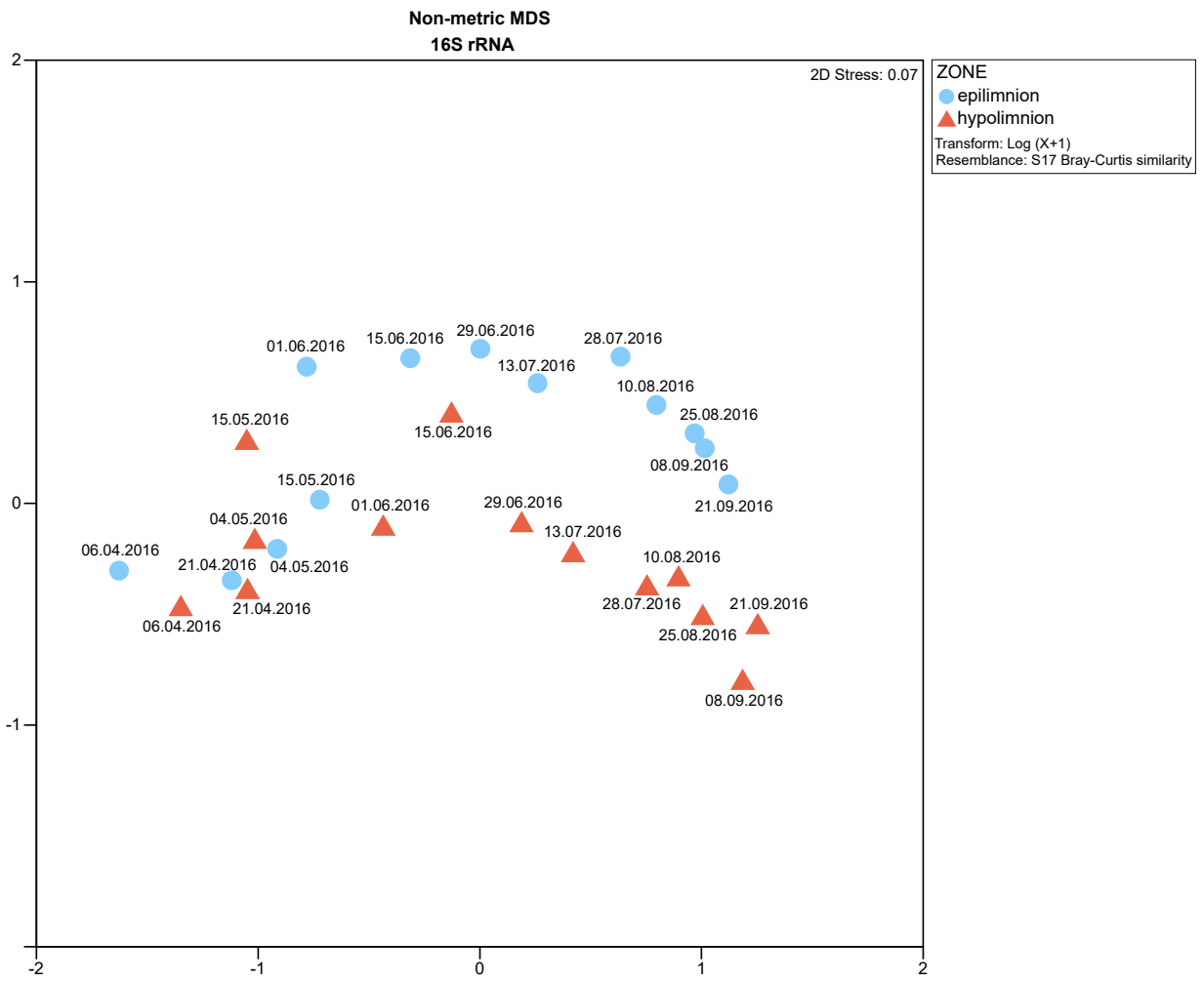
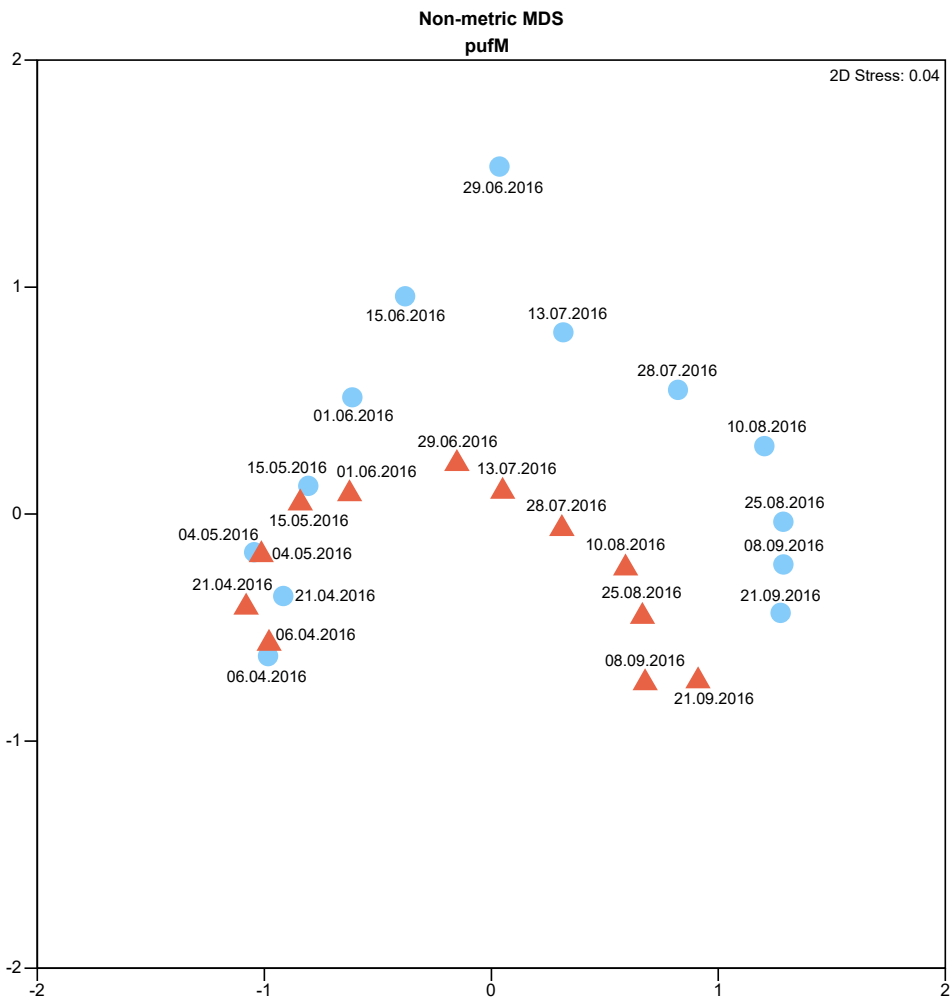
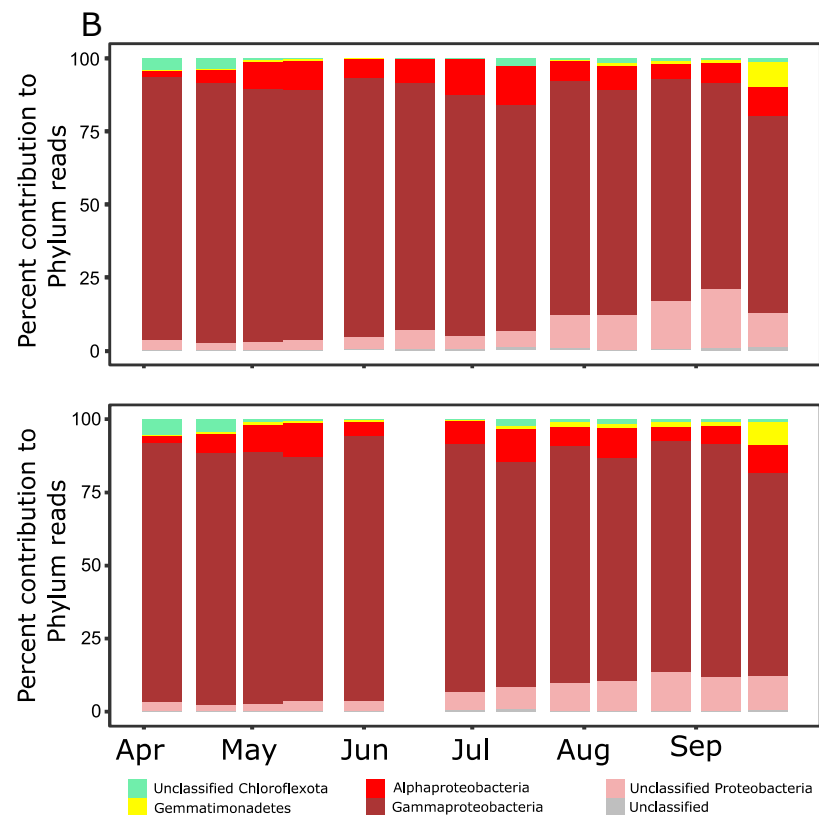
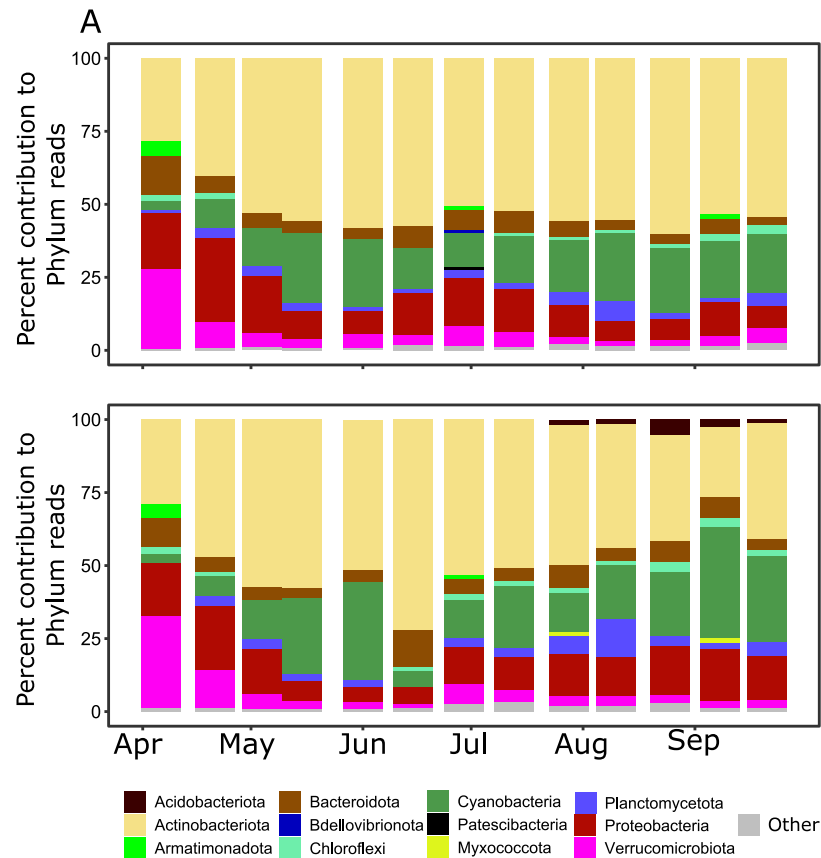


Supplementary Figure S1. Weekly values of environmental variables in epilimnion (blue-circles and line) and hypolimnion (red - triangles and line) of Cep lake. (A) temperature; (B) optical dissolved oxygen; (C) dissolved organic carbon; (D) soluble reactive phosphorous; (E) dissolved nitrogen; and (F) chlorophyll-a.

A**B**

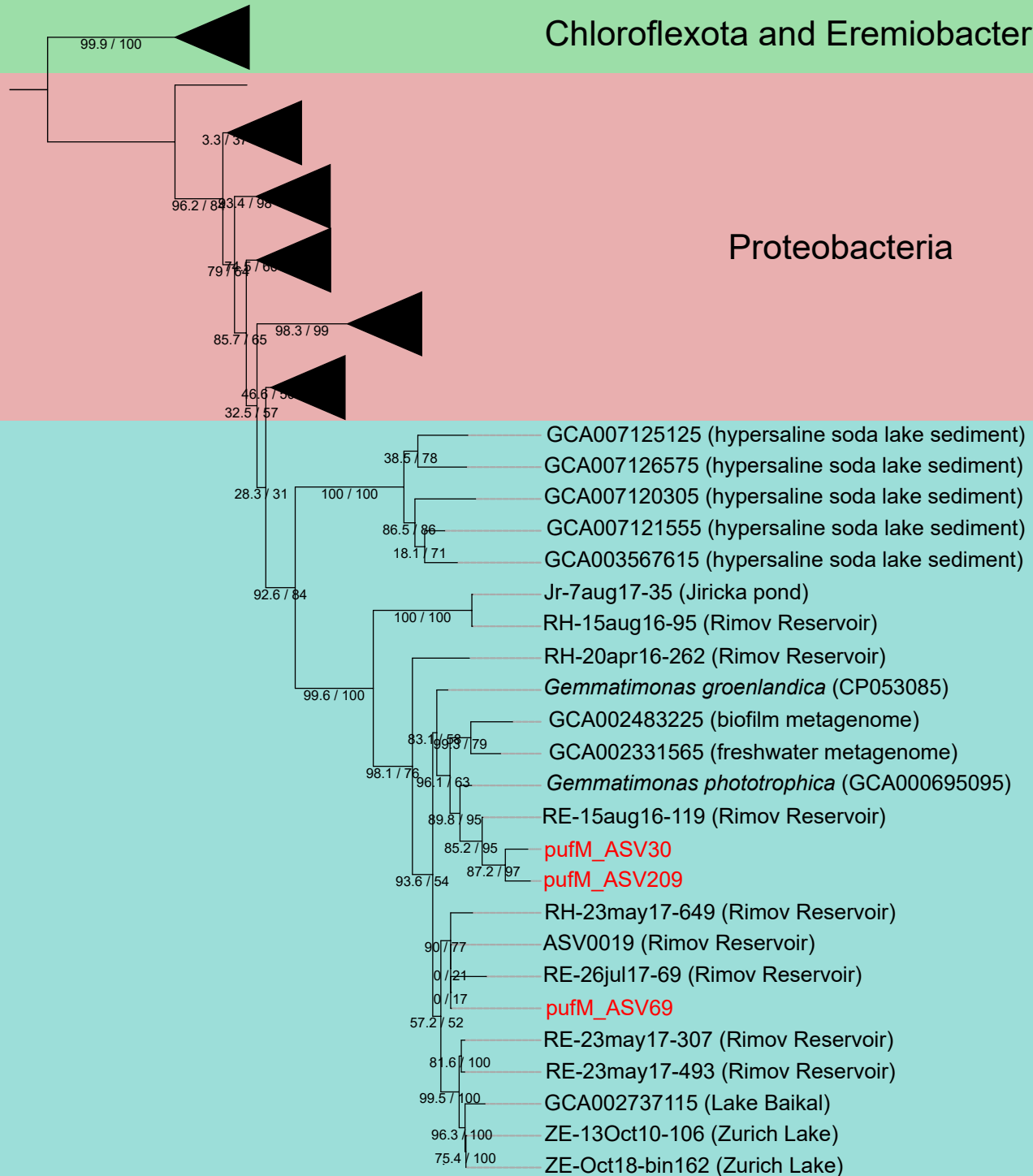
Supplementary Figure S2. Nonmetric multidimensional scaling plots of (A) all bacteria and (B) AAP bacteria based on Bray-Curtis distances.



Supplementary Figure S3. Community contribution at phylum level of (A) total bacteria community and (B) AAP bacteria community for epilimnion (top) and hypolimnion (bottom).

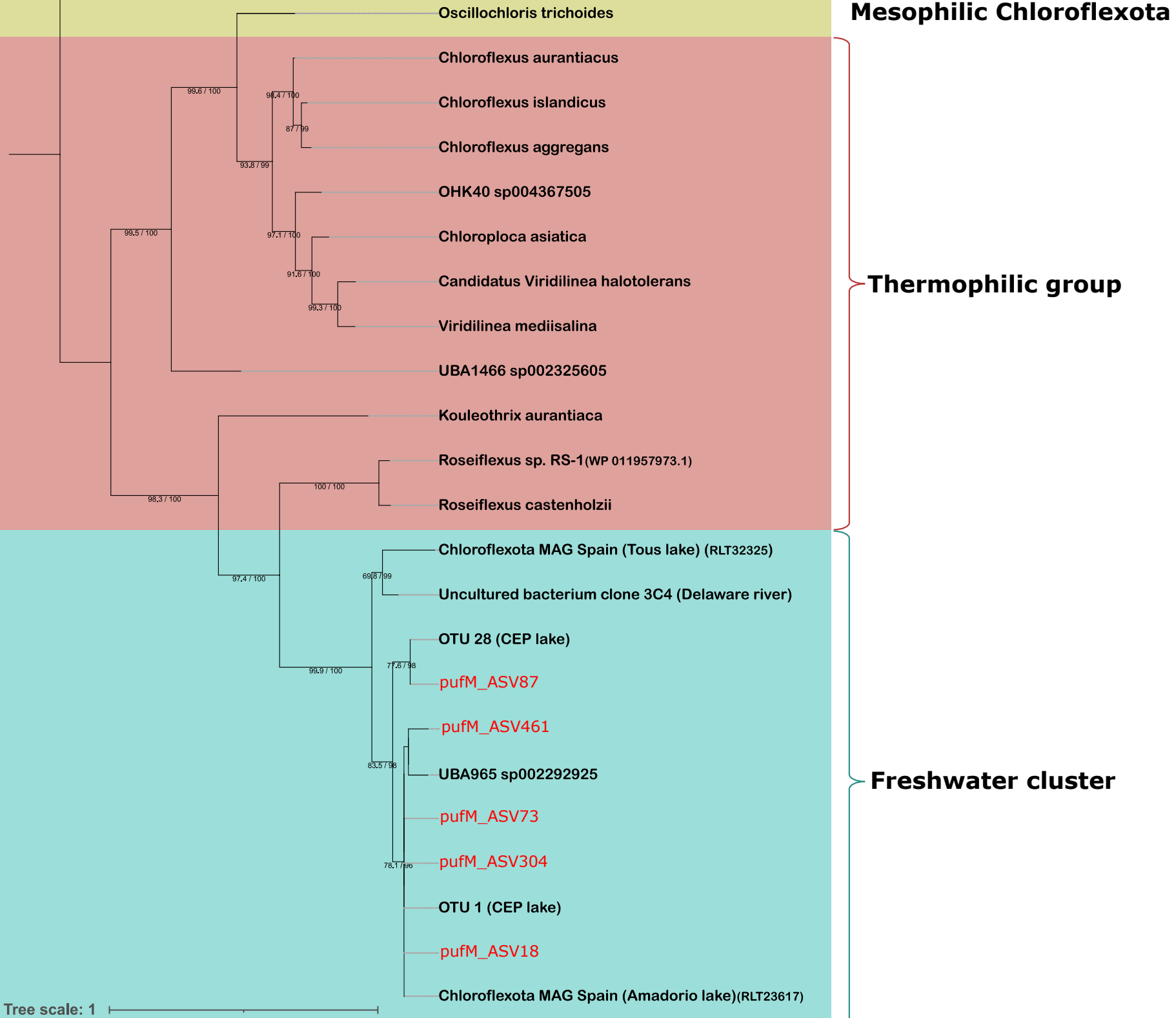
Chloroflexota and Eremiobacteriota

Proteobacteria

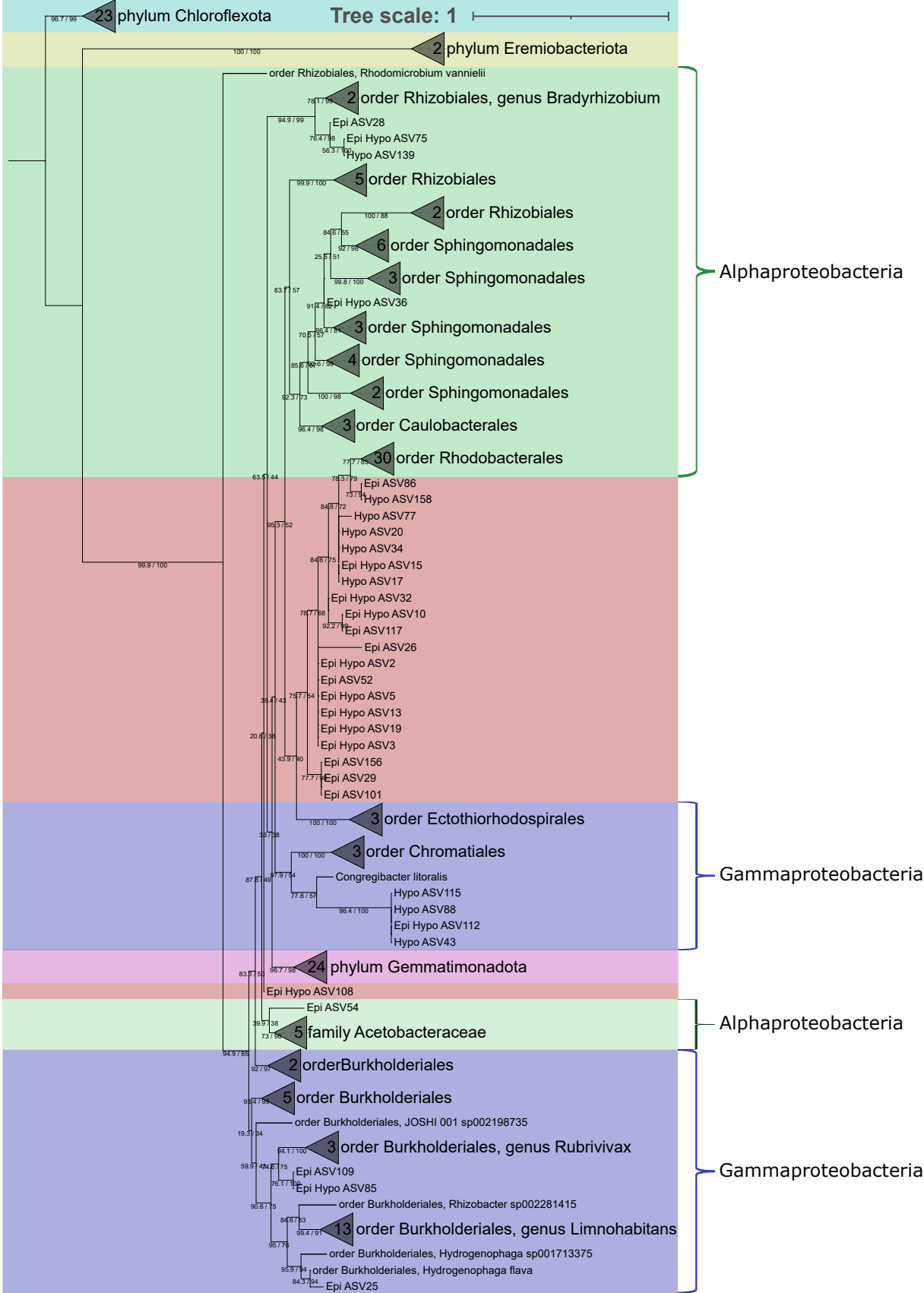


Supplementary Figure S4. Phylogenetic tree showing in detail Gemmatimonadota phylum sequences and unclassified ASVs that clustered inside.

Proteobacteria, Gemmatimonadota and Eremiobacteriota



Supplementary Figure S5. Details of Chloroflexota sequences distribution in the pufM protein Maximum Likelihood phylogenetic tree computed using LG+F+I+G4 substitution model. The analysis involved pufM amino acid sequences of the reference sequences from Proteobacteria, Chloroflexota, Gemmatimonadota and Eremiobacteriota and the targeted unclassified ASVs.



Supplementary Figure S6. Phylogenetic tree showing in detail Proteobacteria phylum sequences and unclassified ASVs that clustered inside.