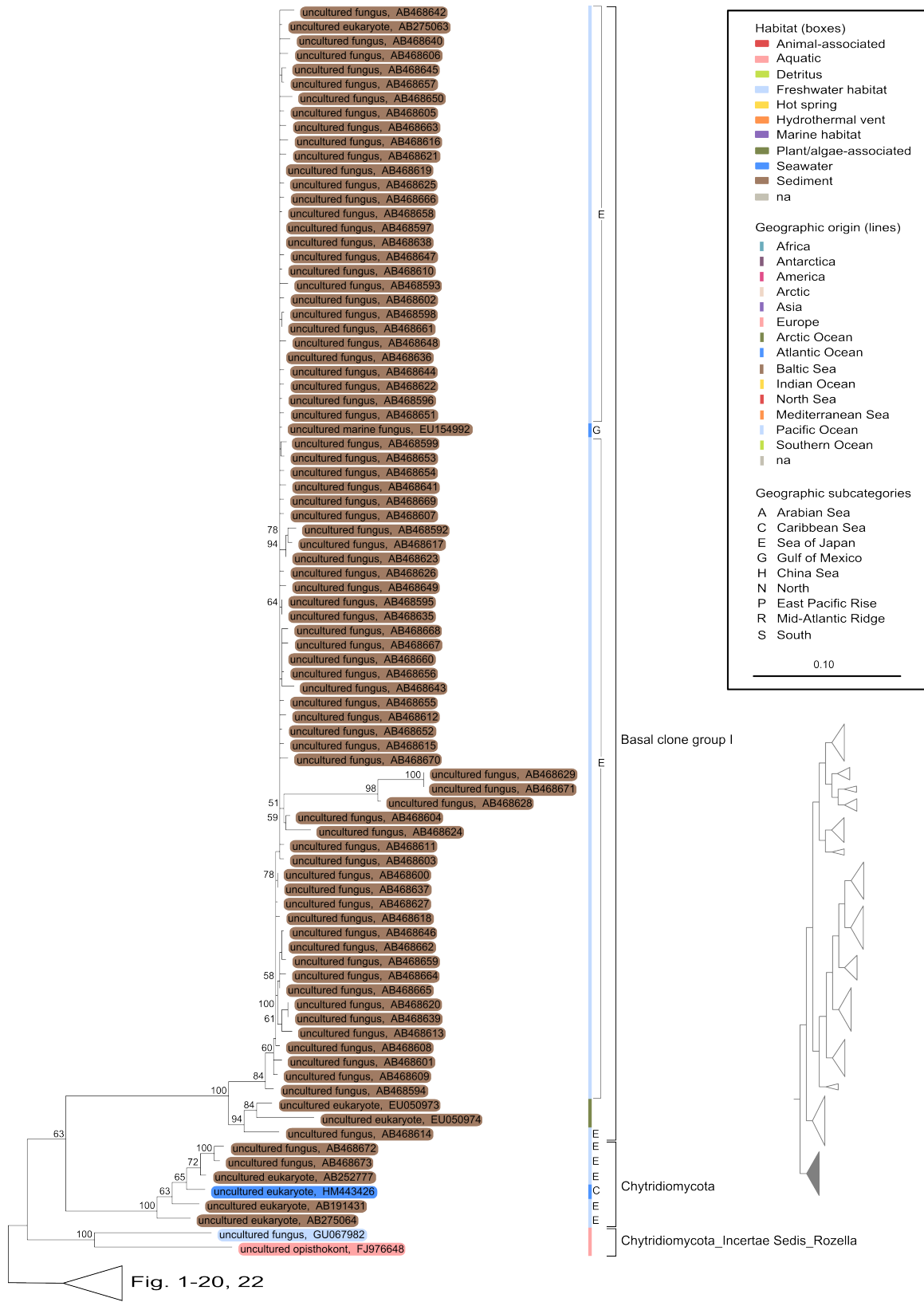


Figure 22: Subsection of basal fungal lineages

