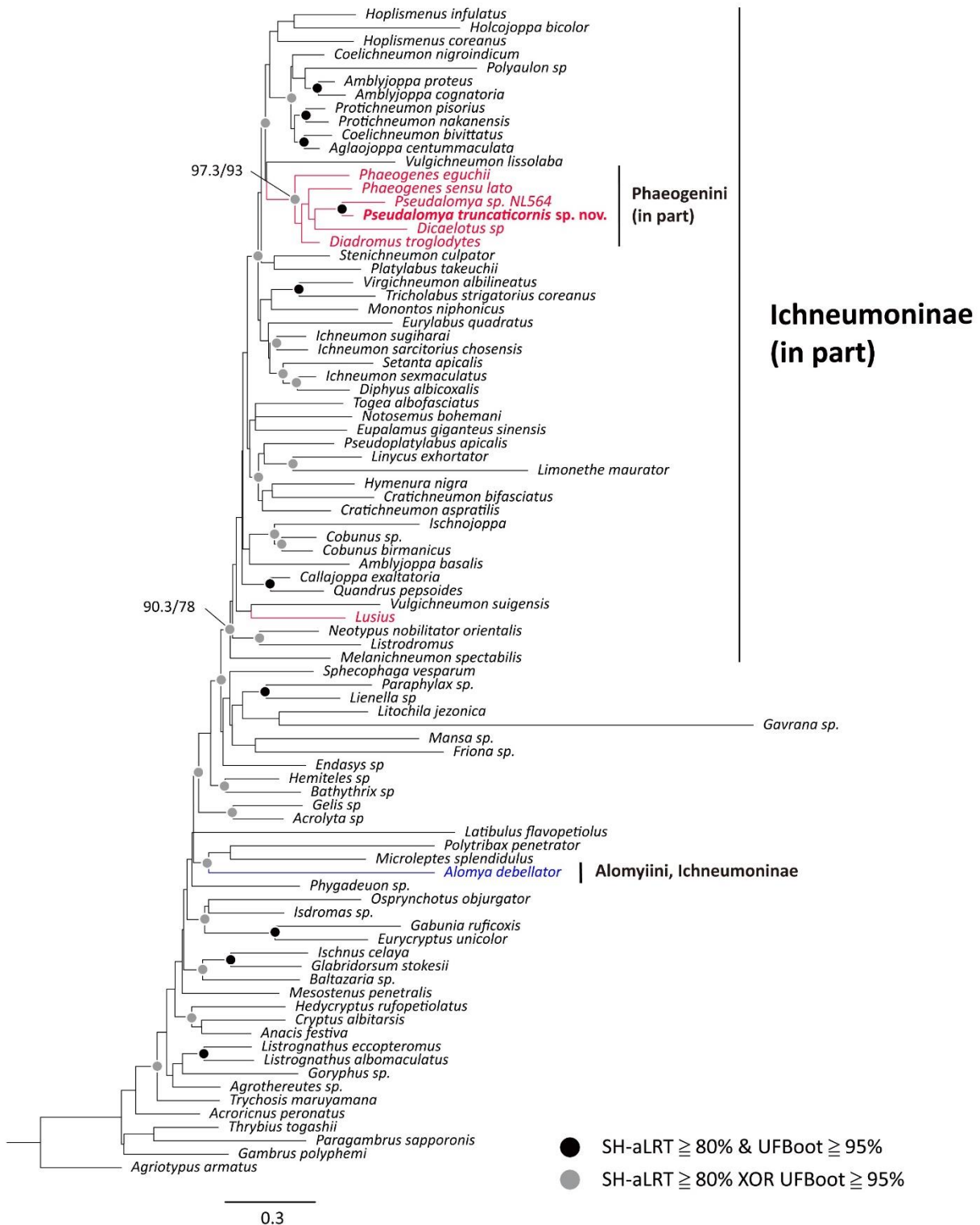
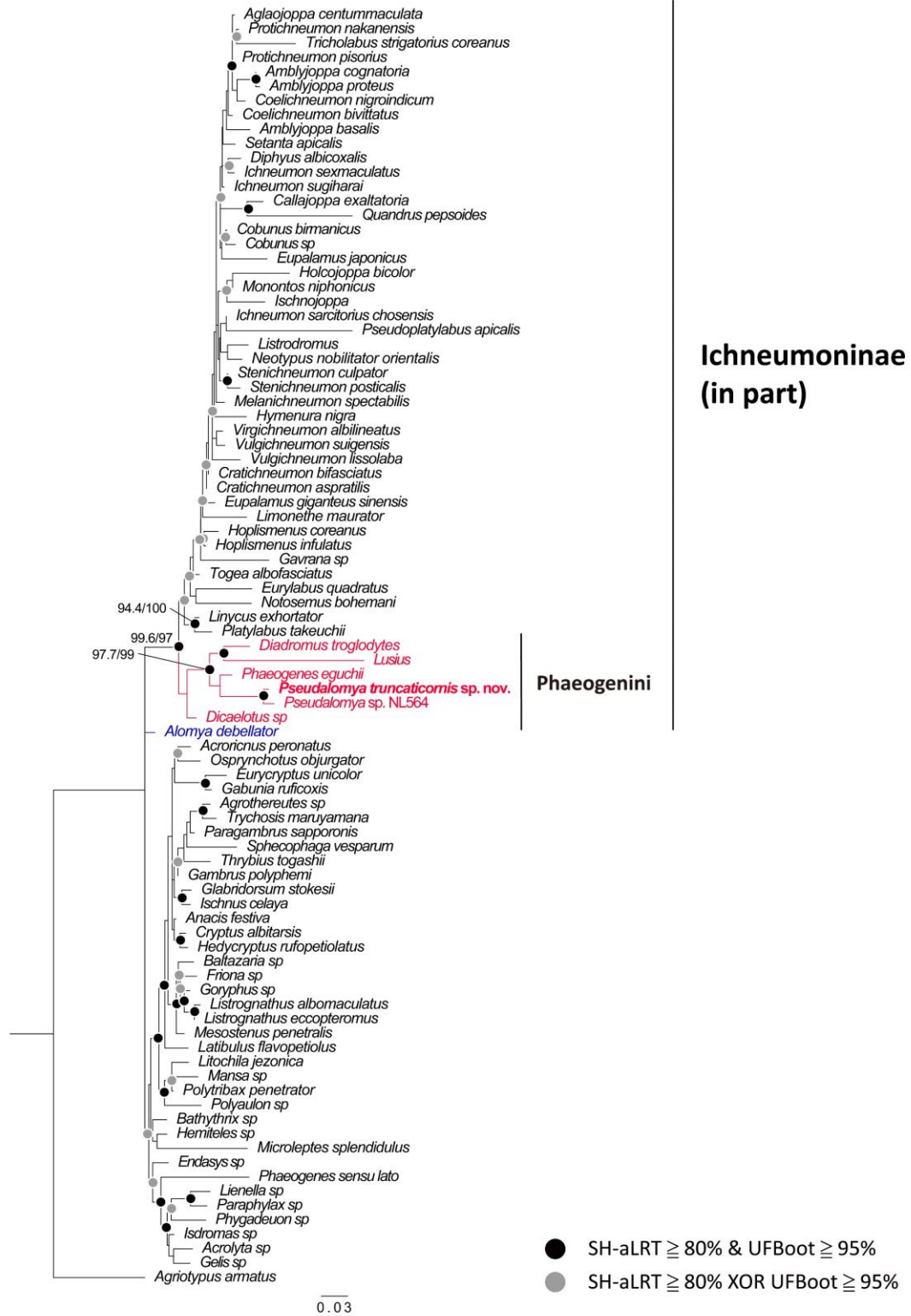


**Supplementary material 4.** Complete maximum likelihood trees reconstructed using the *COI*, *28S*, *18S*, and concatenated *18S+28S+COI* datasets.

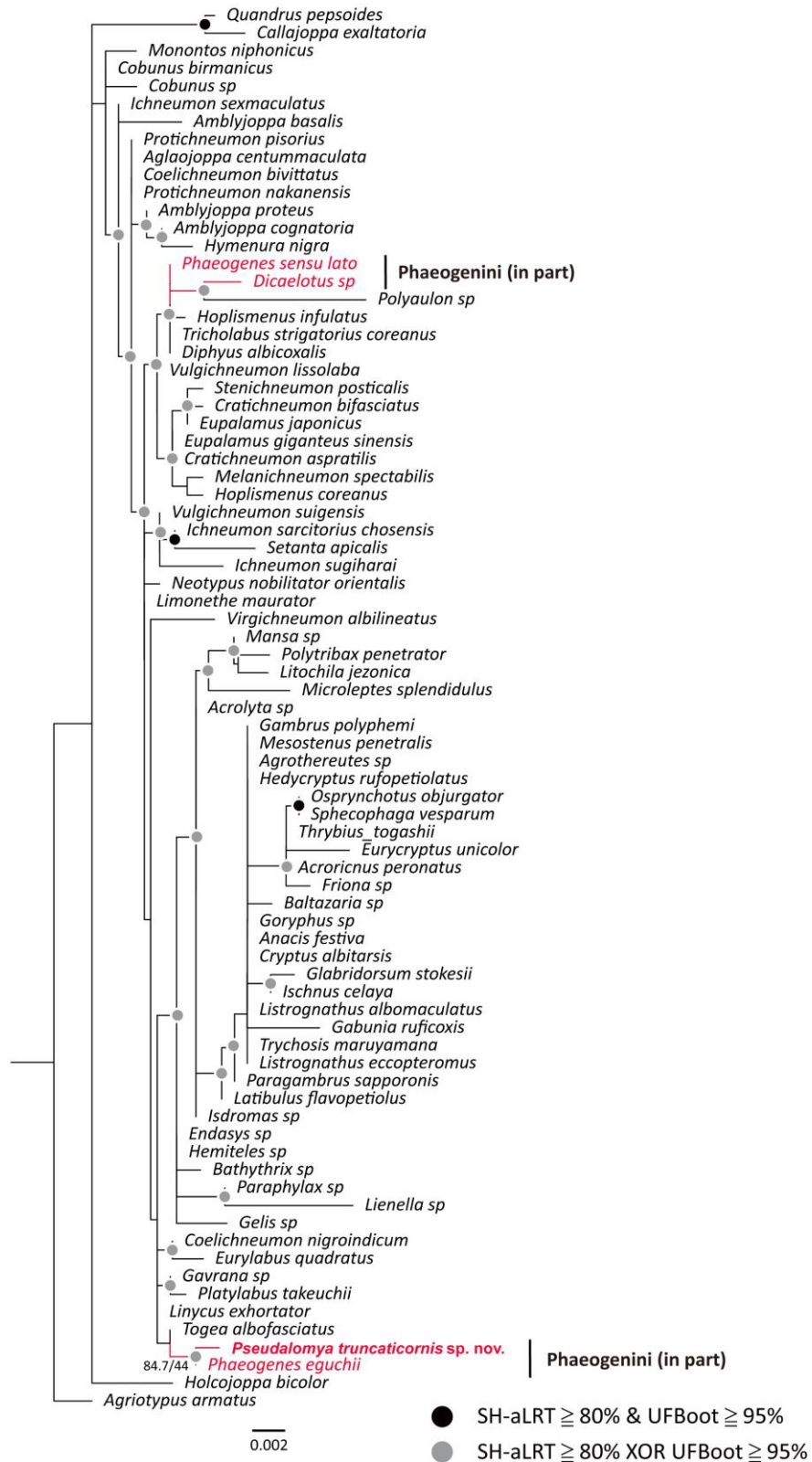
Figures with captions in the .pdf file. All trees were rerooted using the outgroup *Agriotypus armatus*. The red and blue colors indicate Phaeogenini and Alomyini, respectively. Branch lengths of the phylogenetic trees are proportional to the inferred number of nucleotide substitutions per site, except for the branch of the outgroup *Agriotypus armatus*. Circles on the nodes indicate different SH-aLRT/UFBoot values. Nodal support with an SH-aLRT value of <80% and a UFBoot value of <95% is not shown. Abbreviations: SH-aLRT, SH-like approximate likelihood ratio test; UFBoot, ultrafast bootstrap approximation; XOR, one or the other but not both.



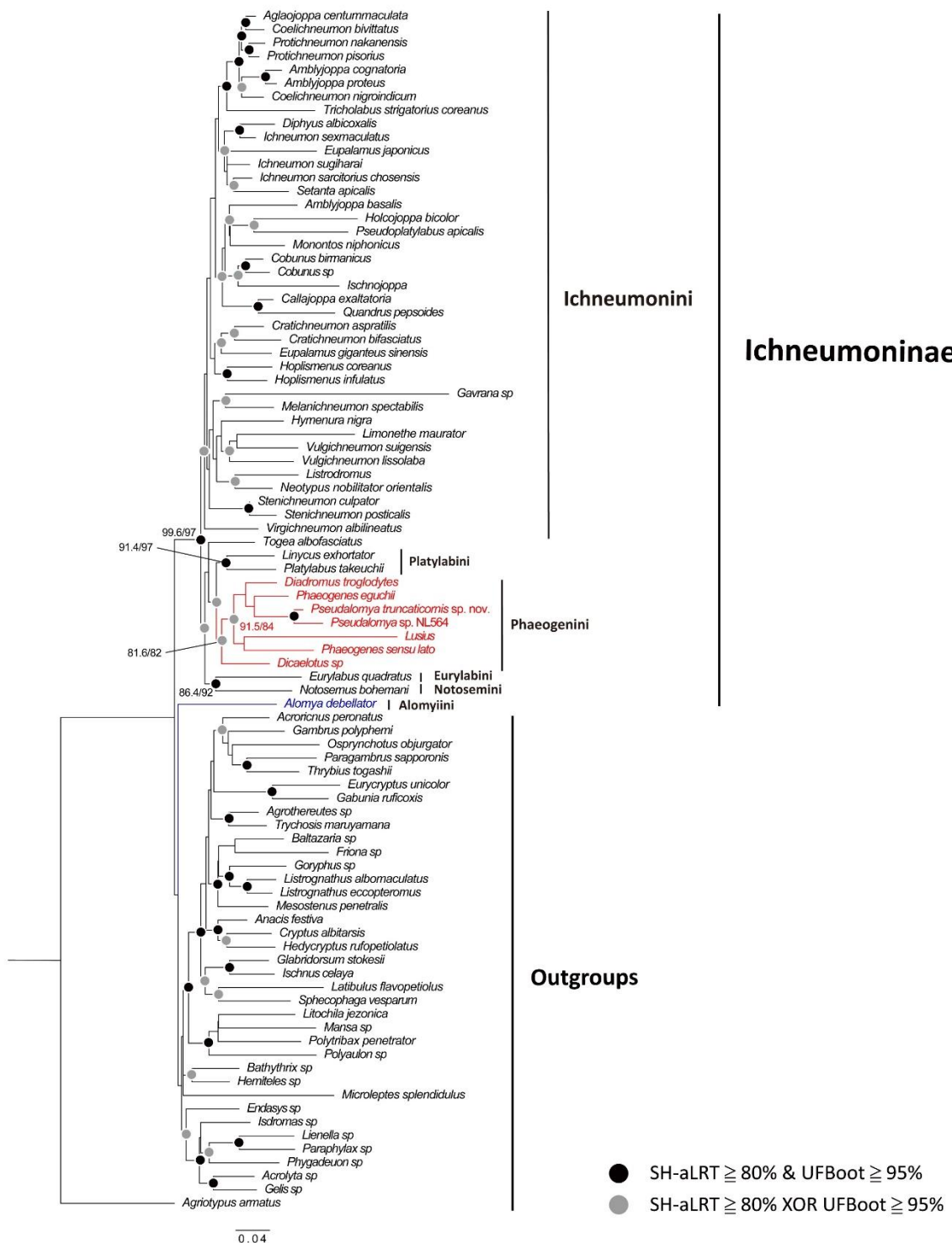
**Figure S1.** Phylogenetic tree of Ichneumoninae based on the *COI* dataset (*COI*: 648 bp, GTR+F+I+G4 (1–648\3 and 2–648\3 bp)).



**Figure S2.** Phylogenetic tree of Ichneumoninae based on the 28S dataset (28S: 625 bp, GTR+F+I+G4 (1–625 bp)).



**Figure S3.** Phylogenetic tree of Ichneumoninae based on the 18S dataset (18S: 1302 bp, TNe+I+G4 (1–1302 bp)).



**Figure S4.** Phylogenetic tree of Ichneumoninae based on the concatenated 18S+28S+COI dataset (2575 bp, 18S: 1302 bp; 28S: 625 bp; COI: 648 bp; SYM+I+G4 (1–1302, 1303–1927, 1928–2575\3 and 1929–2575\3 bp); HKY+F+I+G4 (1930–2575\3 bp)).