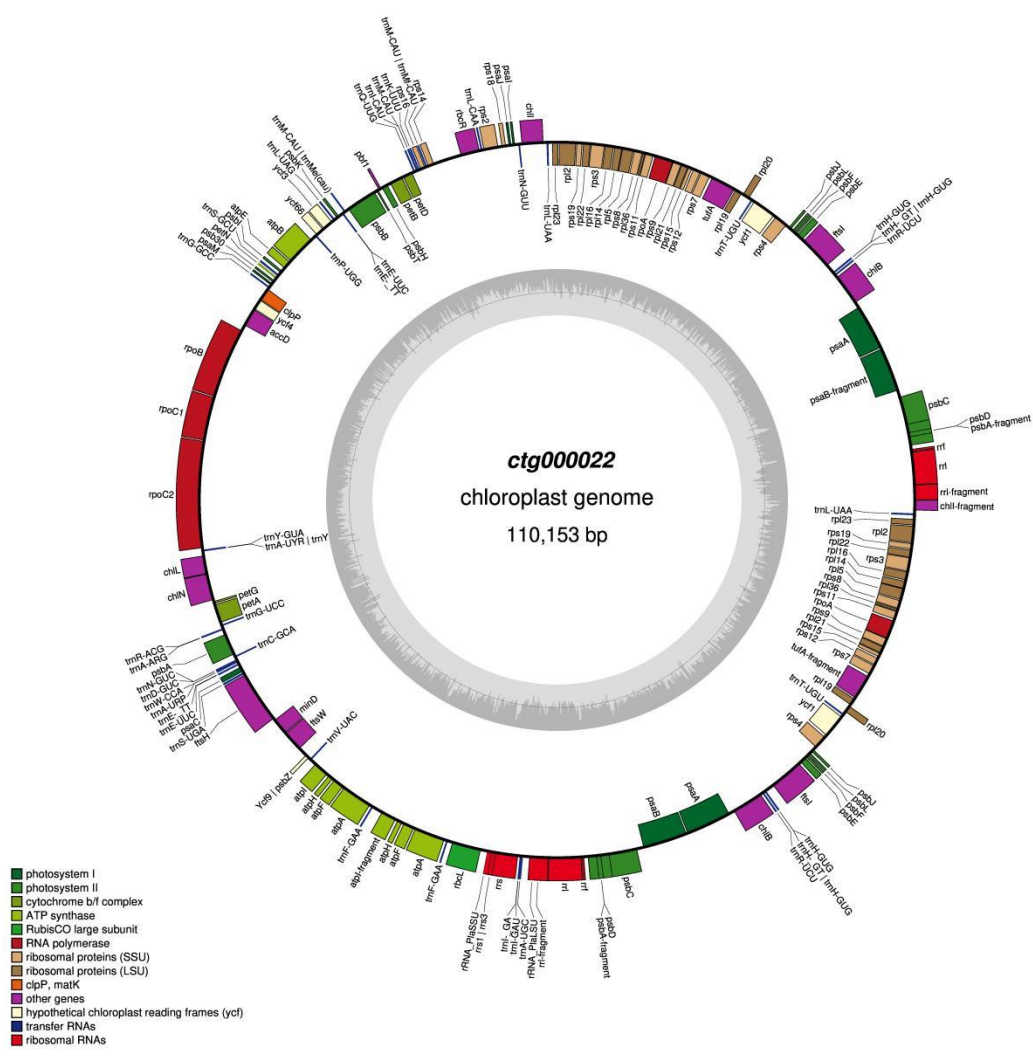


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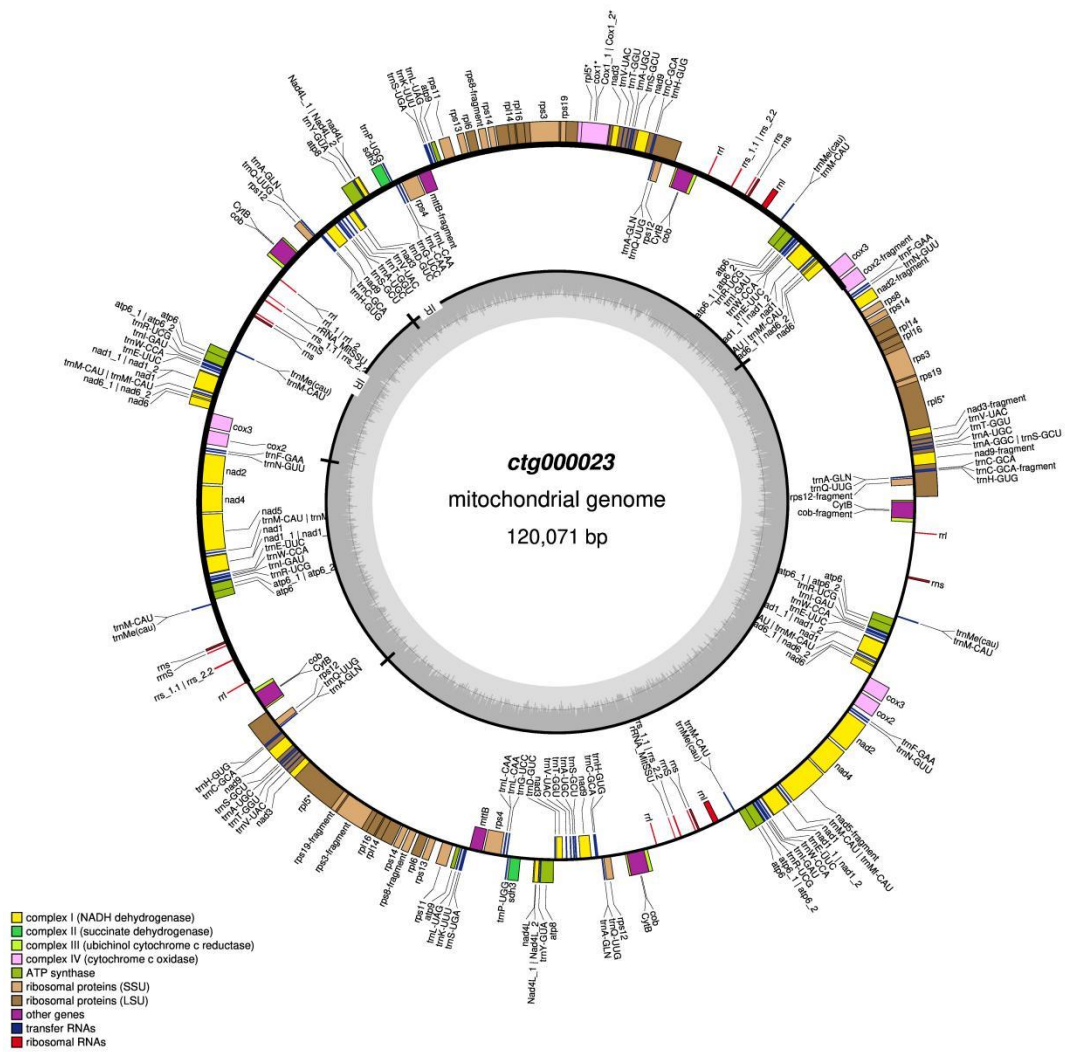
The genome of *Prasinoderma coloniale* unveils the existence of a third phylum within green plants

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Huan Liu^{1,3}

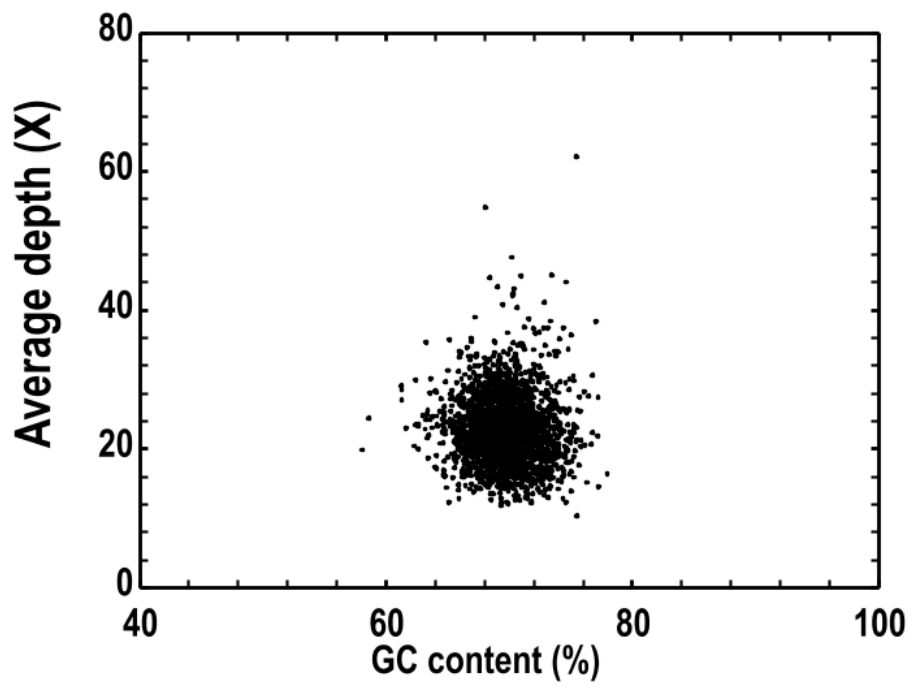
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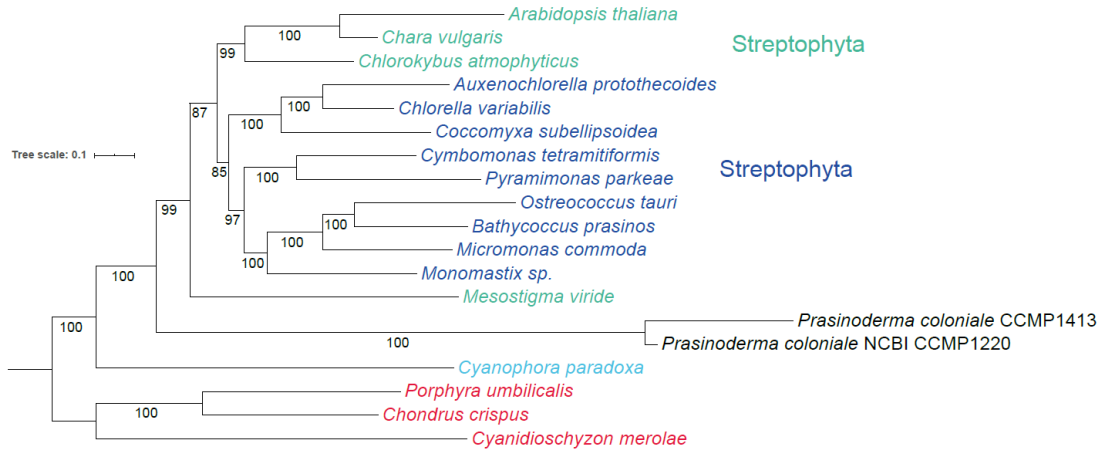
Supplementary Figure 1. The chloroplast circos map of *Prasinoderma coloniale*.



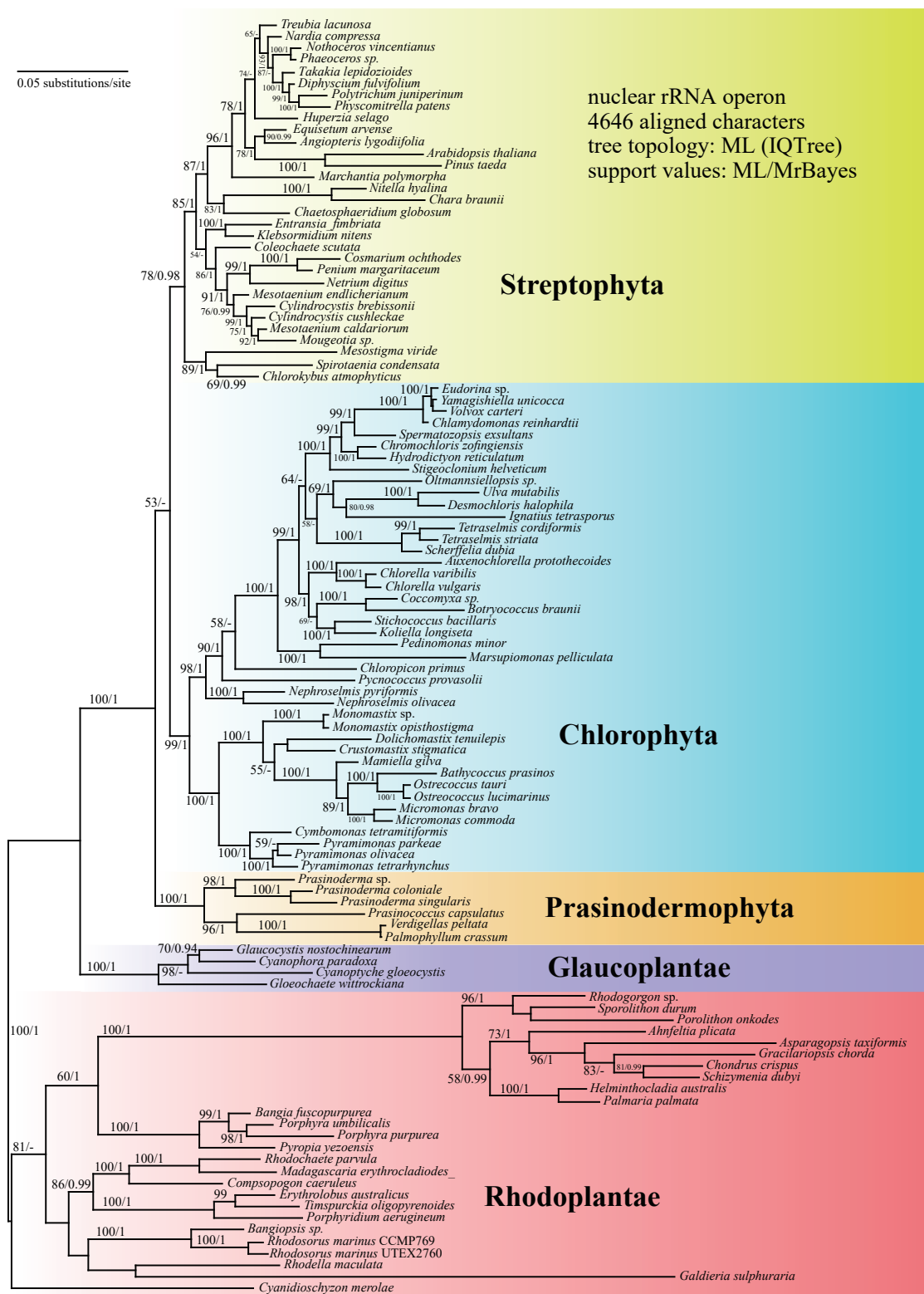
Supplementary Figure 2. The mitochondrial circos map of *Prasinoderma coloniale*.



Supplementary Figure 3. The GC depth distribution of *Prasinoderma coloniale*.

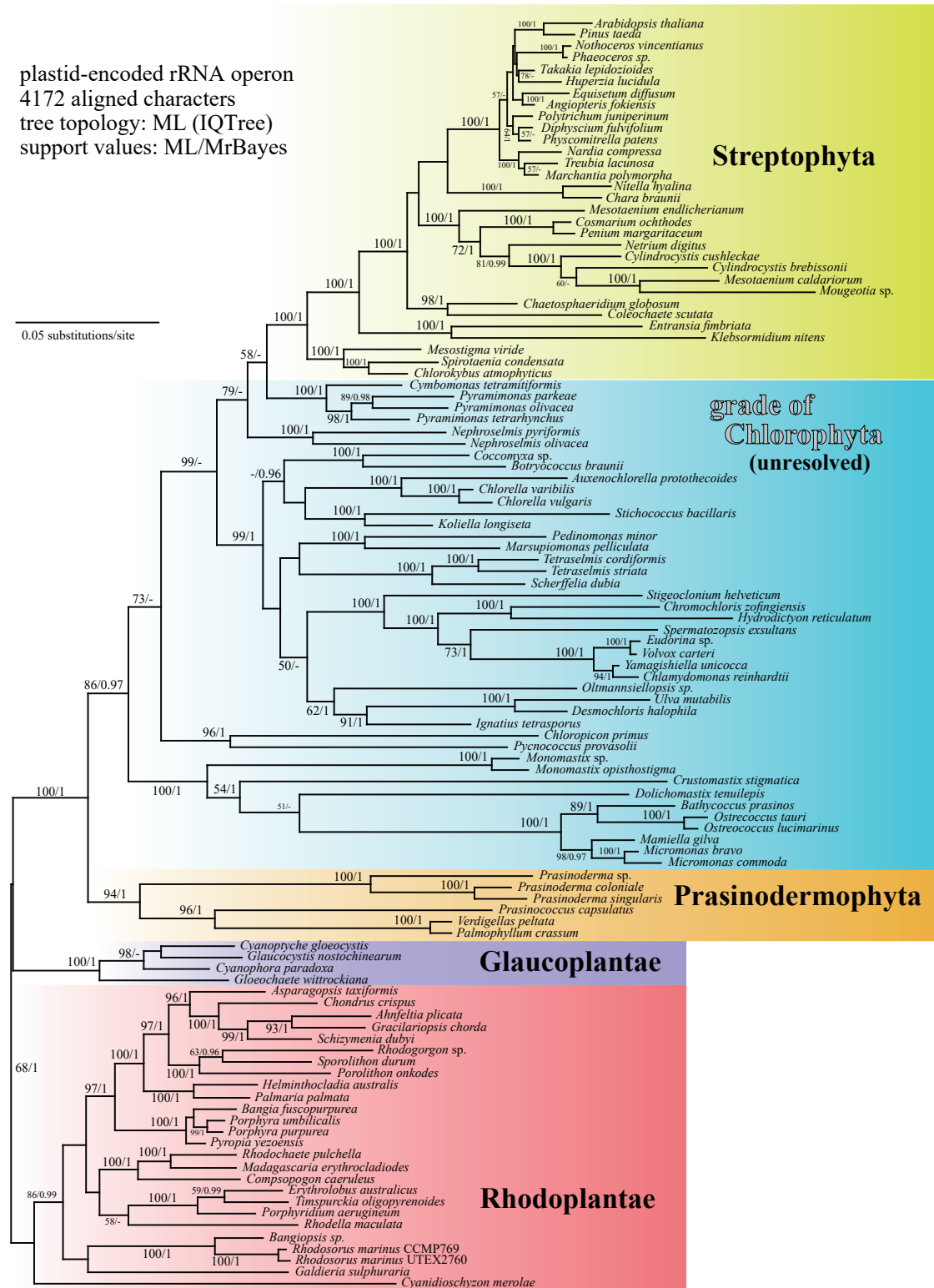


Supplementary Figure 4. The concatenated phylogenetic tree of 19 species with 31 single-copy mitochondria gene place Prasinodermophyta (*Prasinoderma coloniale*) to the sister lineage of other Viridiplantae with high bootstrap support (100.0).

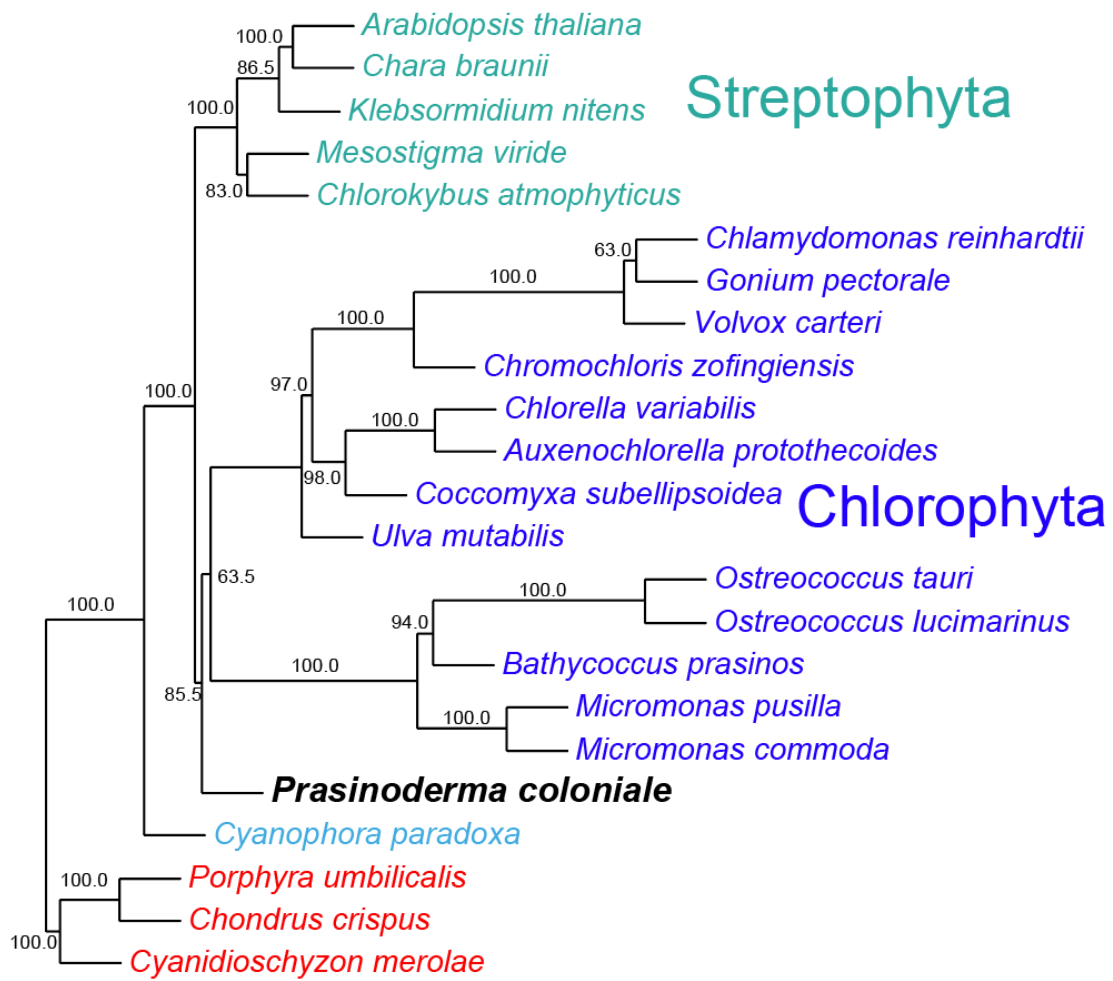


Supplementary Figure 5. The nuclear rRNA operon tree of 109 species with 4,646 aligned characters place Prasinodermophyta (*Prasinoderma coloniale*) to the sister lineage of other Viridiplantae with high bootstrap support (100.0/1).

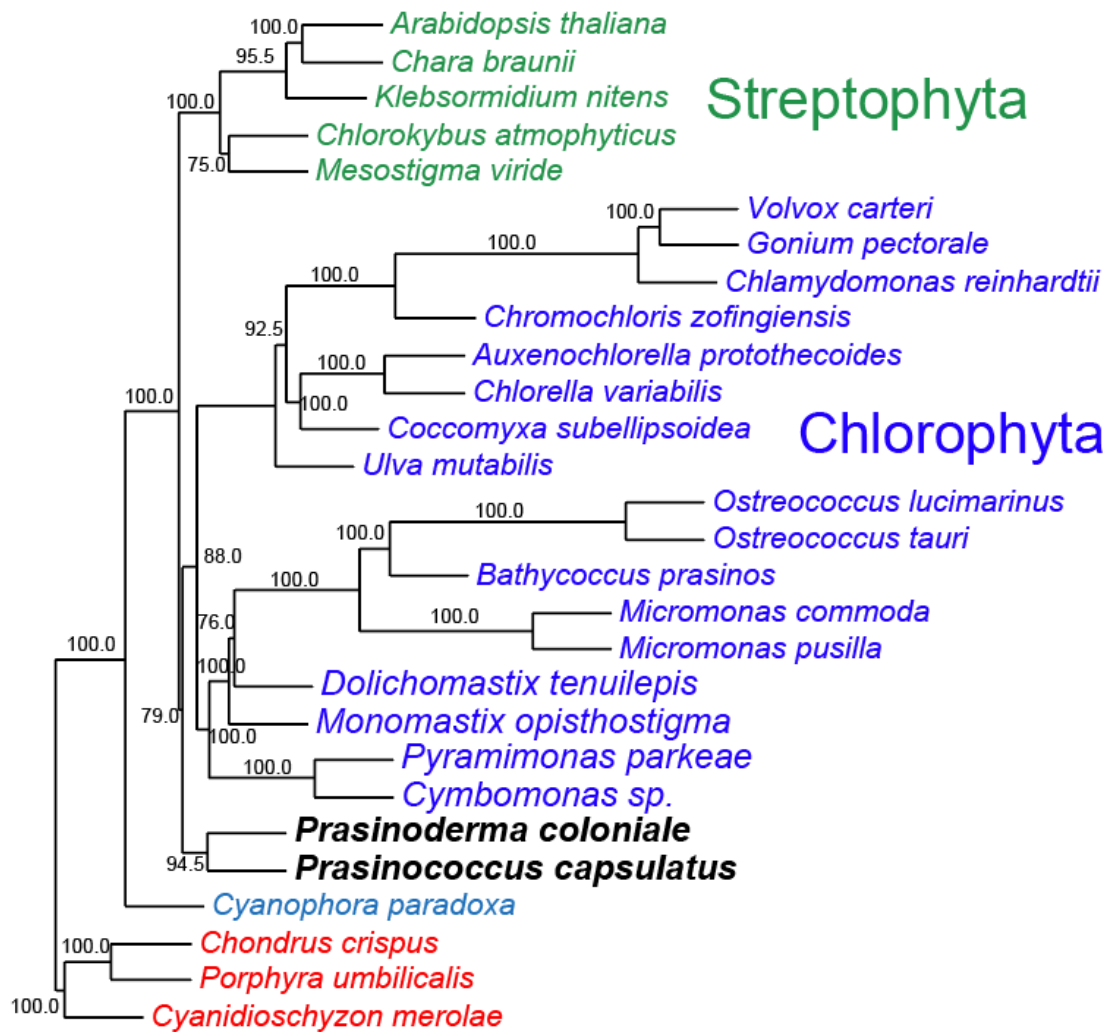
plastid-encoded rRNA operon
 4172 aligned characters
 tree topology: ML (IQTree)
 support values: ML/MrBayes



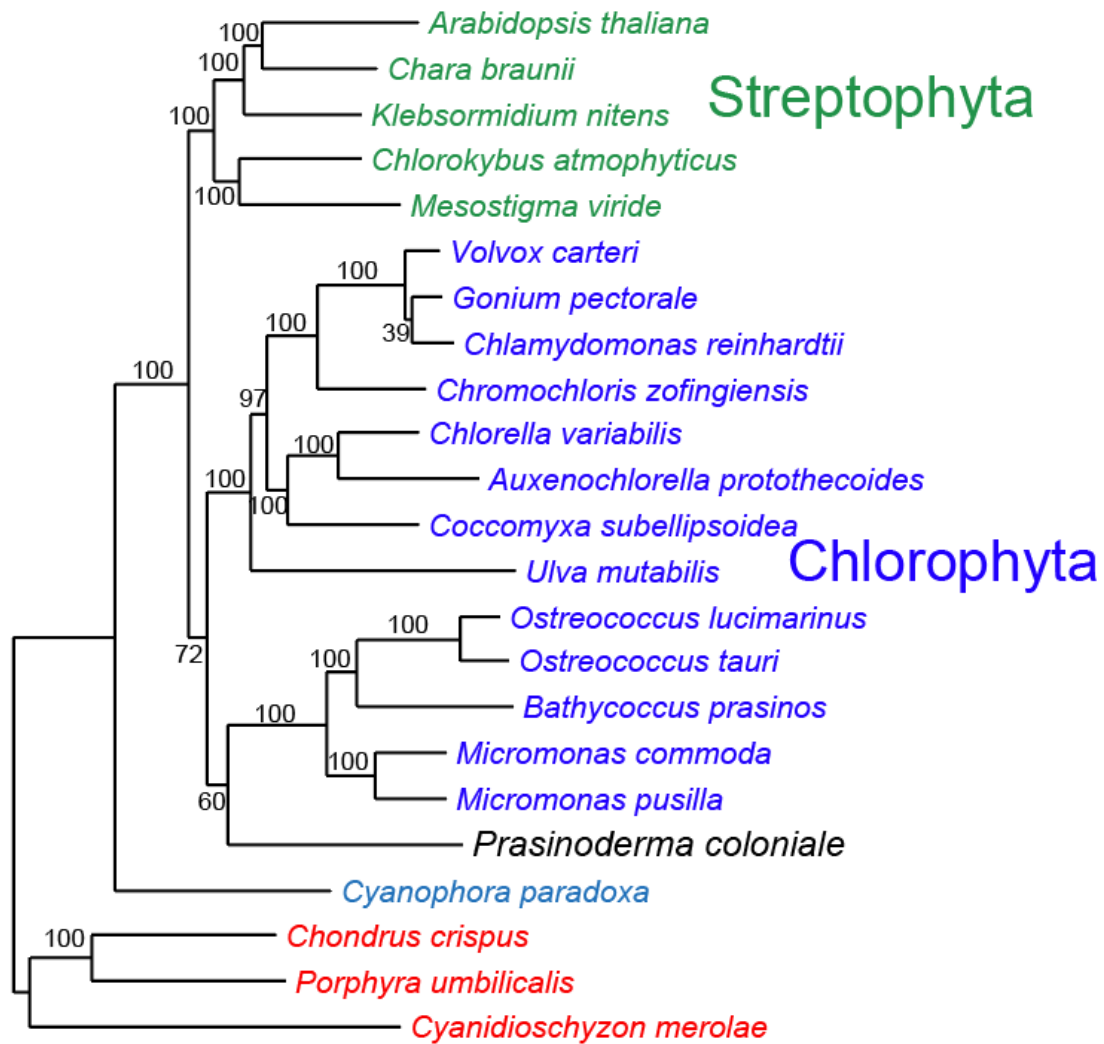
Supplementary Figure 6. The plastid-encoded rRNA operon tree of 109 species with 4,172 aligned characters place Prasinodermophyta (*Prasinoderma coloniale*) to the sister lineage of other Viridiplantae with high bootstrap support (94.0/1).



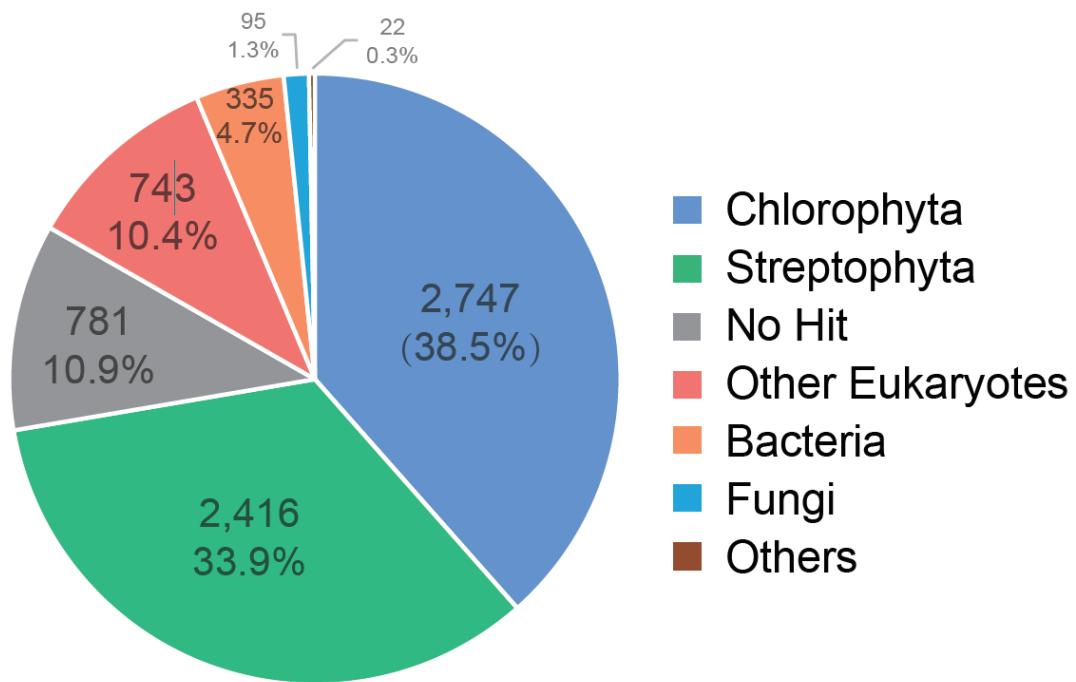
Supplementary Figure 7. The coalescent phylogenetic tree of 23 species with 45 single-copy genes using ASTRAL place Prasinodermophyta (*Prasinoderma coloniale*) to the sister lineage of other Chlorophyta with high support (85.5).



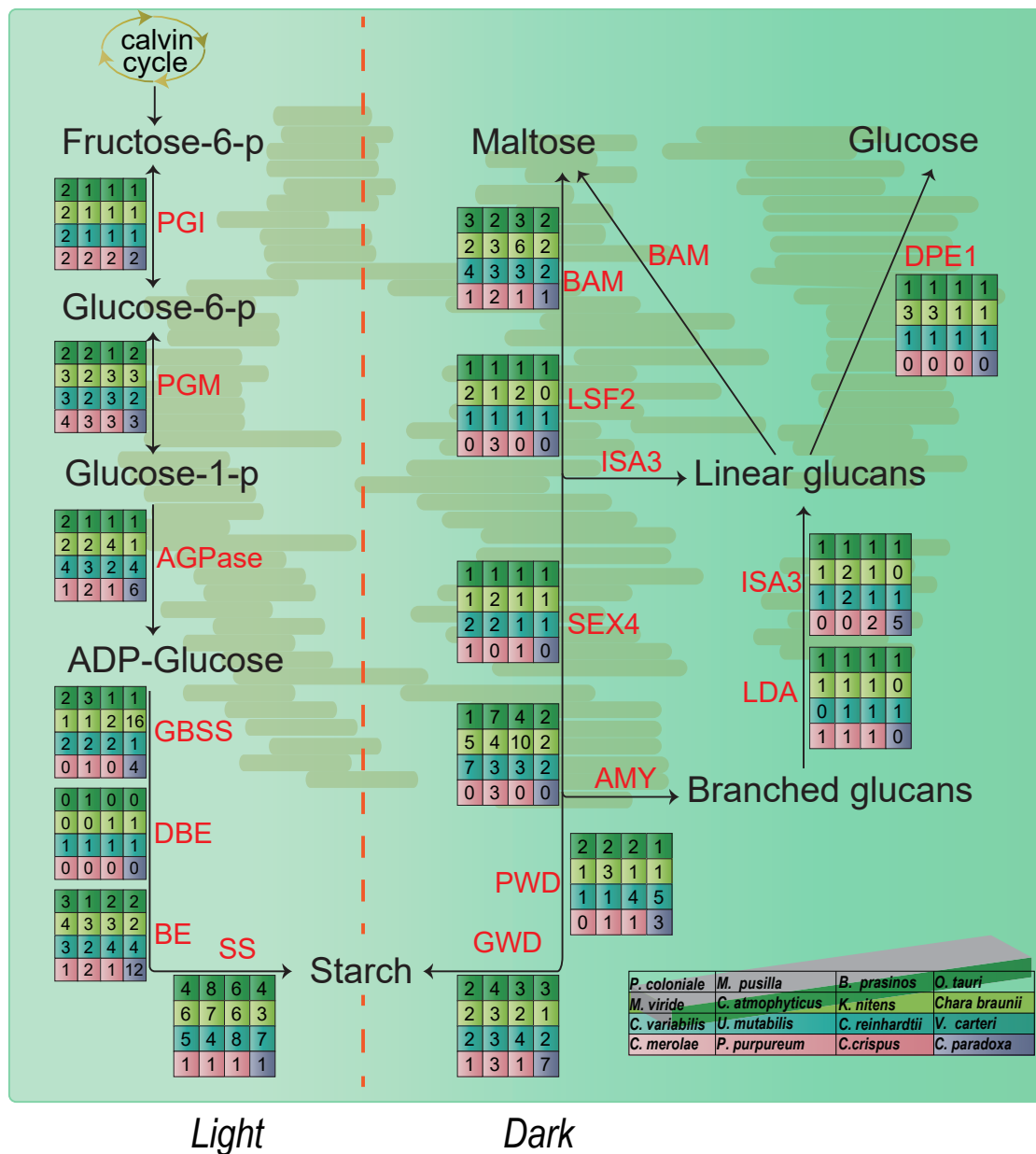
Supplementary Figure 8. The coalescent phylogenetic tree of 28 species with 213 single-copy genes using ASTRAL place *Prasinoderma coloniale* to the sister lineage of other Chlorophyta with relatively lower support (79.0). In order to increase the number of single-copy genes to construct the phylogenetic tree, we allowed gene absence up to 8 species in one gene family. As for the species, 5 transcriptome data were added including *Prasinococcus capsulatus*, *Cymbomonas sp.*, *Pyramimonas parkeae*, *Monomastix opisthostigma*, *Dolichomastix tenuilepis* but removed the *Ostreococcus sp.* RCC809.



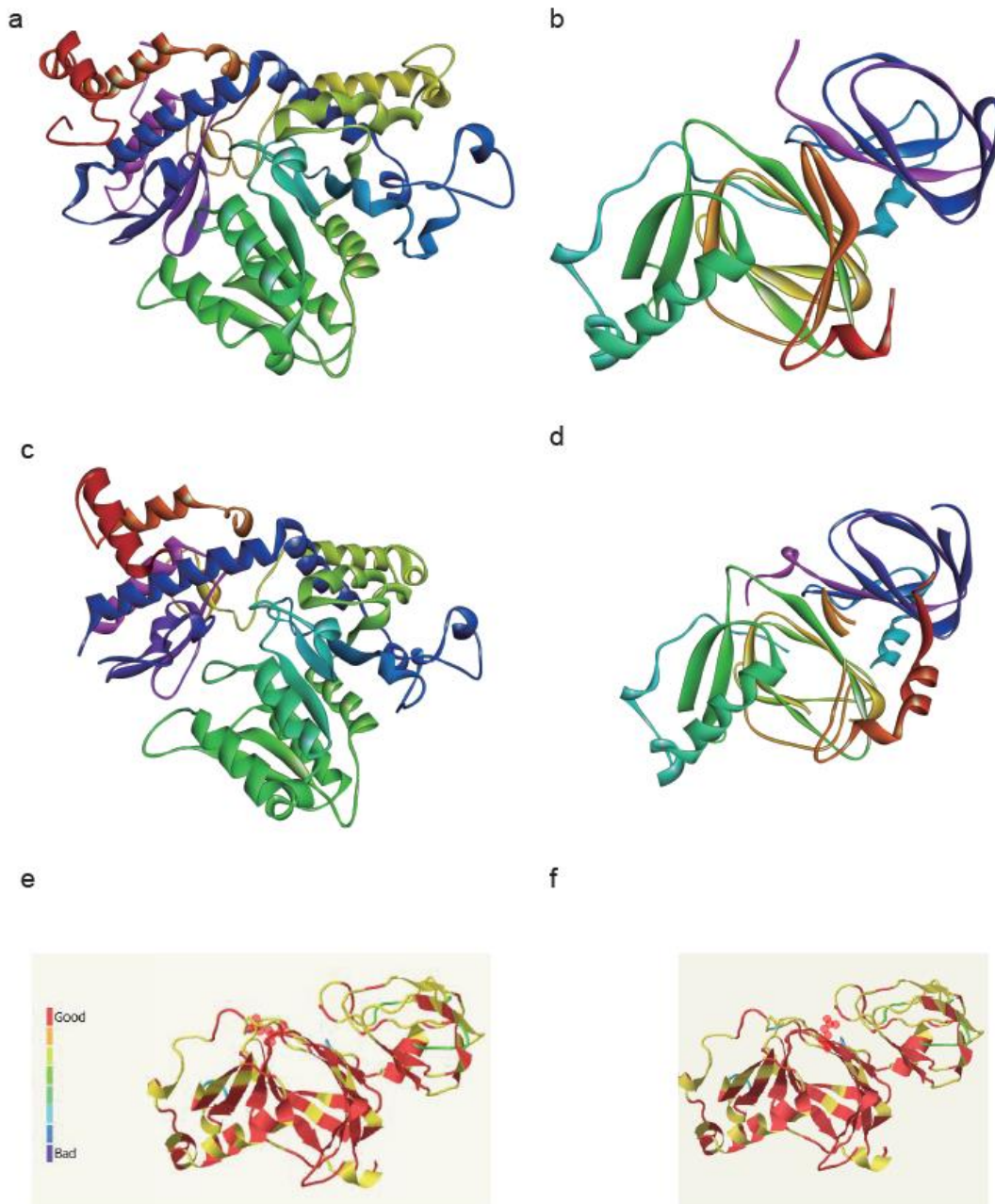
Supplementary Figure 9. The concatenated phylogenetic tree of 23 species with 45 single-copy genes using RAxML place *Prasinoderma coloniale* to the sister lineage of Mamiellales (Mamiellophyceae). PROTCATGTR AA substitution model and 500 bootstraps were used in phylogenetic analysis. The Prasinodermophyta, represented only by *Prasinoderma coloniale*, was resolved as sister to the Mamiellales (Mamiellophyceae) with high support (81). This artificial placement (i.e. *Prasinoderma coloniale* diverging within the Chlorophyta) gained high support by bootstrapping (100).



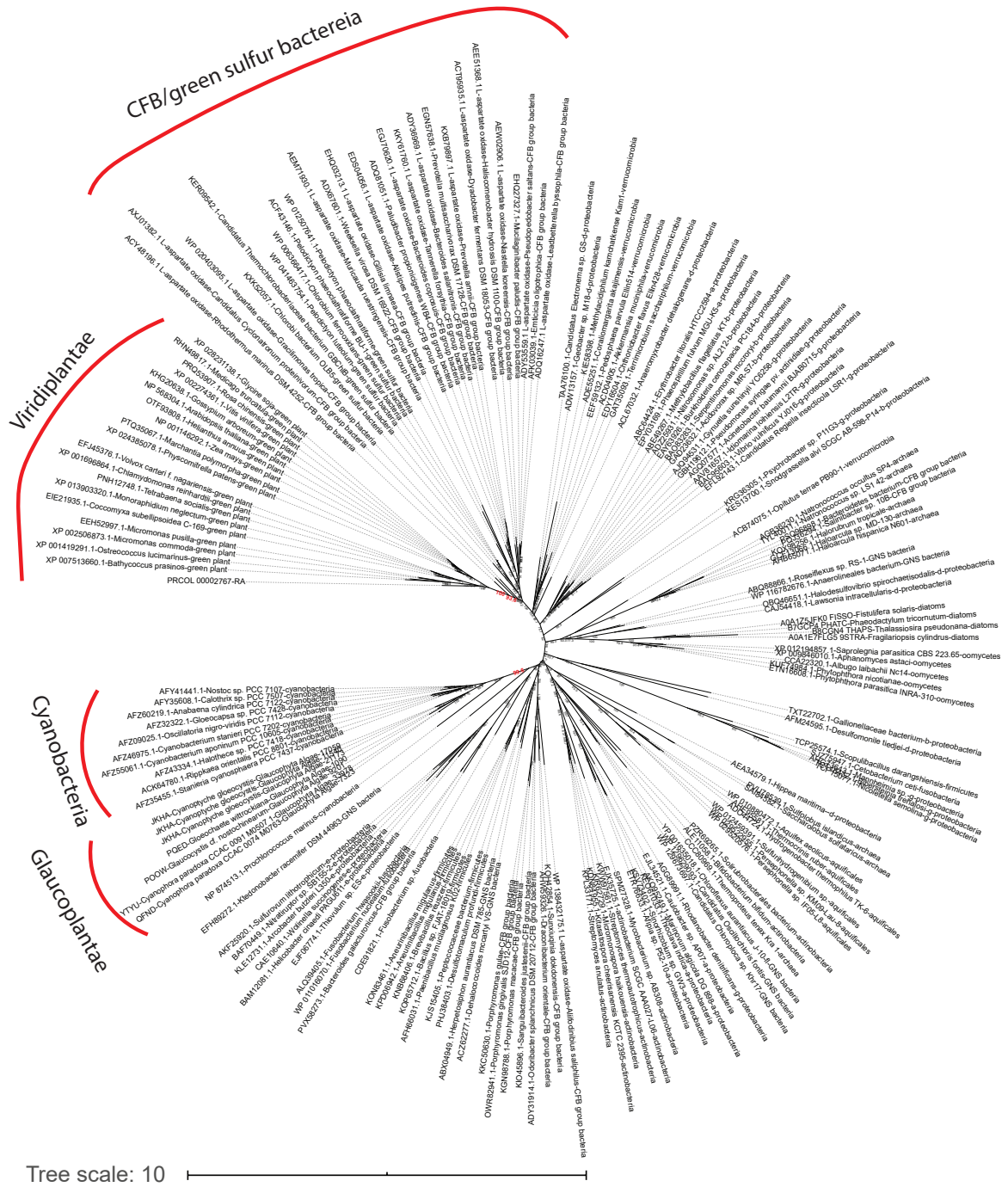
Supplementary Figure 10. Taxon distribution of the best BLAST hits of the *P. coloniale* genes in the NCBI non-redundant protein database.



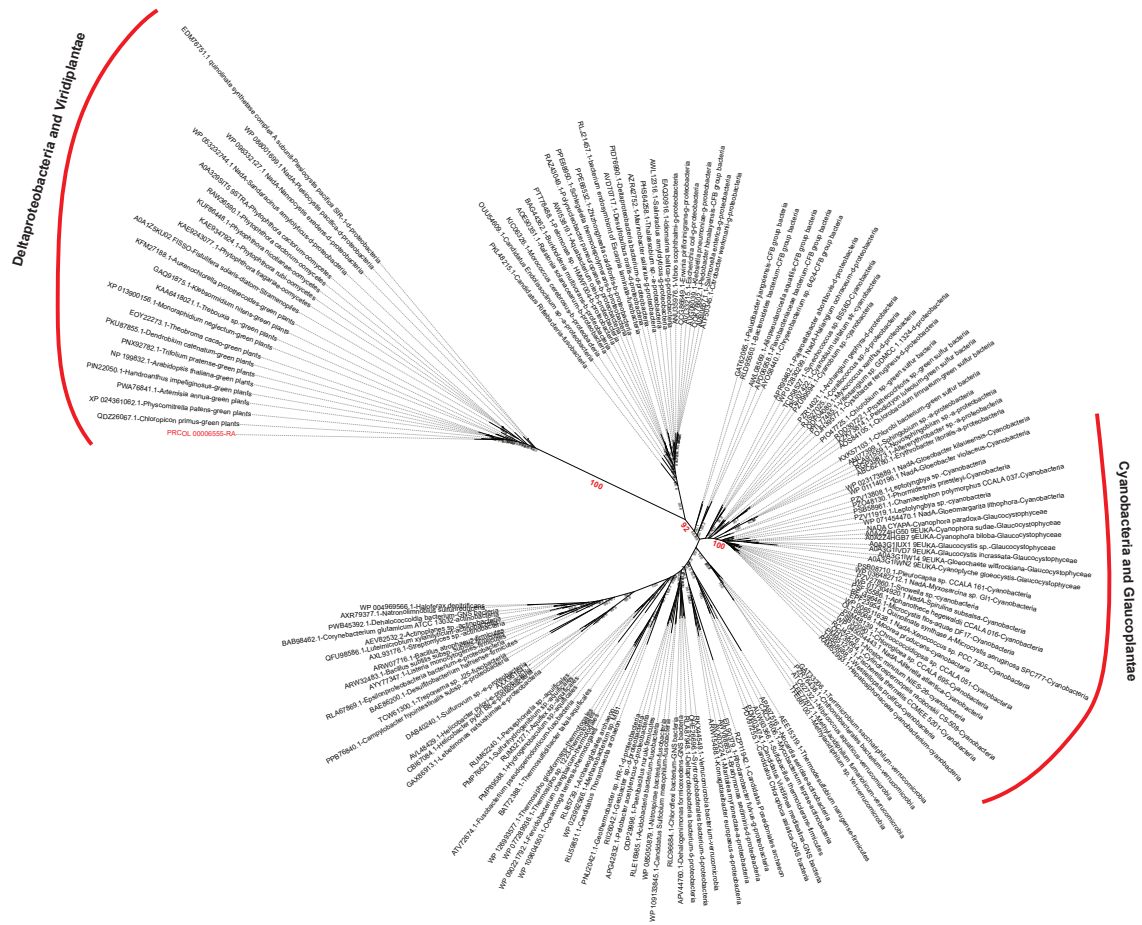
Supplementary Figure 11. Reconstruction the Pathways of starch synthesis and degradation in 16algae genomes. Fructose-6-p, fructose 6-phosphate; Glucose-6-p, glucose 6-phosphate; Glucose-1-p, glucose 1-phosphate; ADP-Glucose, ; PGI, phosphoglucose isomerase; PGM, hosphoglucomutase; AGPase, ADP-glucose pyrophosphorylase; GBSS, granule-bound starch synthase; DBE, debranching enzyme; BE, branching enzyme; SS, Starch synthase; GWD, α -glucan,water dikinase; PWD, phosphoglucan,water dikinase; AMY, α -amylase; SEX4, Phosphoglucan phosphatase DSP4; ISA3, Isoamylase 3; LSF2, Phosphoglucan phosphatase LSF2; BAM, β -amylase; DPE1, Glucanotransferase (dpe1); LDA, Protein LIMIT DEXTRINASE; the gene copy number of each species is shown in the Supplementary Table 16.



Supplementary Figure 12. Structural Features of KYU and HAAO Protein Domains Constructed by Swiss-Model Homology-Based Approach. a) KYU domain based on the crystal structure of *P. coloniale*. b) HAAO domain based on the crystal structure of *P. coloniale*. c) KYU domain based on the crystal structure of human. d). HAAO domain based on the crystal structure of human. e) KYU domain alignment of a and c. f) HAAO domain alignment of b and d.

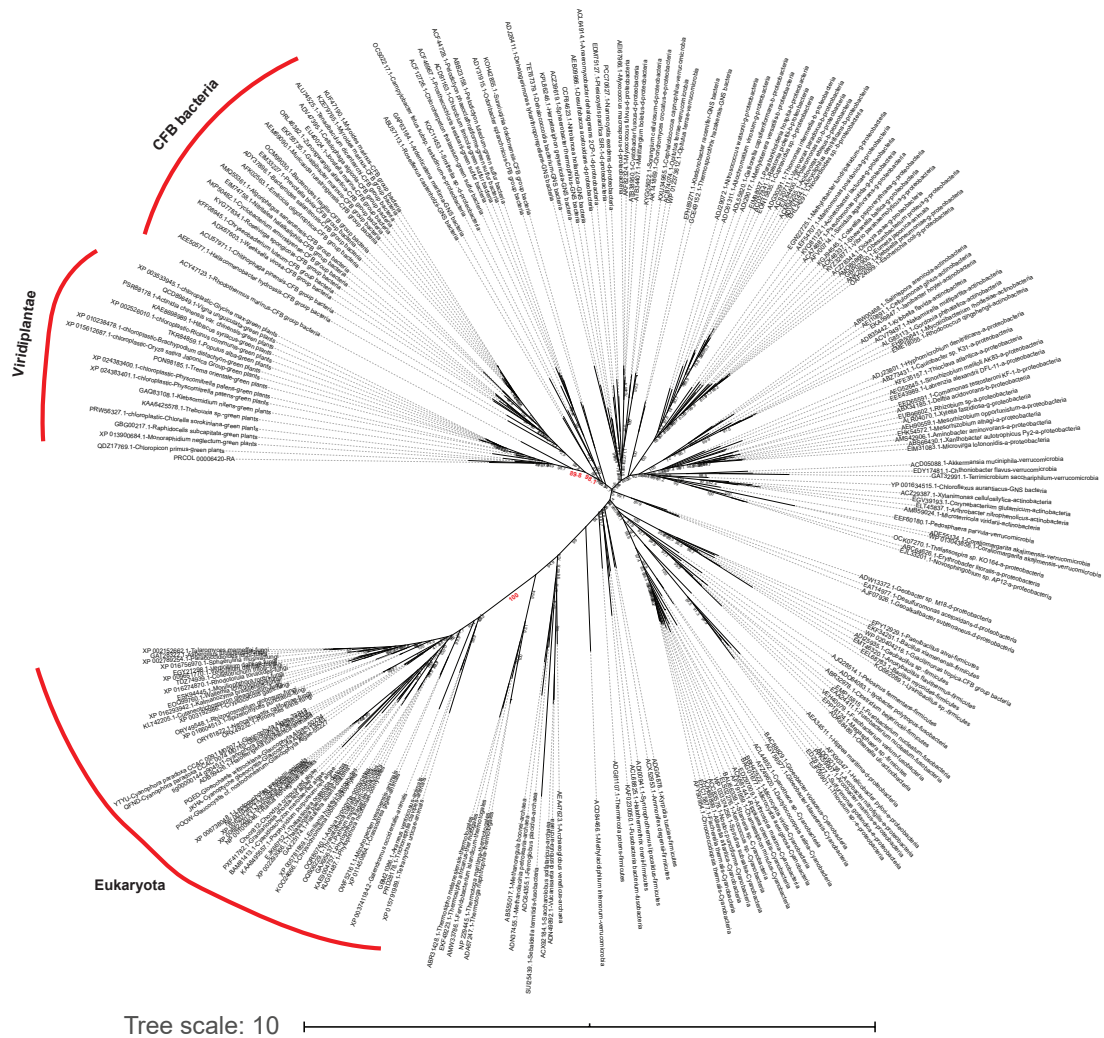


Supplementary Figure 13. The phylogenetic tree of AO (Aspartate oxidase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.

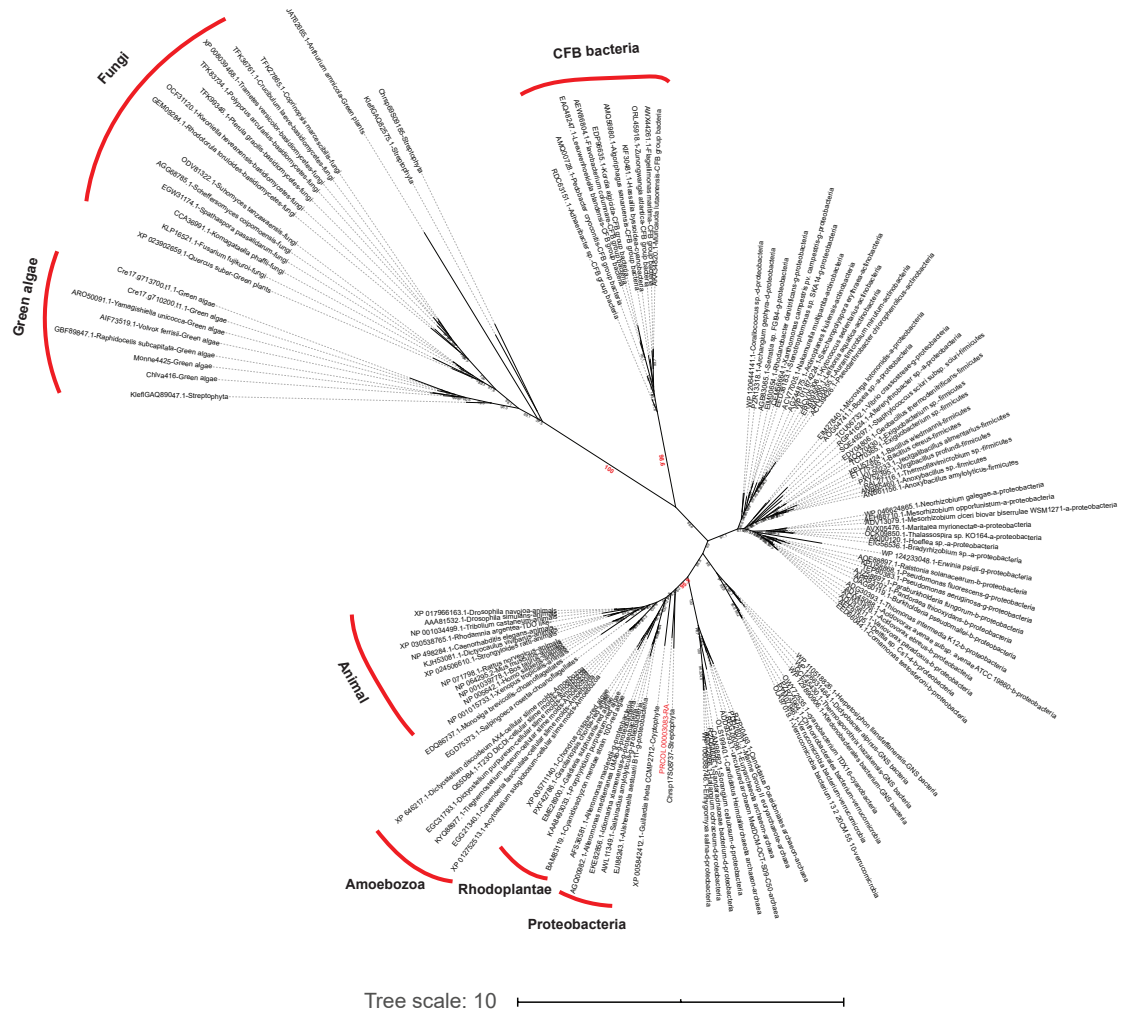


Tree scale: 10

Supplementary Figure 14. The phylogenetic tree of QS (Quinolate synthase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.



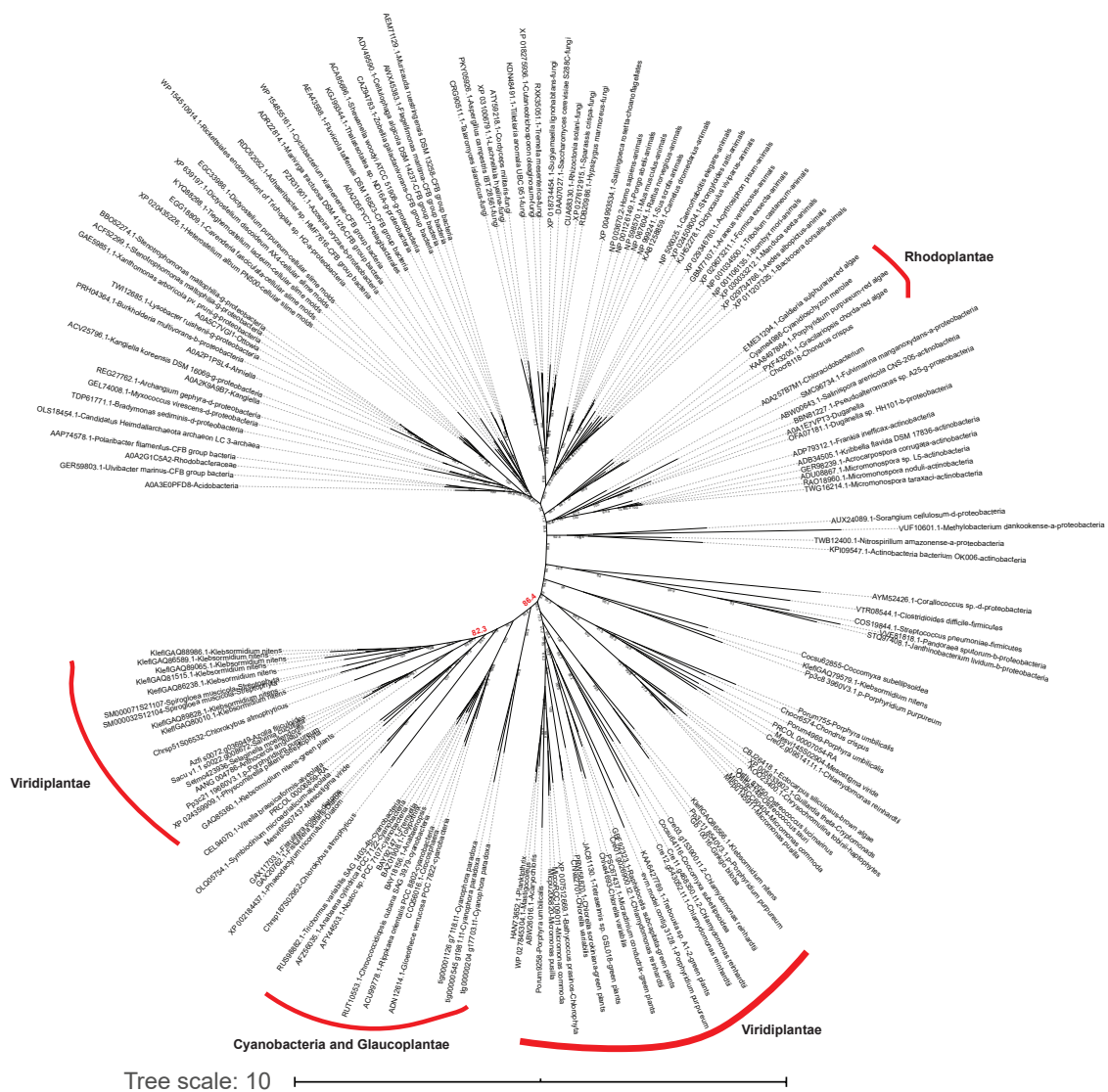
Supplementary Figure 15. The phylogenetic tree of NNP (nicotinate nucleoside pyrophosphatase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.



Supplementary Figure 16. The phylogenetic tree of TDO/IDO (Tryptophan-/Indoleamine 2,3-dioxygenase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.



Supplementary Figure 17. The phylogenetic tree of AFM (Arylformamidase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.

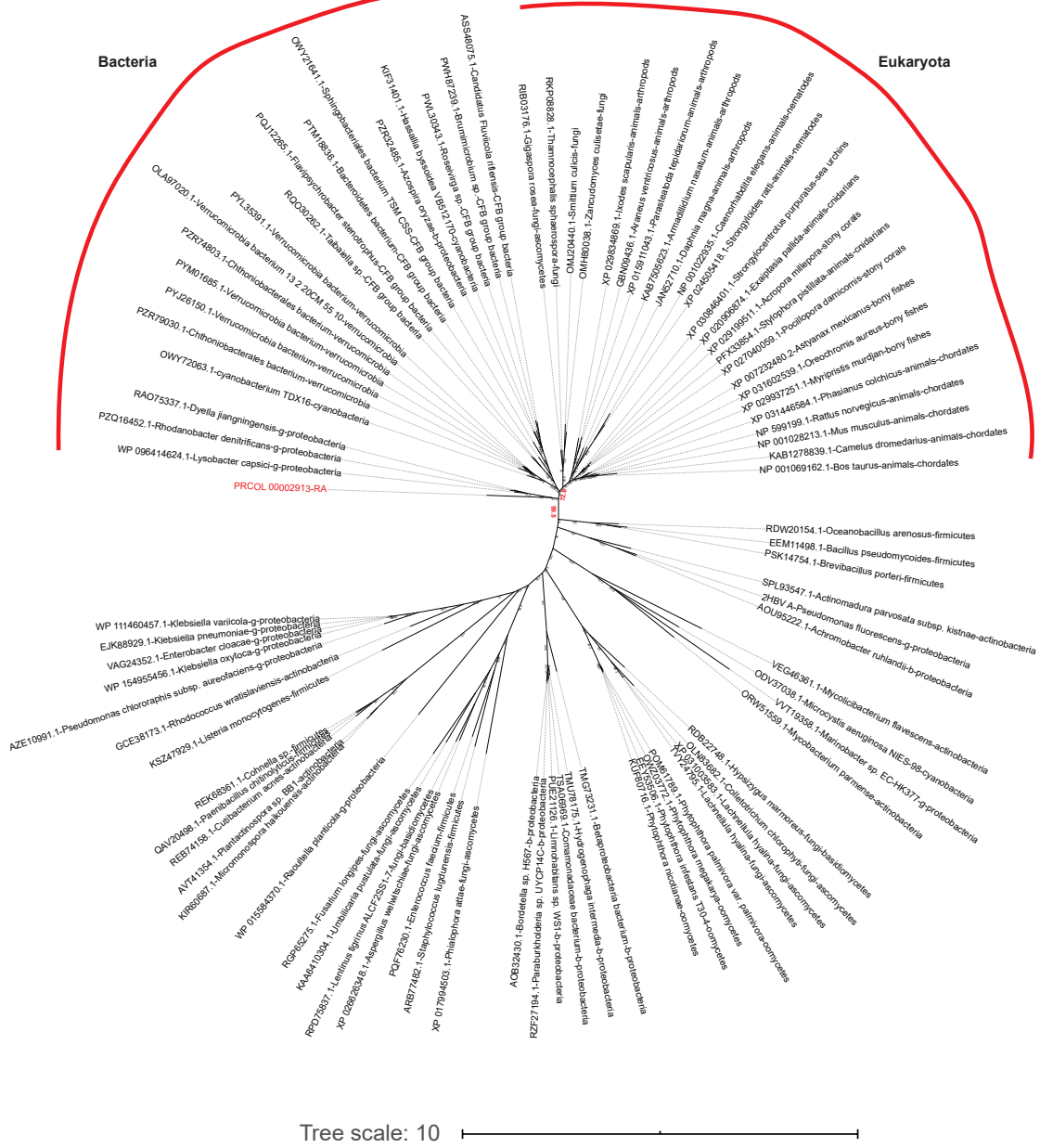


Supplementary Figure 18. The phylogenetic tree of KMO (Kynurenine 3-monooxygenase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.



Tree scale: 10

Supplementary Figure 19. The phylogenetic tree of KYU (kynureninase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.



Supplementary Figure 21. The phylogenetic tree of ACMSD (amino-β-carboxymuconate-semialdehyde-decarboxylase) based on IQ-TREE method, using the best model predicted by IQ-TREE with 5000 replicates. The important bootstraps are highlighted by the red color.