Fig. S1. Flow cytometry cytograms illustrating the identification of the picophytoplankton groups PE-rich *Synechococcus* (red) and photosynthetic picoeukaryotes (PPE; green). (A) Red fluorescence (FL3) versus Forward Scatter (FSC), (B) Orange fluorescence (FL2) versus FL3.
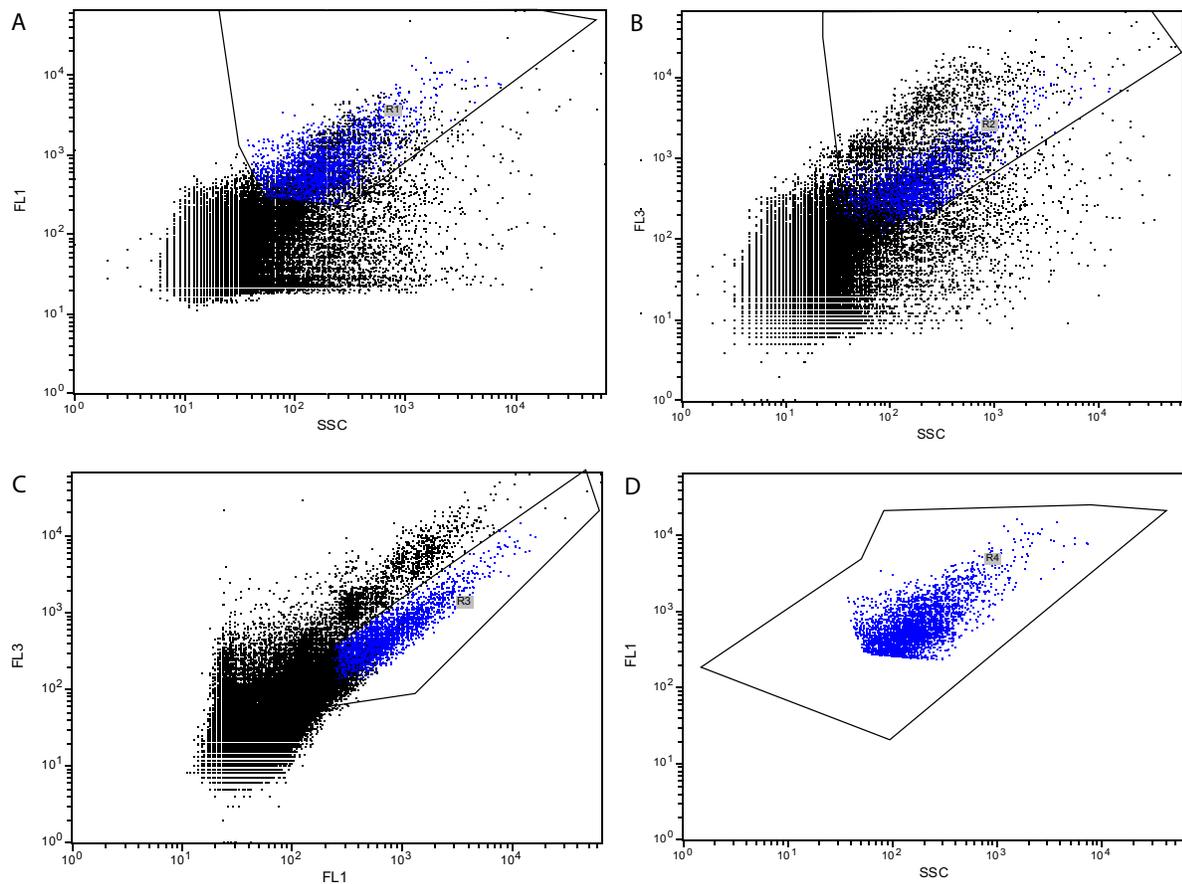
Fig. S2. Flow cytometry cytograms illustrating the identification of heterotrophic nanoflagellates (blue). (A) Side scatter (SSC) versus green fluorescence (FL1) showing all organisms stained by SyberGreen I and the establishment of R1. (B) Representation of intermediate plot of red fluorescence (FL3) versus SSC and R2. (C) FL3 versus FL1 allowing for discrimination of non-autotrophic cells (R3). (D) The heterotrophic nanoflagellates (R4) in FL1 versus SSC.
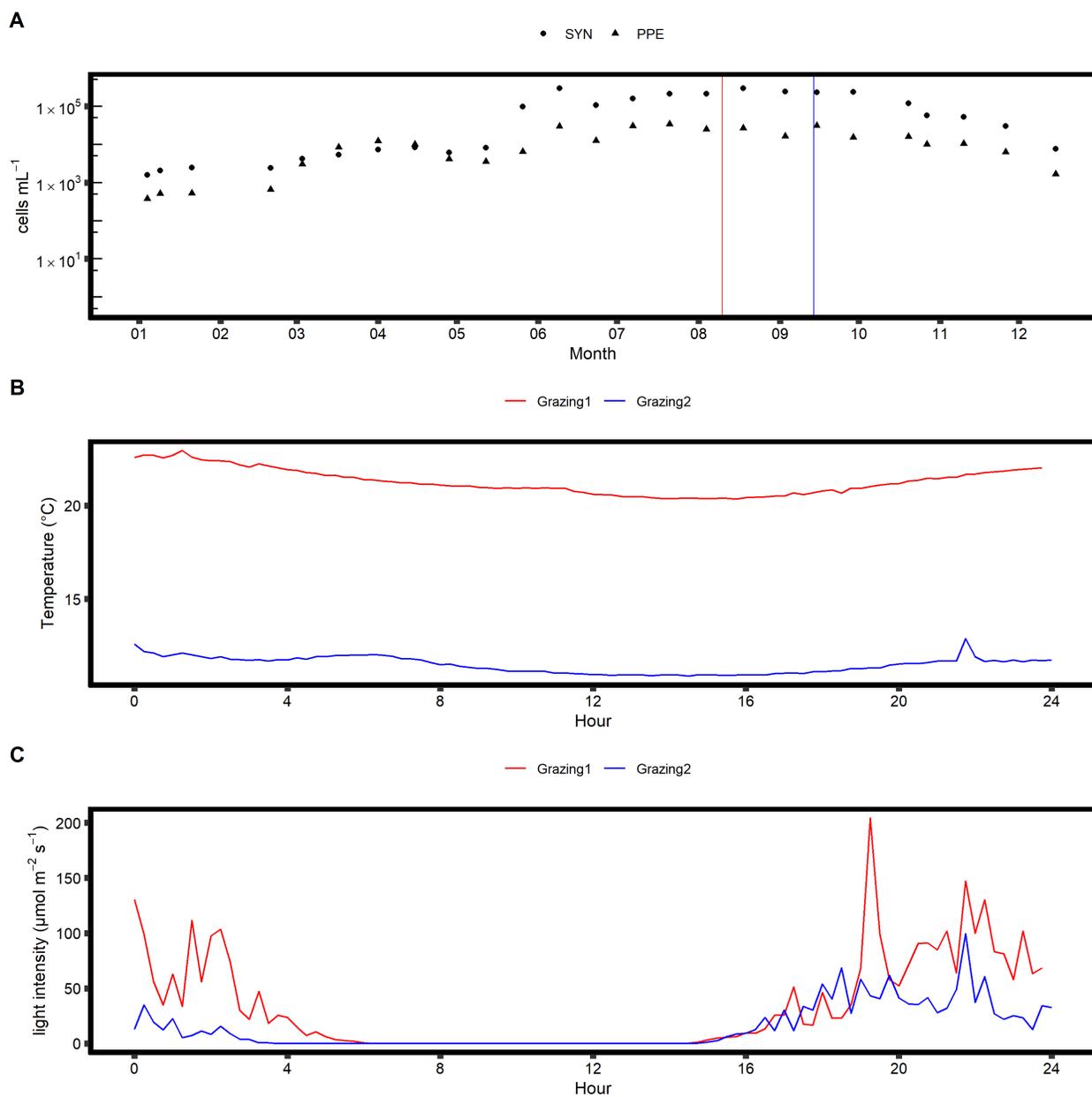
Fig. S3. (A) SYN and PPE cell abundance (cells mL^{-1}) in logarithmic scale at the Linnaeus Microbial Observatory (LMO) during 2020. Experimental dates for Grazing1 (in August) and Grazing2 (in September) are marked with vertical lines. (B) Temperature (°C) during the experiments. (C) Light intensity (μmol m^{-2} s^{-1}) during the experiments.
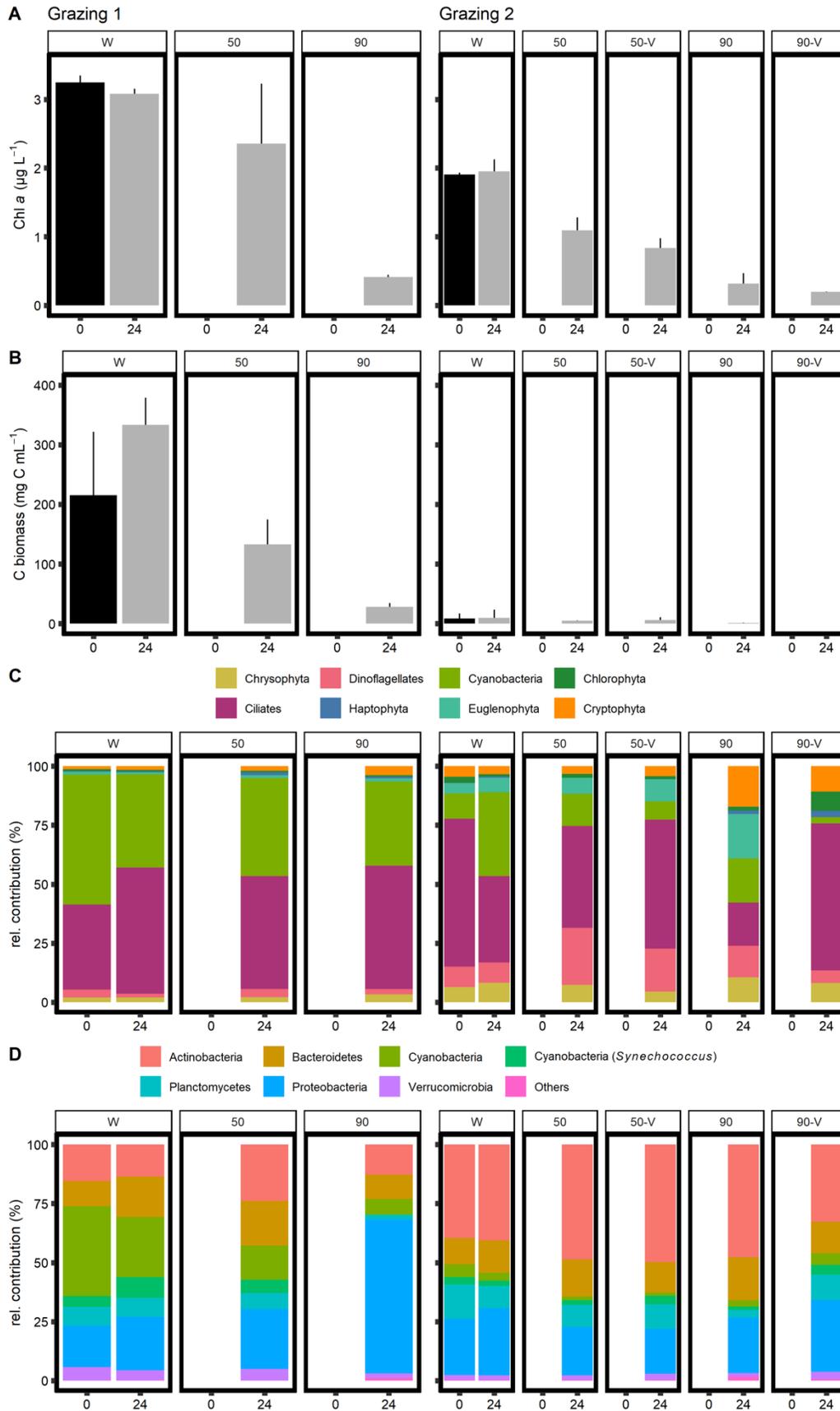
Fig. S4. Biomass and community composition for Grazing1 (left) and Grazing2 (right) at the initial time point (0) and after *in situ* incubation (24). Treatments consisted of a seawater control treatment (W), and seawater diluted to 50% (50) and 90% (90) with grazer free water in Grazing1 and Grazing2. Additionally, Grazing2 presented an extra set of dilutions to 50% (50-V) and 90% (90-V) with virus free water. (A) Chl *a* (μg L^{-1}); mean values±SD (B) Total phytoplankton (>5 μm diameter) carbon biomass (mg C mL^{-1}); mean values±SD, (C) relative contribution of phytoplankton (>5 μm diameter) estimated from microscopy counts shown on phylum level and (D) Bacterial community composition on phylum level as assessed by 16S rRNA gene sequencing. The relative contribution of *Synechococcus* sequences is specified (green).

A

B
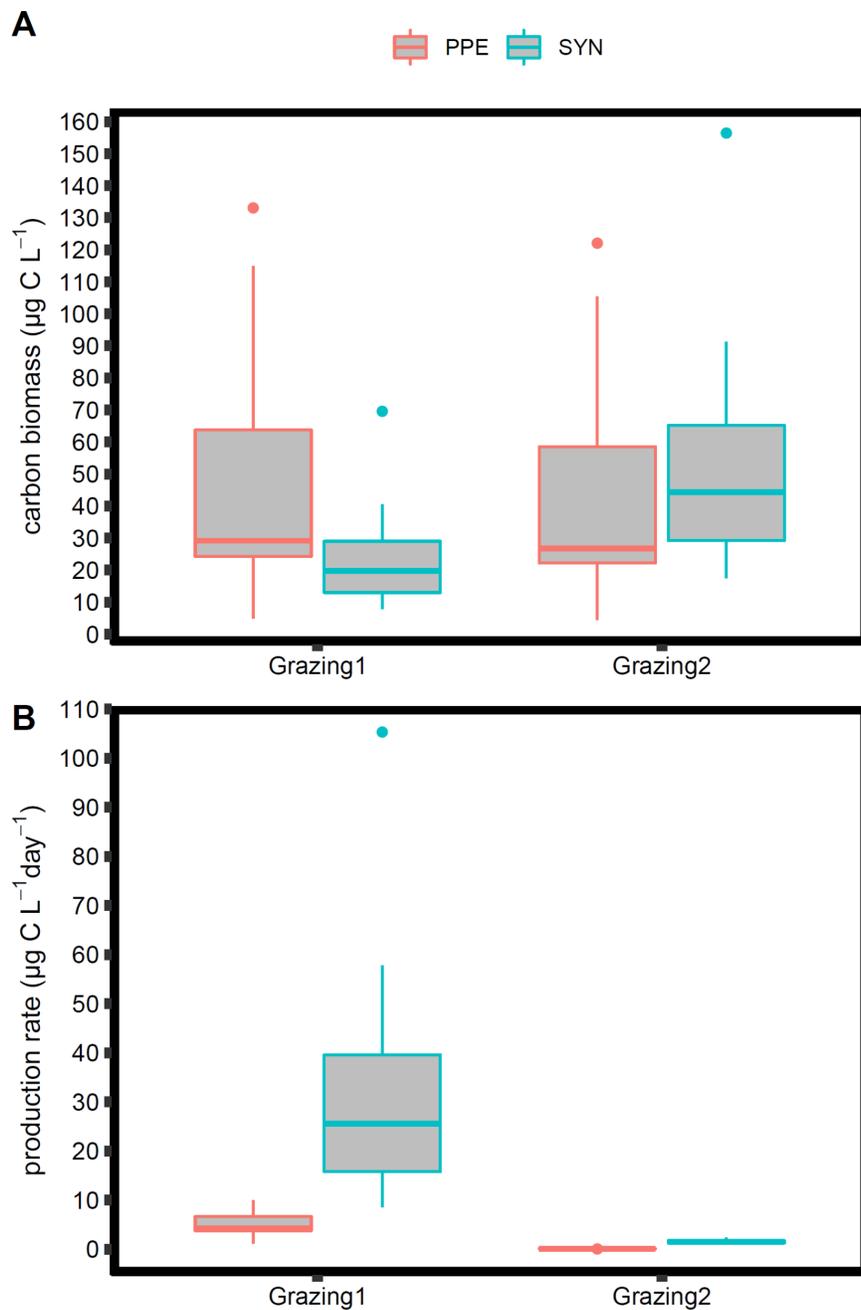
Fig. S5. Picocyanobacteria (SYN) and photosynthetic picoeukaryote (PPE) (A) starting carbon biomass (µg C L^{-1}) and (B) production rates (µg C L^{-1} day^{-1}). Rates were calculated based on all the *C* values available for SYN and PPE from a literature compilation of conversion factors (Alegria Zufia et al., 2021). Boxplots represent median, 25 to 75% interquartile range and non-outlier range; points beyond are outliers.
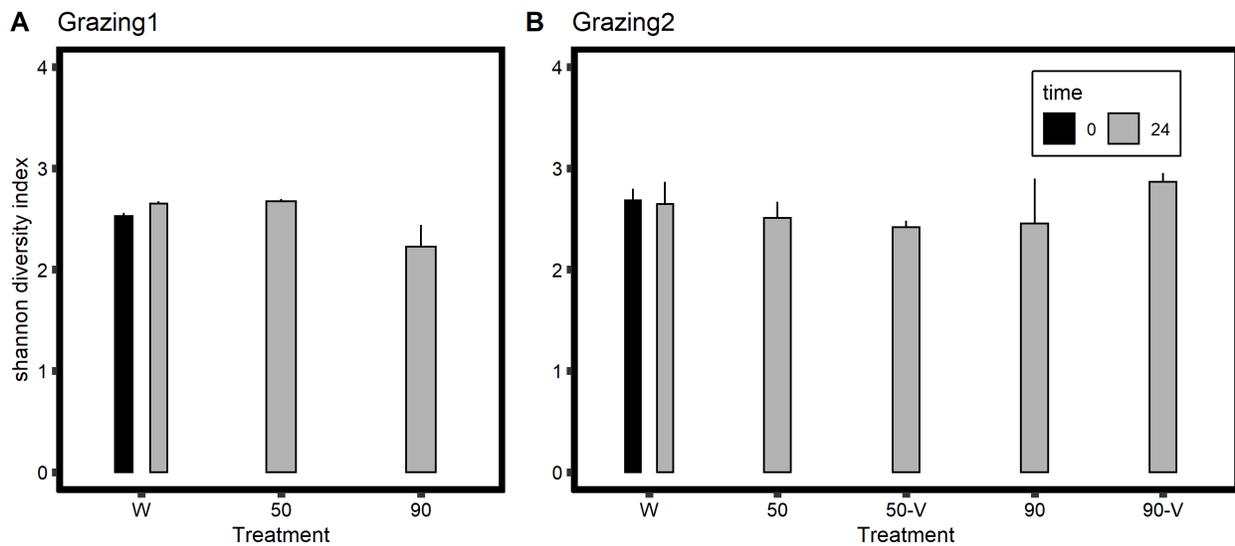
Fig. S6. Shannon biodiversity index for Grazing1 (A) and Grazing2 (B) at the initial time point (0) and after *in situ* incubation (24). Treatments consisted on a non-filtered seawater control treatment (W), and seawater diluted to 50% (50) and 90% (90) with grazers free water in Grazing1 and Grazing2. Additionally, Grazing2 presented an extra set of dilutions to 50% (50-V) and 90% (90-V) with grazers and virus-free water. All values expressed as mean values±SD.
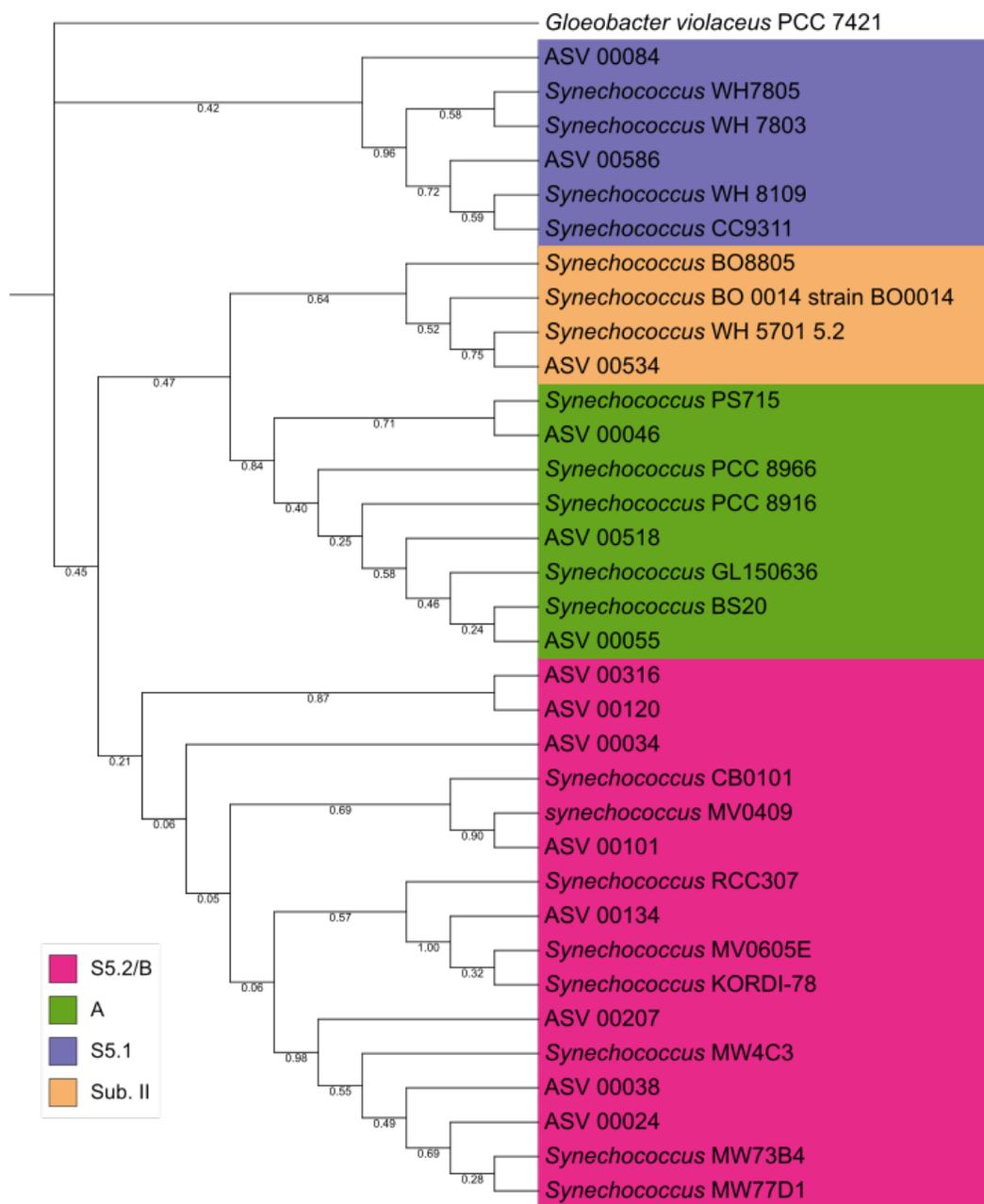
Fig. S7. ML phylogenetic tree following the GTamura-Nei model of V3-V4 rRNA sequences from unicellular picocyanobacteria (1000 bootstraps). Picocyanobacterial (SYN) amplicon sequence variants (ASVs) included in the figure represented >1% of the total bacterial abundance in at least one sample. Phylogenetic SYN clades were identified using references from Huber et al., (2019). *Gloeobacter violaceus* PCC 7421 (NR 074282.1) was used as outgroup.

Table S1. Number of sequences for each sample after each step of the quality control pipeline.

Sample ID	Raw sequences	Filtered sequences	Denoised sequences (%)	Denoised sequences	Merged sequences	Non-chimeric sequences	SYN	PPE
WA-T0-Grazing1	206661	193217	93.49	183360	154212	76877	2682	3051
WB-T0-Grazing1	140767	130856	92.96	119397	89470	32396	1566	717
WC-T0-Grazing1	214336	200299	93.45	189500	158688	77720	4058	3143
WA-T24-Grazing1	158612	147871	93.23	139754	116279	74576	7131	1213
WB-T24-Grazing1	173259	161993	93.5	150486	112316	48783	3998	419
WC-T24-Grazing1	215188	200863	93.34	187716	143221	61784	4951	957
50A-T24-Grazing1	136281	126840	93.07	118504	91399	46043	2273	475
50C-T24-Grazing1	115290	107193	92.98	99083	72324	31728	2028	202
90A-T24-Grazing1	168159	156663	93.16	149244	113964	46947	632	1008
90B-T24-Grazing1	203376	190475	93.66	182469	142786	53670	269	1110
90C-T24-Grazing1	200052	186971	93.46	178377	139386	57388	579	1179
WA-T0-V-Grazing2	140103	130570	93.2	122354	98500	39226	1389	1375
WB-T0-V-Grazing2	142829	132239	92.59	123347	95802	44573	1635	1313
WC-T0-V-Grazing2	118611	110696	93.33	101721	77427	34736	729	1643
WA-T24-V-Grazing2	119192	111173	93.27	103877	81689	25928	443	450
WB-T24-V-Grazing2	172015	160689	93.42	152134	124199	57482	1224	1650
WC-T24-V-Grazing2	134532	124961	92.89	112349	75853	24275	774	300
50A-T24-G-Grazing2	137409	128517	93.53	119531	89562	29367	528	479
50C-T24-G-Grazing2	148867	139316	93.58	131501	105101	37180	885	121
50A-T24-V-Grazing2	160386	149780	93.39	141346	115632	45860	2029	576
50C-T24-V-Grazing2	147290	138046	93.72	130114	101385	33333	905	248
90A-T24-G-Grazing2	196580	183906	93.55	178240	158278	65447	363	773
90B-T24-G-Grazing2	165053	154589	93.66	146250	118543	42085	963	1028
90C-T24-G-Grazing2	252900	236526	93.53	225546	188365	87869	1488	2416
90A-T24-V-Grazing2	278717	259211	93	251049	221998	146013	9960	3109
90B-T24-V-Grazing2	247267	230887	93.38	219087	181302	92116	1251	5870
90C-T24-V-Grazing2	158798	148338	93.41	141012	116014	70018	2972	3207