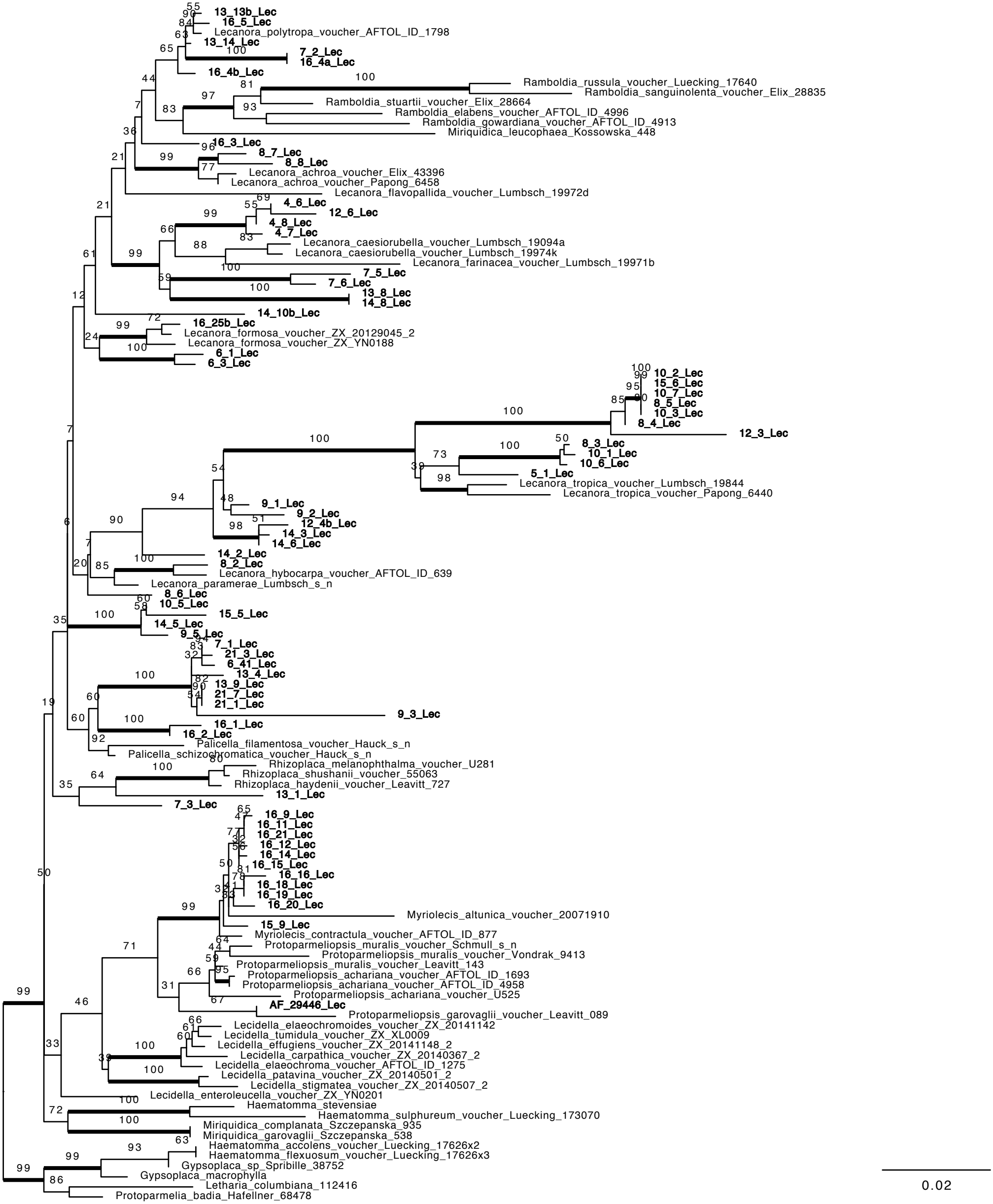

Supplementary figure 7. Single-locus tree for Lecanoraceae nrLSU. Maximum-likelihood tree inferred with the TN+F+R3 substitution model. Support values are UFboot2 with 5000 replicates. Bipartitions with bootstrap support ≥95 are indicated with bold branches. Bold tip names indicate specimens sequenced in this study. Scale indicates substitutions per site.