

Supplementary material

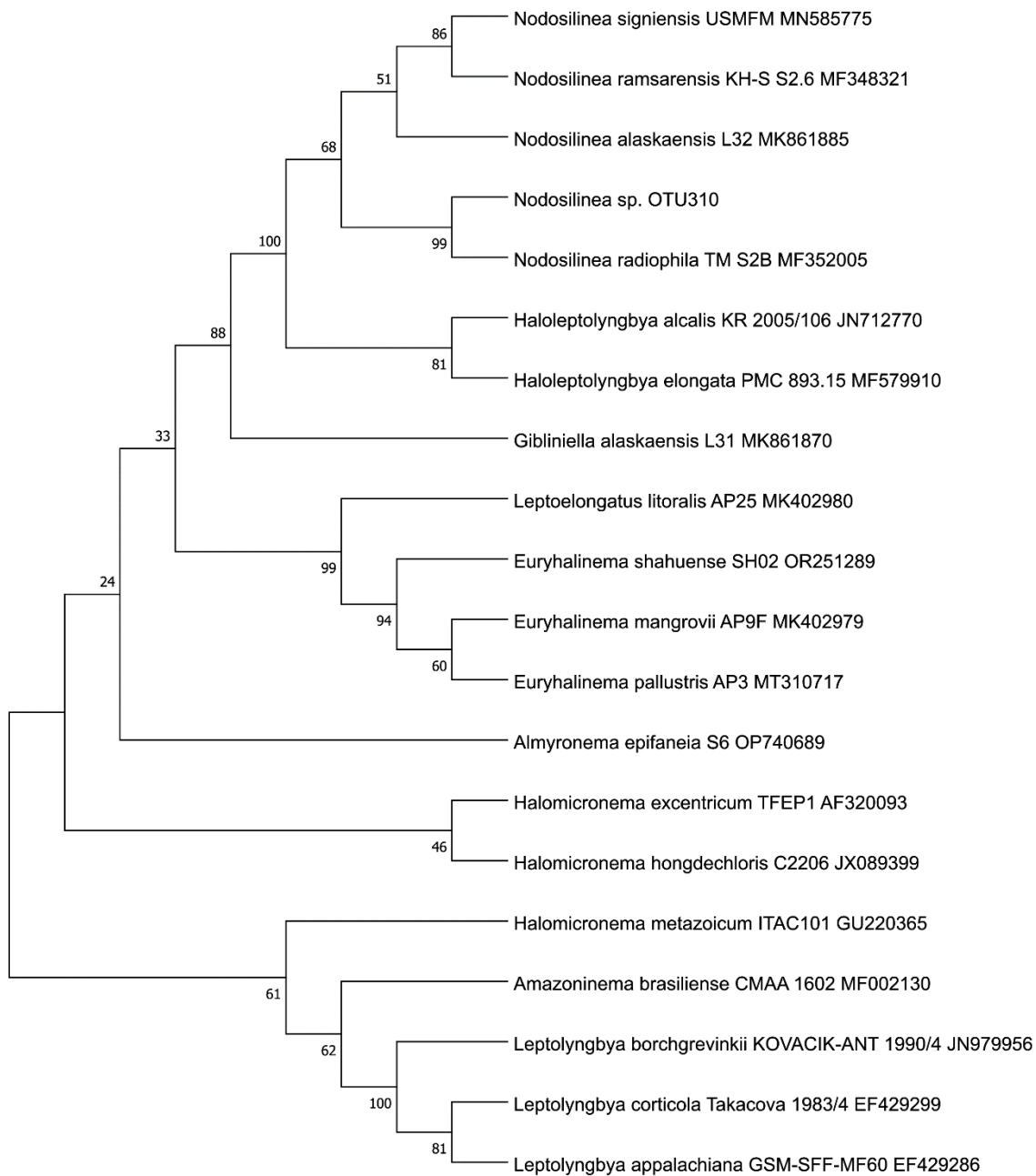


Figure S1. Neighbor-Joining tree based on partial 16S rRNA genes sequences showing the phylogenetic position of the cyanobacterial contaminant OTU310-ES1 among strains from the LPSN database.

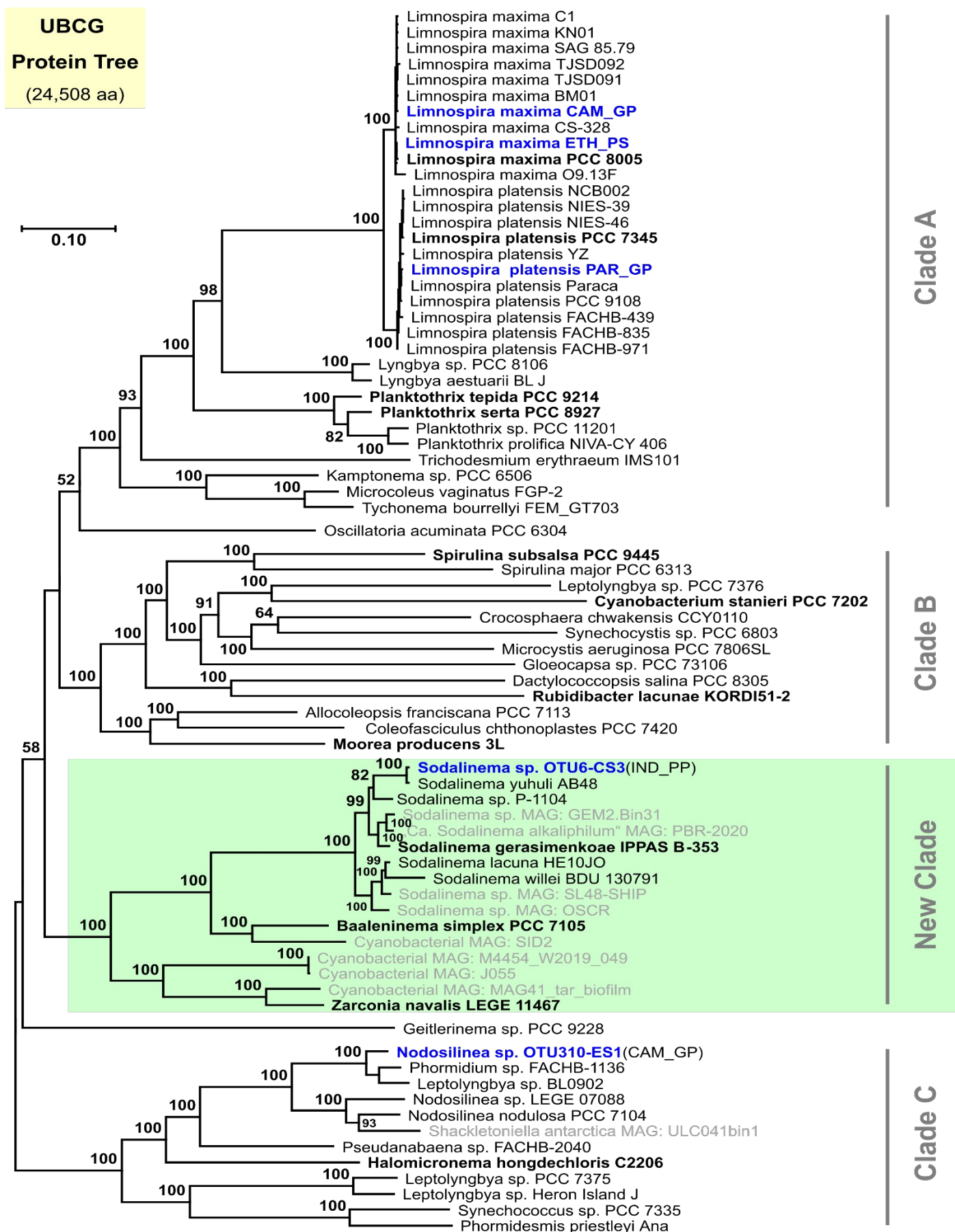


Figure S2: Evolutionary position of the genus *Sodalinema*. Phylogenomic maximum likelihood tree of five cyanobacterial MAGs from the cyanosphere of four spirulina cultures (ETH_PS, CAM_GP, PAR_GP, IND_PP) and 70 reference genomes. The RaxML tree was constructed from 24,508 variable amino acid positions based on a protein alignment of 92 housekeeping genes under the GTR4G model. Bootstrap values are shown at the nodes. Spirulina MAGs are highlighted in blue and bold, type strains are shown in black and bold. Cyanobacterial clades were designated in accordance with Shih et al. 2013; a new clade comprising the taxa *Sodalinema*, *Baaleninema* and *Zarconia* is highlighted with a green box. Accession numbers of all genomes are provided in Table S1.

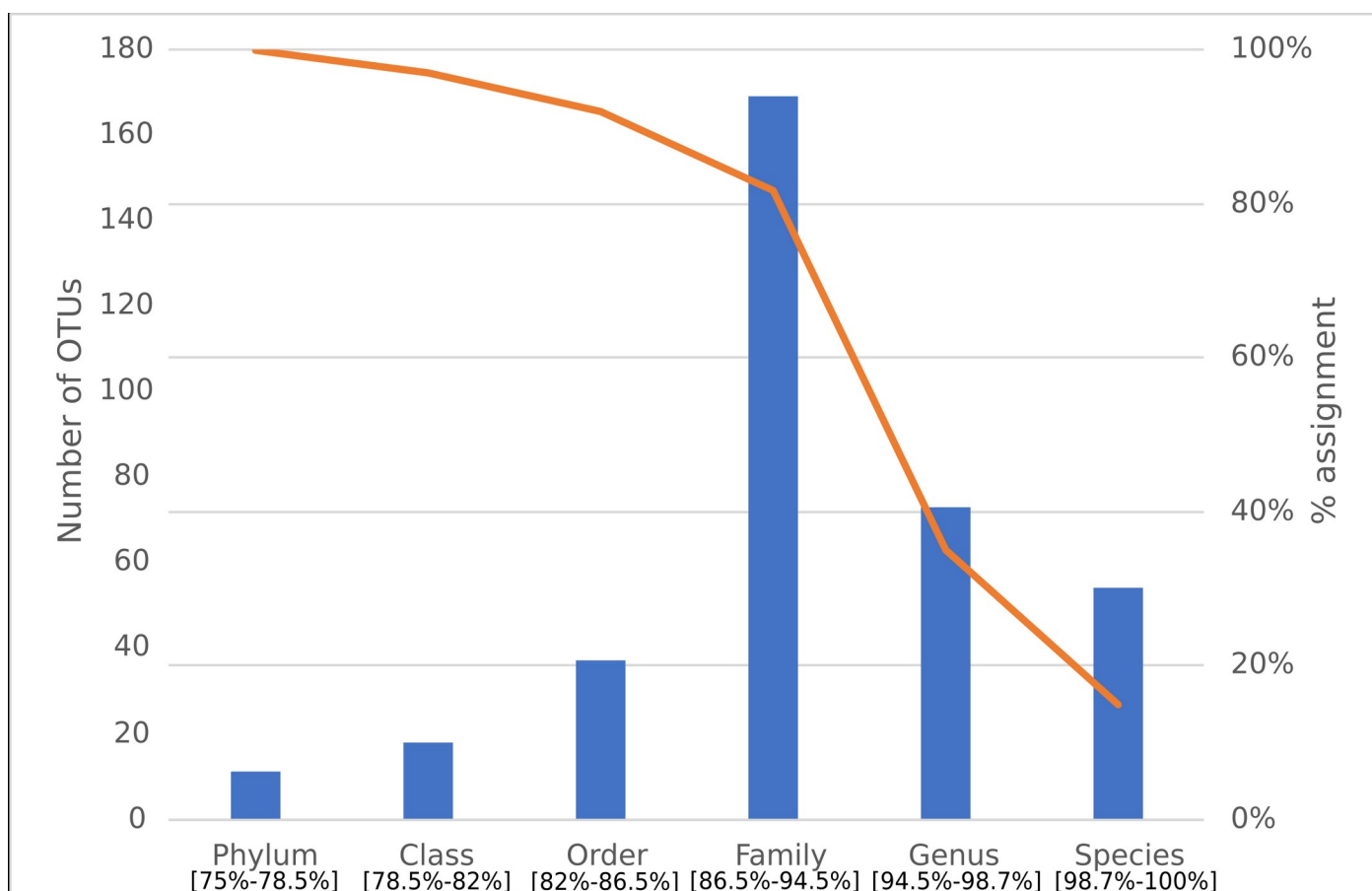


Figure S3. Classification of heterotroph OTUs according to 16S rRNA gene reference sequences from type strains. The histogram shows the distribution of the number of OTUs by 16S rRNA identity range. Numbers in brackets represent 16S rRNA identity thresholds for each taxonomic level. The curve shows the decreasing cumulative percentage of OTUs classified on more specific taxonomic levels.

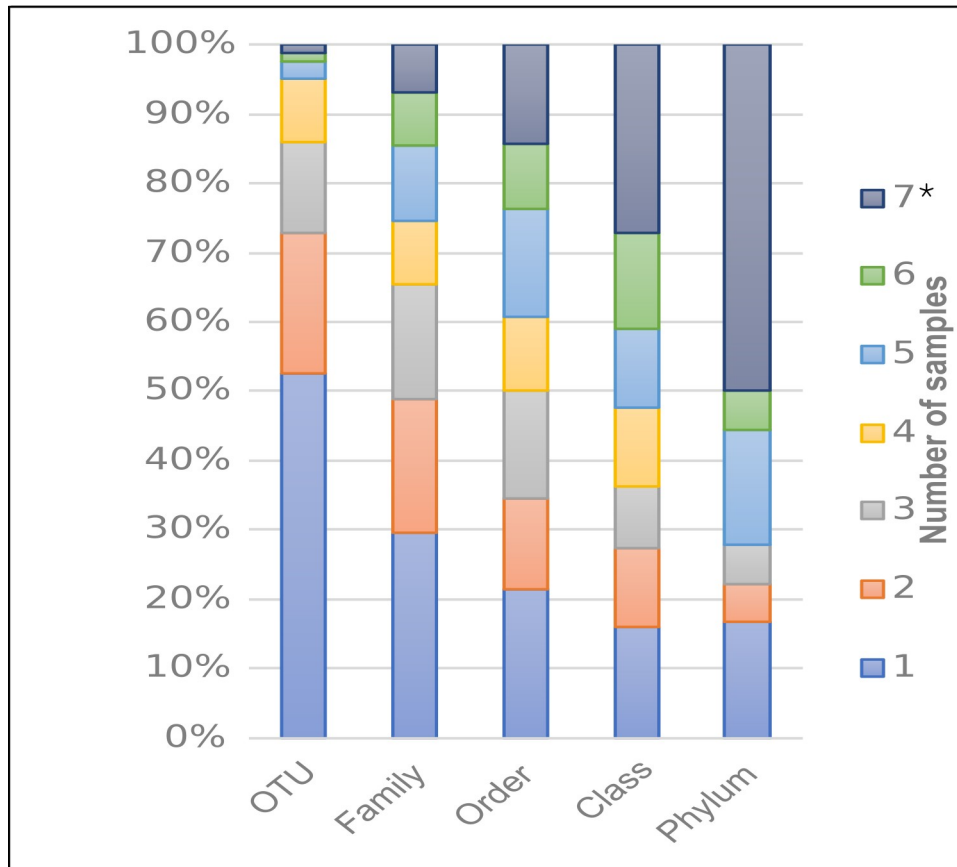


Figure S4. Proportion of unique (1x) and shared (2x - 7x) OTUs from seven spirulina samples based on the taxonomic resolution of OTUs, families, orders, classes and phyla.

* All the samples.