

Supplementary Material

Phylogeography and evolutionary dynamism of marine gastropods from the Lord Howe Island Group

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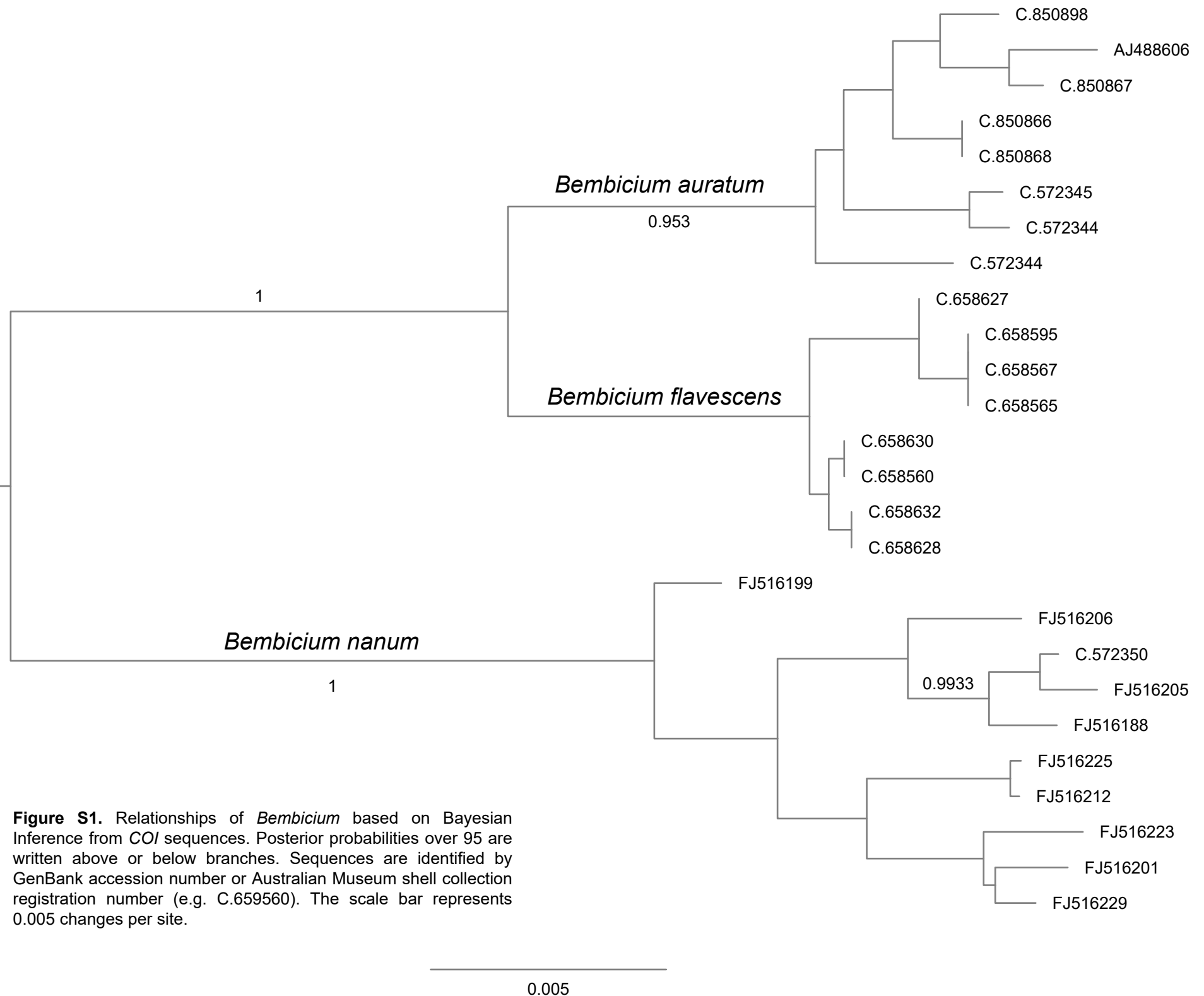


Figure S1. Relationships of *Bembicium* based on Bayesian Inference from COI sequences. Posterior probabilities over 95 are written above or below branches. Sequences are identified by GenBank accession number or Australian Museum shell collection registration number (e.g. C.659560). The scale bar represents 0.005 changes per site.

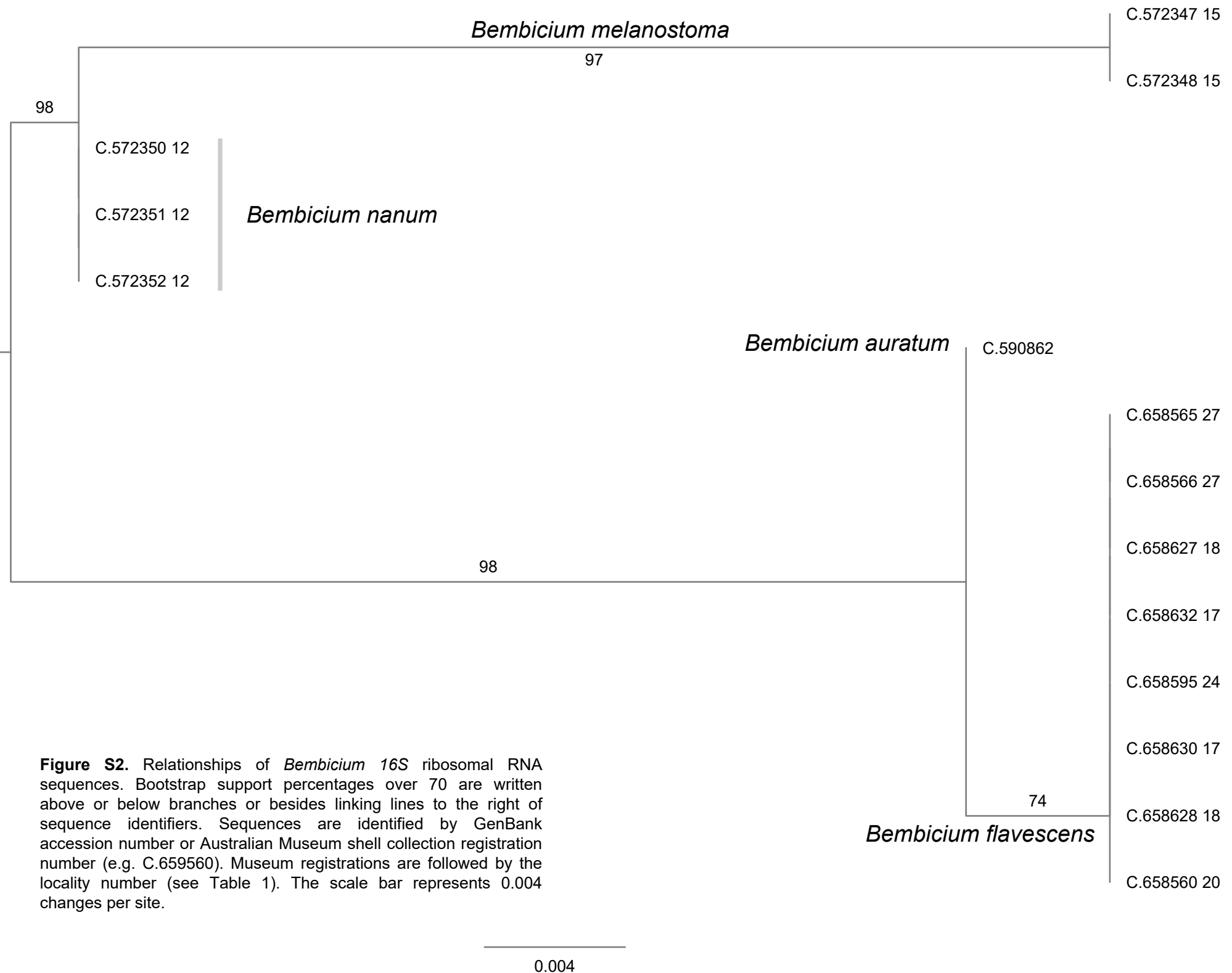


Figure S3. Relationships of *Bembicium* based on concatenated *COI* and *16S* ribosomal RNA sequences. Bootstrap support percentages over 70 are written above or below branches or besides linking lines to the right of sequence identifiers. Sequences are identified by GenBank accession number or Australian Museum shell collection registration number (e.g. C.659560). The scale bar represents 0.04 changes per site. Specimens without hatch marks were sequenced only for *COI*, specimens with a single hatch mark were sequenced only for *16S* rRNA and specimens with two hatch marks were sequenced for both *COI* and *16S* rRNA.

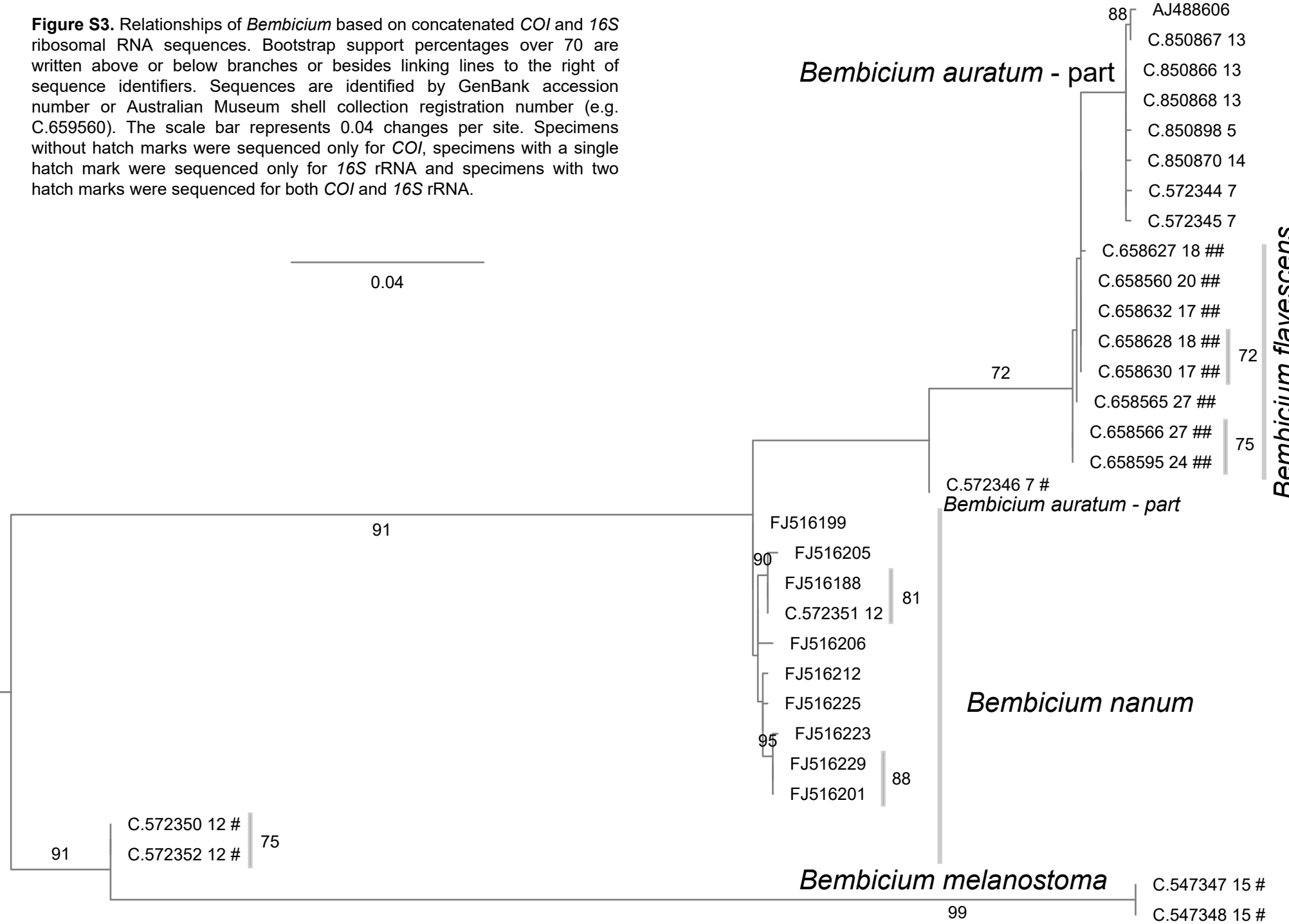
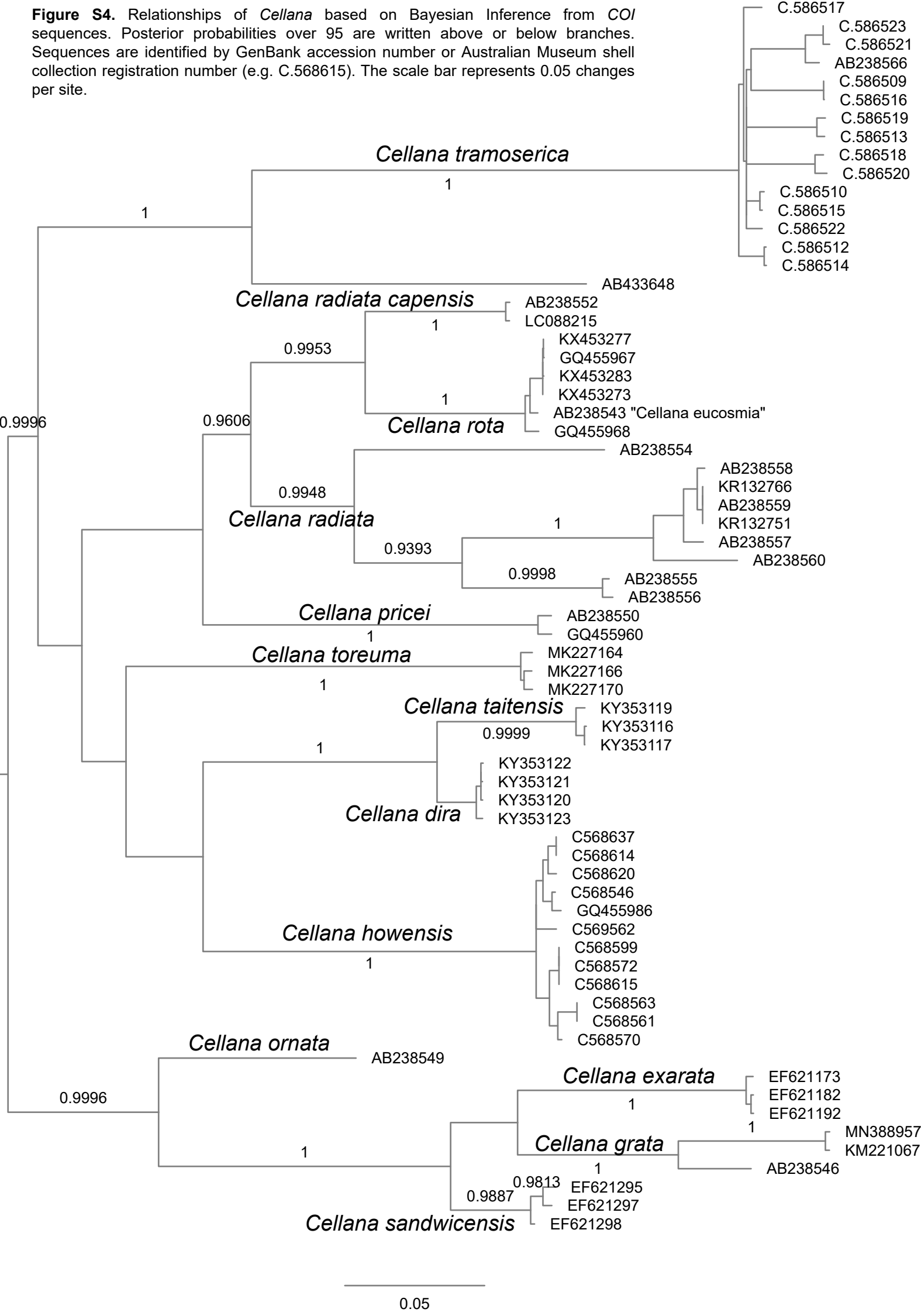


Figure S4. Relationships of *Cellana* based on Bayesian Inference from COI sequences. Posterior probabilities over 95 are written above or below branches. Sequences are identified by GenBank accession number or Australian Museum shell collection registration number (e.g. C.568615). The scale bar represents 0.05 changes per site.



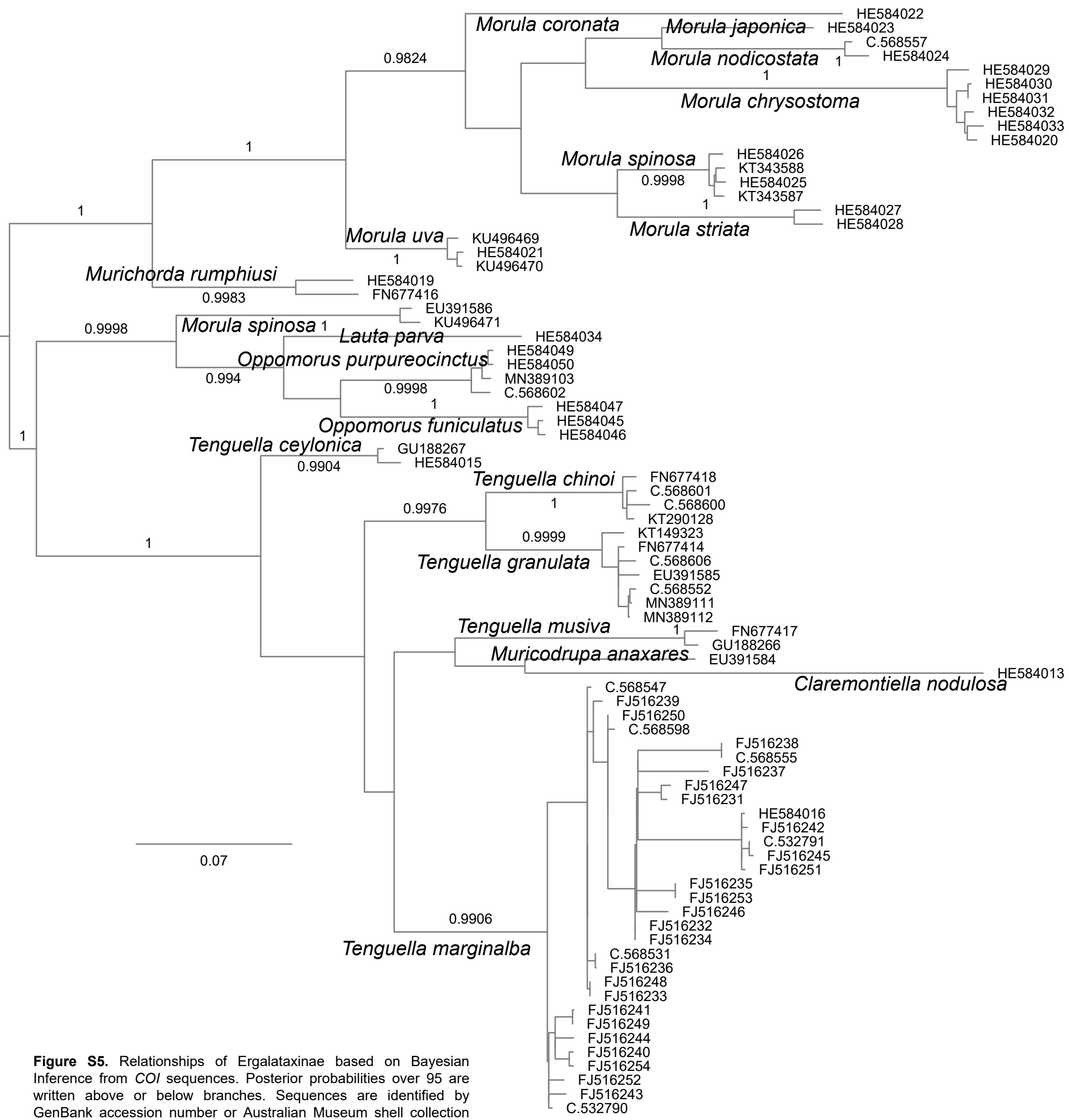


Figure S5. Relationships of Ergalataxinae based on Bayesian Inference from COI sequences. Posterior probabilities over 95 are written above or below branches. Sequences are identified by GenBank accession number or Australian Museum shell collection registration number (e.g. C.568552). The scale bar represents 0.07 changes per site.