

Supplementary material I

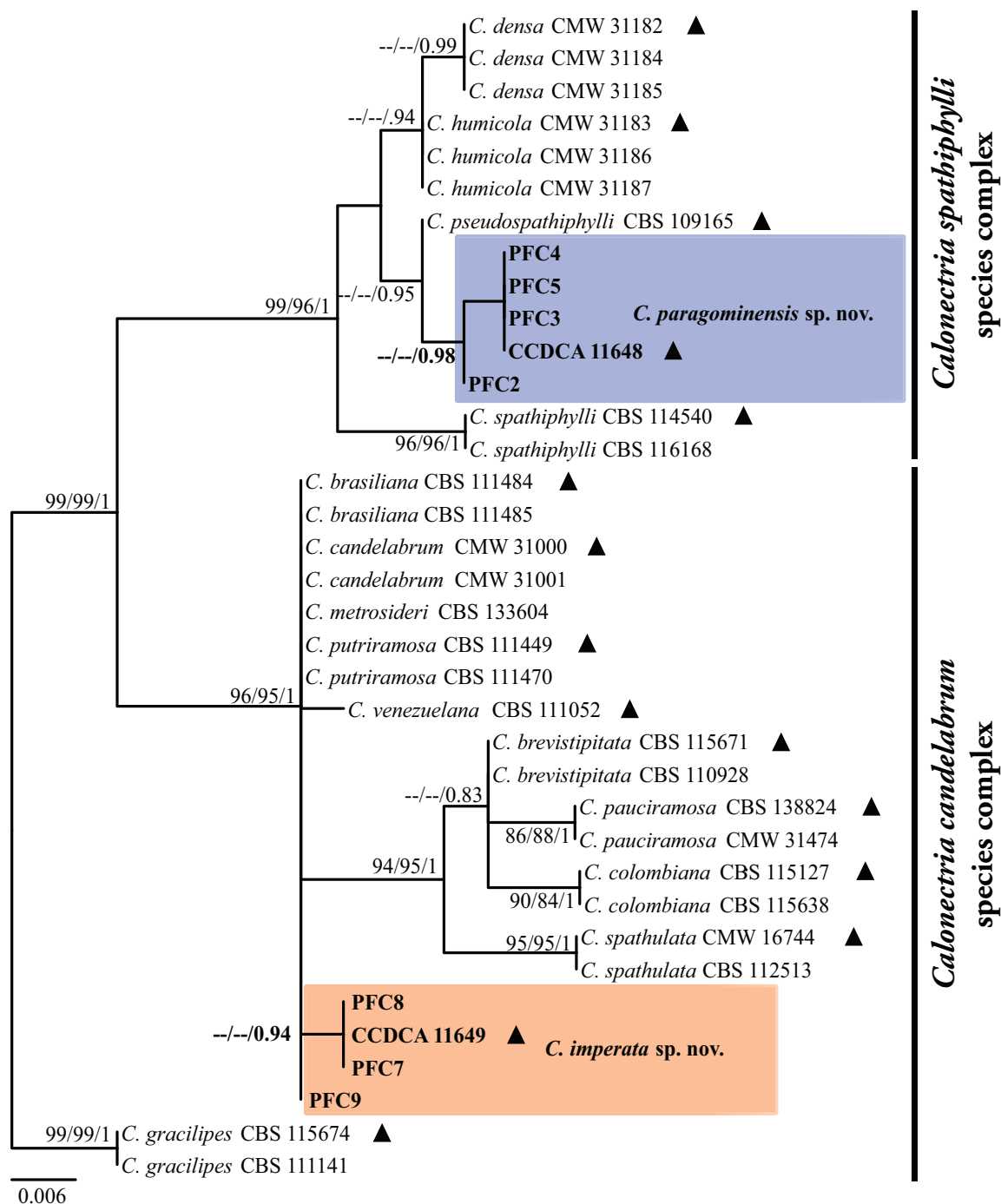


Figure S1. Phylogenetic tree based on maximum likelihood analysis of *act* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.

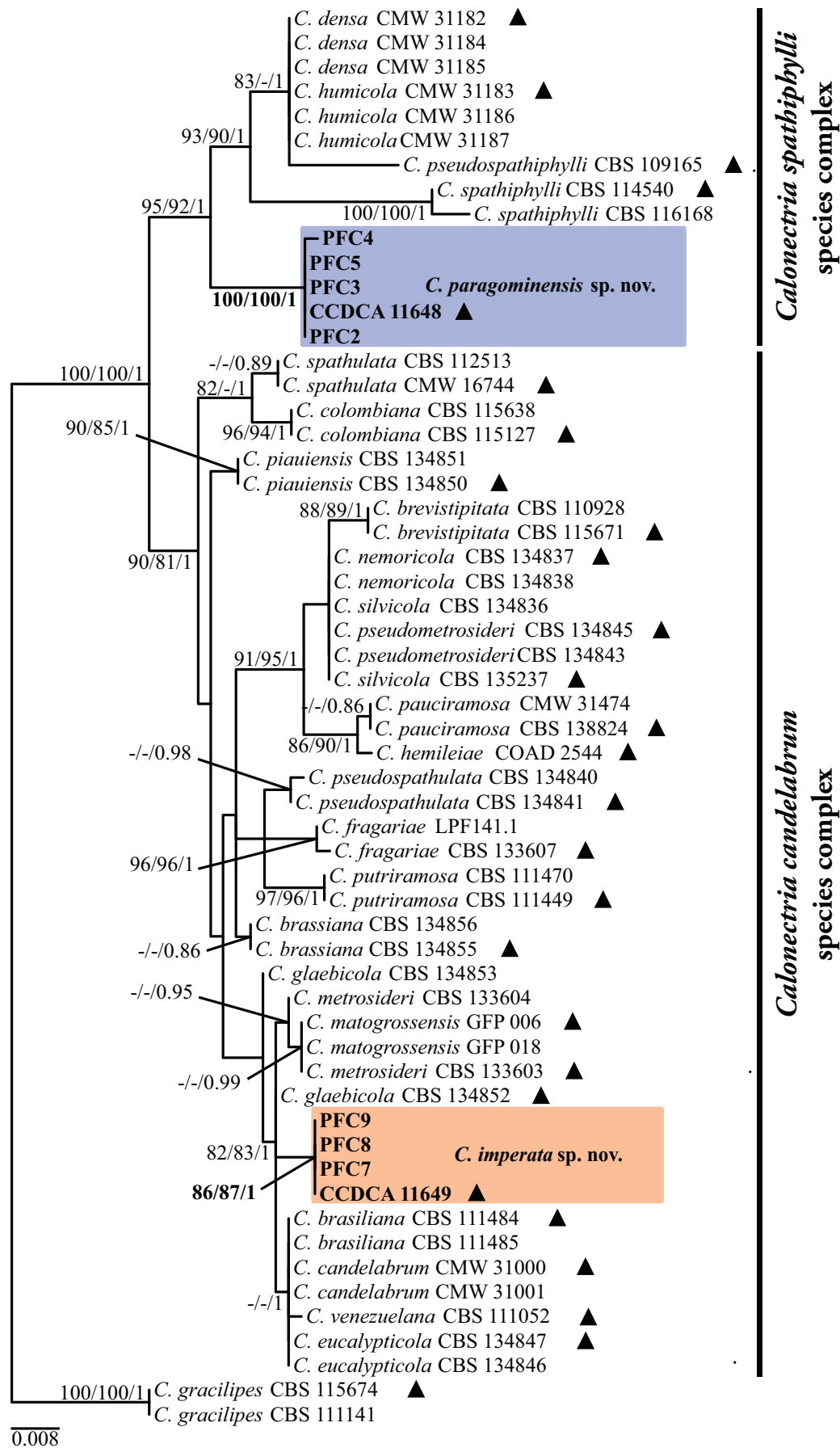


Figure S2. Phylogenetic tree based on maximum likelihood analysis of *cmdA* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.

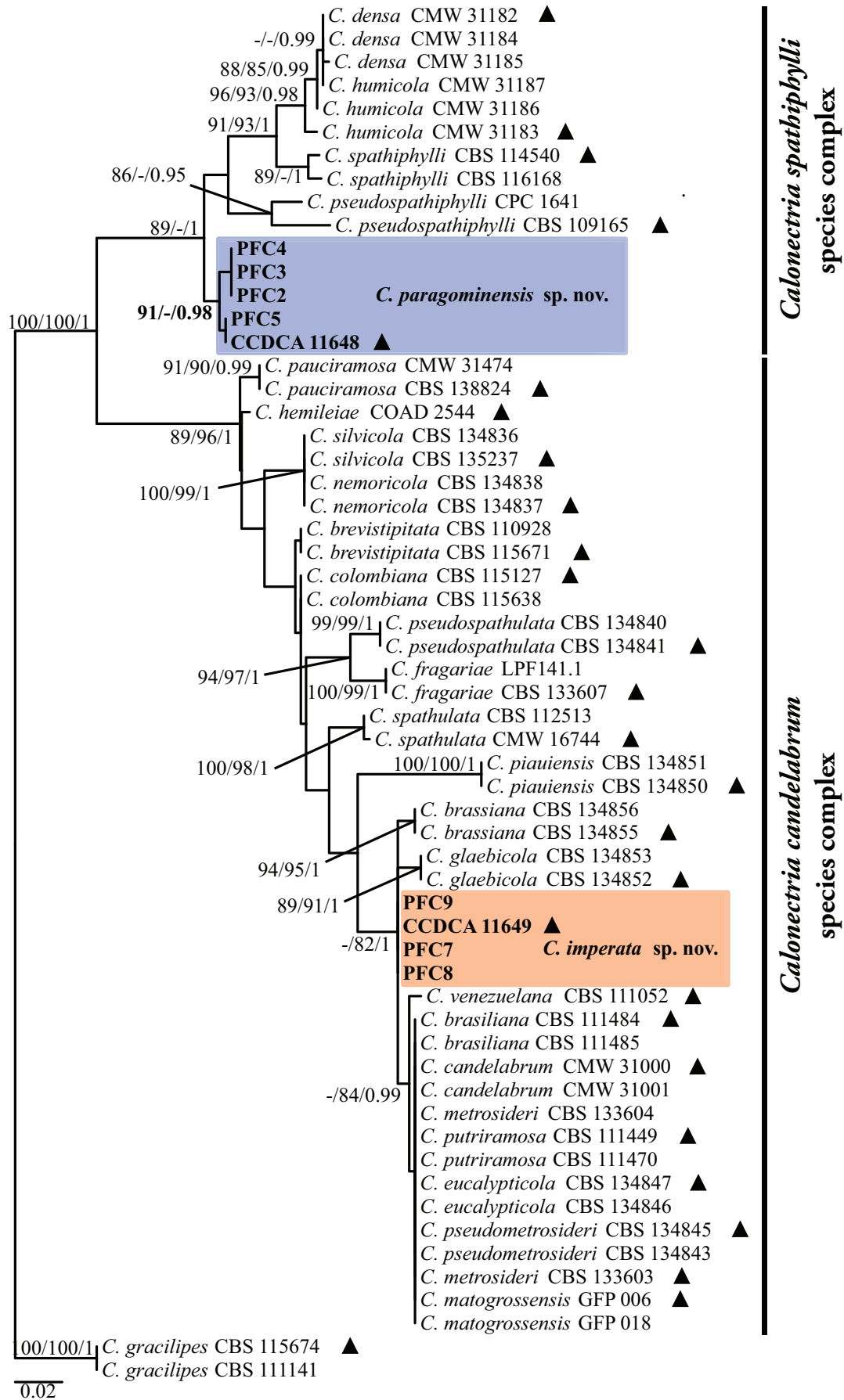


Figure S3. Phylogenetic tree based on maximum likelihood analysis of *his3* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.

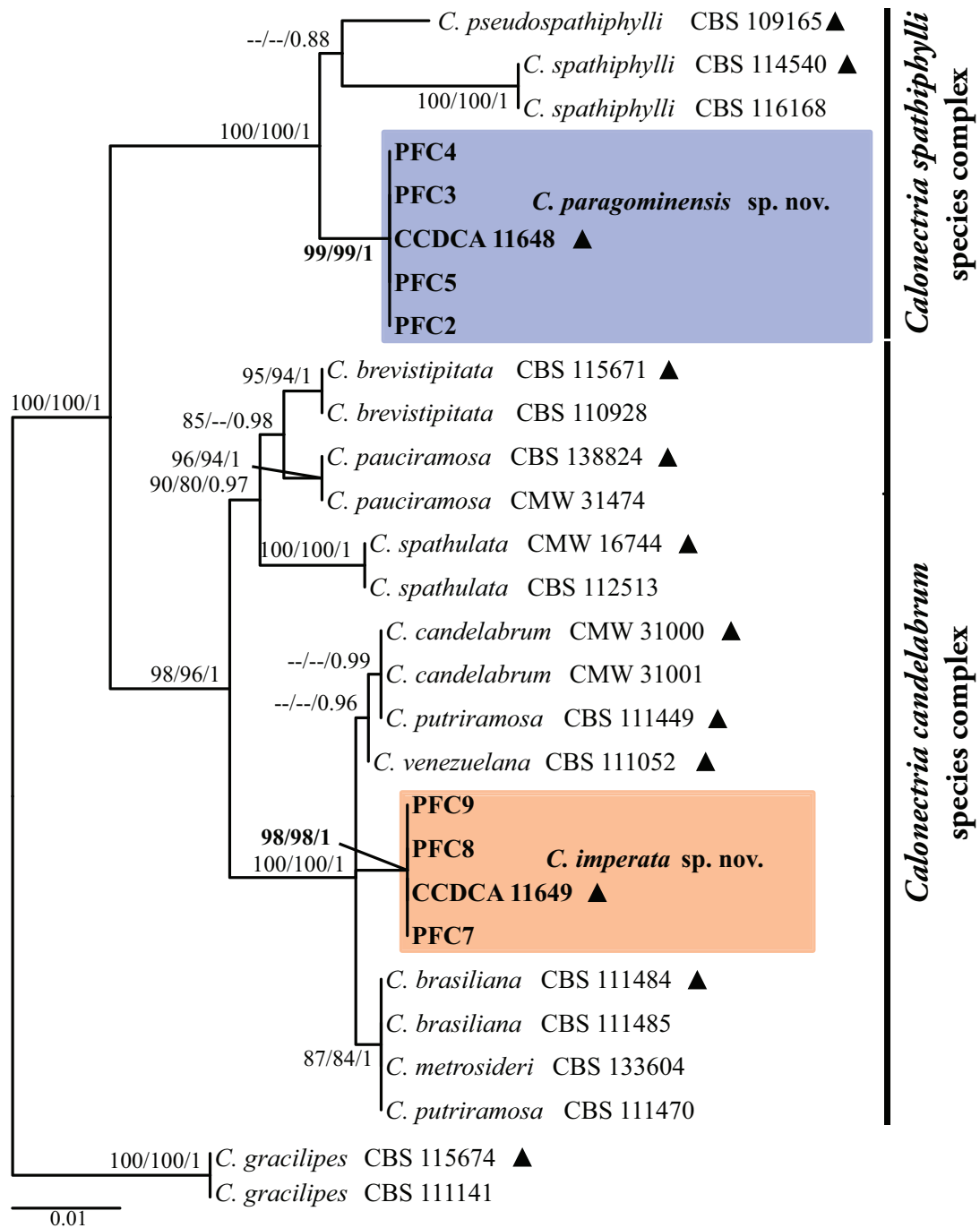


Figure S4. Phylogenetic tree based on maximum likelihood analysis of *rpb2* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.

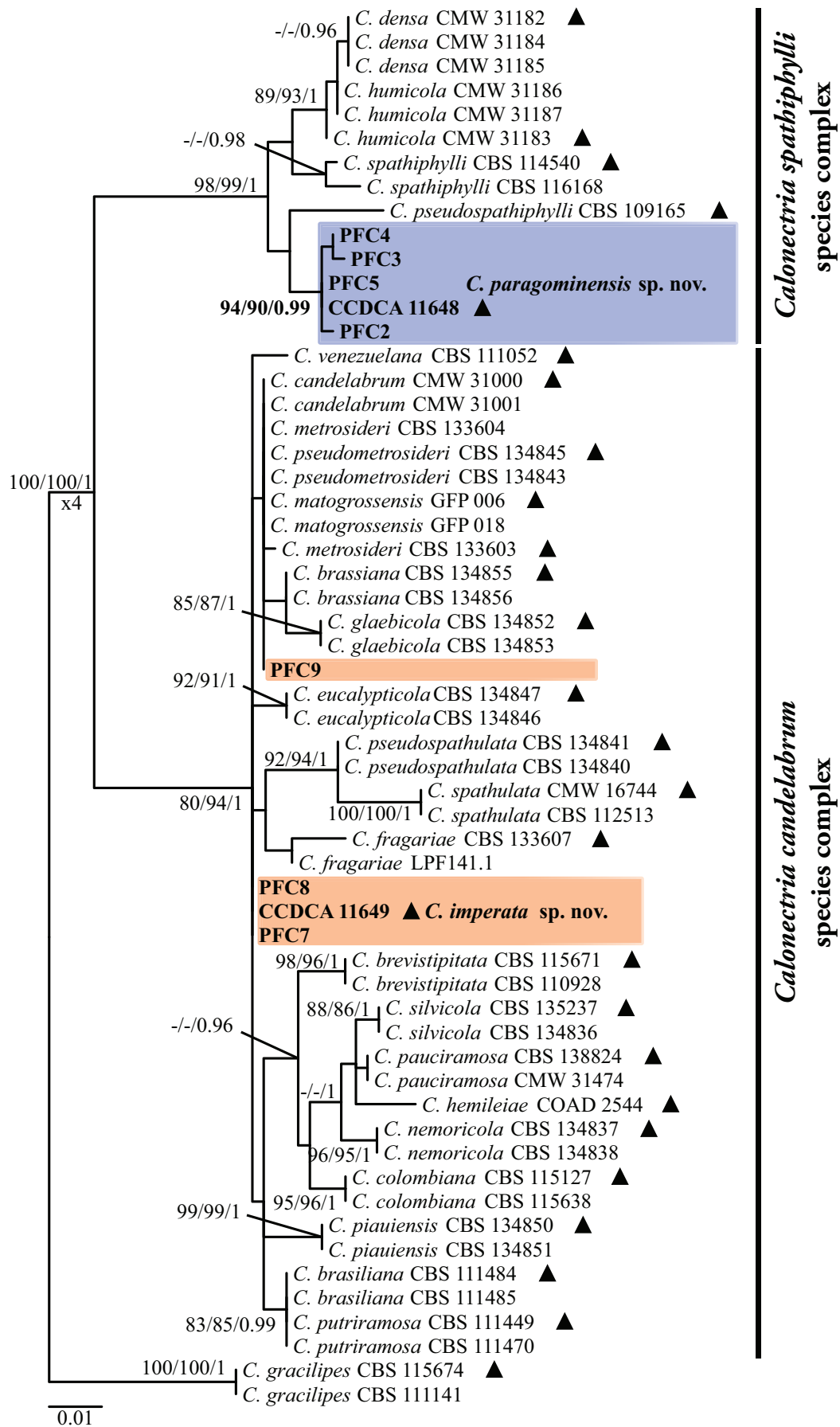


Figure S5. Phylogenetic tree based on maximum likelihood analysis of *tef1* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.

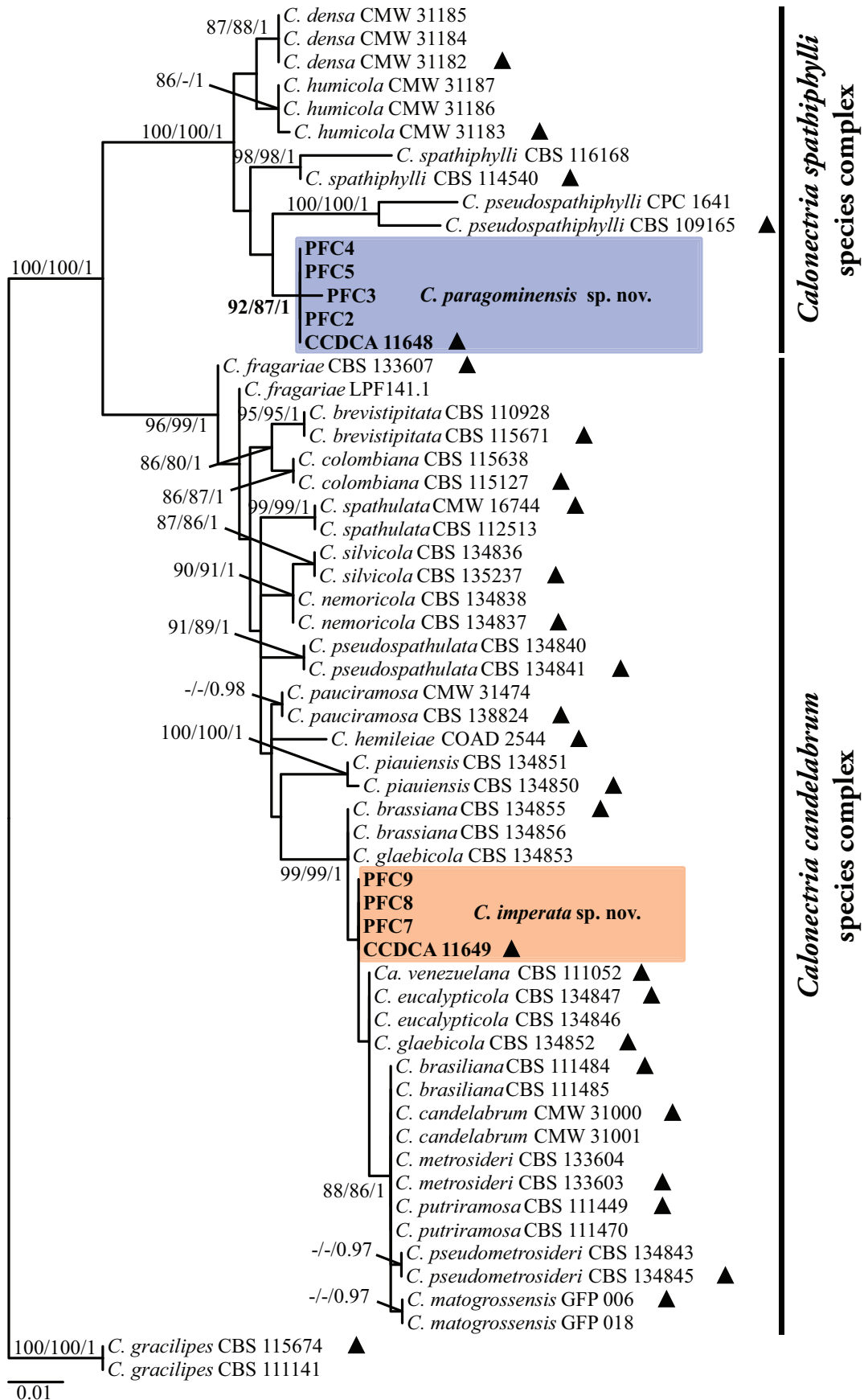


Figure S6. Phylogenetic tree based on maximum likelihood analysis of *tub2* gene region. Bootstrap support values $\geq 80\%$ for maximum parsimony (MP), Ultrafast bootstrap support values $\geq 95\%$ for maximum likelihood (ML), and posterior probability (PP) values ≥ 0.95 from BI analyses are presented at the nodes (MP/ML/PP). Bootstrap values below 80% (MP), 95% (ML) and posterior probabilities below 0.80 are marked with “-”. Ex-type isolates are indicated by “▲”, isolates highlighted in bold were sequenced in this study, and novel species are in blue and orange. *C. gracilipes* was used as outgroup. The scale bar indicates the number of nucleotide substitutions per site.