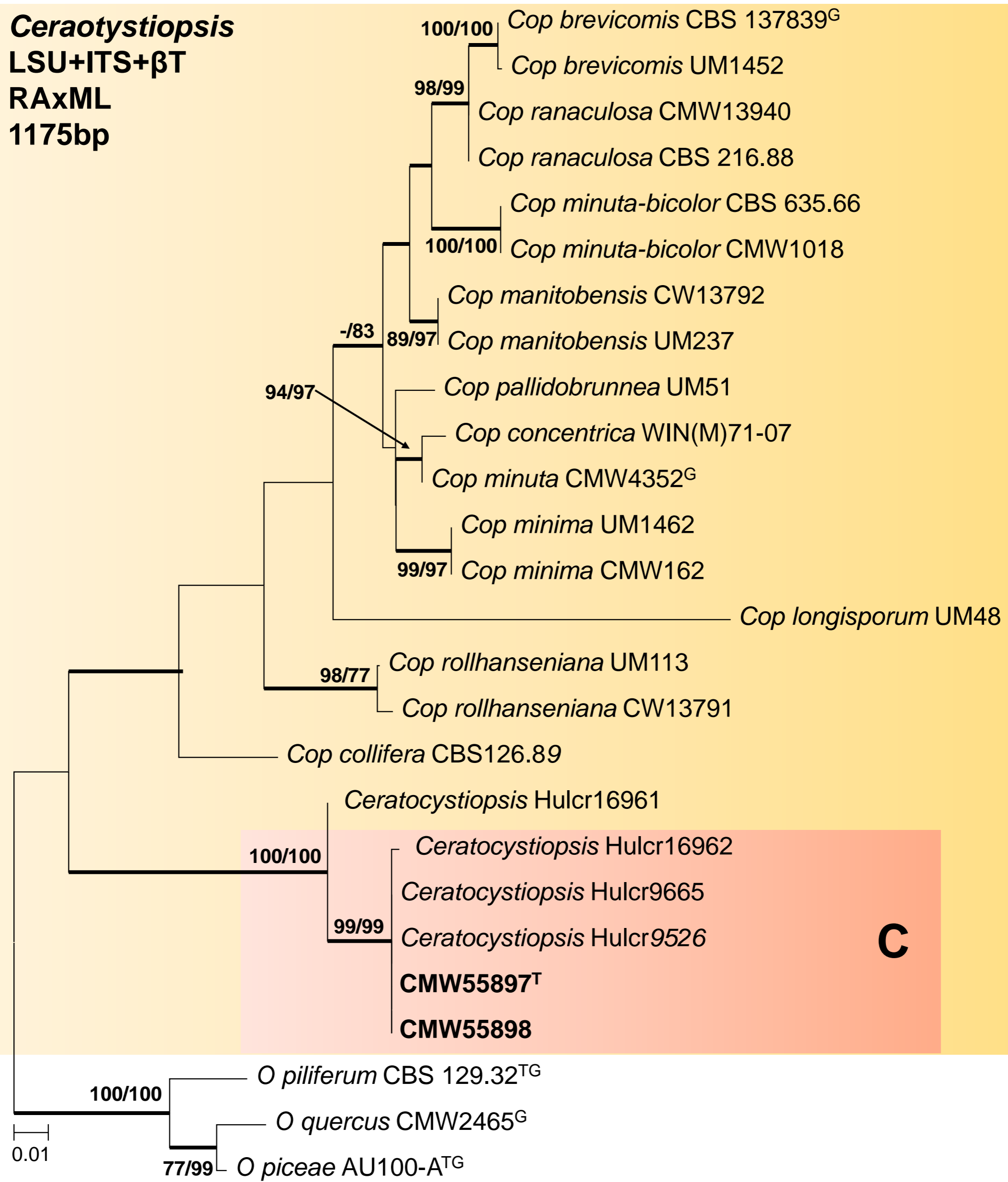


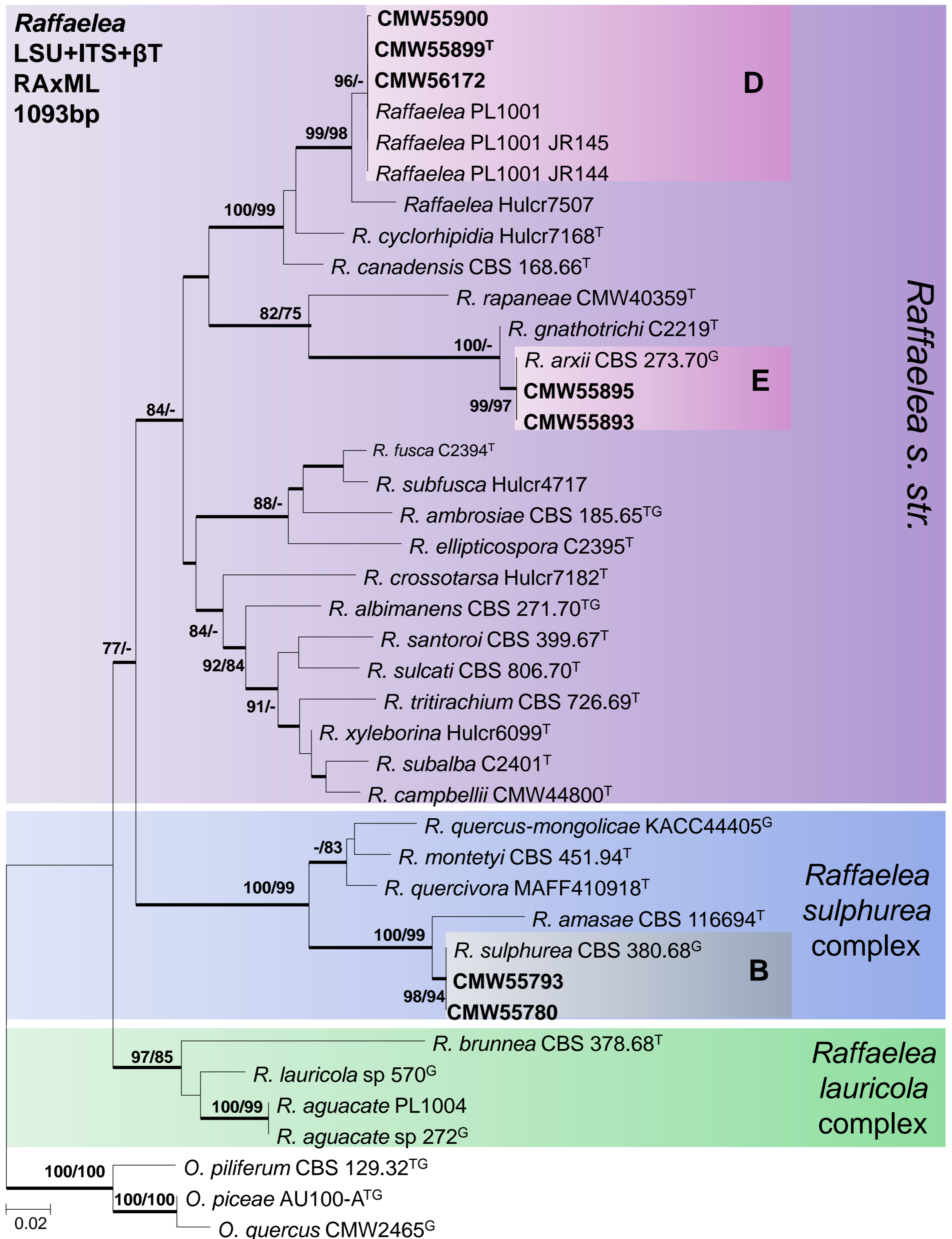
Ceraotystiopsis
LSU+ITS+βT
RAXML
1175bp



Ceratocystiopsis

Supplementary Figure 1

RAXML phylogenies derived from analyses of the combined LSU, ITS and βT *Ceratocystiopsis* datasets including all major taxa described in the genus. Bold branches indicate posterior probabilities $\geq 95\%$. Bootstrap values $\geq 75\%$ for maximum likelihood and maximum parsimony analyses are indicated at nodes as ML/MP. G=sequence extracted from available genome. T=Ex-Type isolate.



Supplementary Figure 2

RAXML phylogenies derived from analyses of the combined LSU, ITS and βT *Raffaelea* datasets including all major taxa described in the genus. Bold branches indicate posterior probabilities ≥ 95 %. Bootstrap values ≥ 75 % for maximum likelihood and maximum parsimony analyses are indicated at nodes as ML/MP. G=sequence extracted from available genome. T=Ex-Type isolate.