

Journal of Plant Research

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?

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Online Resource 4. Phylogenetic trees of chloroplast-encoded rRNA and proteins.

16S-23S rRNA, a combined tree of 16S rRNA and 23S rRNA; 33 proteins (33P in [Fig. 5](#)), a combined tree with 33 chloroplast-encoded proteins in [Tajima et al. 2016](#), re-analyzed with the LG model; PsaA, Photosystem I reaction center protein; PsaB, Photosystem I core protein; PsaAB, a tree including selected PsaA and PsaB; PsaD and PsaE, nuclear-encoded Photosystem I proteins; Set A48, a combined tree of 23 chloroplast-encoded photosynthesis-related proteins conserved in 48 organisms (in the Gclust dataset CPBACT10); Set A53, a combined tree of 23 chloroplast-encoded house-keeping proteins conserved in 53 organisms; Set A53 selected (A53-2), a combined tree of 9 selected proteins in the set A53; Set B42, 53 chloroplast-encoded proteins conserved in red algae and bacteria (42 species); Set F35, 20 chloroplast-encoded proteins conserved in macrophytic red algae (35 species); Set B37, 24 chloroplast-encoded proteins conserved in red algae and cyanobacteria (37 species); Set E48, three chloroplast-encoded chlorophyll synthesis enzymes conserved in 48 organisms; RbcL, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; RpoA, RNA polymerase subunit α ; RpoB (two pages), RNA polymerase subunit β ; RpoC (two pages), RNA polymerase subunit β' in bacteria, and subunits β' and β'' that are split in cyanobacteria and chloroplasts.

16S-23S rRNA
 BI (4x4 + pair, nst6, invgamma)



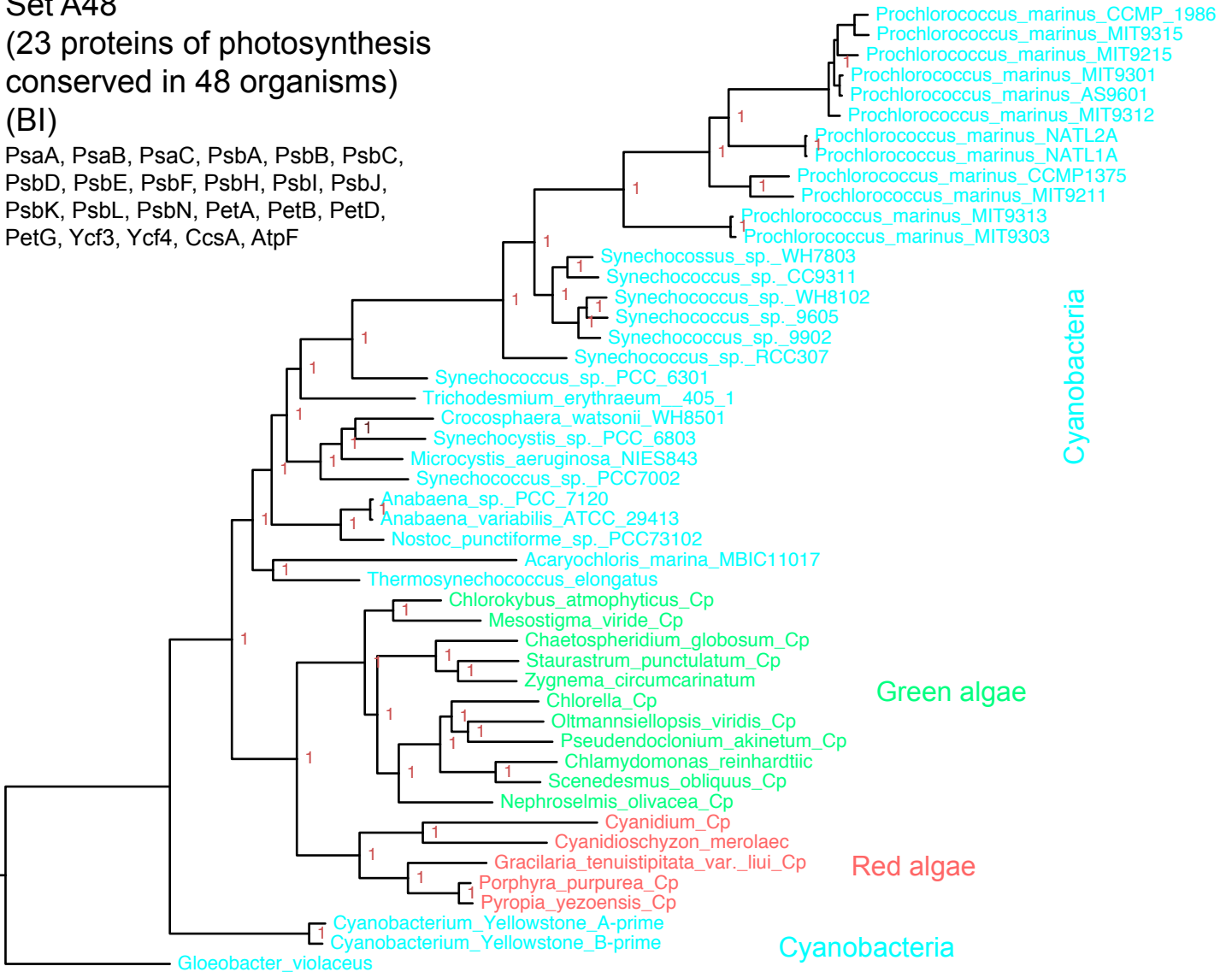
0.1

Set A48

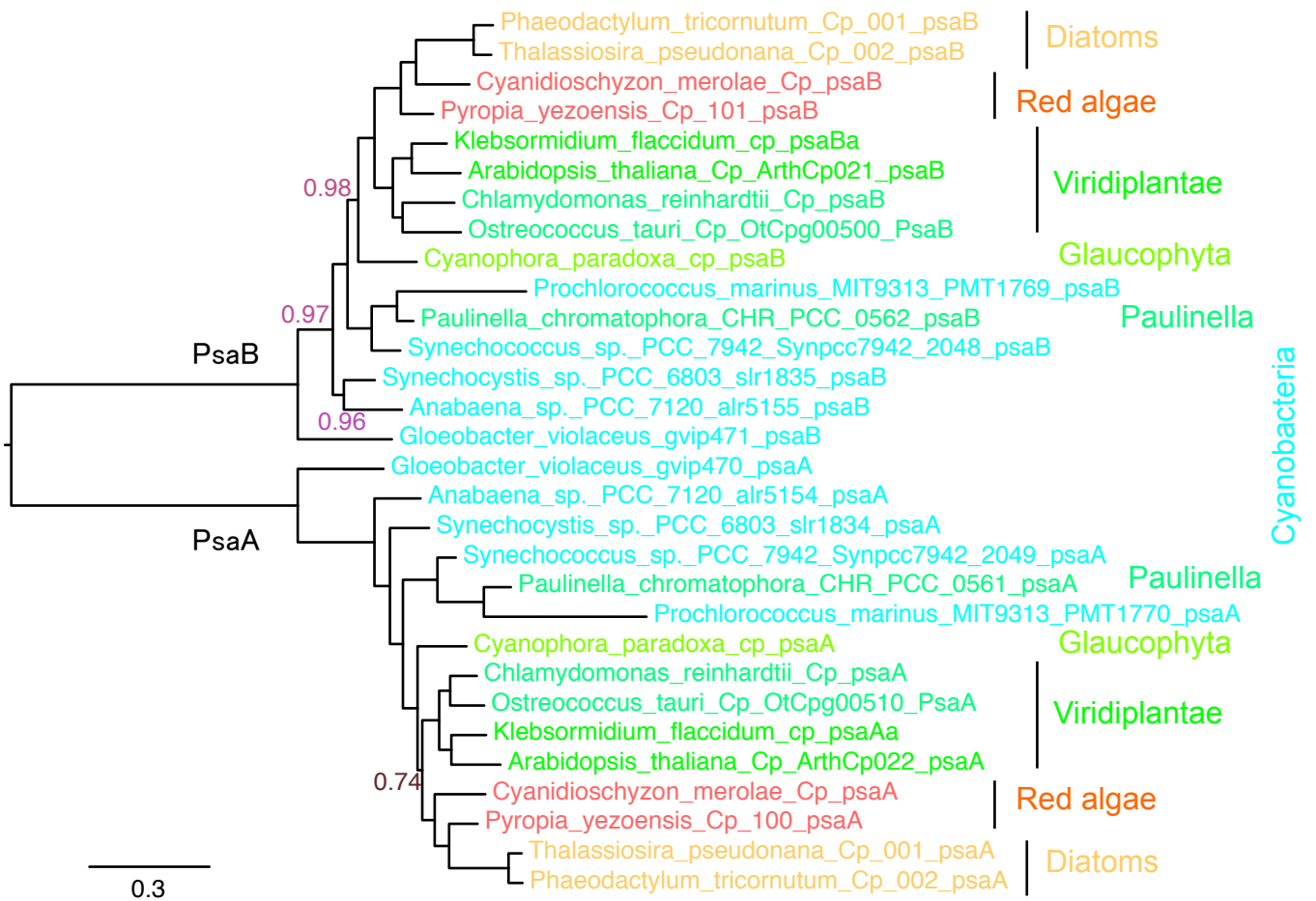
(23 proteins of photosynthesis conserved in 48 organisms)

(BI)

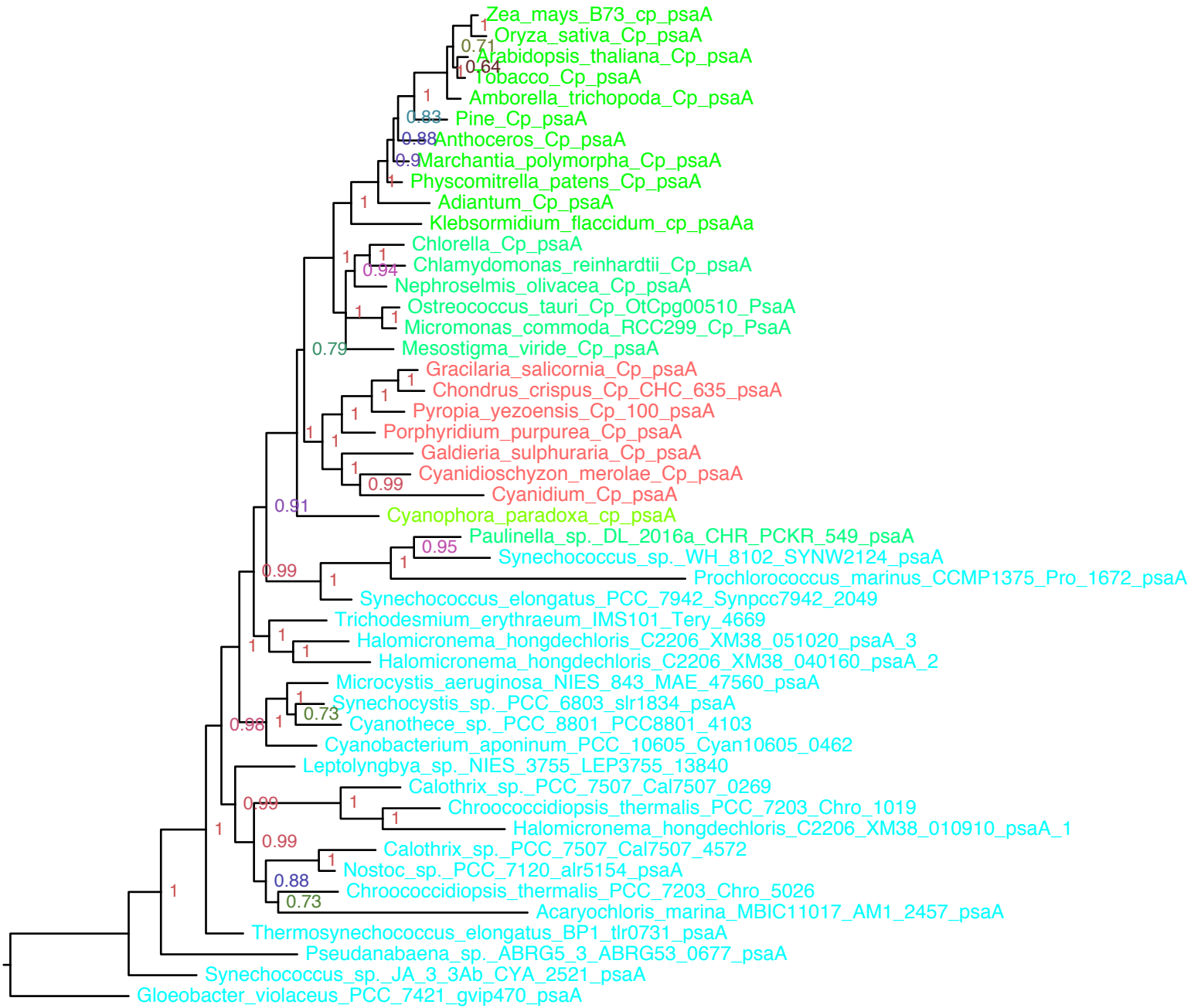
PsaA, PsaB, PsaC, PsbA, PsbB, PsbC, PsbD, PsbE, PsbF, PsbH, PsbI, PsbJ, PsbK, PsbL, PsbN, PetA, PetB, PetD, PetG, Ycf3, Ycf4, CcsA, AtpF



PsaAB tree
(BI)

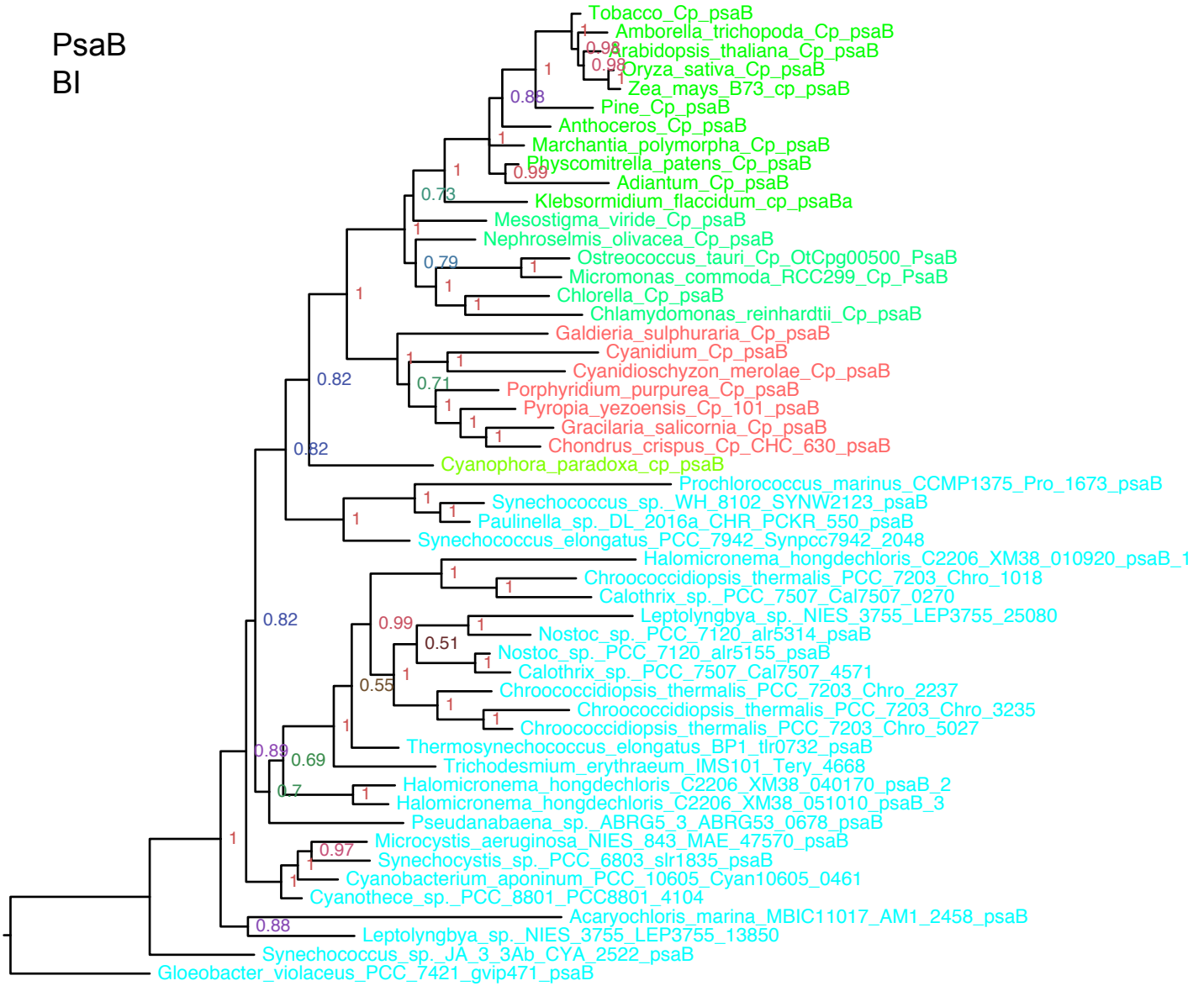


PsaA
BI



0.1

PsaB
BI



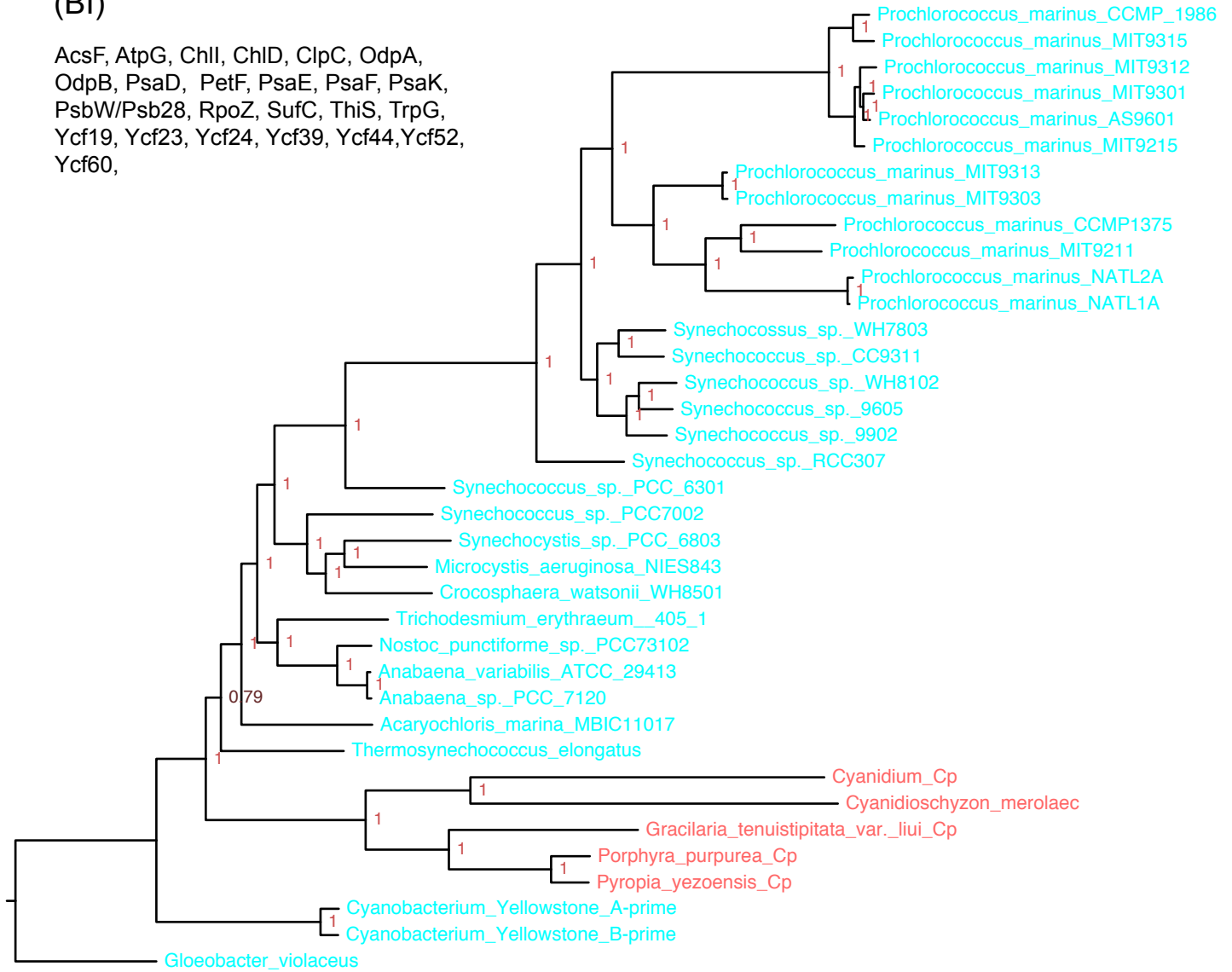
0.07

Set B37

(24 proteins conserved in red algae)

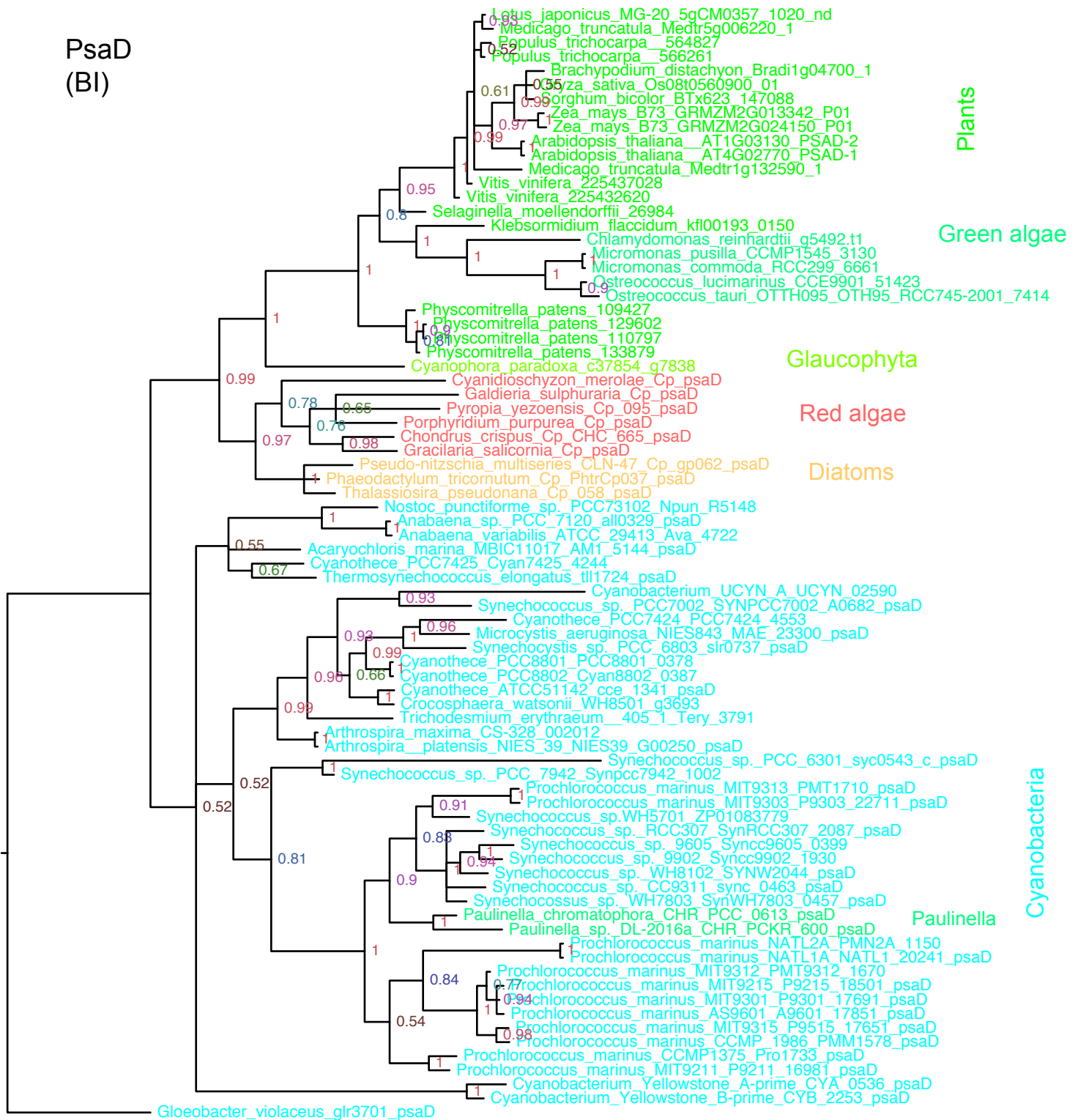
(BI)

AcsF, AtpG, ChlI, ChlD, ClpC, OtpA, OtpB, PsaD, PetF, PsaE, PsaF, PsaK, PsbW/Psb28, RpoZ, SufC, ThiS, TrpG, Ycf19, Ycf23, Ycf24, Ycf39, Ycf44, Ycf52, Ycf60,



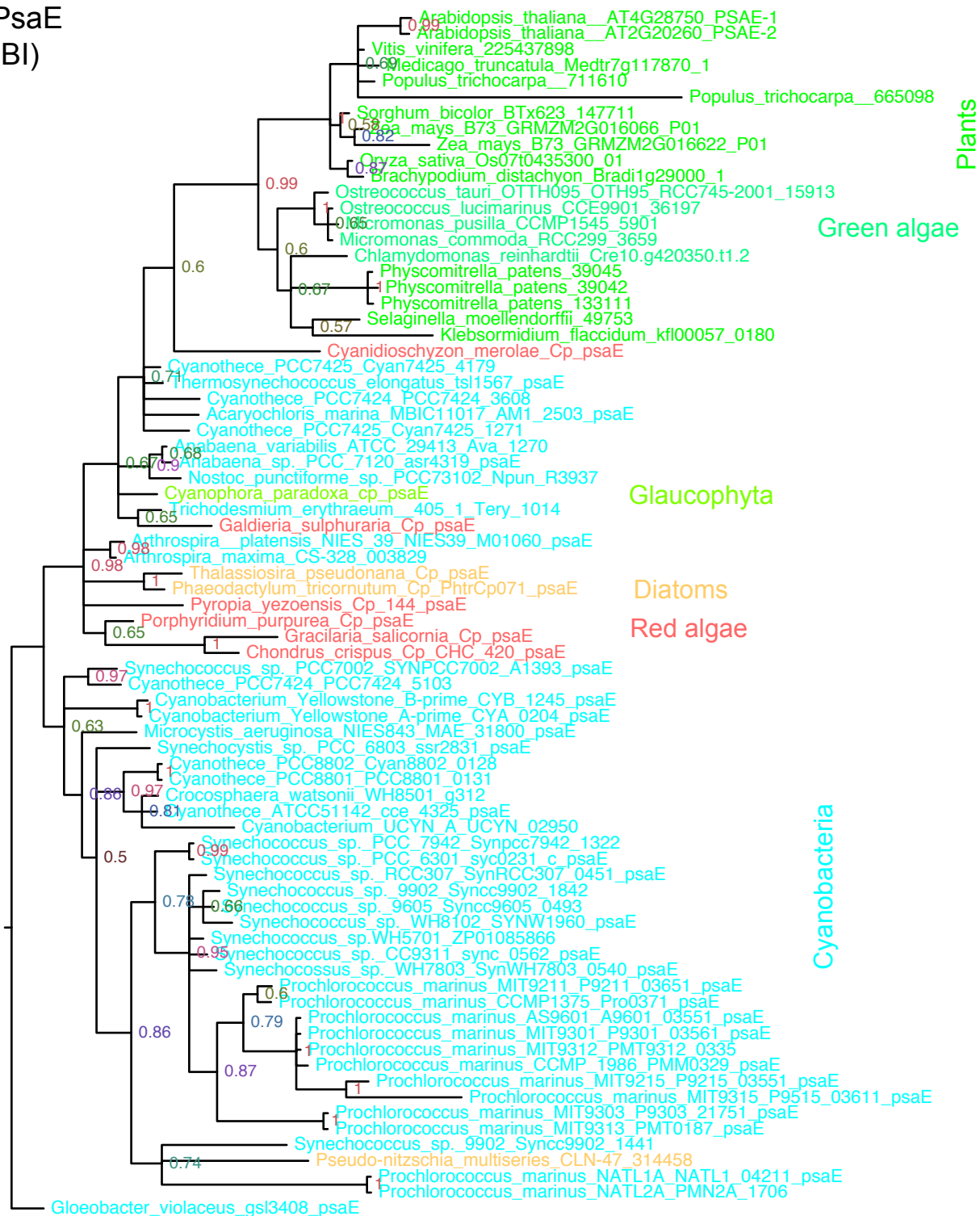
0.2

PsaD
(BI)



0.2

PsaE
(BI)



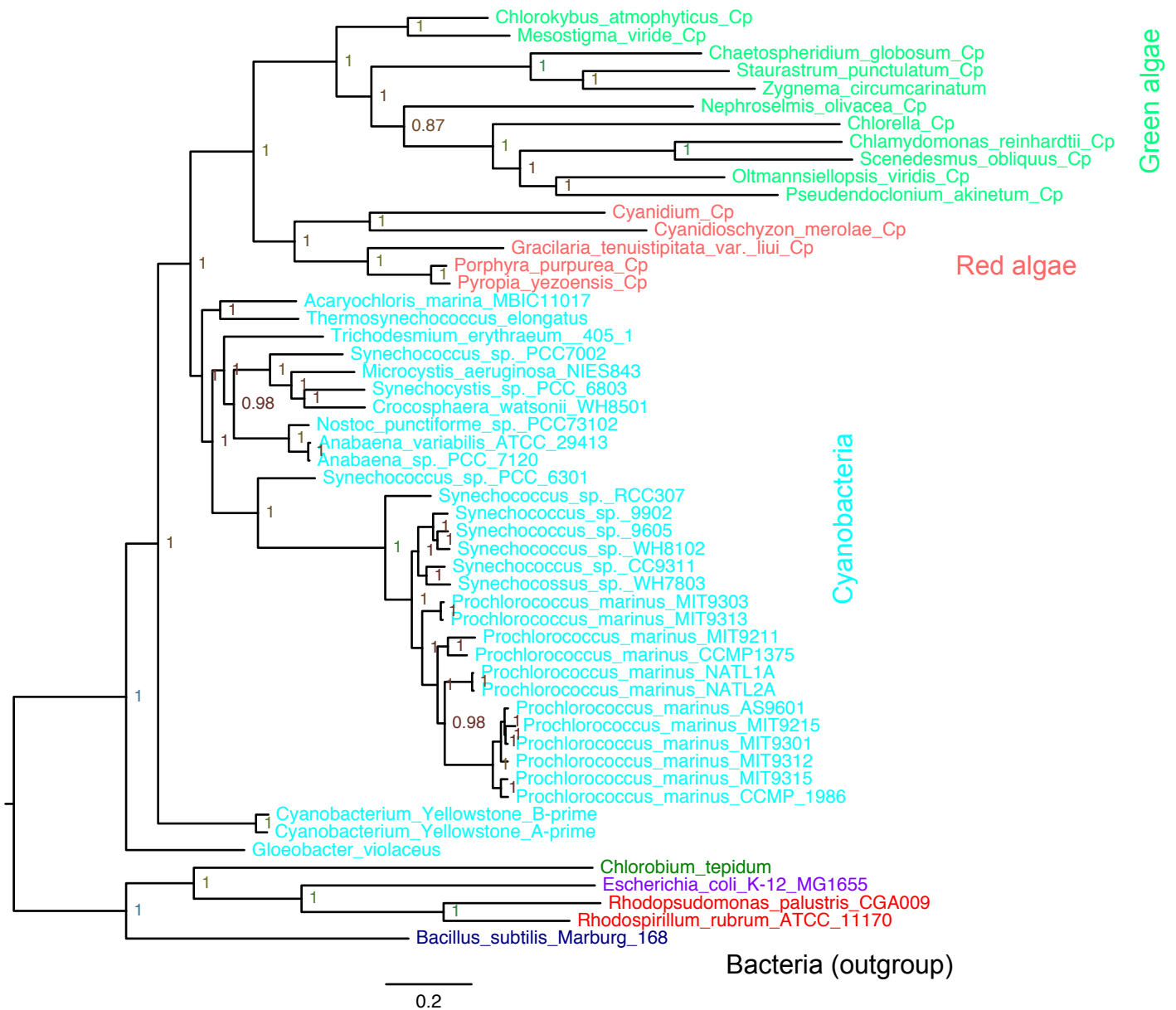
0.3

Set A53

(23 proteins of house-keeping proteins conserved in 53 organisms)

(BI)

AtpA, AtpB, AtpE, AtpH, Atpl, Rps2, Rps3, Rps4,
Rps7, Rps8, Rps11, Rps12, Rps14, Rps18,
Rps19, rpl2, Rpl14, Rpl16, Rpl20, Rpl23, rpoA,
RpoB, RpoC (C1+C2)

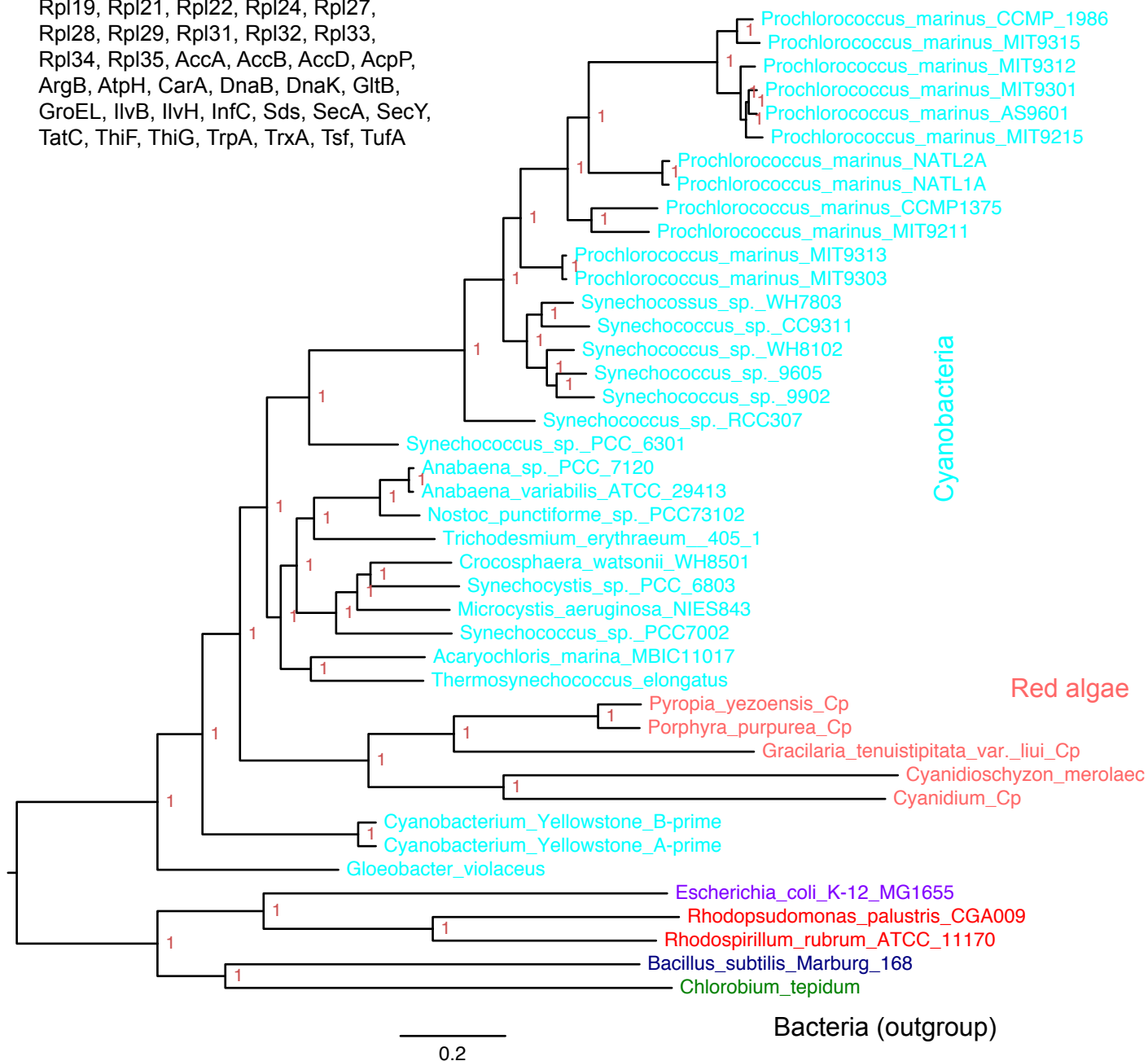


Set B42

(53 proteins conserved in red algae and bacteria)

(BI)

Rps5, Rps6, Rps9, Rps10, Rps13,
 Rps16, Rps17, Rps20, Rpl1, Rpl3, Rpl4,
 Rpl5, Rpl6, Rpl11, Rpl12, Rpl13, Rpl18,
 Rpl19, Rpl21, Rpl22, Rpl24, Rpl27,
 Rpl28, Rpl29, Rpl31, Rpl32, Rpl33,
 Rpl34, Rpl35, AccA, AccB, AccD, AcpP,
 ArgB, AtpH, CarA, DnaB, DnaK, GltB,
 GroEL, IlvB, IlvH, InfC, Sds, SecA, SecY,
 TatC, ThiF, ThiG, TrpA, TrxA, Tsf, TufA

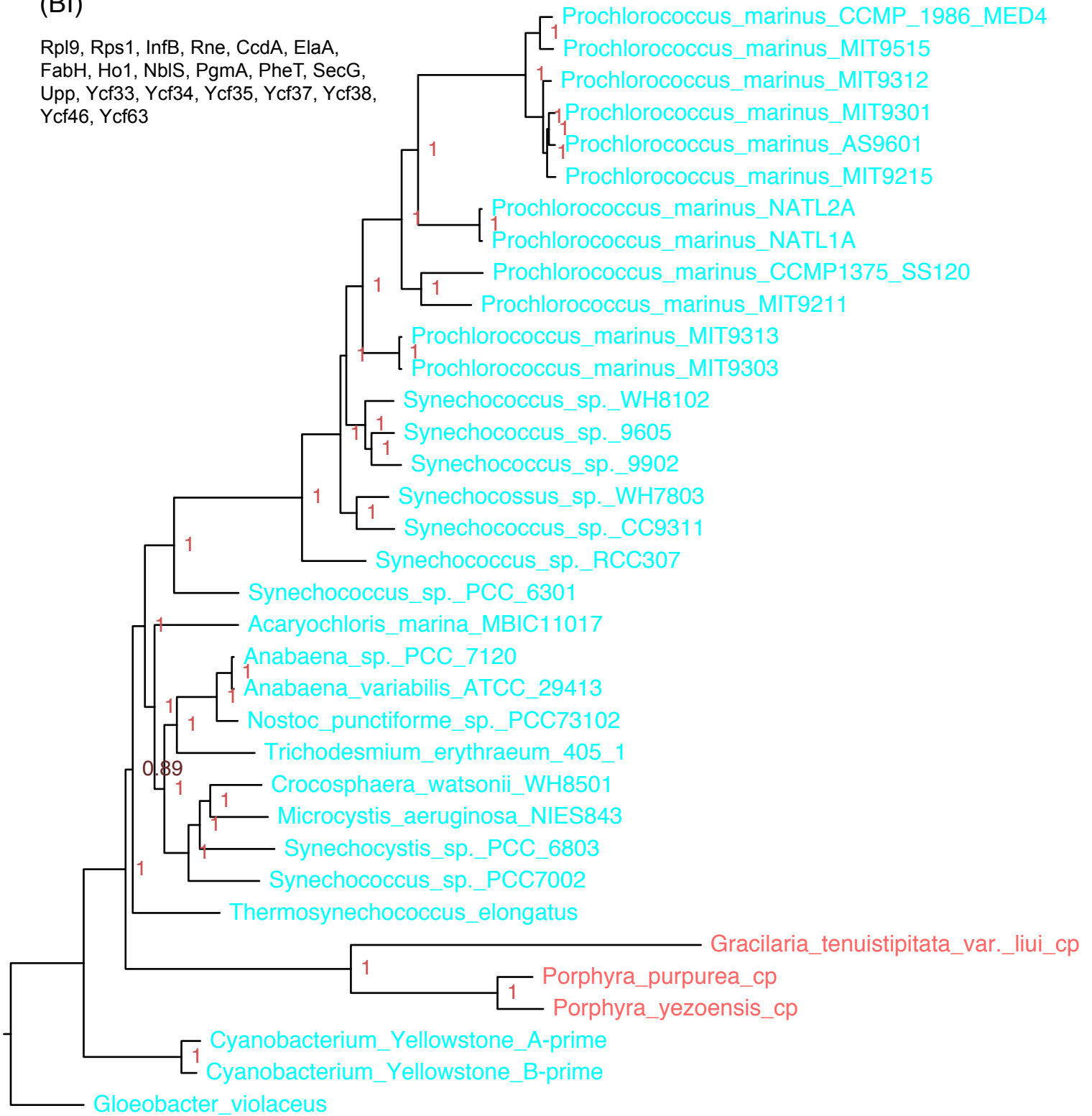


Set F35

(20 proteins conserved in
35 red macrophytes)

(BI)

Rpl9, Rps1, InfB, Rne, CcdA, ElaA,
FabH, Ho1, NblS, PgmA, PheT, SecG,
Upp, Ycf33, Ycf34, Ycf35, Ycf37, Ycf38,
Ycf46, Ycf63



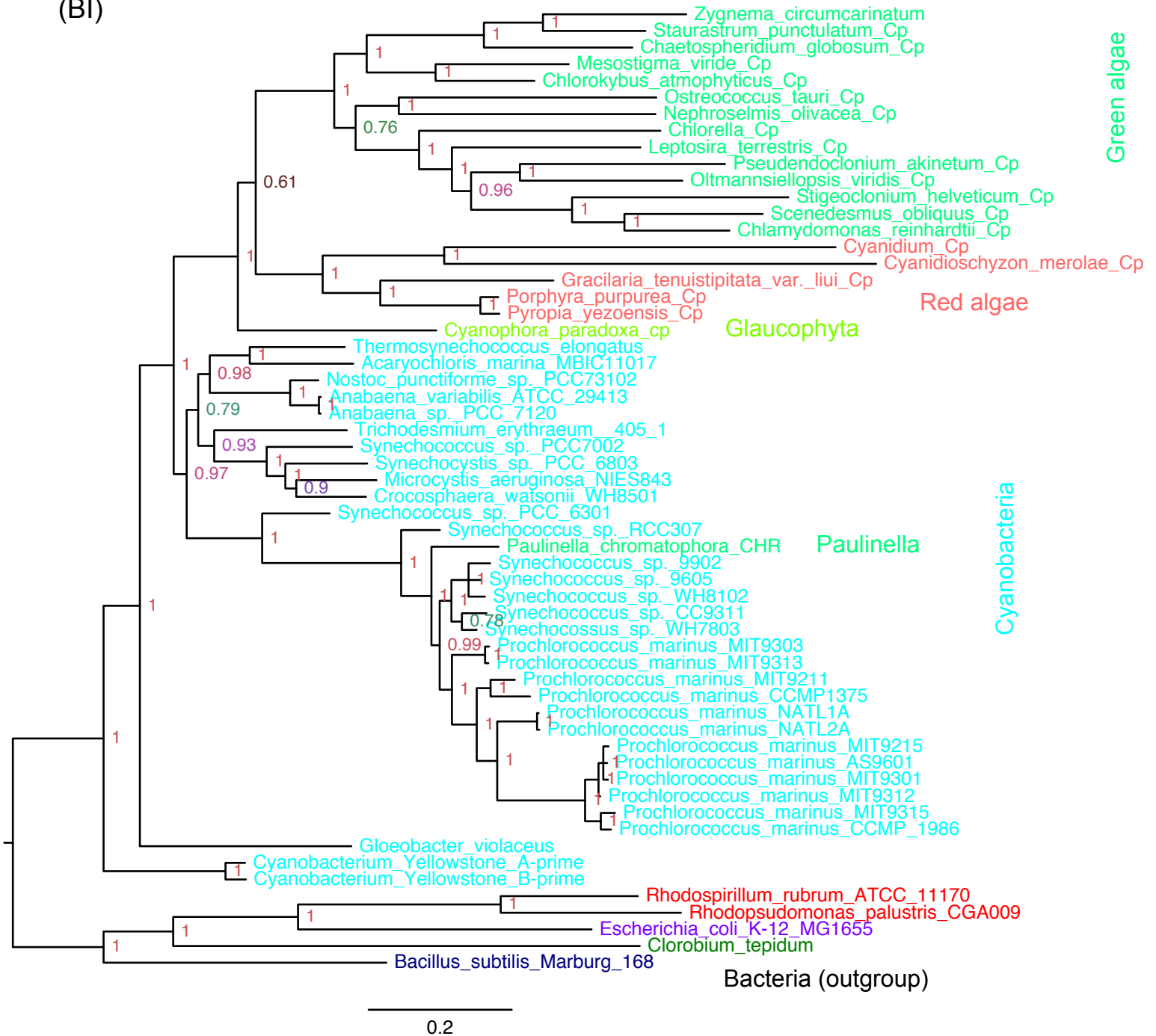
0.3

Set A53 selected

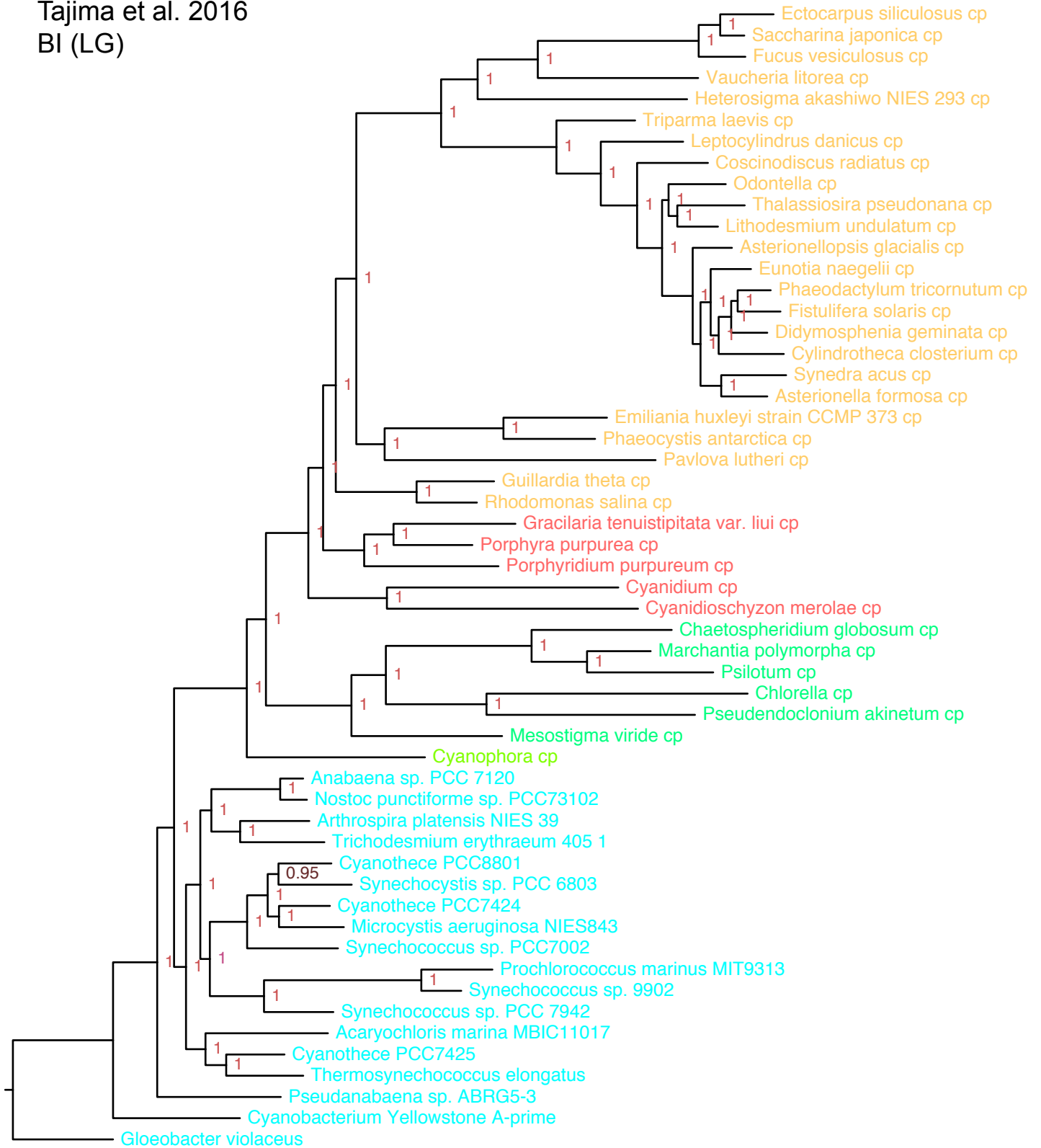
Rpl2, Rps12, Rps19, Rpl14, Rpl16,

Rpl20, Rps8, Rps11, Rps18

(BI)



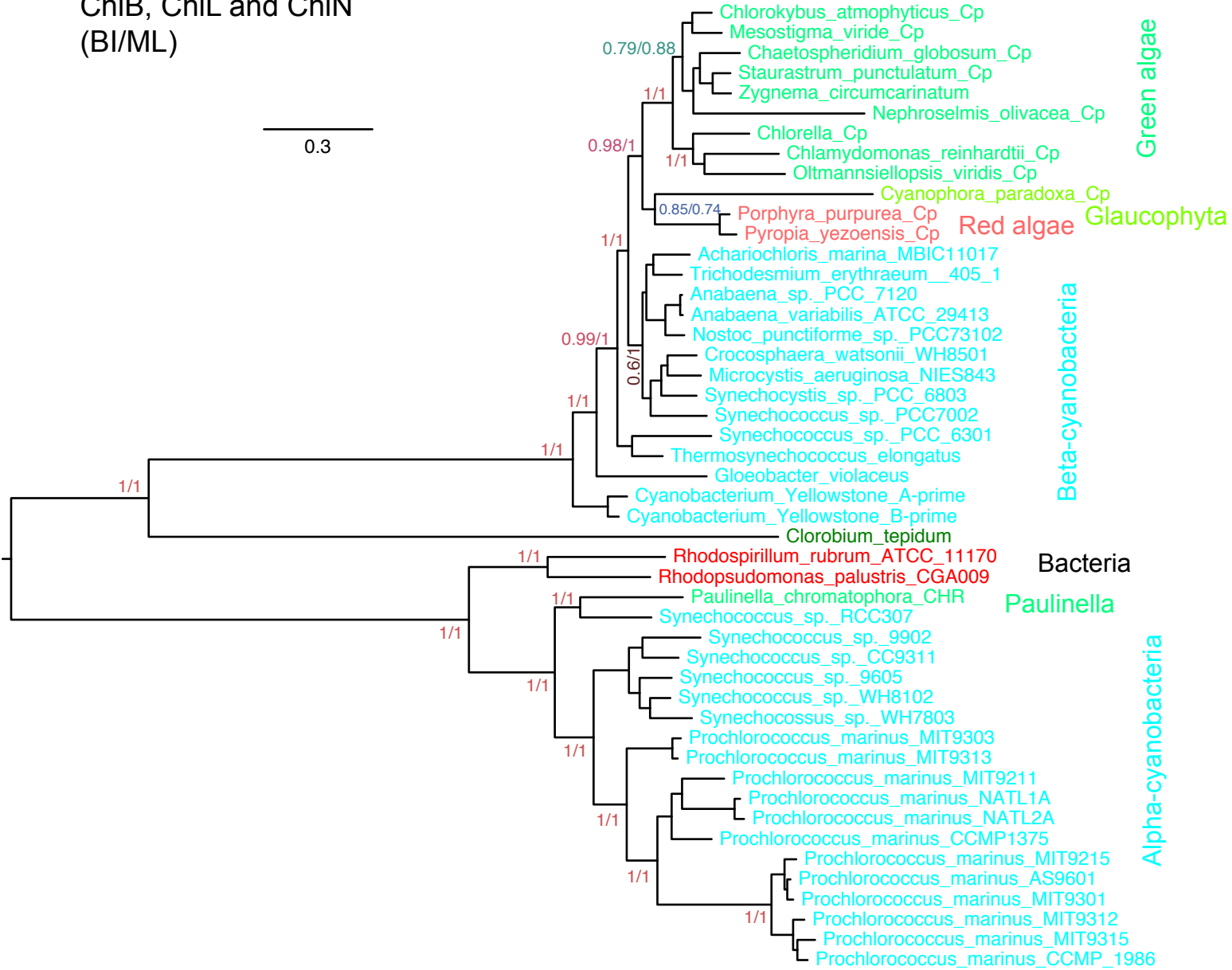
33 proteins
Tajima et al. 2016
BI (LG)



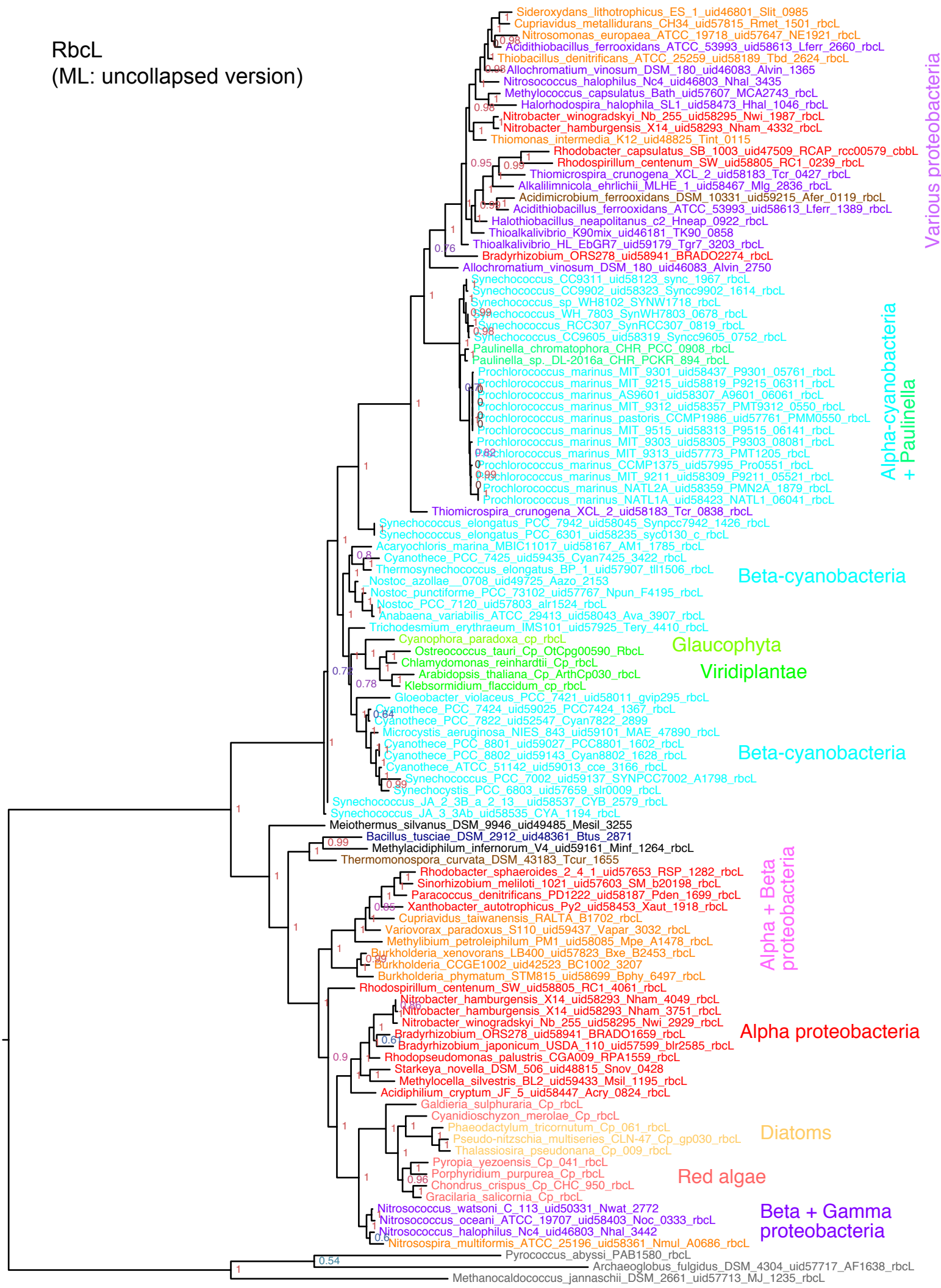
0.2

Set E48
ChIB, ChIL and ChIN
(BI/ML)

0.3



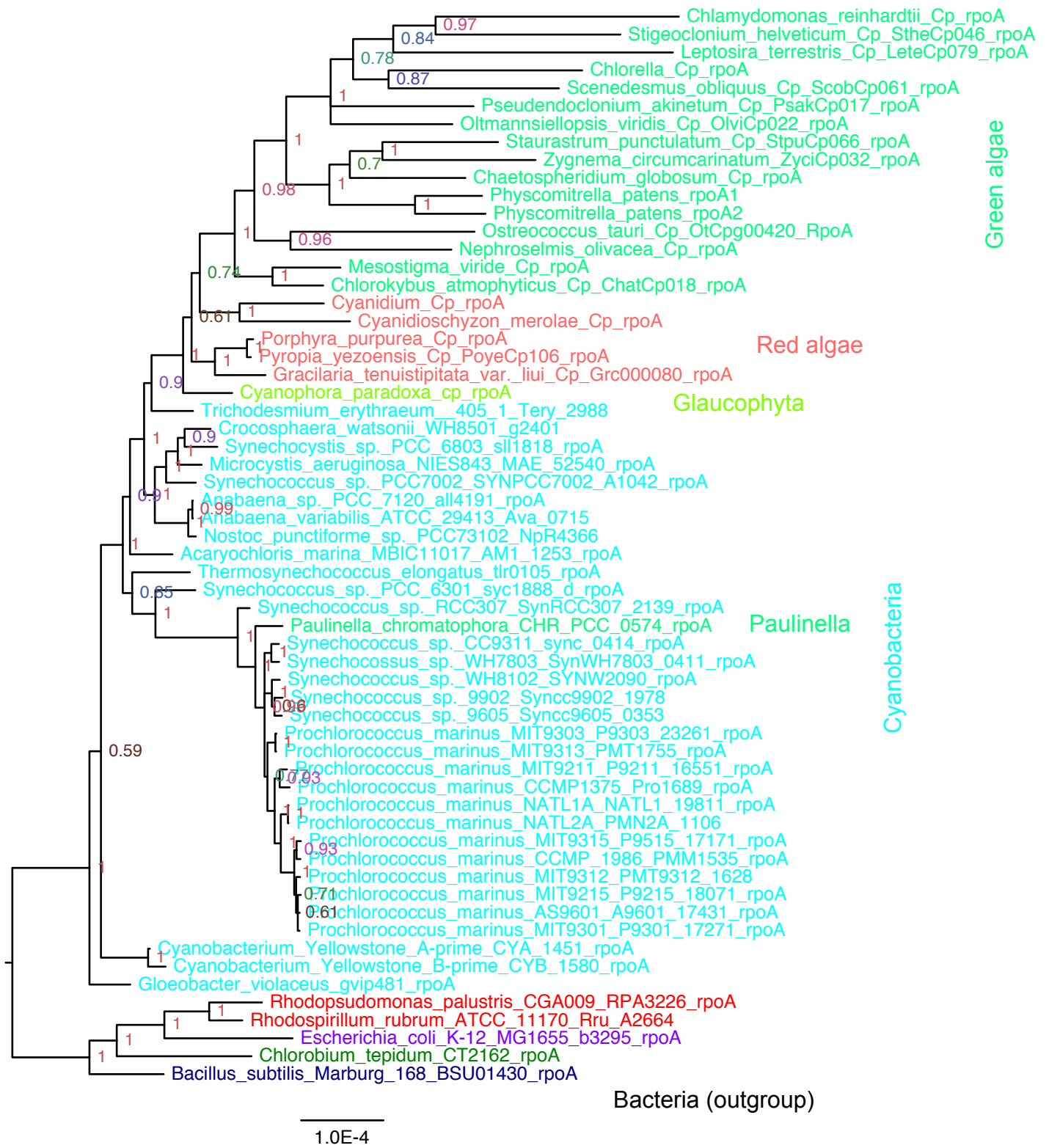
RbcL
(ML: uncollapsed version)



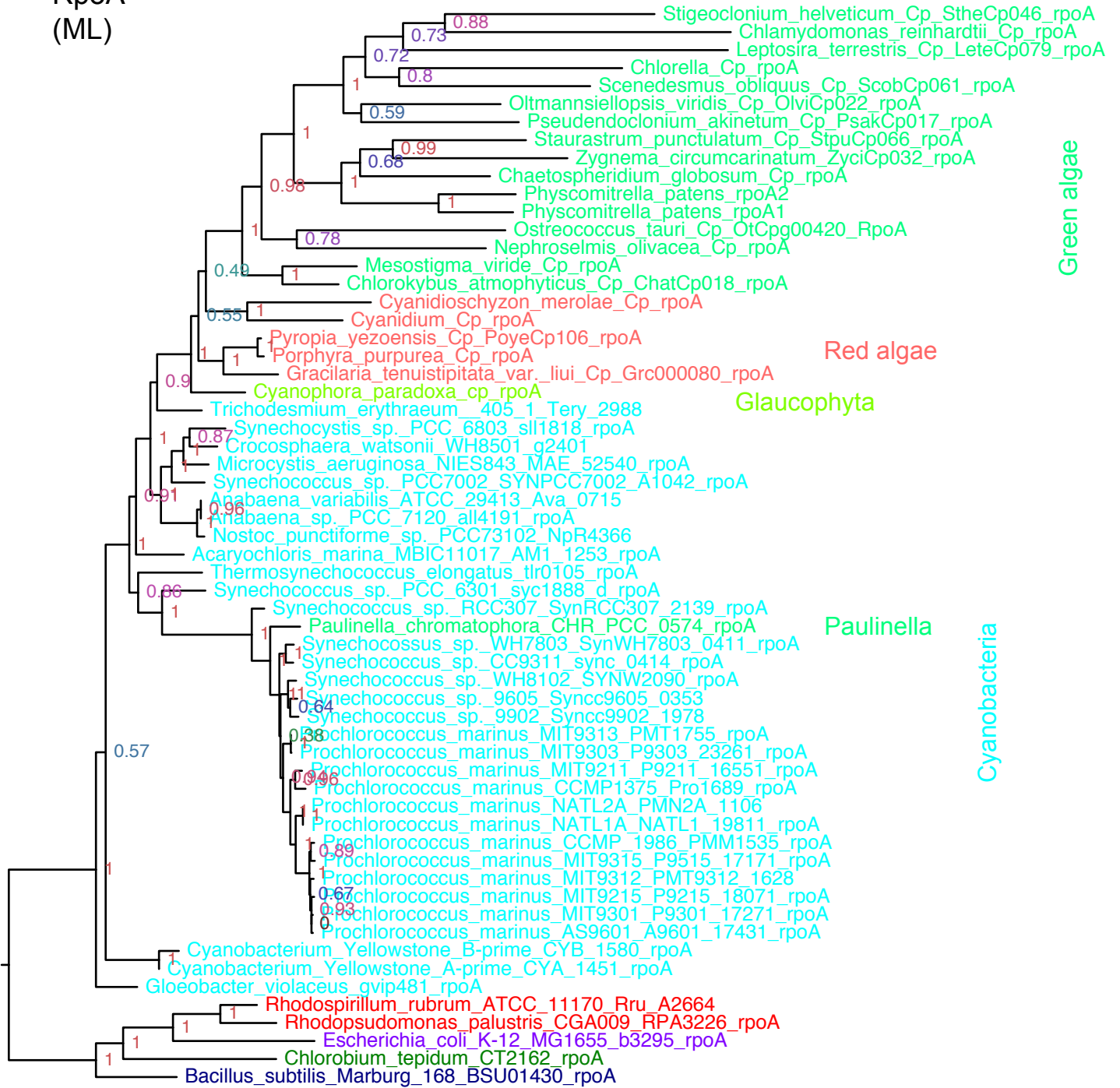
0.4

Archaea (outgroup)

RpoA
(BI)



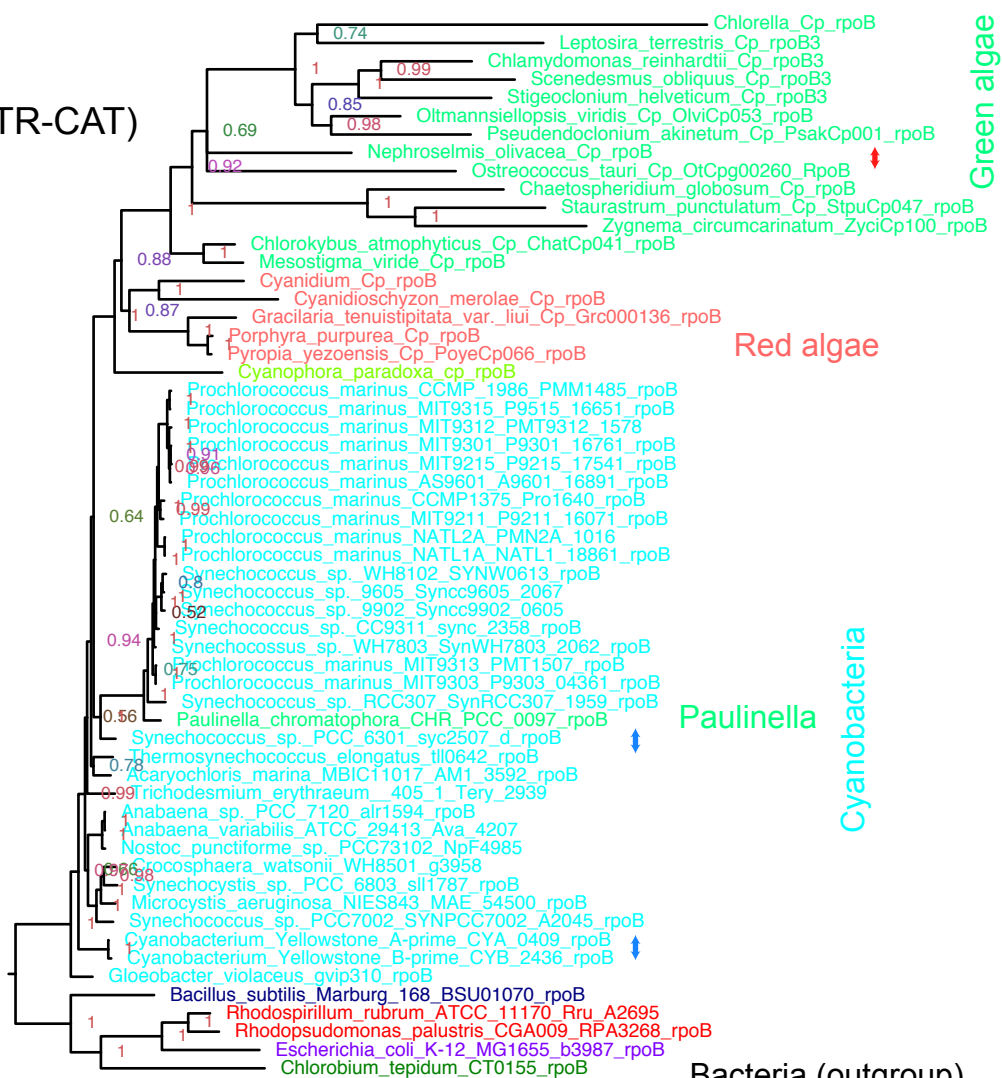
RpoA
(ML)



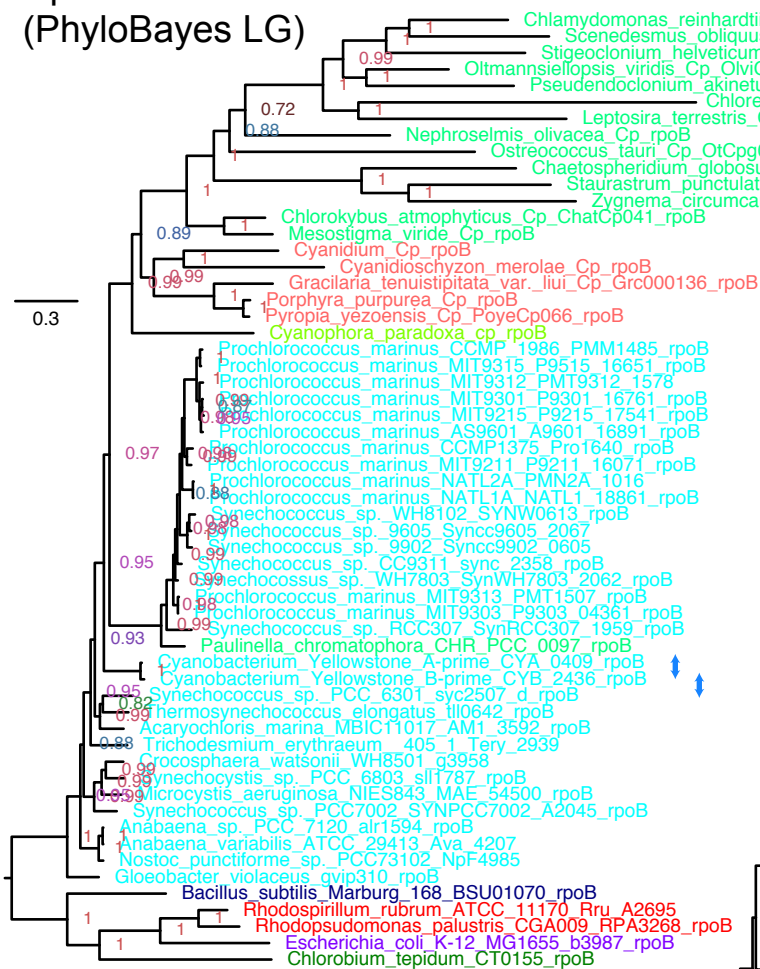
Bacteria (outgroup)

0.4

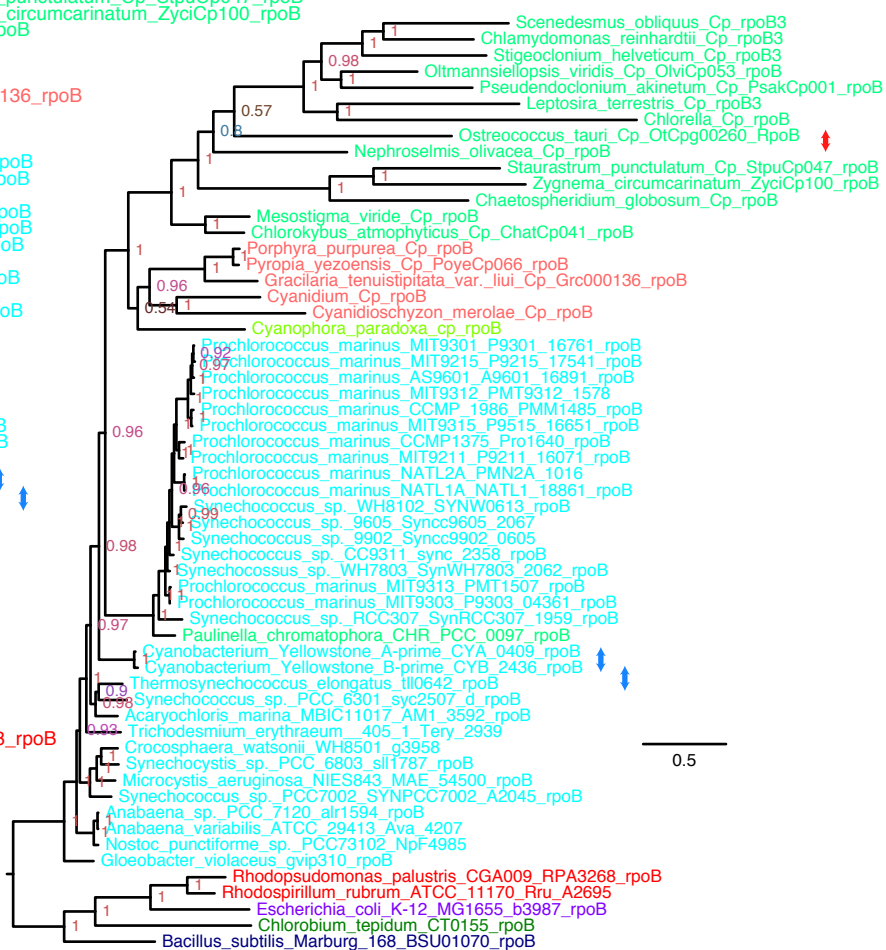
RpoB
(PhyloBayes GTR-CAT)



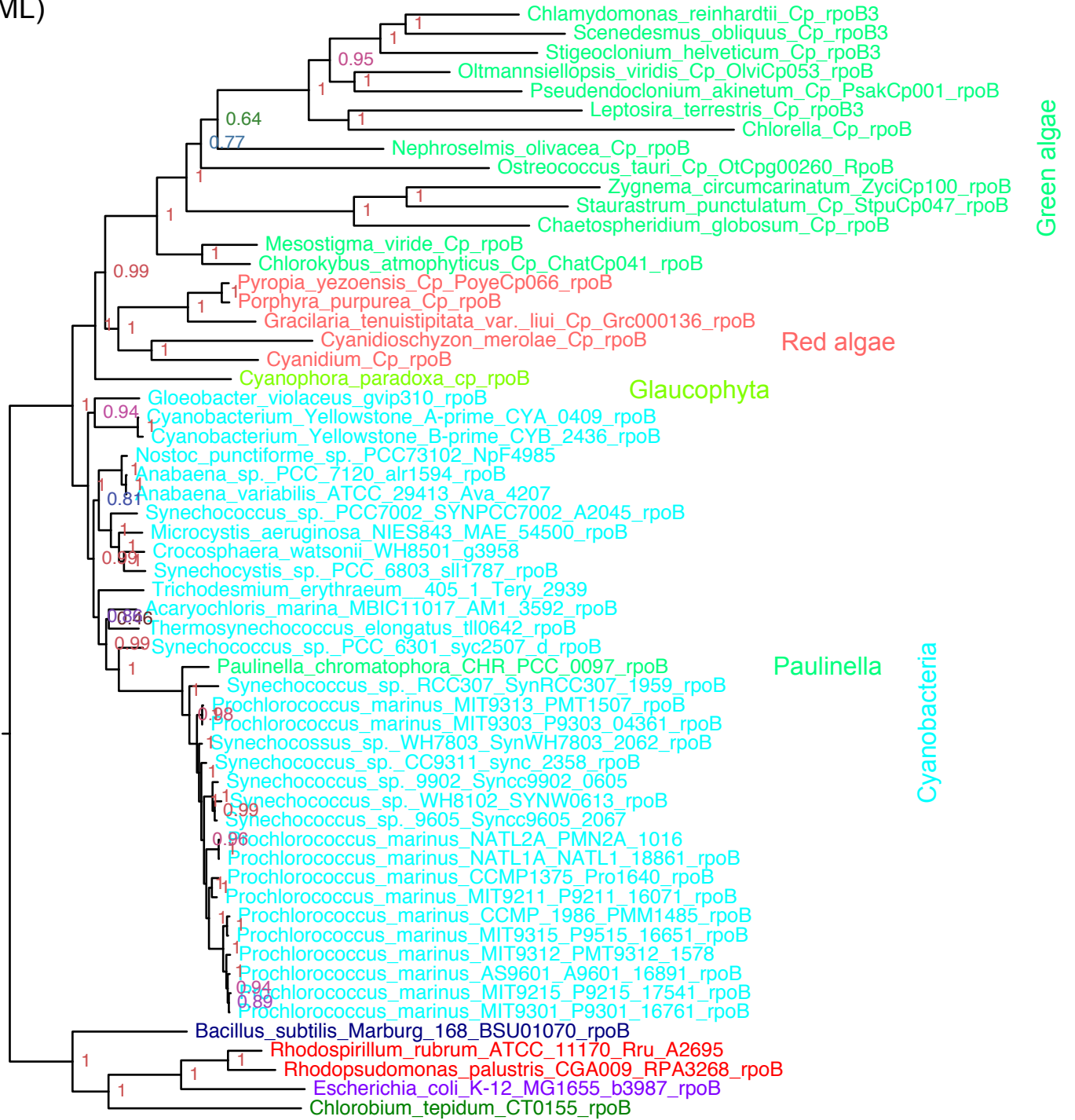
RpoB
(PhyloBayes LG)



RpoB
(MrBayes LG)



RpoB
(ML)



Green algae

Red algae

Glaucophyta

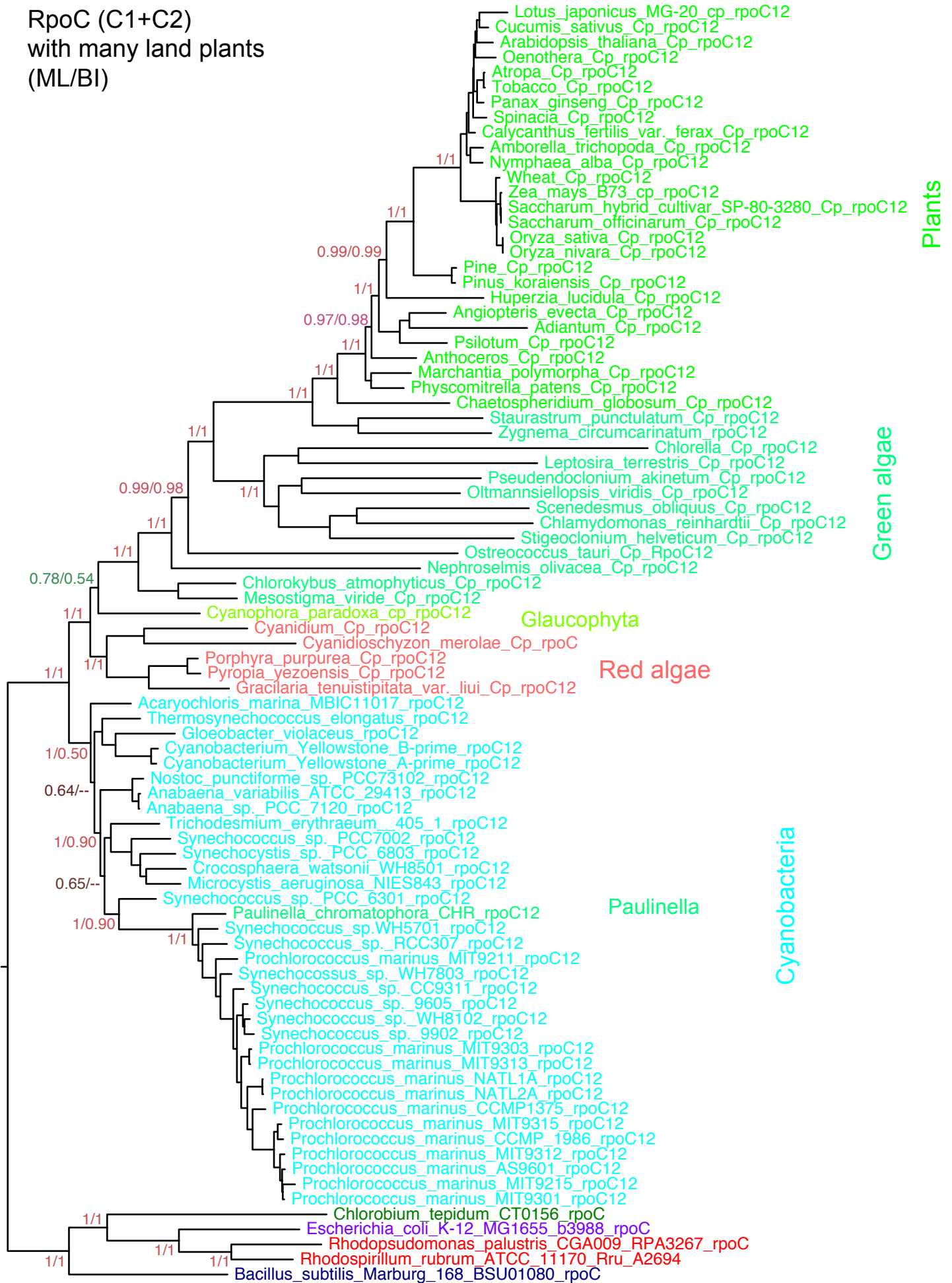
Paulinella

Cyanobacteria

Bacteria (outgroup)

0.3

RpoC (C1+C2)
with many land plants
(ML/BI)



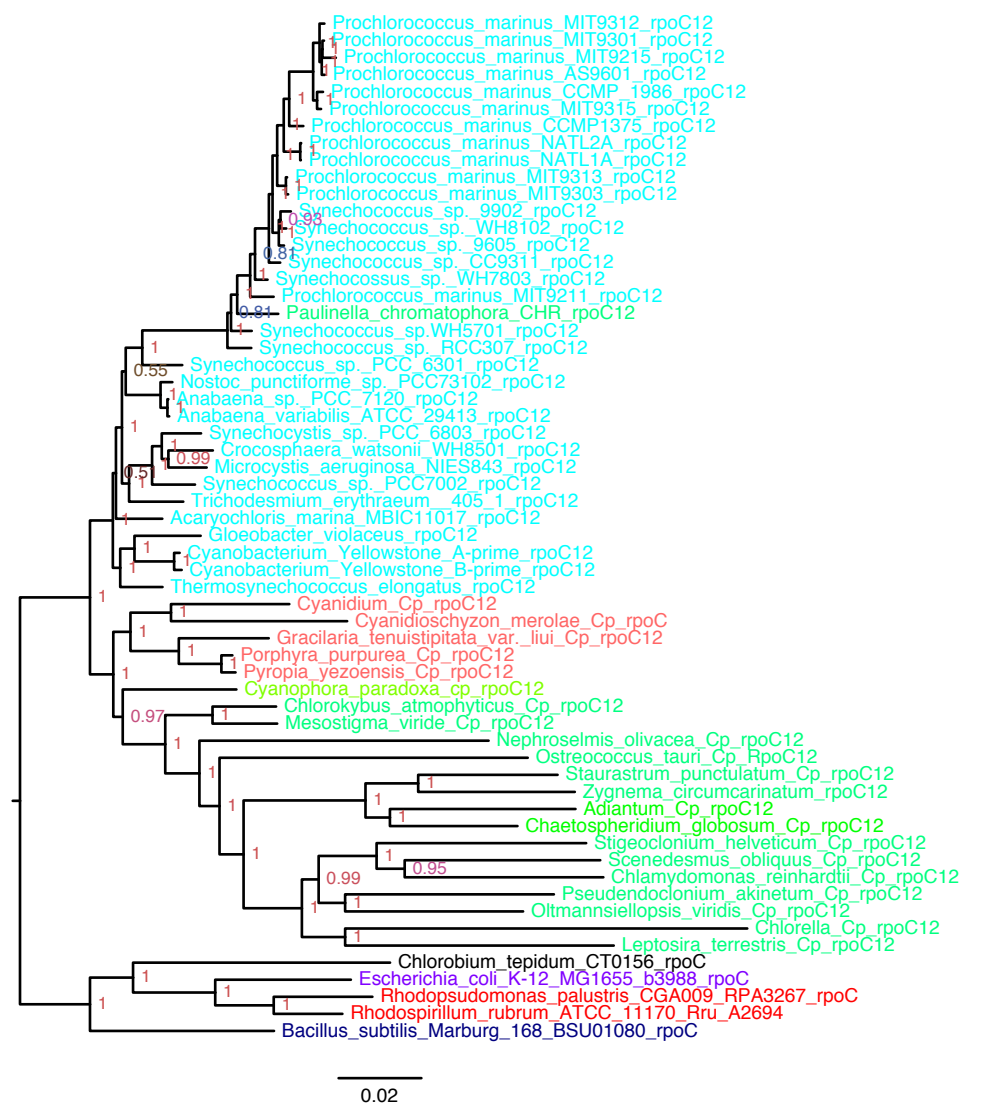
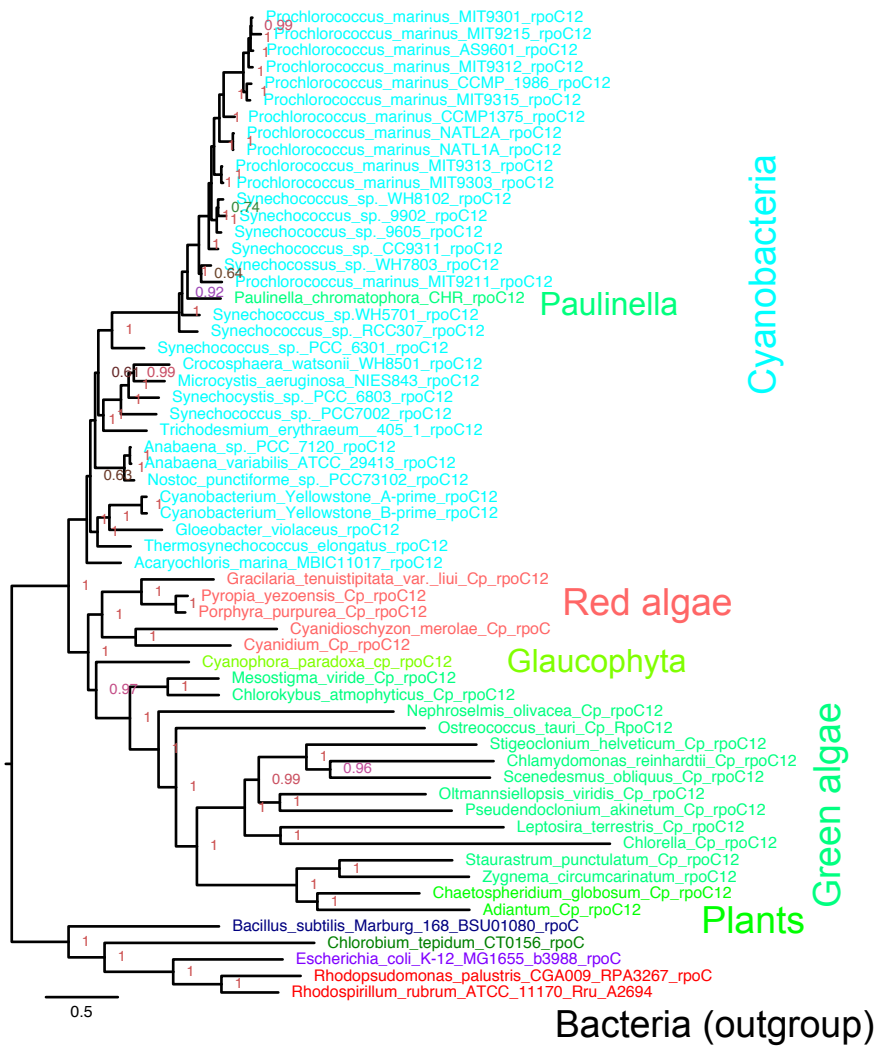
0.4

Bacteria (outgroup)

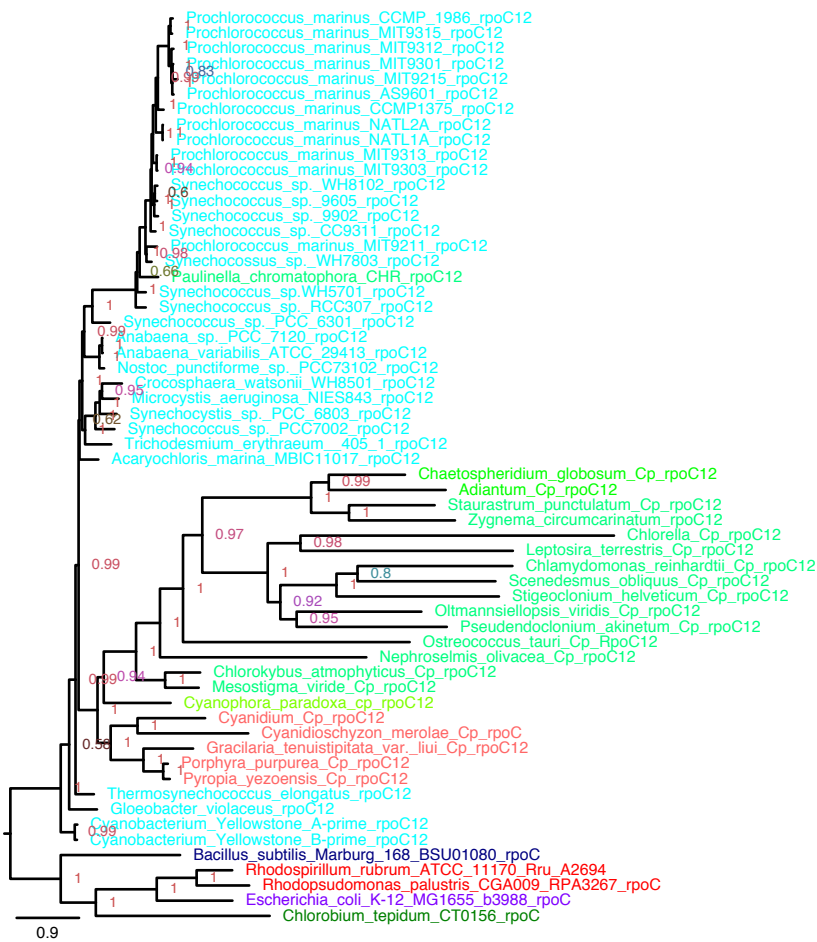
RpoC

(ML, LG)

(MrBayes, LG)



(PhyloBayes, CAT+GTR)



PBP (Cluster 705 in Gclust2012_42)

(BI/ML)

