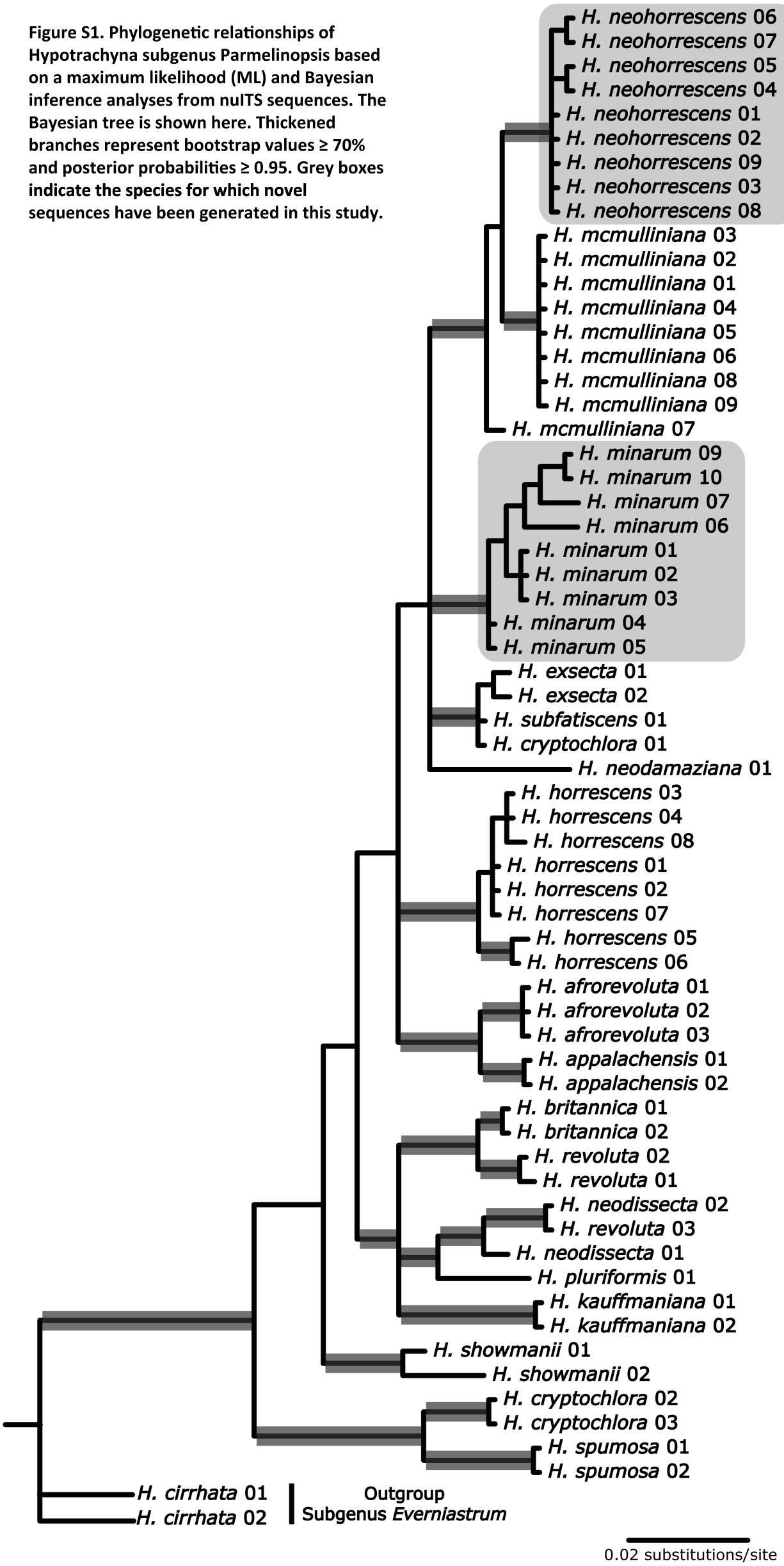Figure S1. Phylogenetic relationships of Hypotrachyna subgenus Parmelinopsis based on a maximum likelihood (ML) and Bayesian inference analyses from nuITS sequences. The Bayesian tree is shown here. Thickened branches represent bootstrap values ≥ 70% and posterior probabilities ≥ 0.95. Grey boxes indicate the species for which novel sequences have been generated in this study.