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Online Resources

Complex origins of chloroplast membranes with photosynthetic machineries: Multiple transfers of genes from divergent organisms at different times or a single endosymbiotic event?

Naoki Sato

University of Tokyo

naokisat@bio.c.u-tokyo.ac.jp

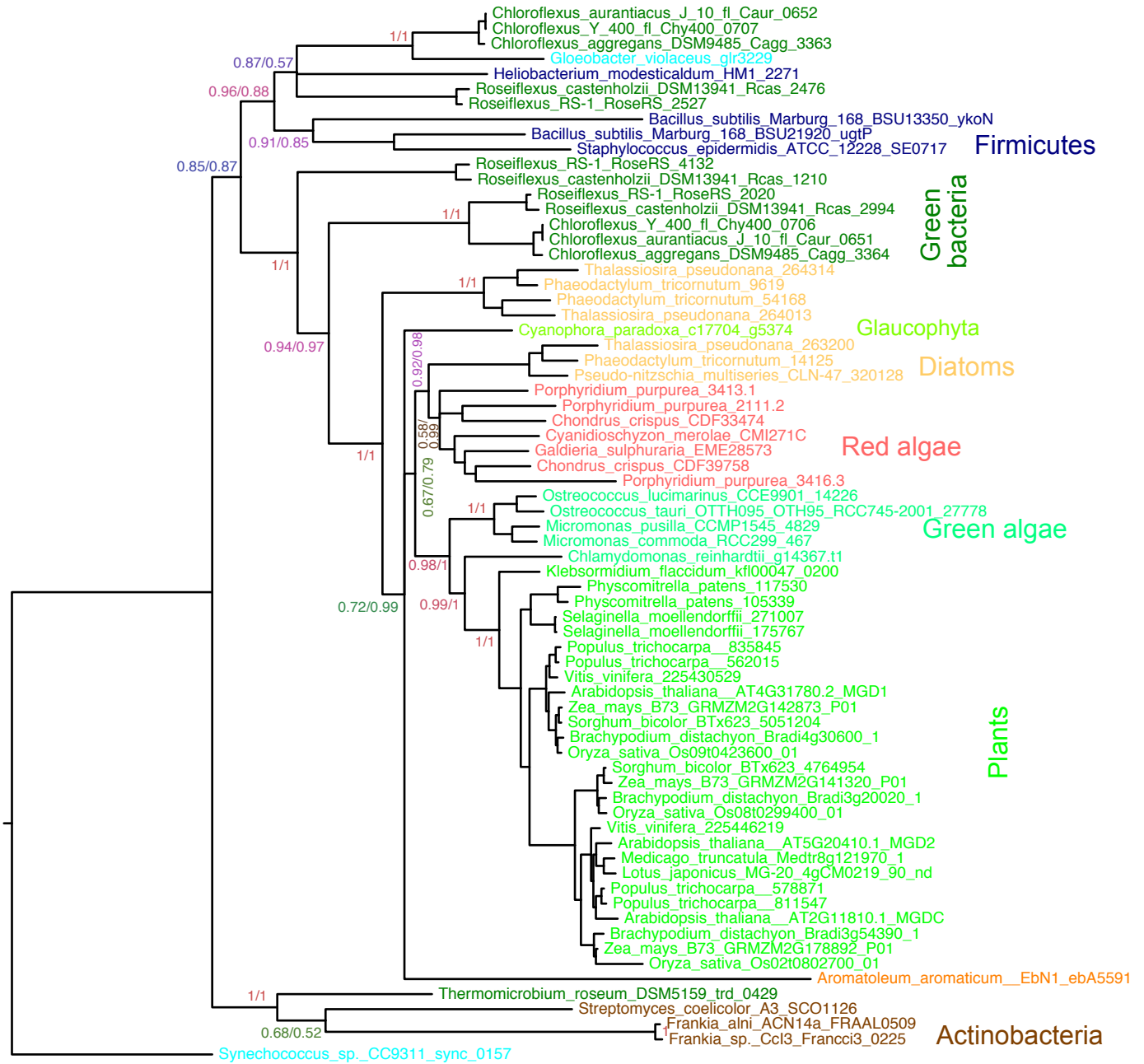
Phylogenetic trees are grouped in 6 PDF files (Online Resources 2 – 7).

Online Resource 2. Phylogenetic trees of enzymes involved in chloroplast lipid biosynthesis.

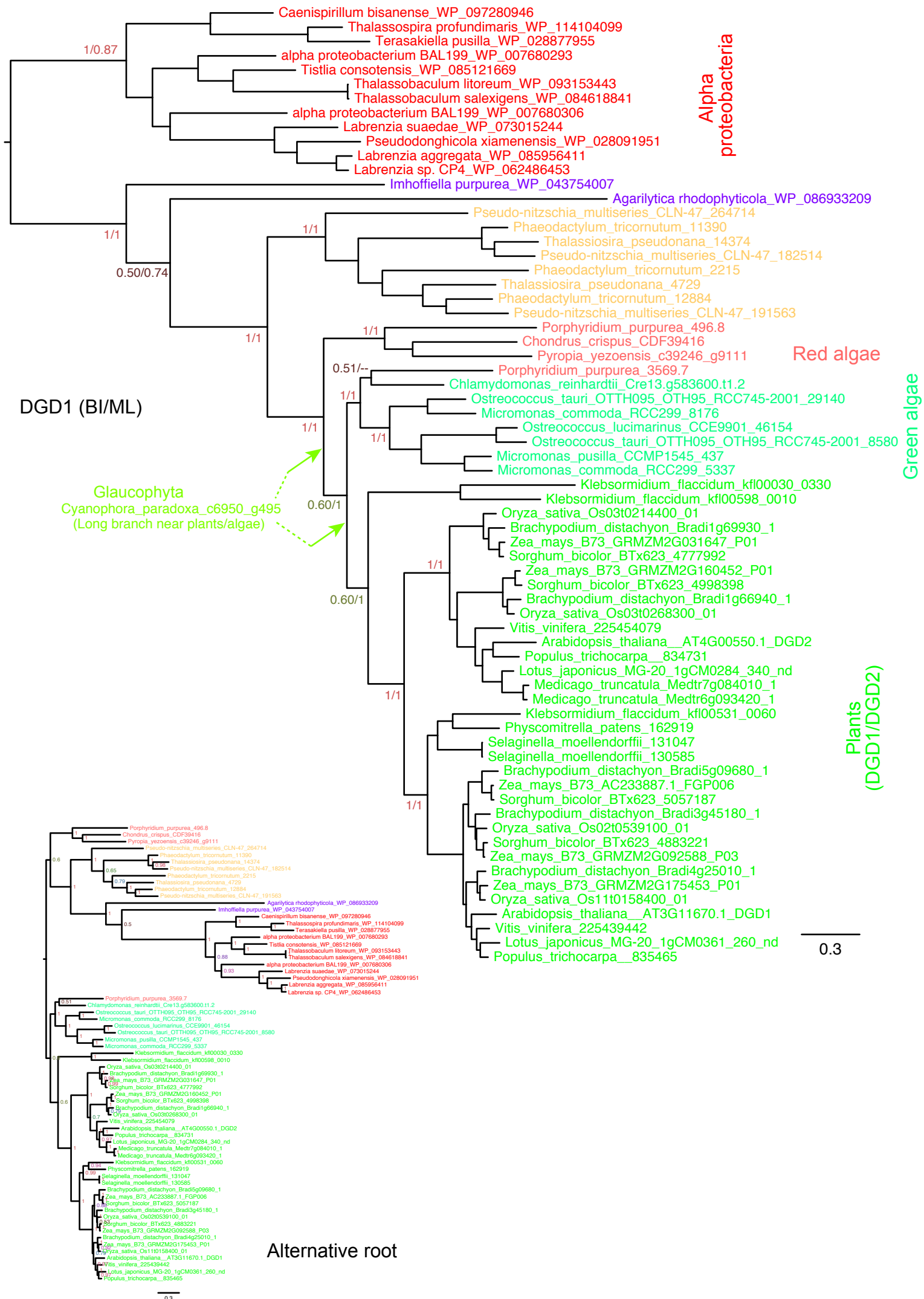
This PDF file includes phylogenetic trees of the following enzymes: MDG1, monogalactosyl diacylglycerol synthase in plants/algae; DGD1, digalactosyl diacylglycerol synthase in plants/algae; MgdA, monoglucosyl diacylglycerol synthase in cyanobacteria; monoglucosyl diacylglycerol epimerase in cyanobacteria; DgdA, digalactosyl diacylglycerol synthase in cyanobacteria; CDS, CDP diacylglycerol synthase; PGPS, phosphatidylglycerol phosphate synthase (including eukaryotic CLS, cardiolipin synthase); PGPP1, phosphatidylglycerol phosphate phosphatase; SqdB/SQD1, UDP sulfoquinovose synthase; SqdX/SQD2, sulfoquinovosyl diacylglycerol synthase. Locate the enzymes in the biosynthetic pathway in [Fig. 1 panels B and C](#).

Three types of phylogenetic methods were tested depending on enzymes: BI, Bayesian Inference method by MrBayes version 3.2.6 with LG model; PB, Bayesian Inference method by PhyloBayes version 4.1 with CAT model; ML, Maximum Likelihood method by PhyML version 4 with LG model. A combination of numbers on each major branch indicates branch support values. For simplicity, support values are not shown for minor branches. "1.00" was shown as "1" for short. Taxa are consistently color-coded according to the color scheme in the FigTree software throughout this paper (the original RGB intensities are shown in each parenthesis): Green (or Spring) (0, 255, 0), land plants; Sea Foam (0, 255, 128), green algae and *Paulinella*; Lime(128, 255, 0), *Cyanophora*; Salmon (255, 102, 102), red algae; Cantaloupe (255, 204, 102), diatoms; Red (or Maraschino) (255, 0, 0), α -proteobacteria; Tangerine (255, 128, 0), β -proteobacteria; Grape (128, 0, 255), γ -proteobacteria; Cyan (or Turquoise) (0, 255, 255), cyanobacteria; Clover (0, 128, 0), green bacteria; Midnight (0, 0, 128), Firmicutes; Aluminum (153, 153, 153), Archaea; Mocha (128, 64, 0), actinobacteria; Steel (102, 102, 102), protists; Black (0, 0, 0), other bacteria and animals. This color code is used in all subsequent phylogenetic trees in Online Resources.

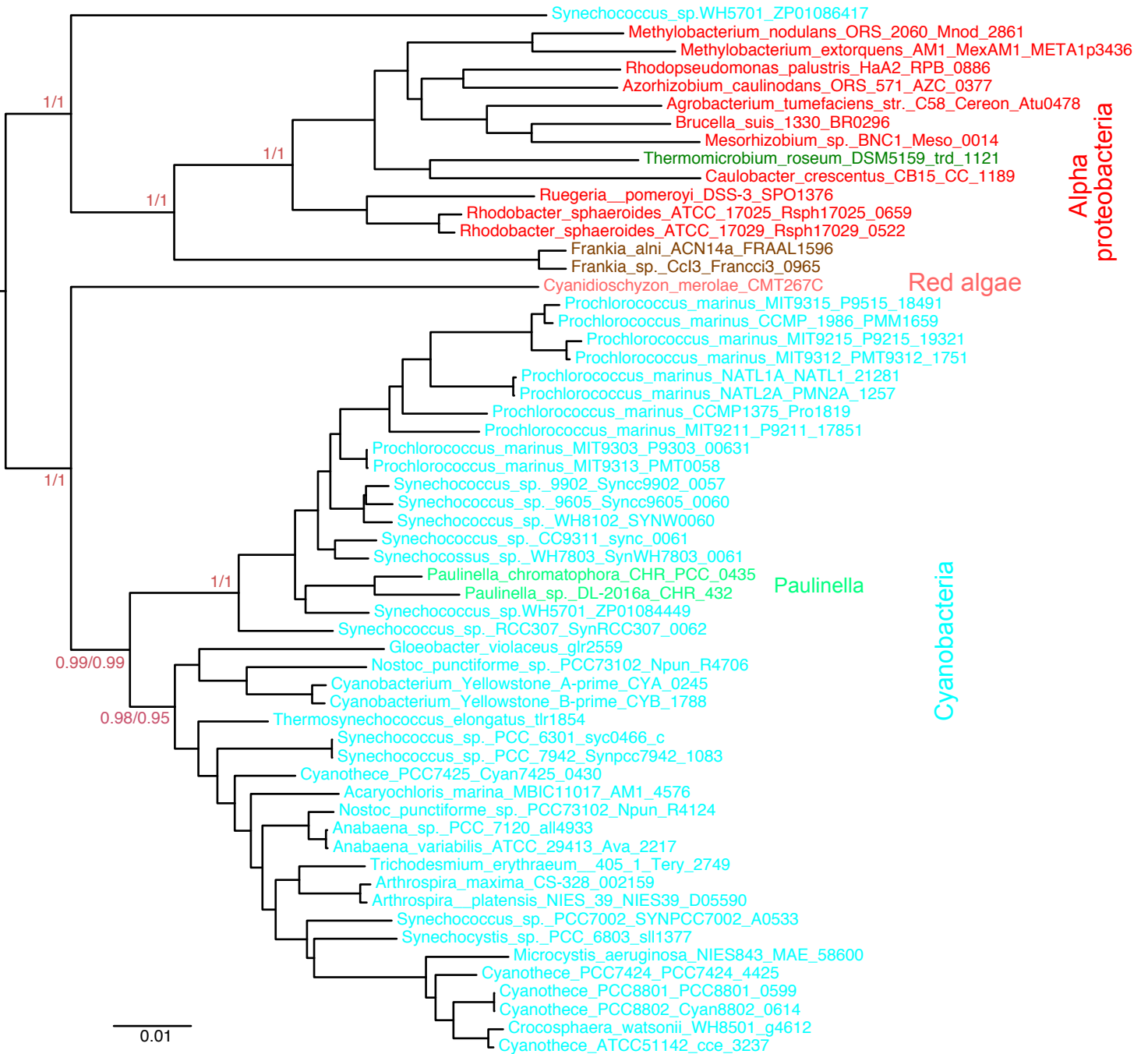
MGD1 (BI/ML)



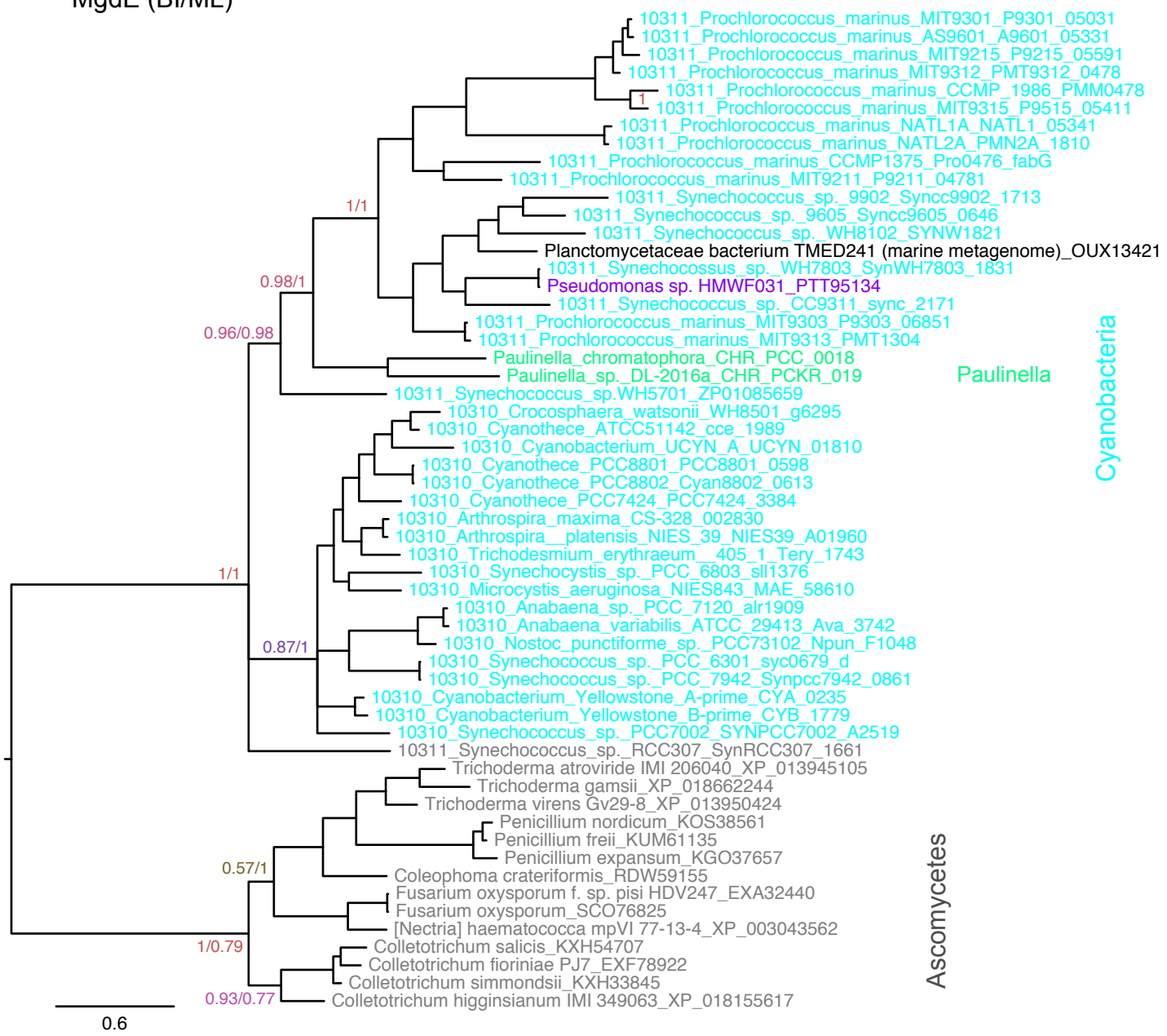
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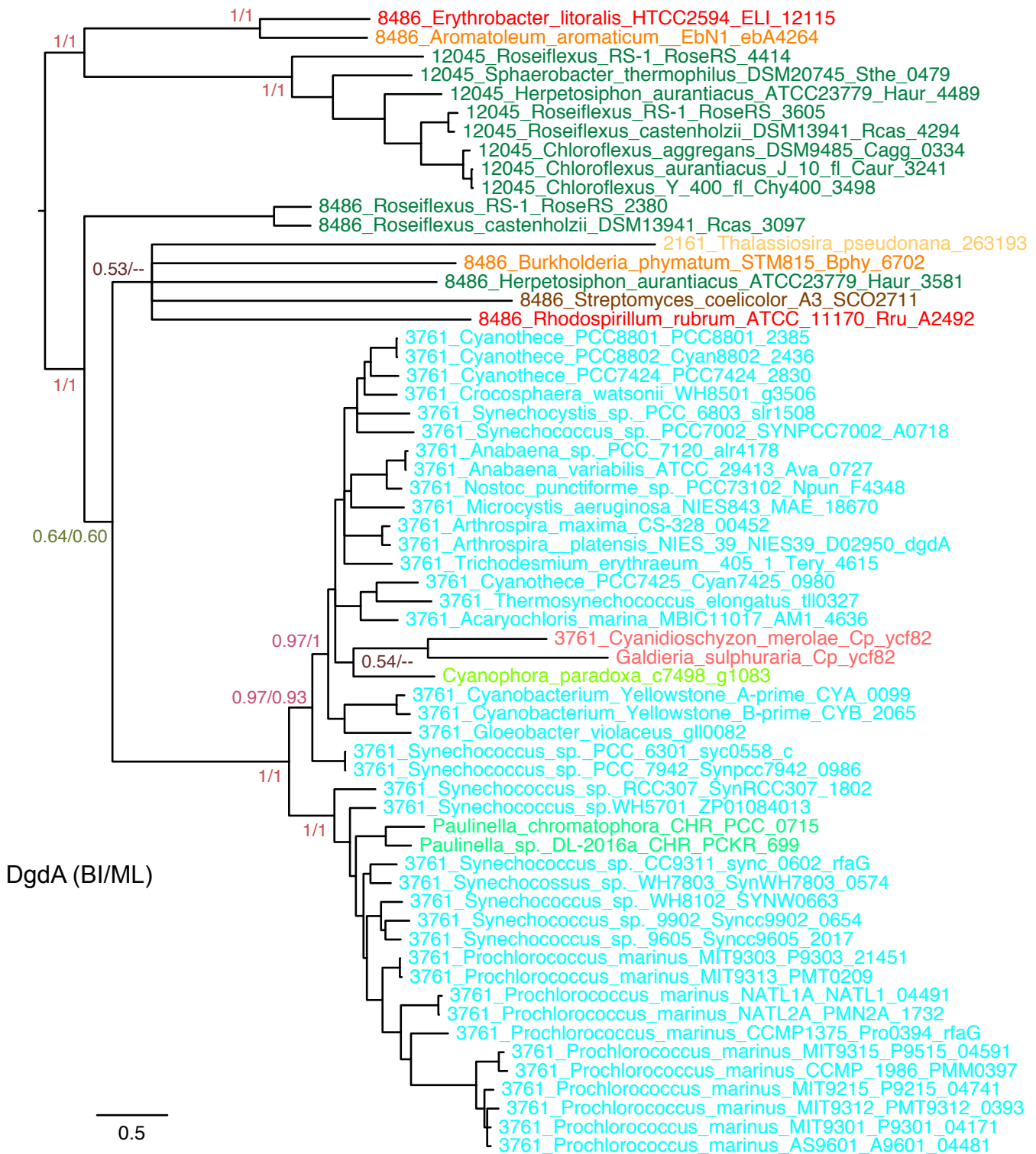


MgdA (BI/ML)



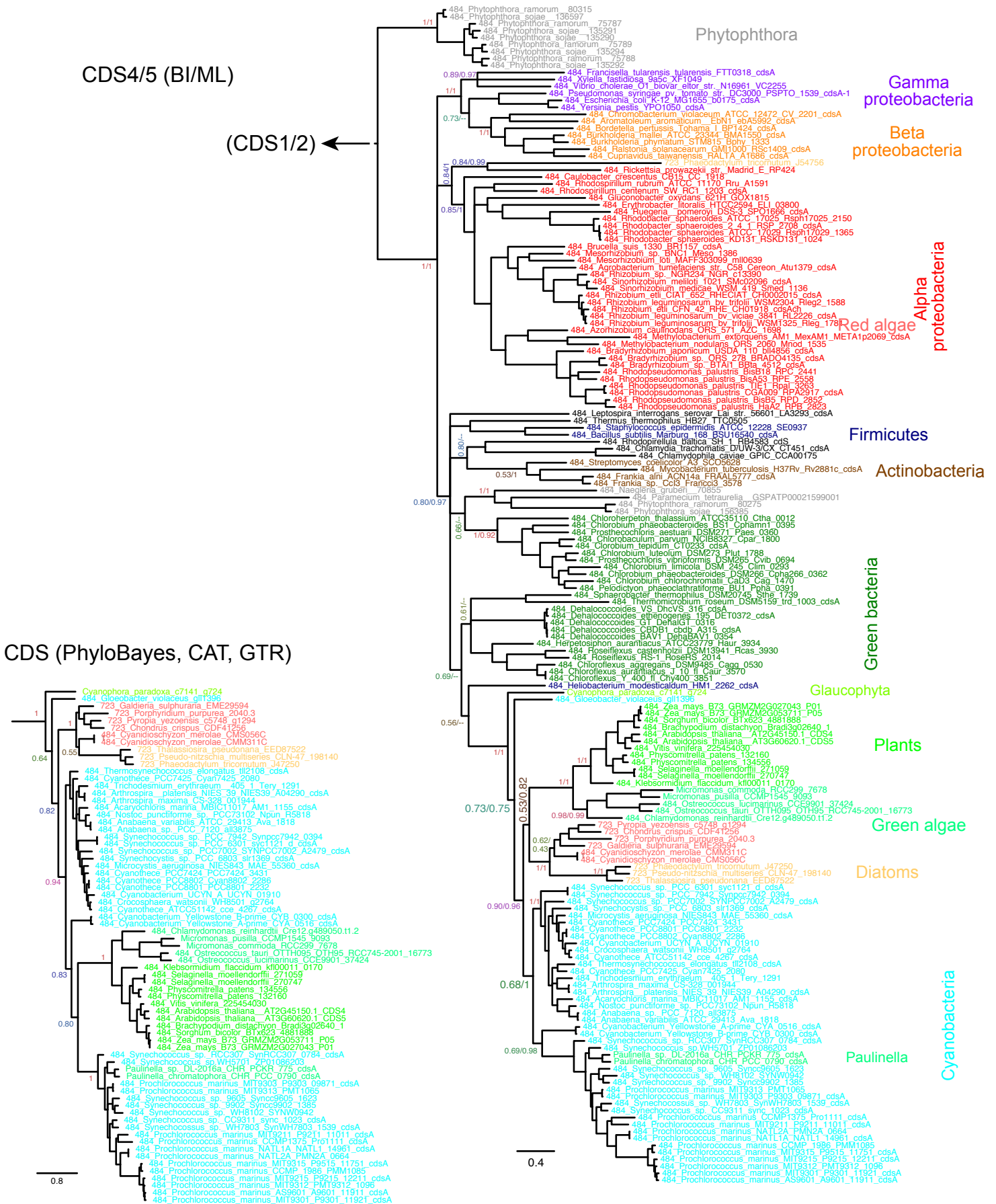
MgdE (BI/ML)



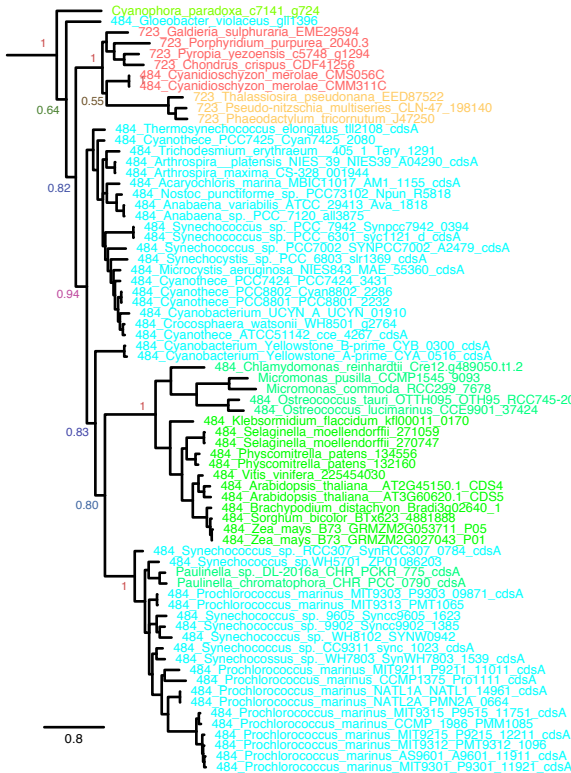


CDS4/5 (BI/ML)

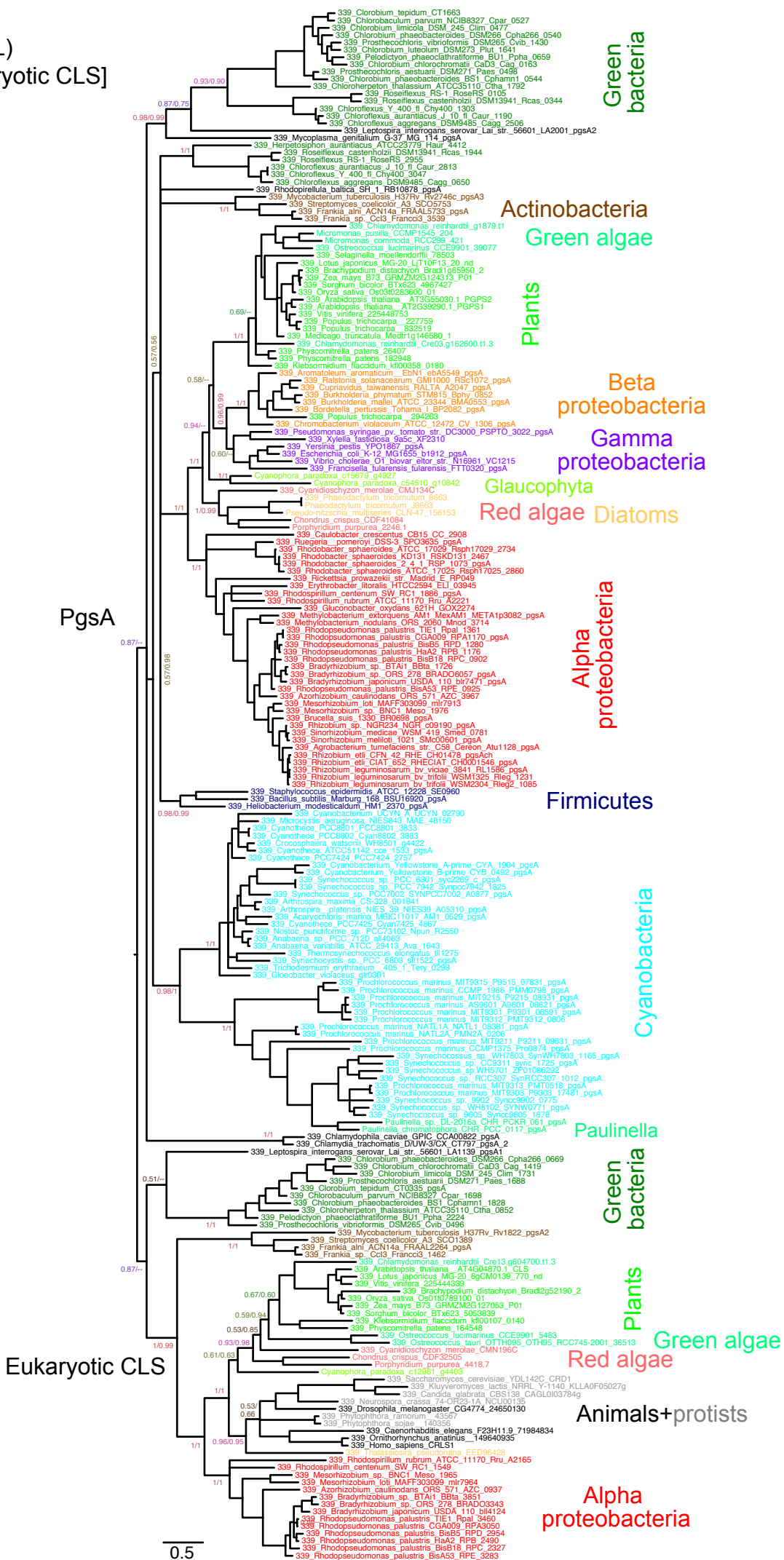
(CDS1/2) ←



CDS (PhyloBayes, CAT, GTR)



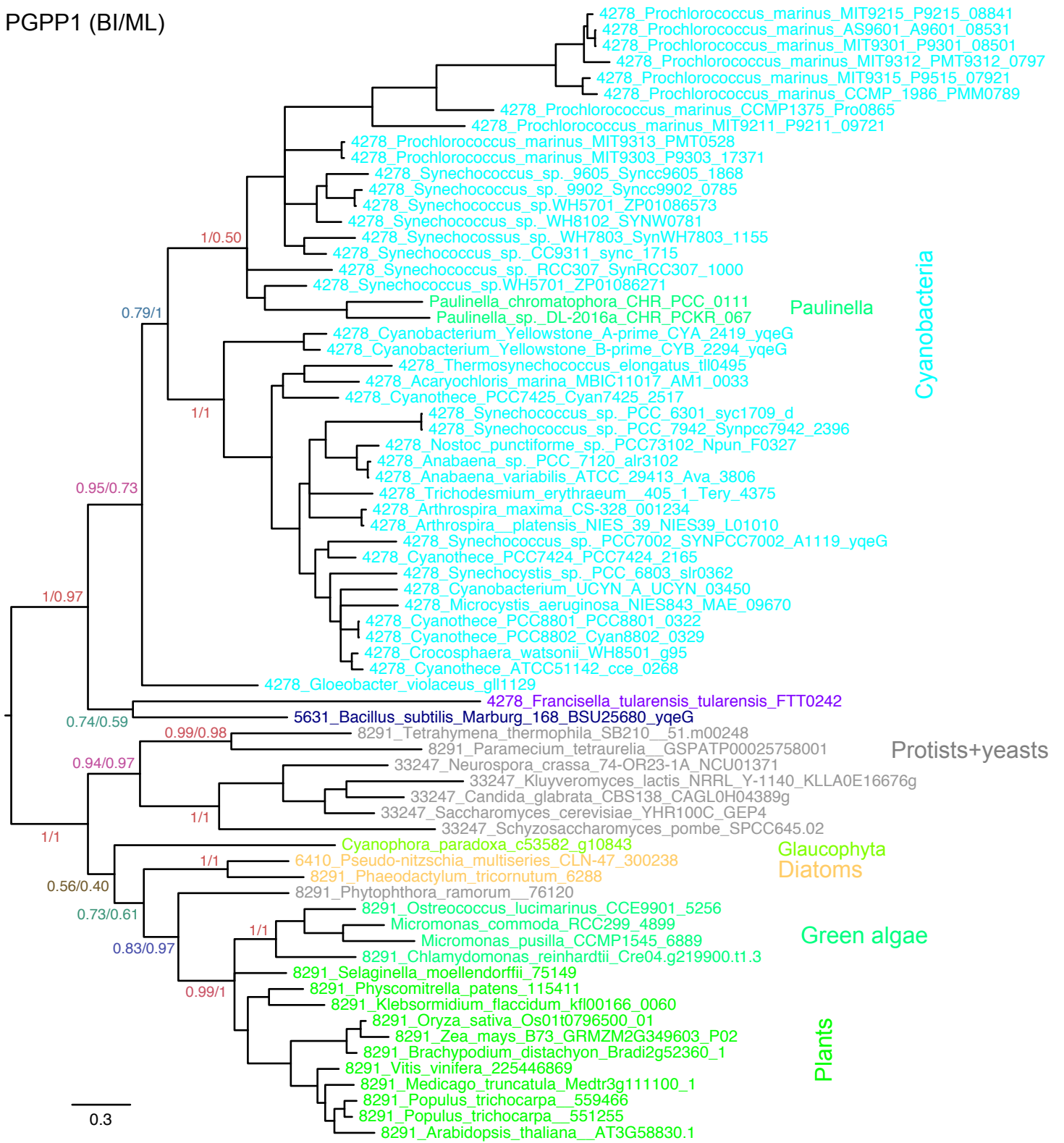
PGPS (BI/ML)
[PgsA, Eukaryotic CLS]



Eukaryotic CLS

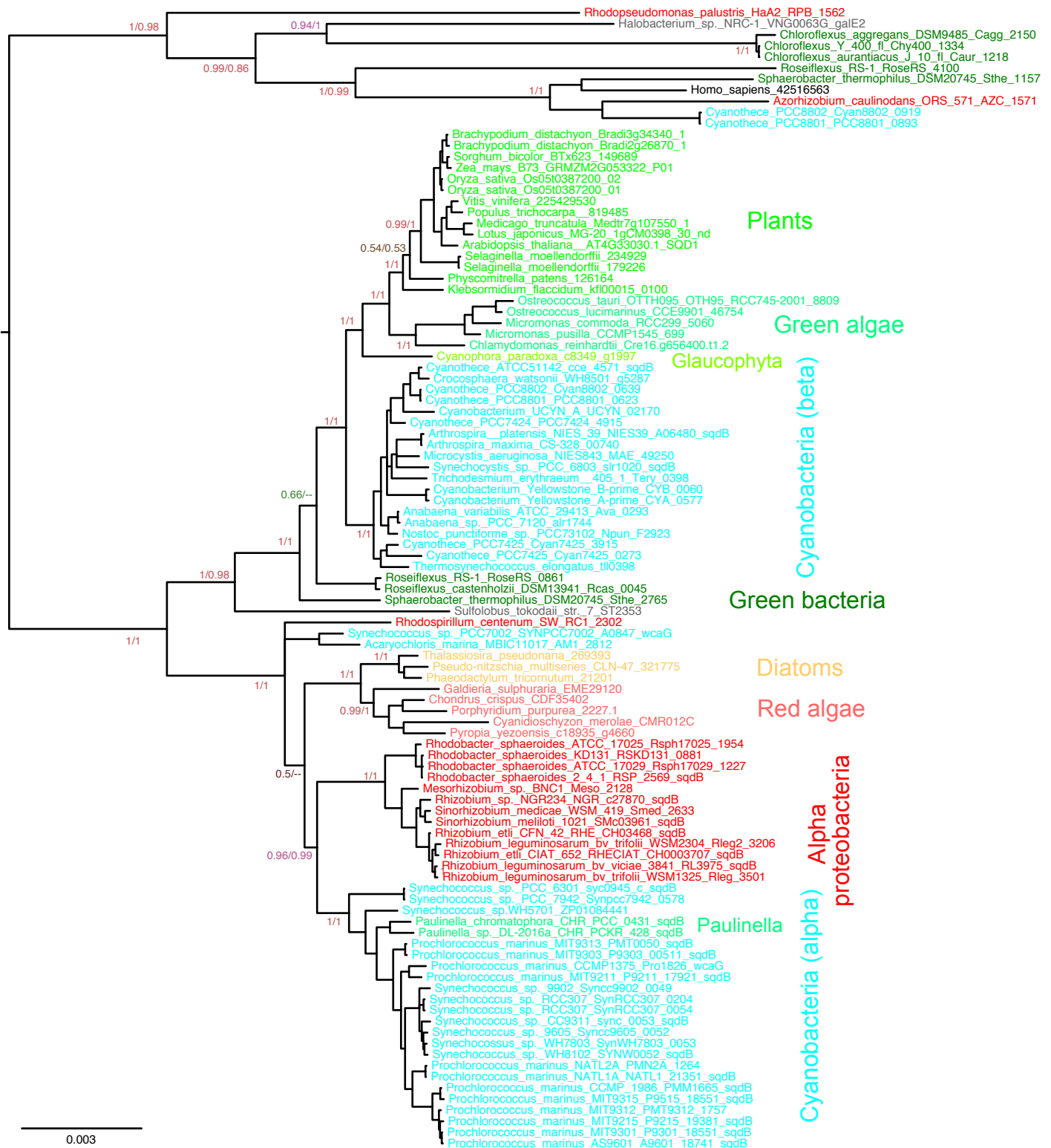
0.5

PGPP1 (BI/ML)



SQD1/SqdB (BI/ML)

Similar splitting of green and red lineages in PhyloBayes, CAT, GTR



SqdX/SQD2 (BI/ML/PB)

