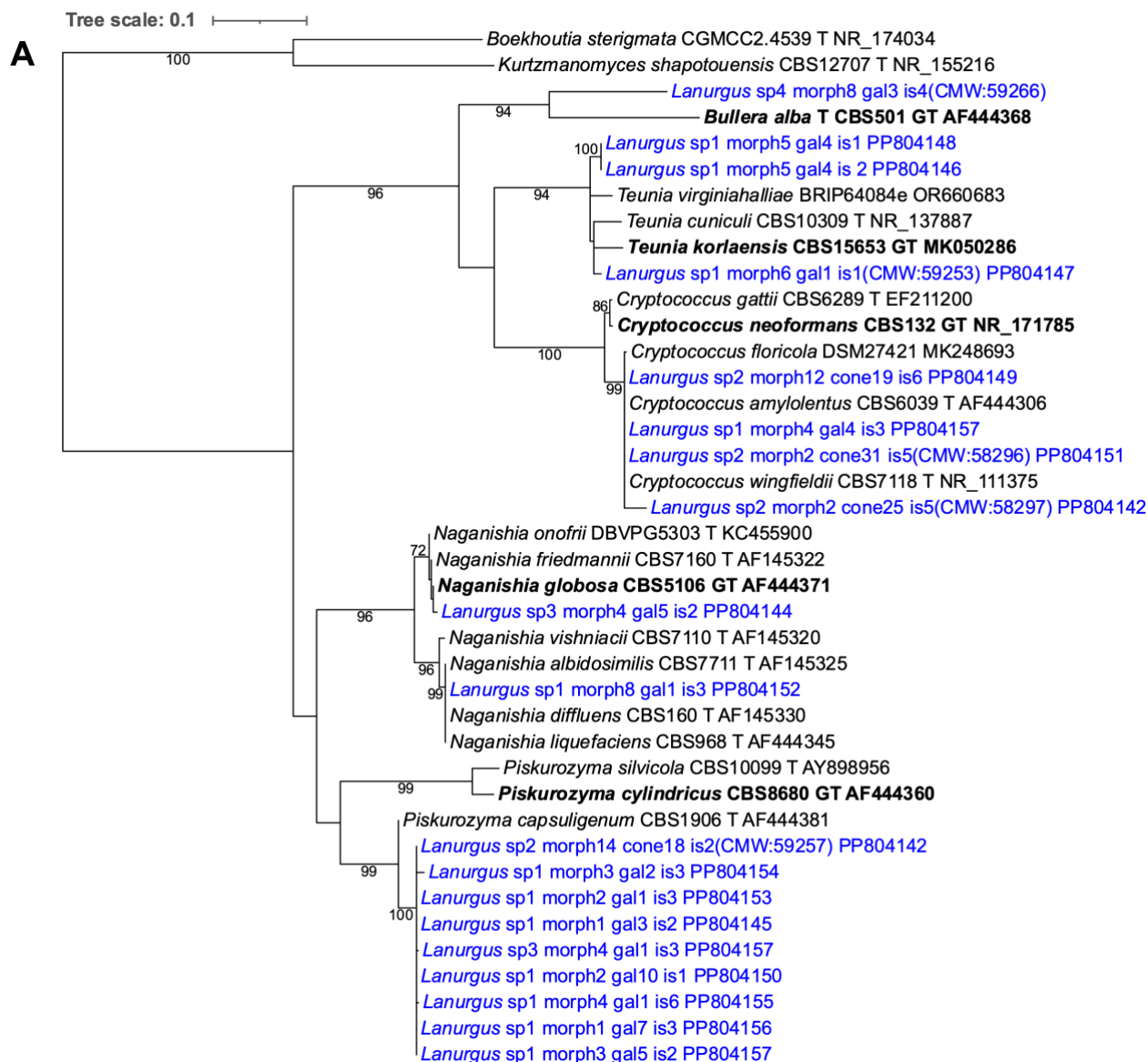


## SUPPLEMENTARY FIGURES

Figure S1A



**Figure S1:** Maximum likelihood phylogenetic analyses of the internal transcribed spacer (ITS) region sequences generated in this study (shown in blue). Type strain reference isolates of species that were identified as close relatives during BLASTn searches, any species closely related to those hits, and the type species of each genus (GT; if available), were included. Phylogenetic trees were determined for the commonly occurring (A) Tremellomycete, (B) Saccharomycete, (C) Sordariomycete and (D) Exobasidiomycete species.

Figure S1B

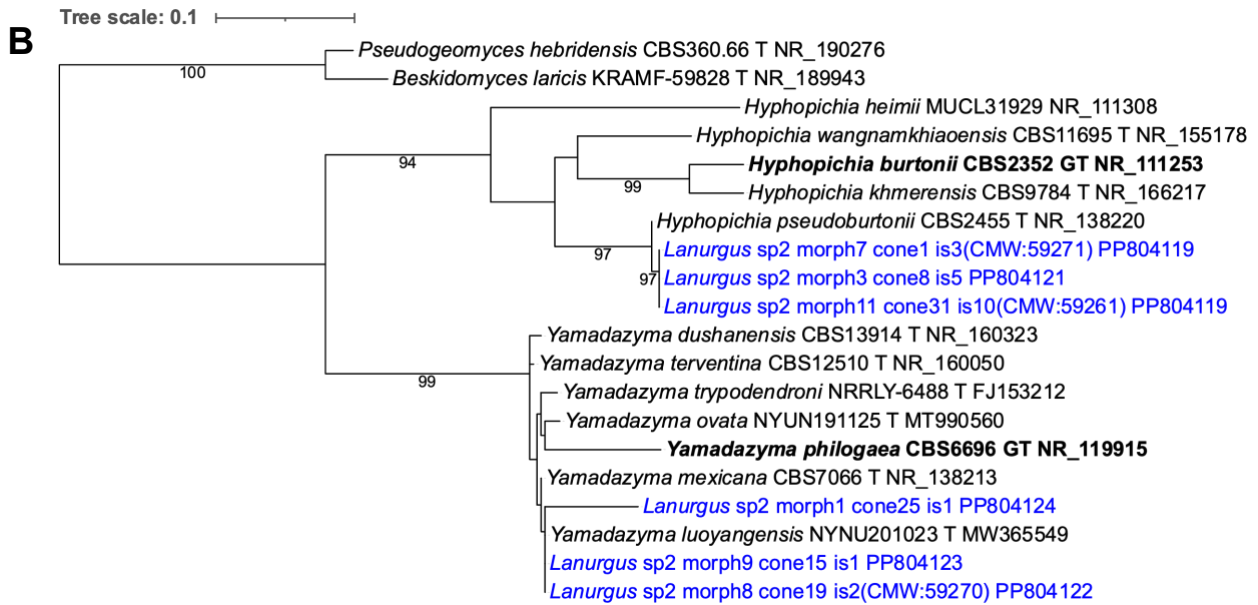


Figure S1C

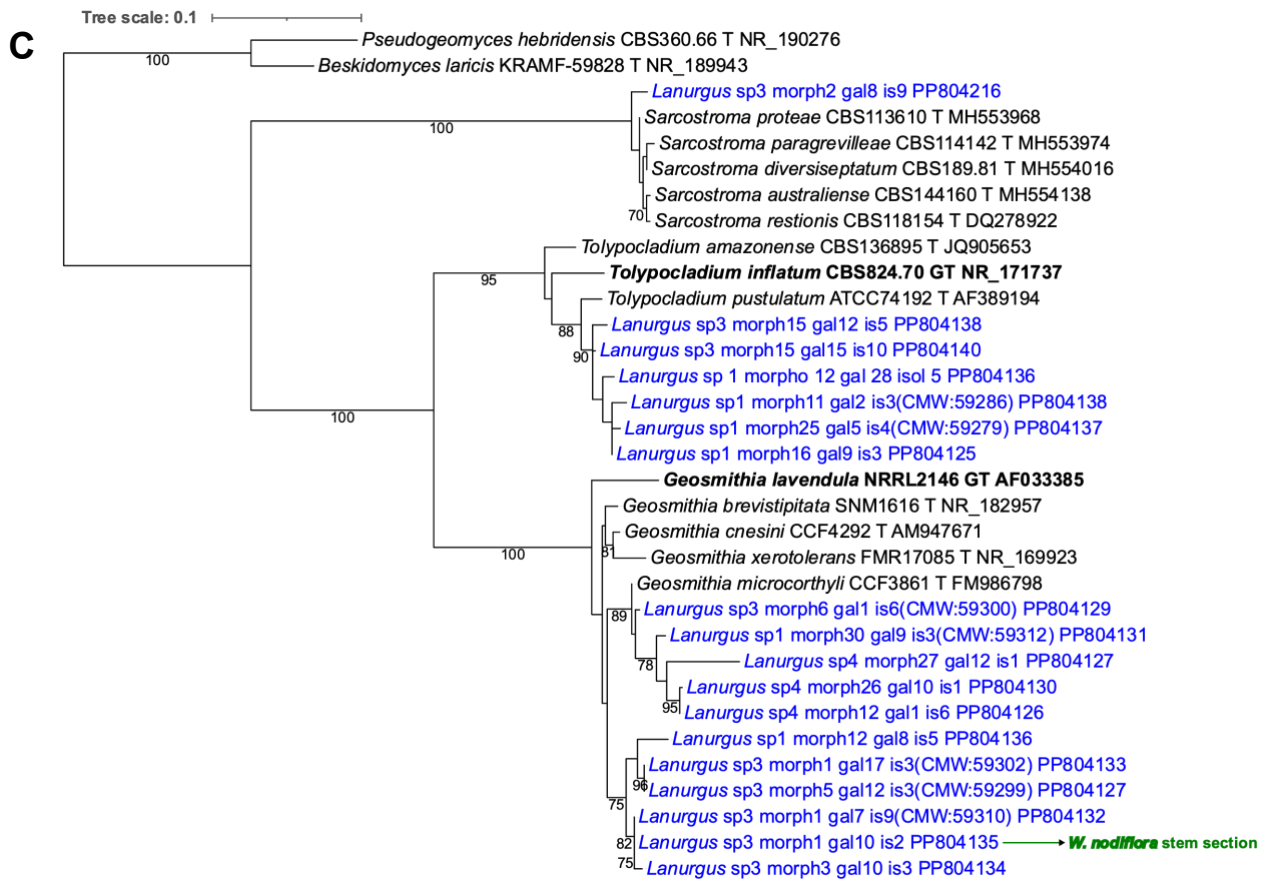


Figure S1D

