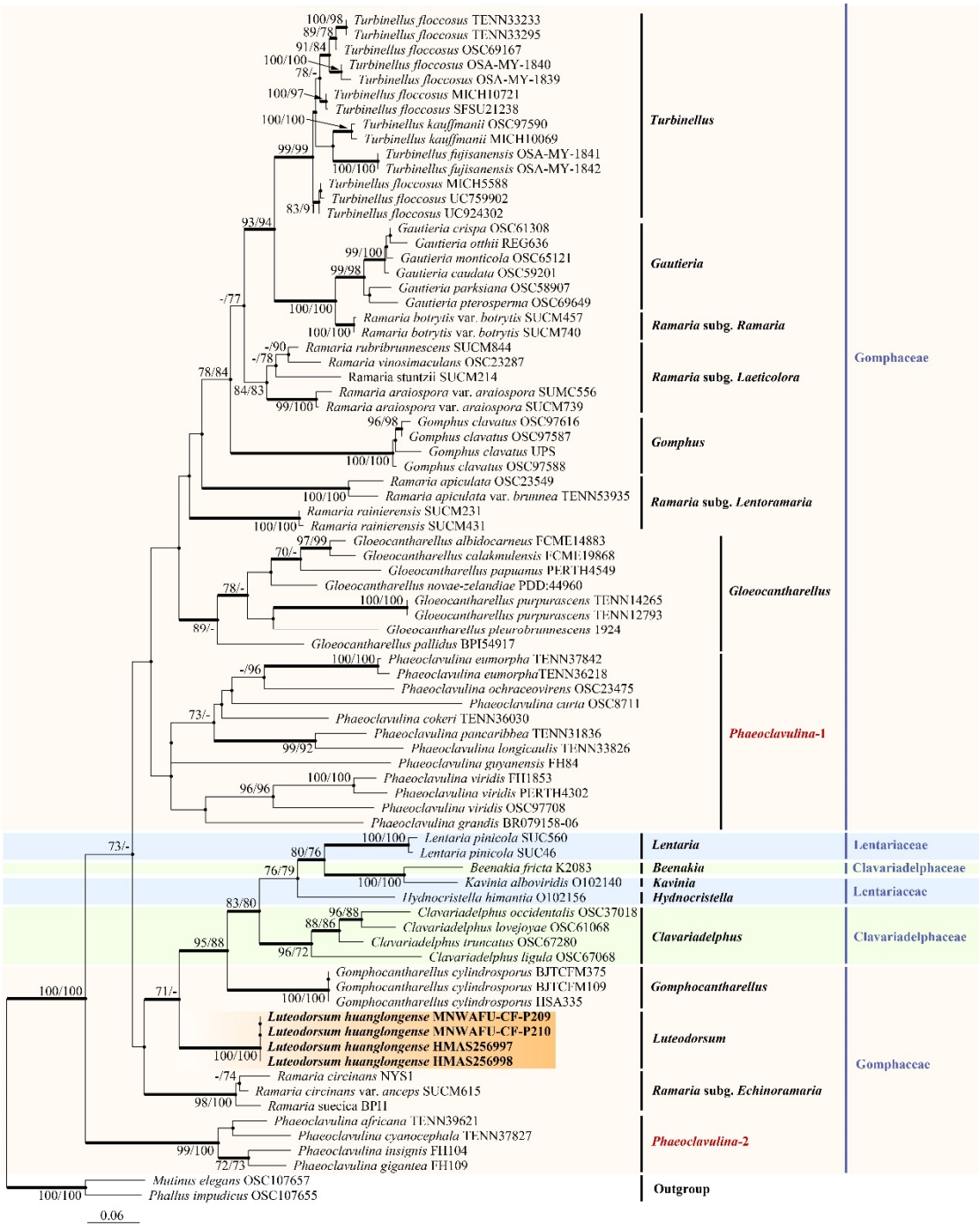
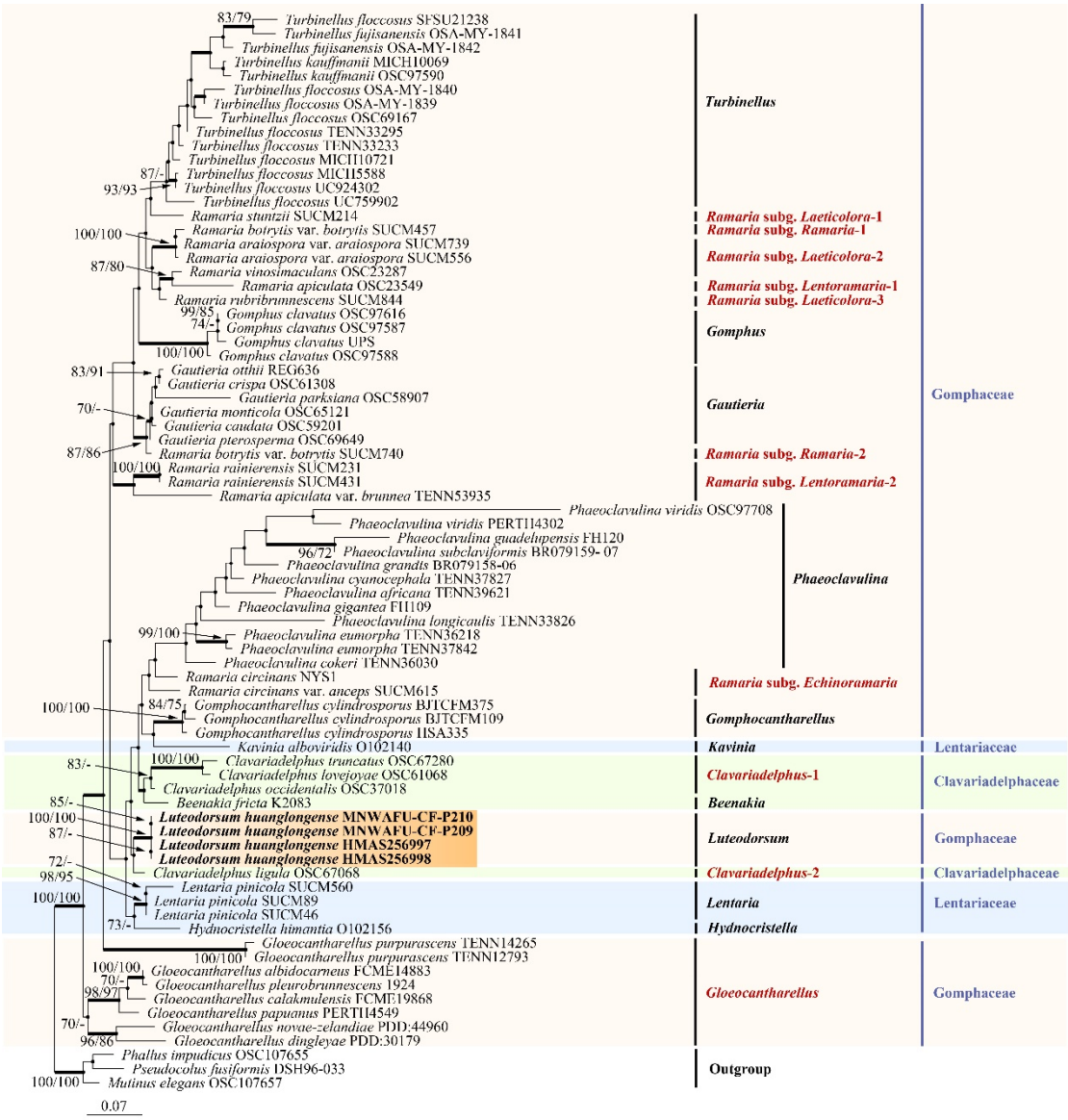
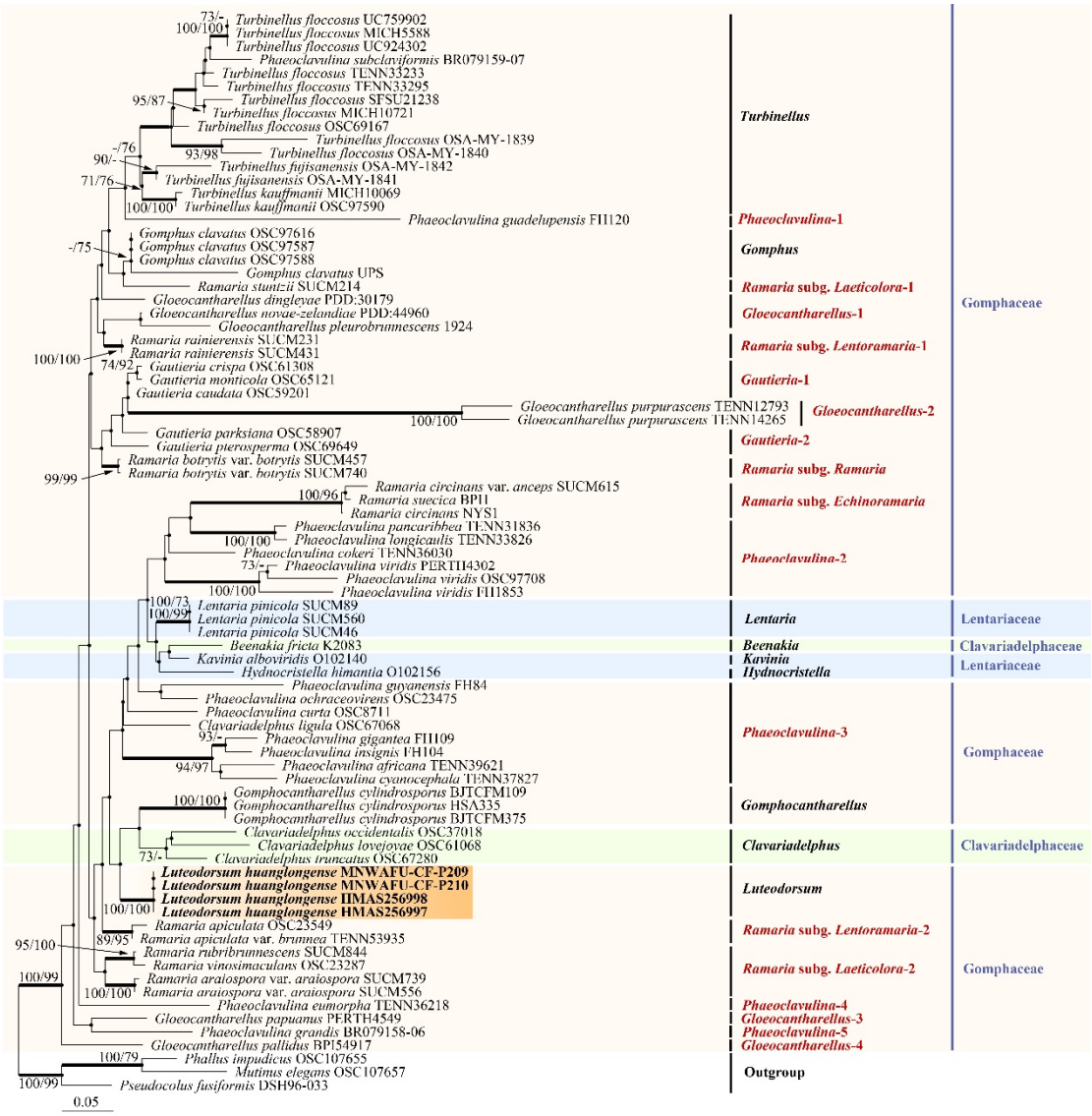


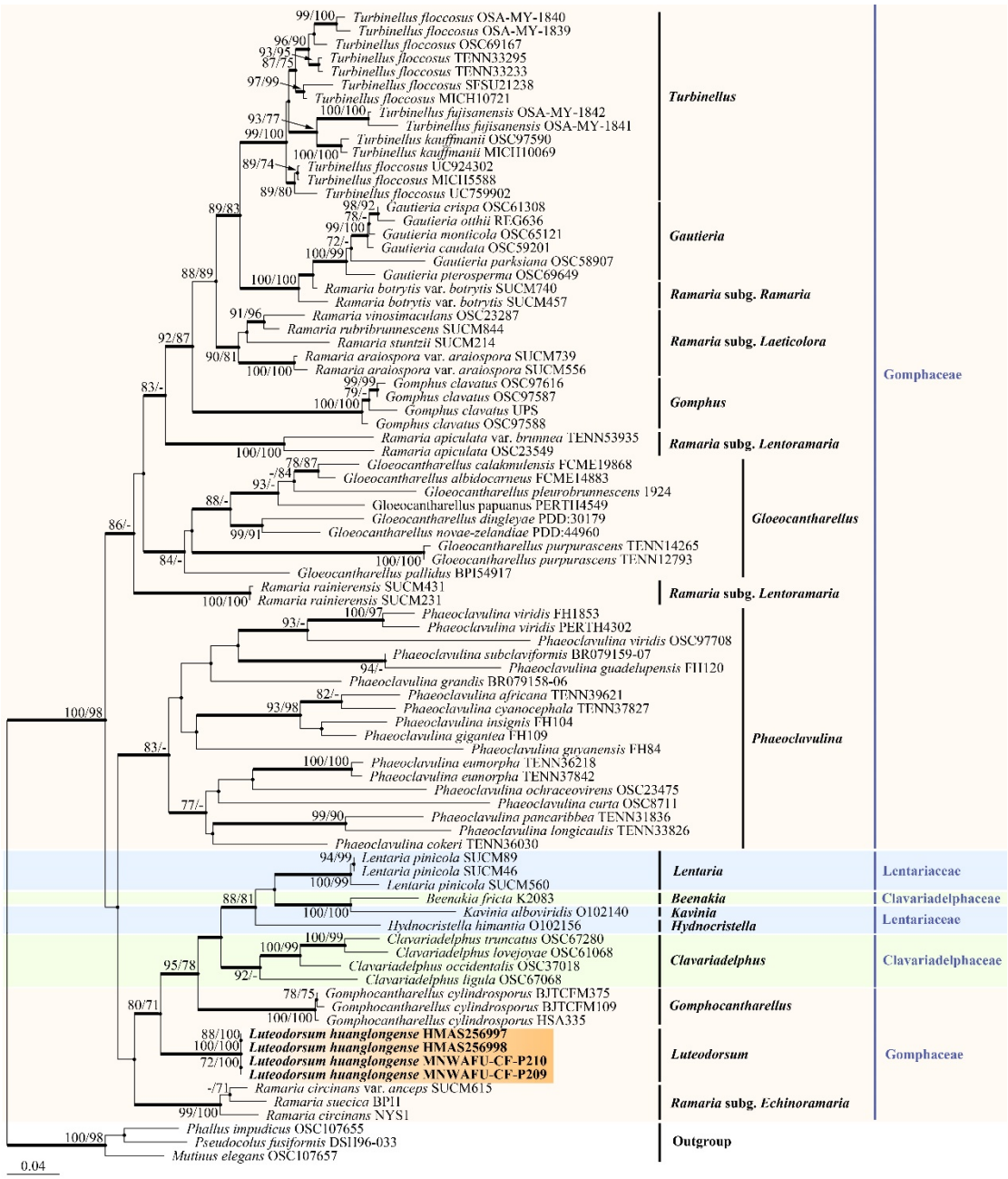
Supplementary Figure S1. Phylogenetic tree generated from a maximum likelihood analysis based on atp6 sequences, depicting the phylogenetic relationships of Gomphales. *Phallus impudicus*, and *Mutinus elegan* were used as outgroups. The nodes above the branches indicate the maximum likelihood bootstrap support (MLBS) values (≥70%) and maximum parsimony bootstrap support (MPBS) values (≥70%). The branches that presented a Bayesian posterior probability (BPP) ≥0.95 are thicker. The novel sequences are highlighted in bold and orange shade.



Supplementary Figure S2. Phylogenetic tree generated from a maximum likelihood analysis based on mtSSU sequences, depicting the phylogenetic relationships of Gomphales. *Phallus impudicus*, *Mutinus elegans*, and *Pseudocolus fusiformis* were used as outgroups. The nodes above the branches indicate the maximum likelihood bootstrap support (MLBS) values (≥70%) and maximum parsimony bootstrap support (MPBS) values (≥70%). The branches that presented a Bayesian posterior probability (BPP) ≥0.95 are thicker. The novel sequences are highlighted in bold and orange shade.



Supplementary Figure S3. Phylogenetic tree generated from a maximum likelihood analysis based on LSU sequences, depicting the phylogenetic relationships of Gomphales. *Phallus impudicus*, *Mutinus elegans*, and *Pseudocolus fusiformis* were used as outgroups. The nodes above the branches indicate the maximum likelihood bootstrap support (MLBS) values (≥70%) and maximum parsimony bootstrap support (MPBS) values (≥70%). The branches that presented a Bayesian posterior probability (BPP) ≥0.95 are thicker. The novel sequences are highlighted in bold and orange shade.



Supplementary Figure S4. Phylogenetic tree generated from a maximum likelihood analysis based on combined atp6 and mtSSU sequences, depicting the phylogenetic relationships of Gomphales. *Phallus impudicus*, *Mutinus elegans*, and *Pseudocolus fusiformis* were used as outgroups. The nodes above the branches indicate the maximum likelihood bootstrap support (MLBS) values (≥70%) and maximum parsimony bootstrap support (MPBS) values (≥70%). The branches that presented a Bayesian posterior probability (BPP) ≥0.95 are thicker. The novel sequences are highlighted in bold and orange shade.