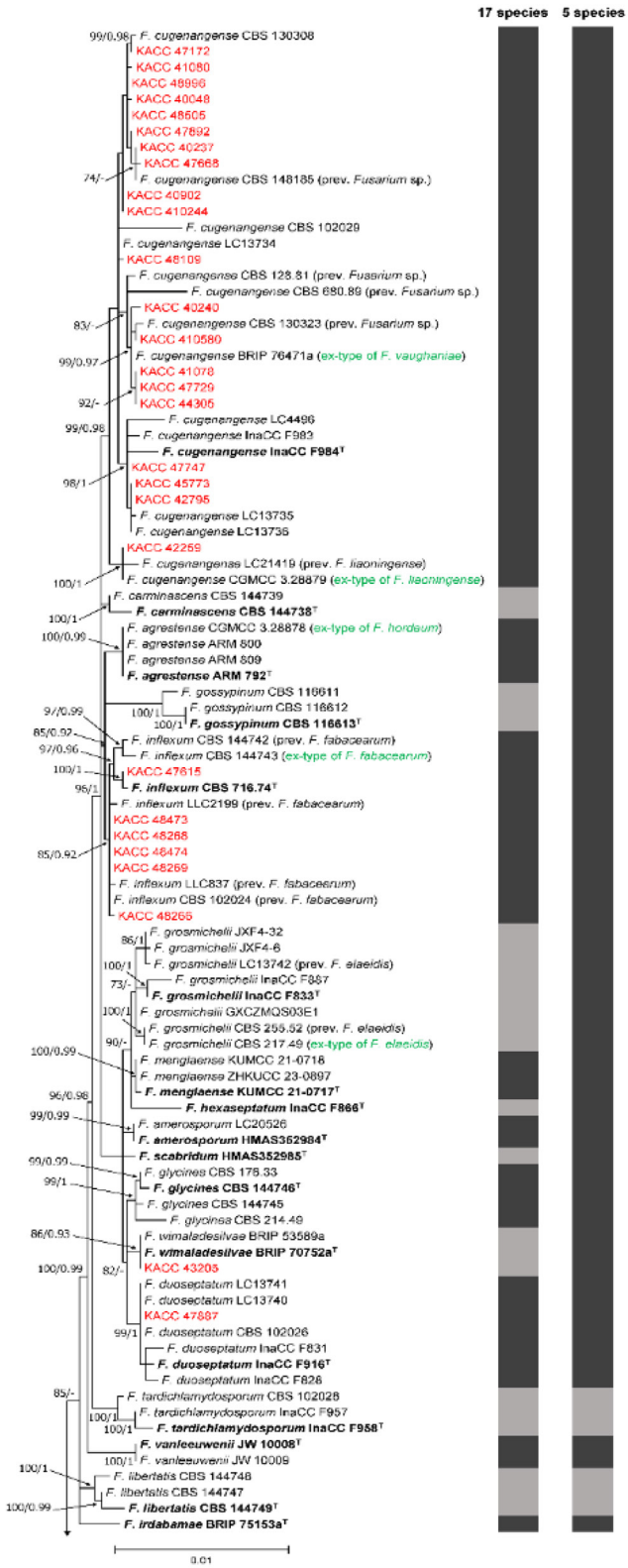

Supplementary Fig. 7. Alternative species delimitation hypotheses used in the BPP analyses. Two delimitation scenarios for the *F. inflexum* lineage and related taxa were generated from a maximum likelihood phylogeny inferred from a concatenated reduced five-locus dataset (*tef1, rpb1, rpb2, CaM,* and *tub2*). Putative lineages are represented by alternating light and dark gray boxes under each delimitation hypothesis.