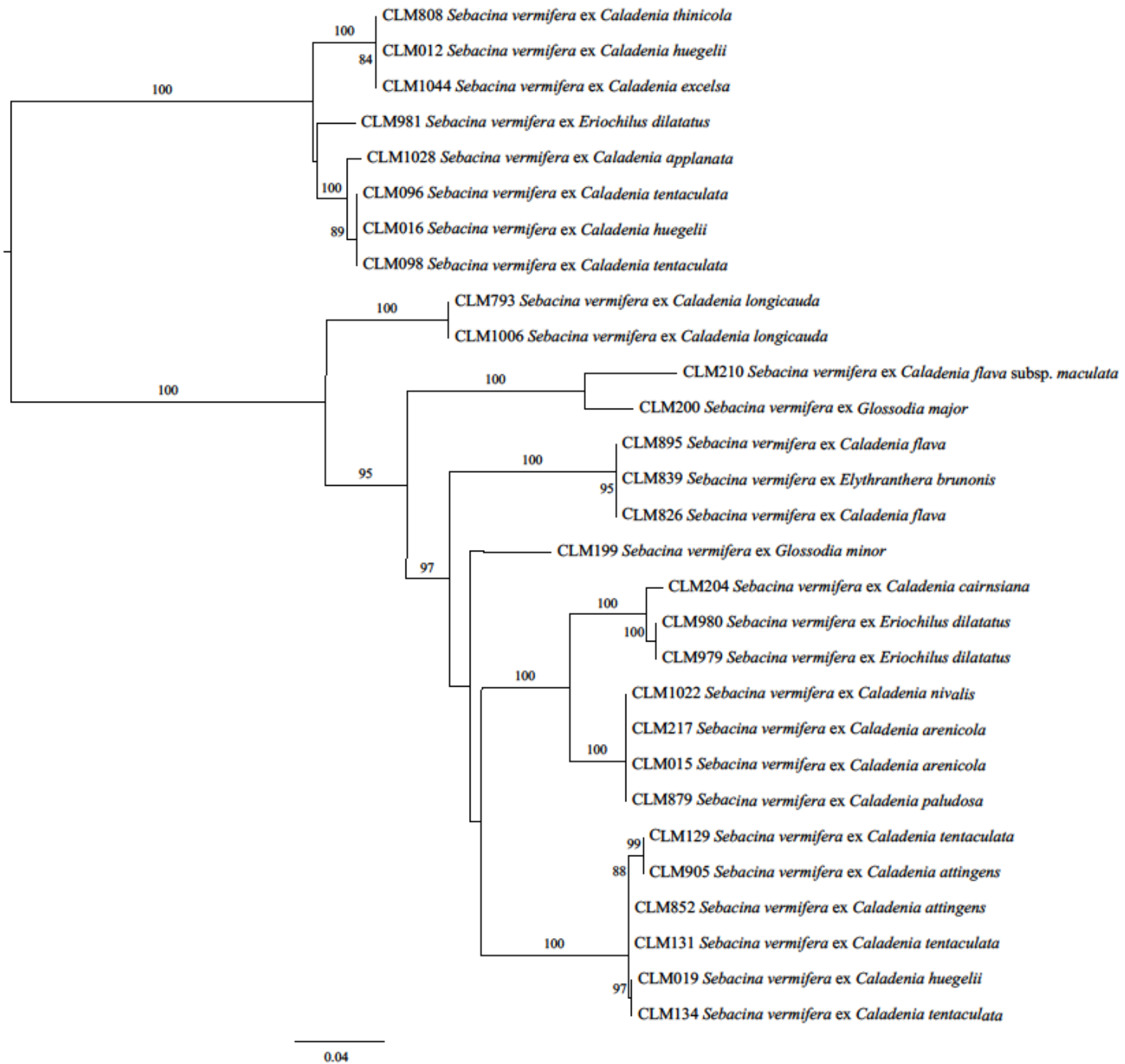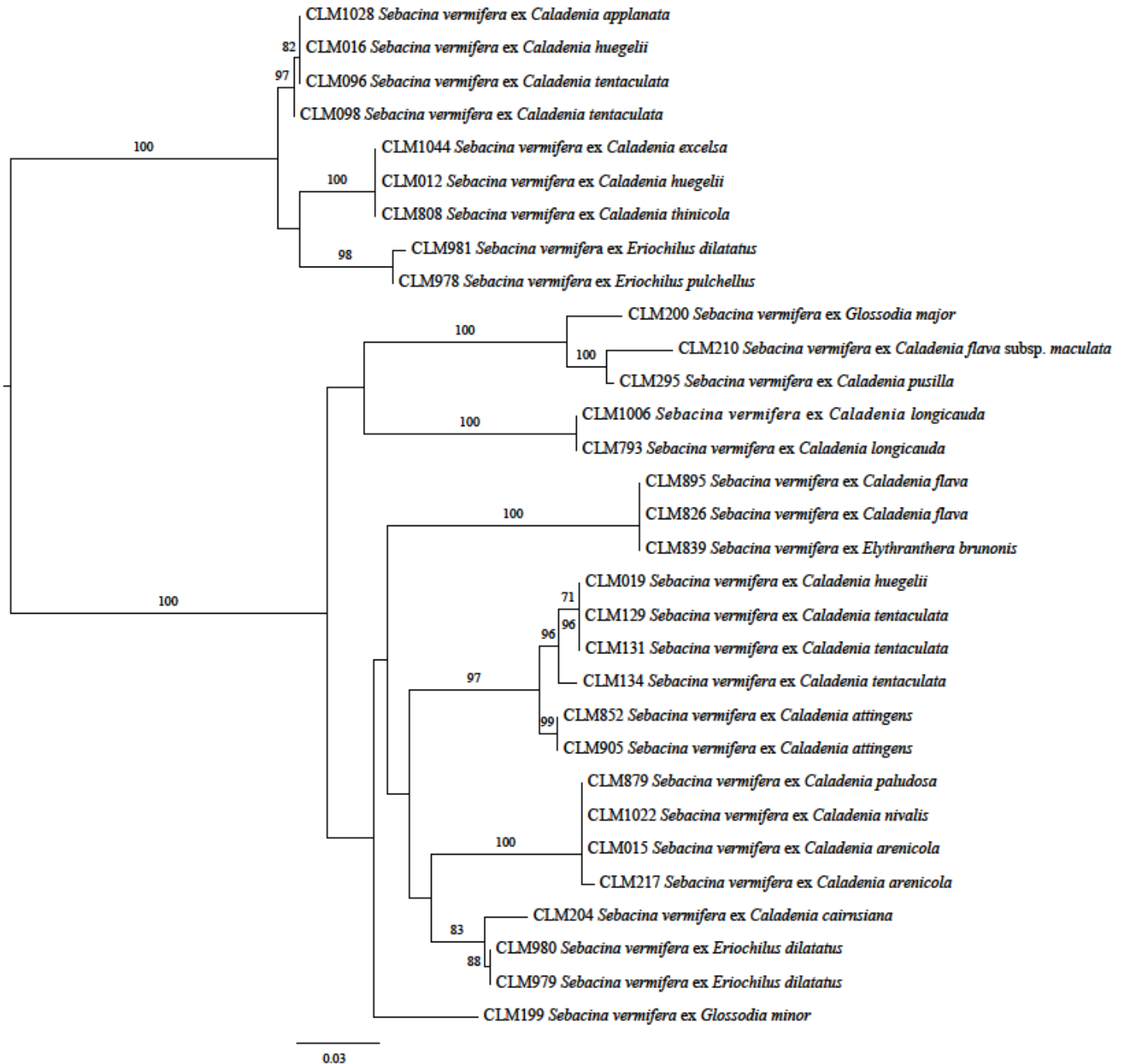**Appendix S1.** Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C11804. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.
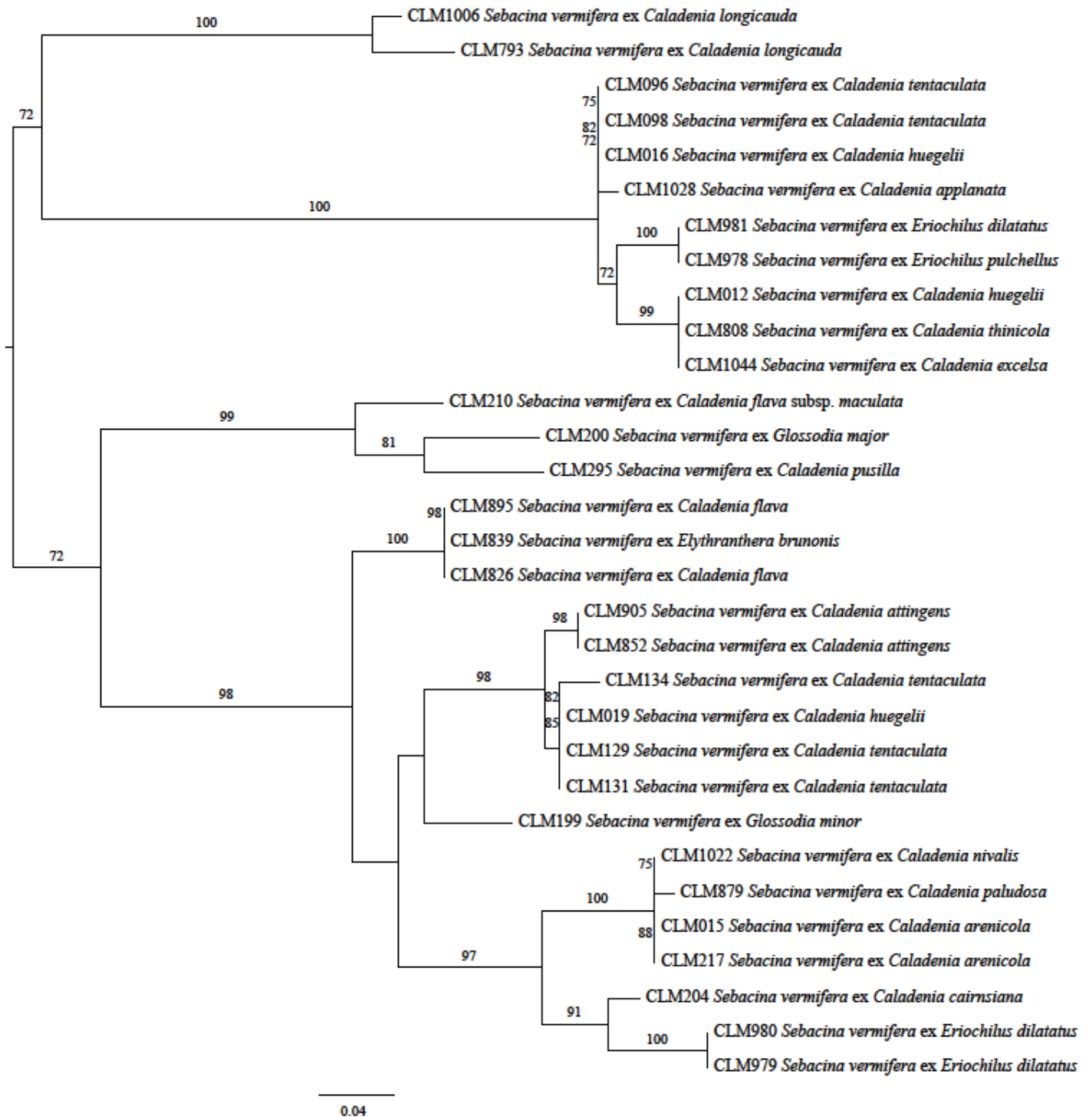
Appendix S2. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C43566. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.
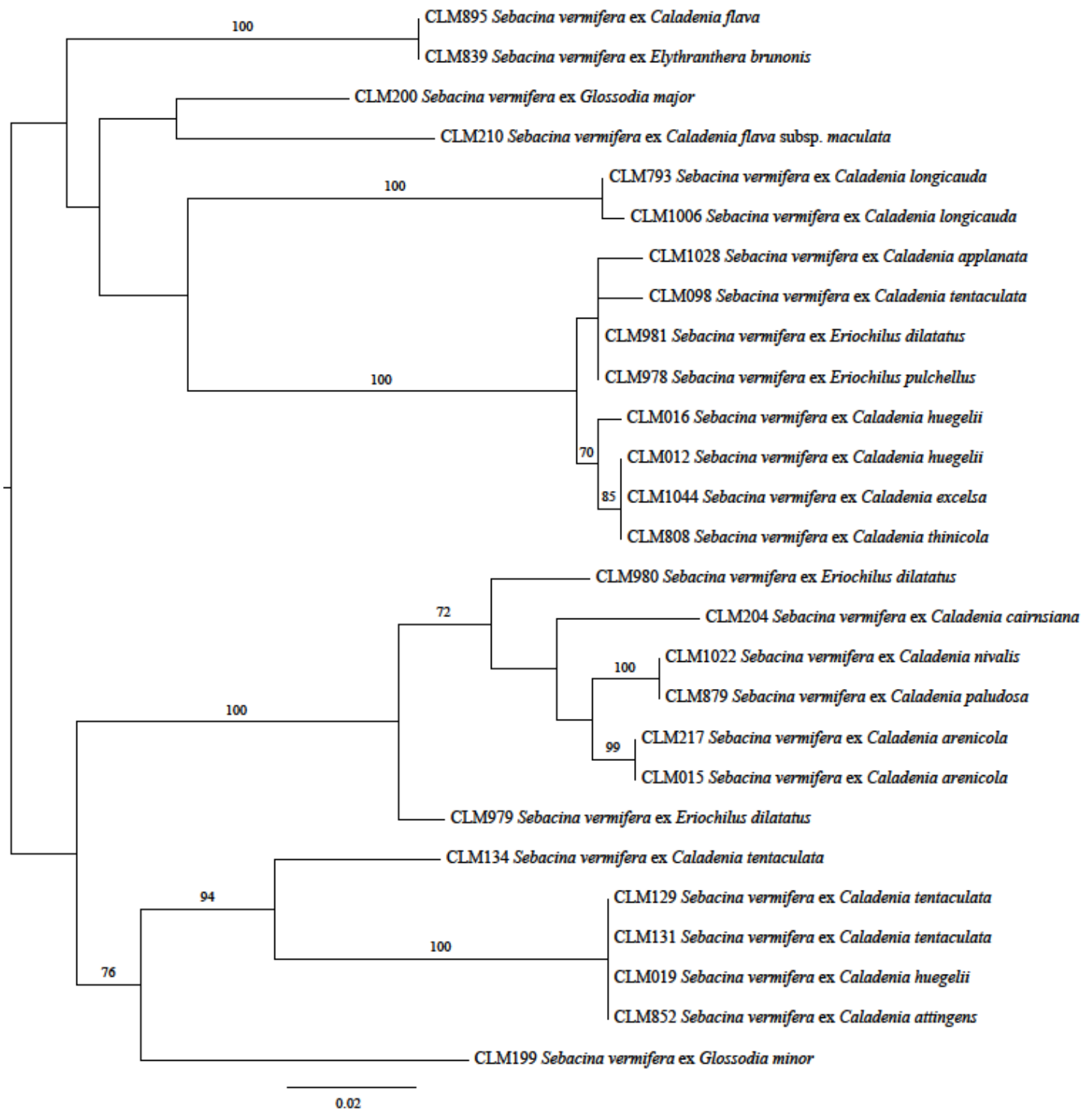
Appendix S3. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C28586. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.
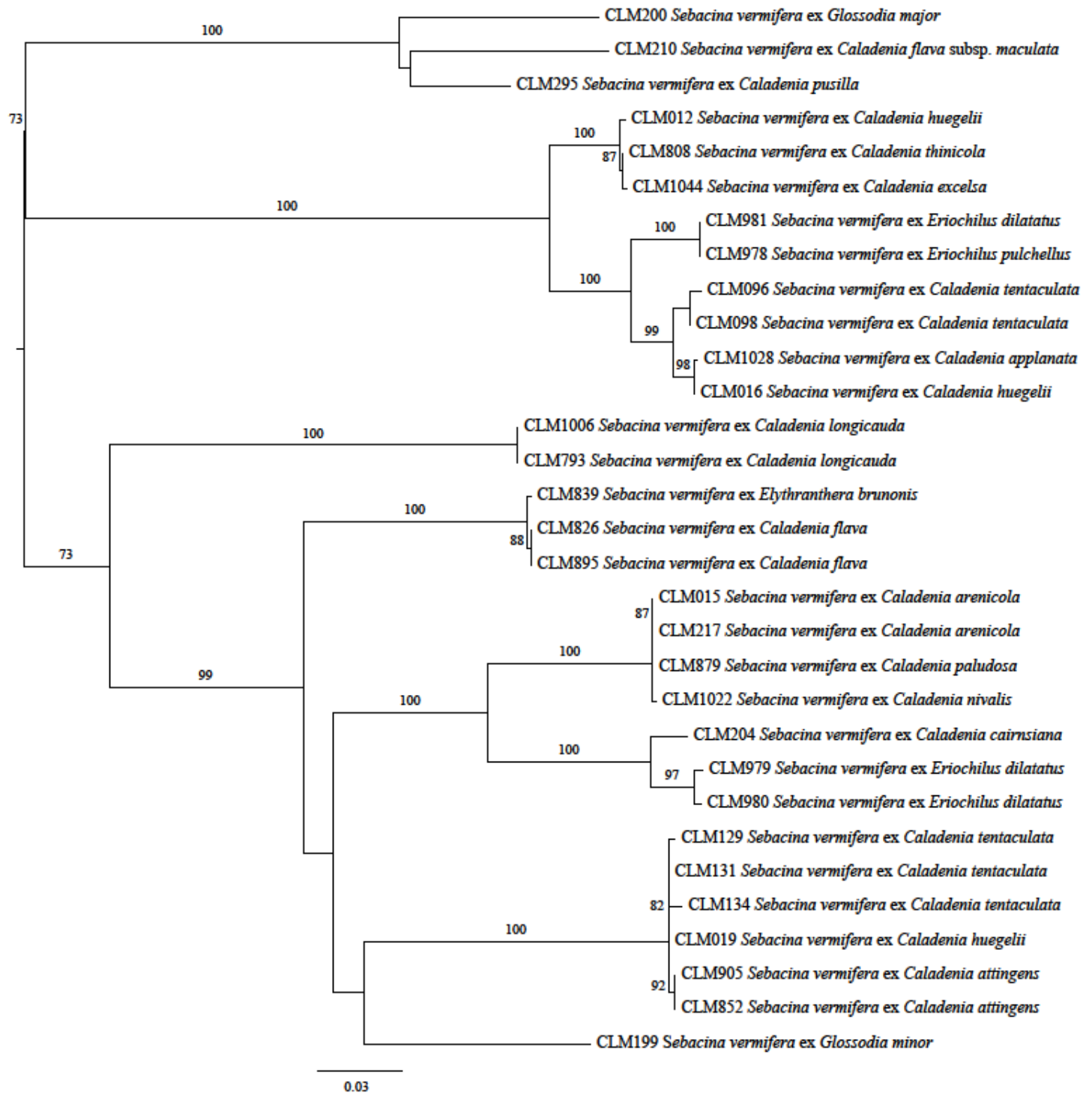
Appendix S4. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C19981. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.
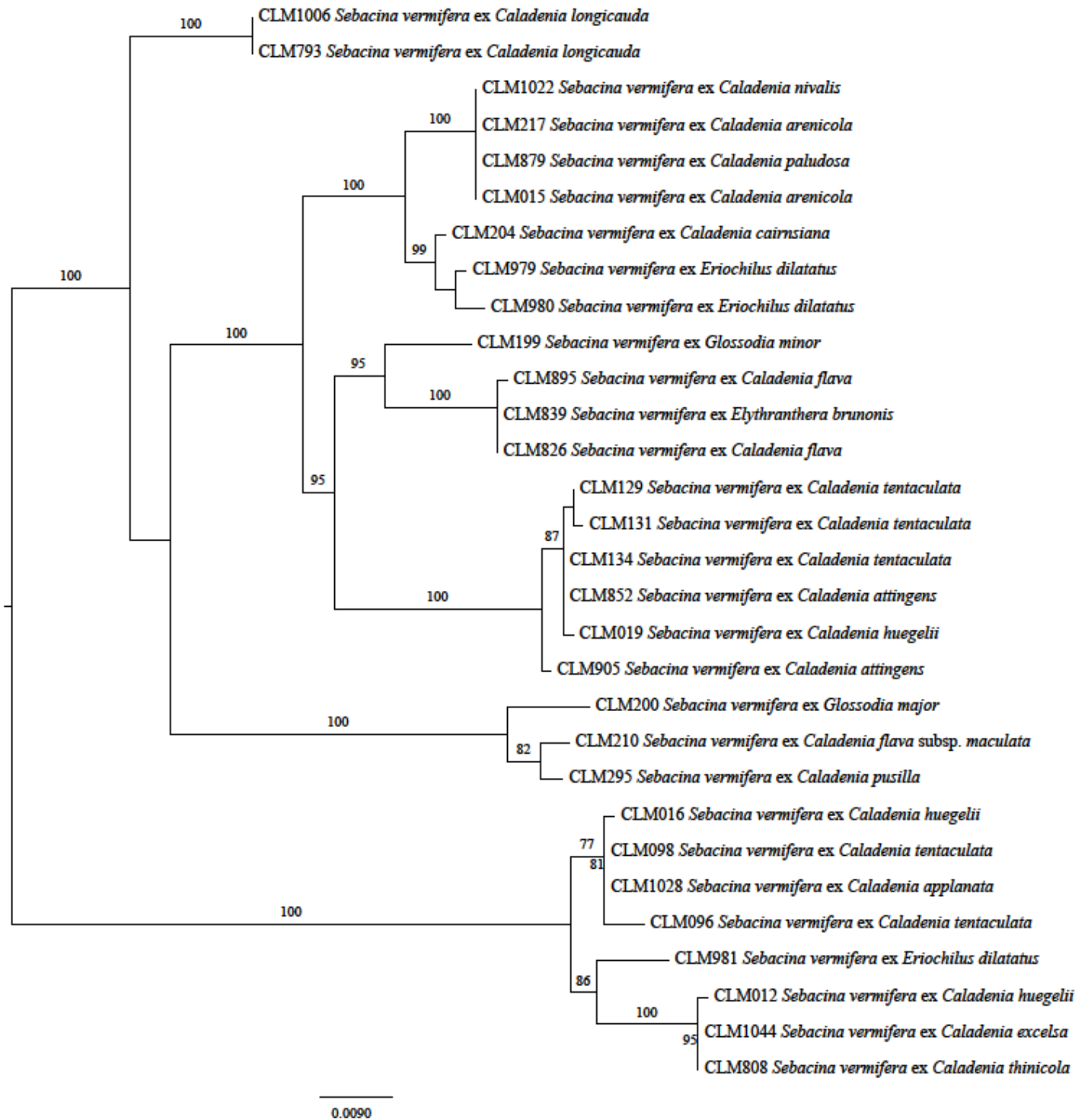
Appendix S5. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C11488. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.

Appendix S6. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C5129+C16699. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.

Appendix S7. Midpoint rooted maximum likelihood tree for *Sebacina vermifera* obtained for locus C2745. The tree with the highest log likelihood is shown. The numbers above the branches are maximum likelihood bootstrap values. Bootstrap values of ≥70% are shown. The branch length is proportional to the inferred divergence level. The bar indicates substitutions per site.