Supplementary figures S4-S8: phylogenetic trees

Fig. S4. Phylogenetic tree of *Prorocentrum* genus showing the position of *P. venetum* (this study, in bold), based on 18S-D3 rDNA sequences; two taxa belonging to the order Peridiniales were used as outgroups. In the box, a subtree with the same topology focusing on the two sister clades (containing taxa related to *P. micans* and *P. venetum*, respectively) is provided to better show the genetic distances between and within species clades. The tree construction was performed by the maximum likelihood algorithm with the substitution models HKY85, TN93 and GTR, which yielded identical topologies. Branch support was assessed by one thousand bootstrap resampling; for clarity, the value obtained with the analysis with the HKY85 model is shown at the main nodes (often the highest of the three models), and only values that differ by more than ± 40 are indicated as HKY85|TN93|GTR. The branch length is proportional to the number of substitutions per site (the scale bar represents the number of nucleotide substitutions per site).

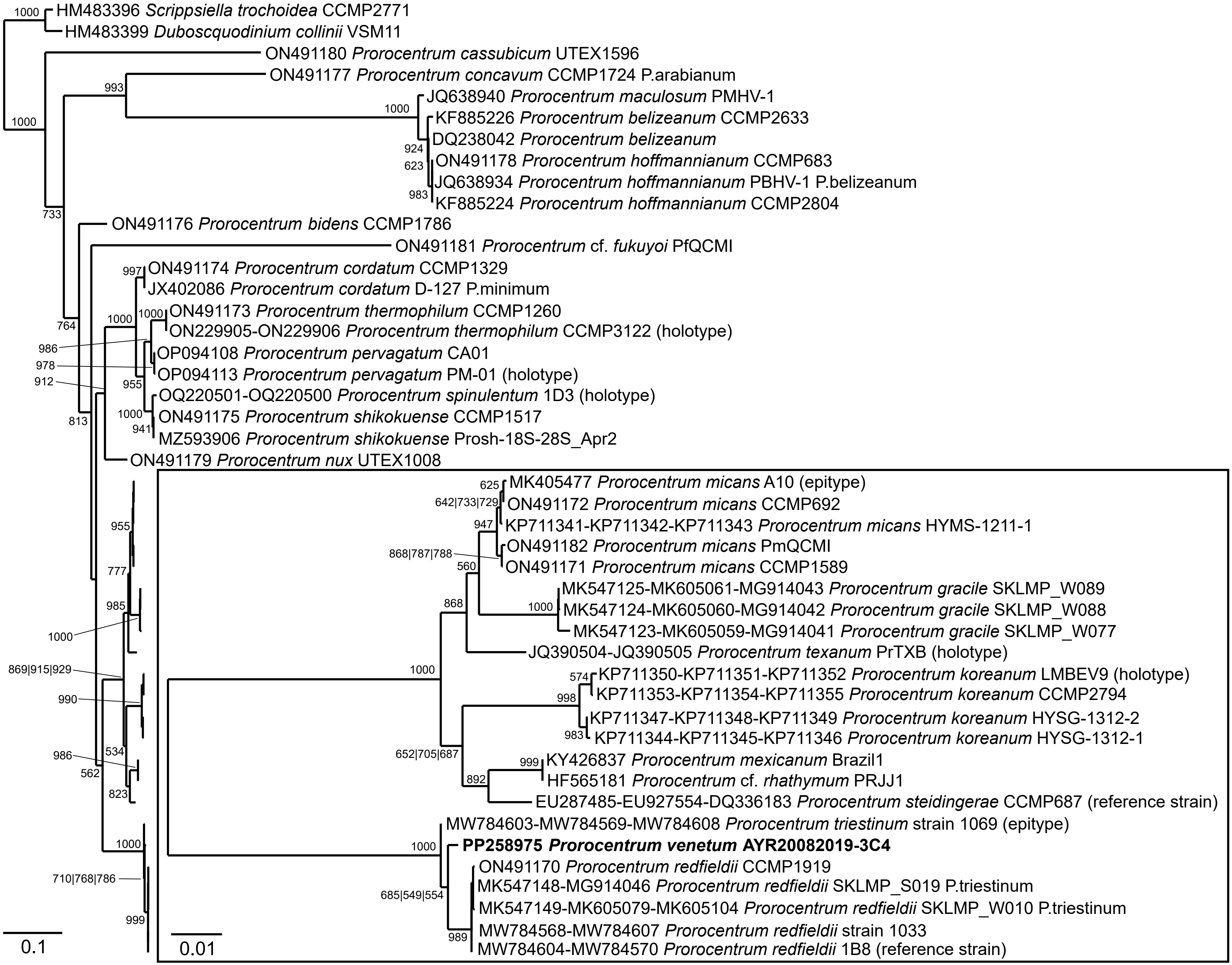
Fig. S5. Phylogenetic tree of *Prorocentrum* genus showing the position of *P. venetum* (this study, in bold), based on 18S-D3 rDNA sequences; two taxa belonging to the order Peridiniales were used as outgroups. In the box, a subtree with the same topology focusing on the two sister clades (containing taxa related to *P. micans* and *P. venetum*, respectively) is provided to better show the genetic distances between and within species clades. The tree construction was performed by a Bayesian algorithm with the HKY85 and GTR substitution models, which yielded similar topologies. The Bayesian branch support (posterior probability value) obtained with the analysis with the HKY85 model is shown at the main nodes (often the highest of the two models); for clarity, only values that differ by more than ± 0.050 are indicated as HKY85|GTR. The branch length is proportional to the number of substitutions per site (the scale bar represents the number of nucleotide substitutions per site).

Fig. S6. Phylogenetic tree based on a selection of 18S rDNA sequences belonging to the two sister clades encompassing taxa related to *P. micans* and *P. venetum*. The tree construction was performed by the maximum likelihood algorithm with the substitution models HKY85, TN93 and GTR, which yielded identical topologies. Branch support was assessed by the aLRT method; for clarity, the value obtained with the analysis with the HKY85 model is shown at the main nodes (often the highest of the three models), and only values that differ by more than ± 0.020 are indicated as HKY85|TN93|GTR. The branch length is proportional to the number of substitutions per site (the scale bar represents the number of nucleotide substitutions per site).

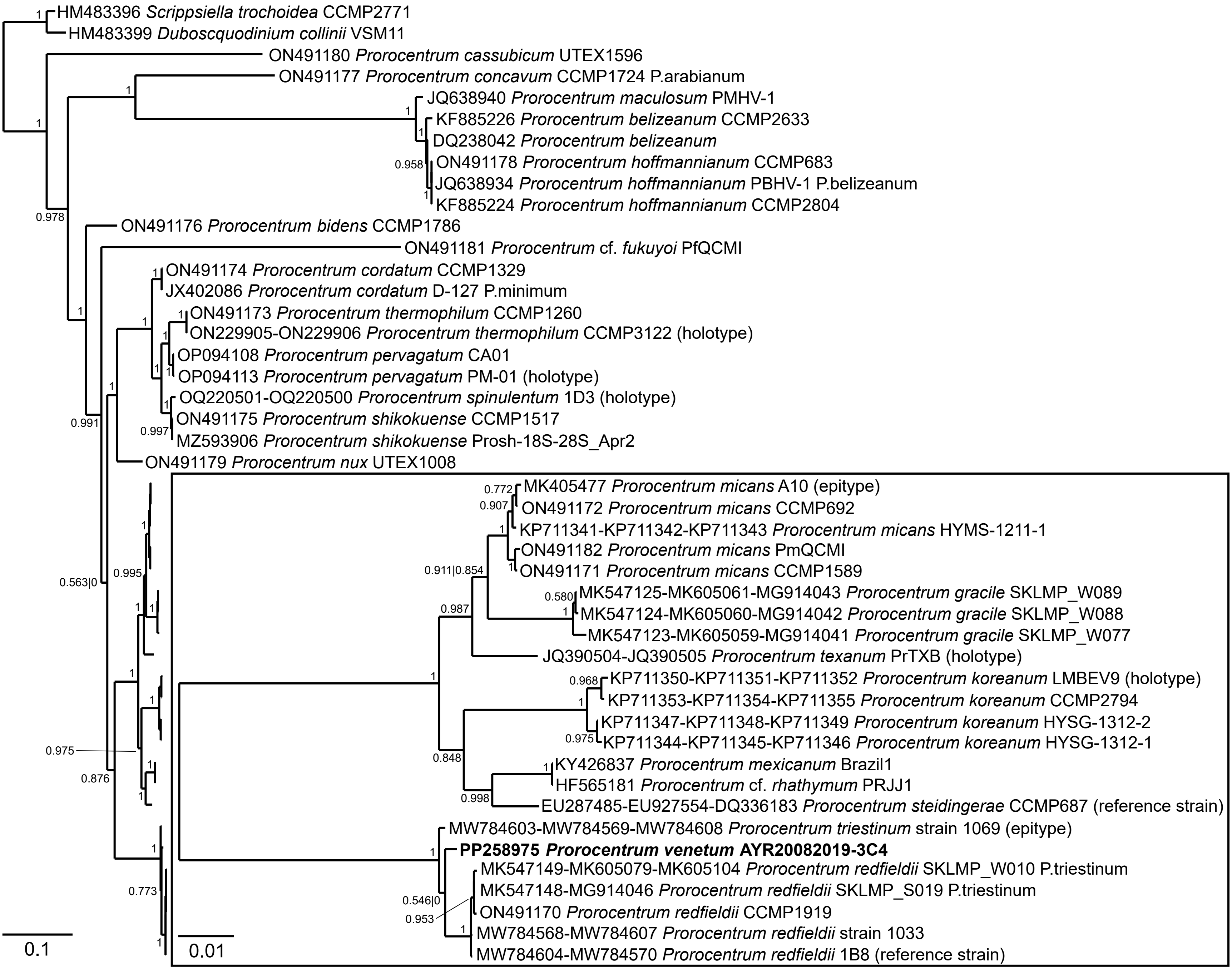
Fig. S7. Phylogenetic tree based on a selection of D1-D2 region of 28S rDNA sequences belonging to the two sister clades encompassing taxa related to *P. micans* and *P. venetum*. The tree construction was performed by the maximum likelihood algorithm with the substitution models HKY85, TN93 and GTR, which yielded identical topologies. Branch support was assessed by the aLRT method; for clarity, the value obtained with the analysis with the HKY85 model is shown at the main nodes (often the highest of the three models), and only values that differ by more than ± 0.020 are indicated as HKY85|TN93|GTR. The branch length is proportional to the number of substitutions per site (the scale bar represents the number of nucleotide substitutions per site).

Fig. S8. Phylogenetic tree based on a selection of sequences from the ITS region (including ITS1, 5.8S rDNA and ITS2) belonging to the two sister clades encompassing taxa related to *P. micans* and *P. venetum*. The tree construction was performed by the maximum likelihood algorithm with the substitution models HKY85, TN93 and GTR, which yielded identical topologies. Branch support was assessed by the aLRT method; for clarity, the value obtained with the analysis with the HKY85 model is shown at the main nodes (often the highest of the three models), and only values that differ by more than ± 0.020 are indicated as HKY85|TN93|GTR. The branch length is proportional to the number of substitutions per site (the scale bar represents the number of nucleotide substitutions per site).

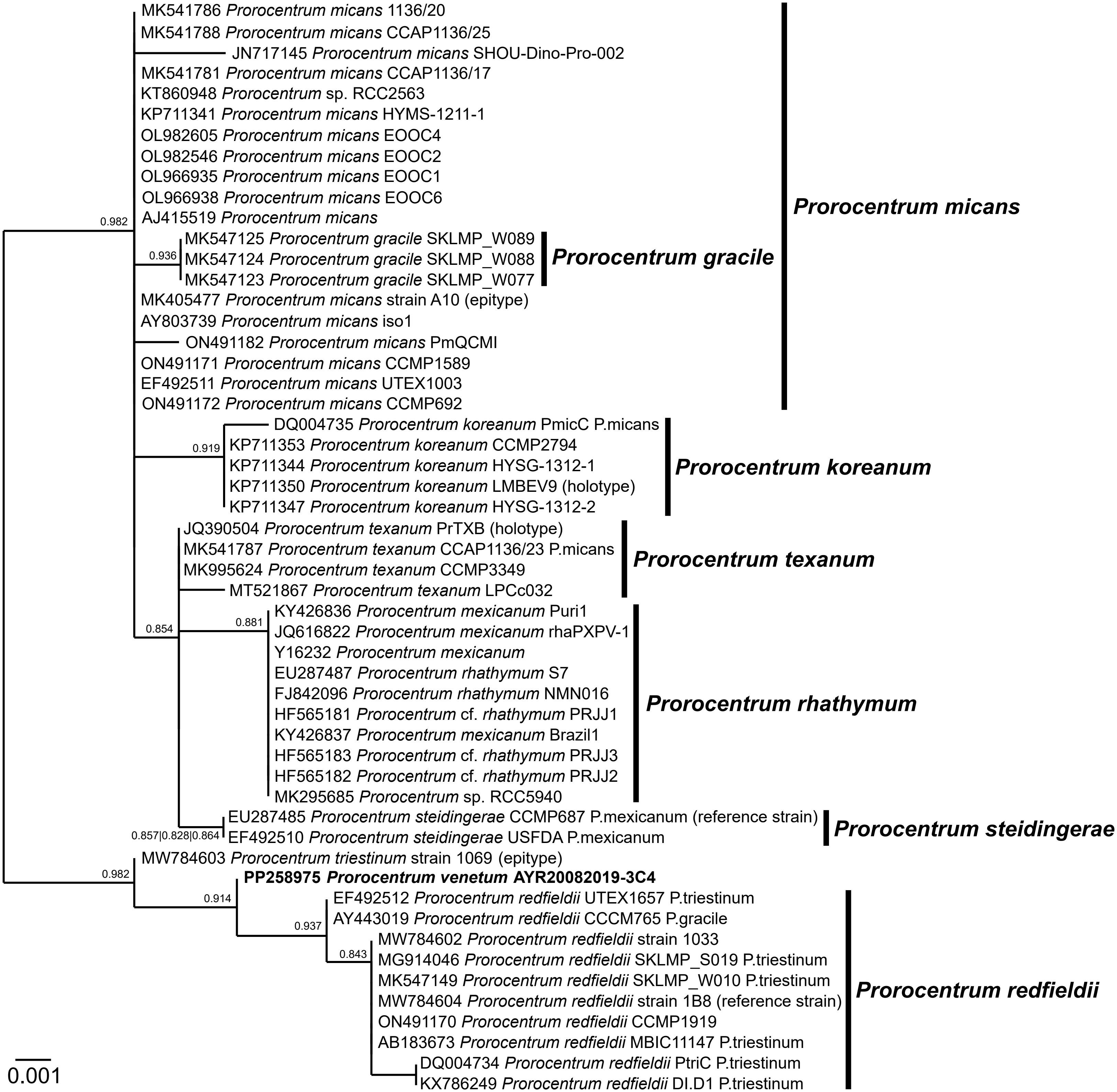
Supplementary Fig. S4. Phylogenetic tree based on 18S-D3 rDNA sequences (ML with bootstrap support)



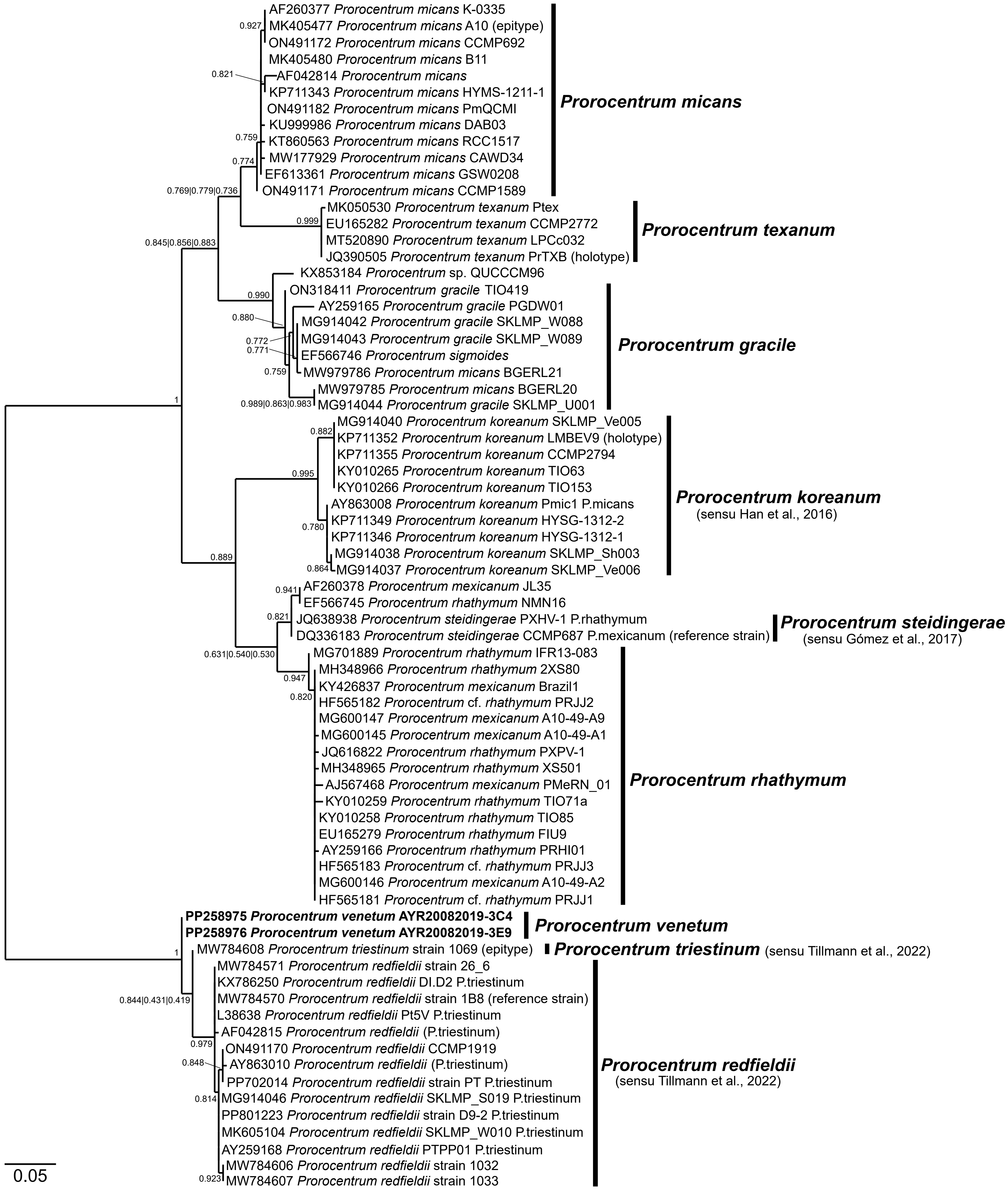
Supplementary Fig. S5. Phylogenetic tree based on 18S-D3 rDNA sequences (MrBayes, posterior probability support)



Supplementary Fig. S6. Phylogenetic tree based on 18S rDNA sequences



Supplementary Fig. S7. Phylogenetic tree based on D1-D2 28S rDNA sequences



Supplementary Fig. S8. Phylogenetic tree based on ITS rDNA sequences