

Fig. S1. Phylogenomics of Cyanobacteria phyla. The maximum likelihood phylogenetic tree was estimated on 31 universal single-copy genes from 650 genomes implementing IQ-TREE under LG + Γ model. The names of 163 genomes reported in this study were highlighted in green color. Colored circles at tips of branches reflect ecological habitats of strains. Light blue circles on internal branches indicate nodes with bootstrap support lower than 70%. Color codes were assigned to order groups. The known oxygenic cyanobacteria group was labelled as Oxyphotobacteria. Monophyletic taxonomic groups were also labelled for clarity.