Supplementary Material

Fig. S1:

Experimental setup: Primary production (PP) was measured at three different light scenarios (100%, 75%, and 50%). For PP, triplicate samples and one blank (dark) were incubated at each of the three light intensities. For bacterial production (BP), triplicate samples and one blank were incubated in the dark. Two identical setups were established at two different temperatures (Δ0°C and Δ+6°C).

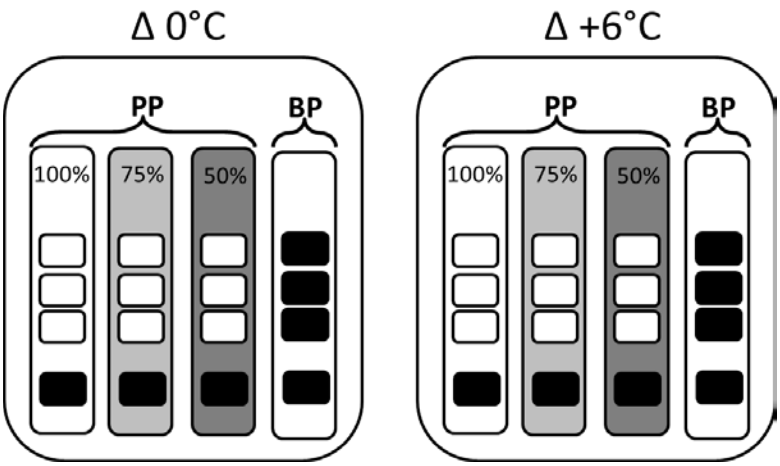

Fig. S2:

Bacterial α-diversity expressed as the number of OTUs and the Shannon index of the bacterial communities at all stations.

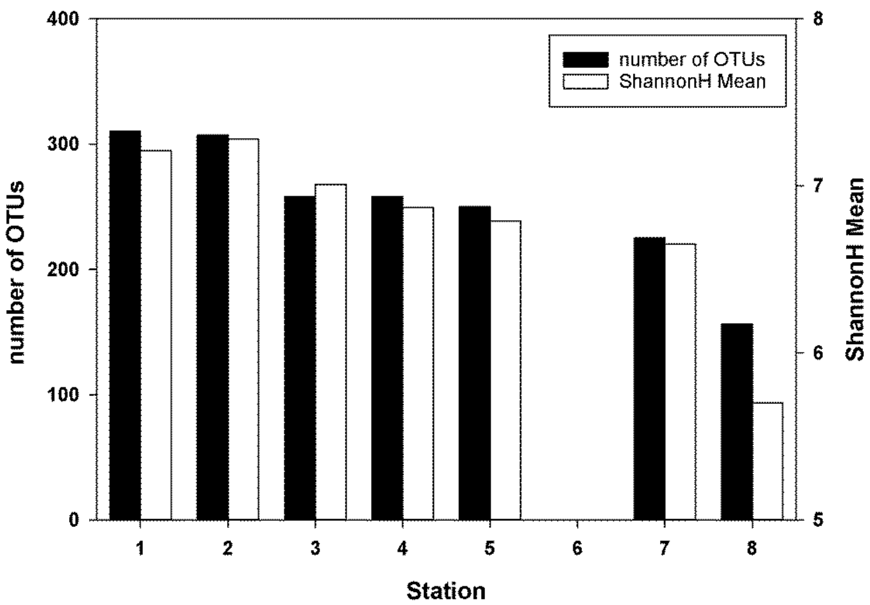

Fig. S3:

Primary production (PP), measured at different light intensities (50, 75, 100%) at the stations 1 to 8, and in the incubations at in situ temperature (Δ0°C) and with a warming of Δ6°C.

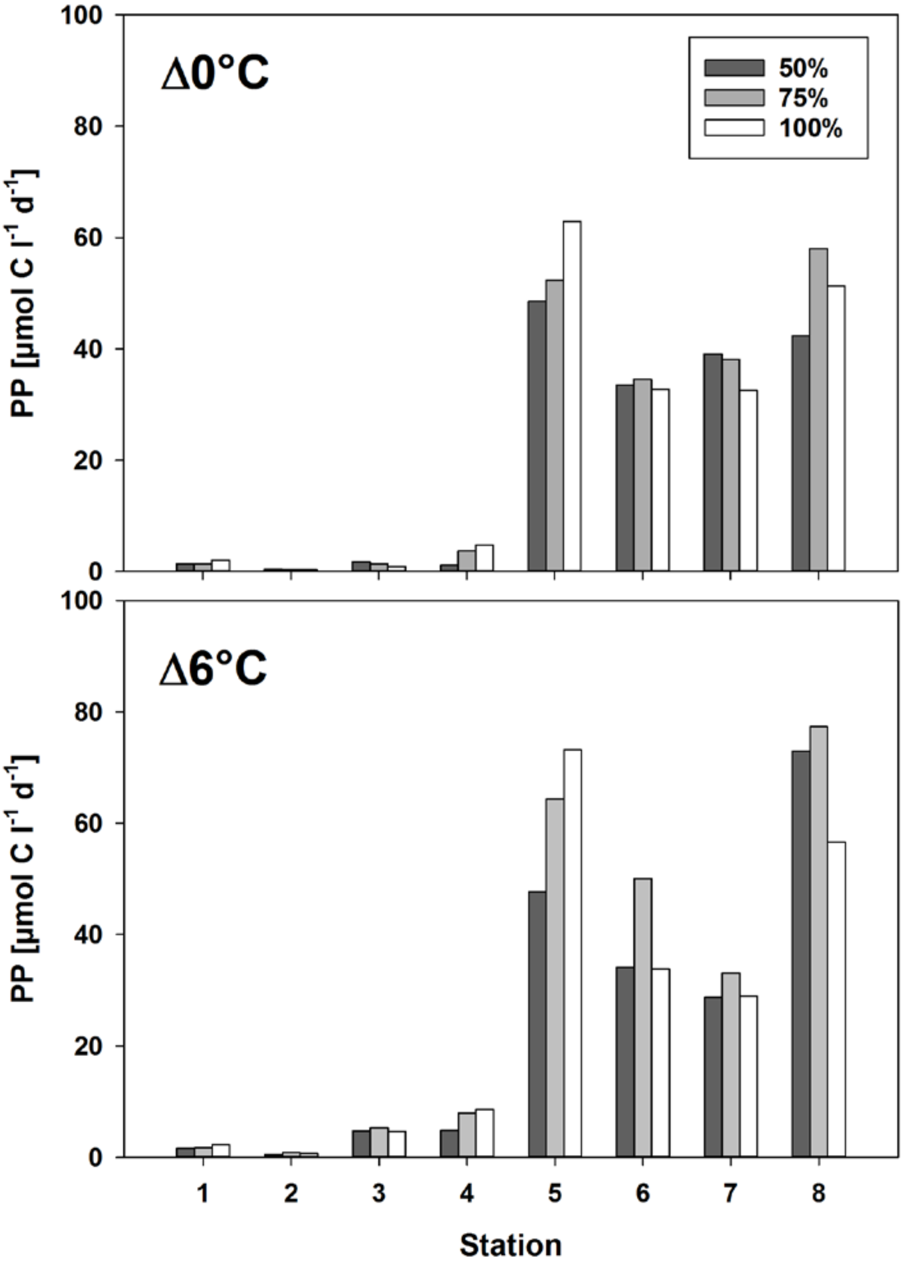

Table S1: Overview of the phylogenetic affiliation of 16S rRNA gene sequences, including the closest cultured relatives and their relative abundance (%), at the respecitve stations.

OTU	St. 1	St. 2	St. 3	St. 4	St. 5	St. 7	St. 8	Class/phyla	Closest cultured relative	Similarity%
OTU99_000009	0	1.32	0	0	1.29	2.06	0.47	*Actinobacteria*	*Actinobacterium* SCGC AAA043-M07	99
OTU99_000043	0.21	1.62	0	0.47	2.21	0.38	3.38	*Actinobacteria*	*Bacterium* HTCC4091	98
OTU99_000036	4.34	0.88	0	0.47	0.37	0	0	*Actinobacteria*	*Actinobacterium* SCGC AAA208-D13	95
OTU99_000110	0	0	0	0	0.46	0	4.38	*Actinobacteria*	*Candidatus* Aquiluna rubra	99
OTU99_000221	0	0.73	0.45	0.76	0.55	2.13	0.24	*Actinobacteria*	*Actinobacterium* SCGC AAA043-L13	94
OTU99_000187	3.49	1.54	0	0	0	0	0	*Actinobacteria*	*Actinobacterium* SCGC AAA278-P20	94
OTU99_000056	0	0	0	0	0	5.03	0.95	*Bacteroidetes*	*Bacterium* DG1021	95
OTU99_000012	0.71	0.88	0	0.38	1.48	0.91	16.77	*Bacteroidetes*	*Flavobacteria bacterium* Yb008	99
OTU99_000157	0	0	0	0	0	0	3.32	*Bacteroidetes*	*Bacteroidetes bacterium* SCGC AAA160-E08	99
OTU99_000031	0.78	2.13	1.36	1.70	2.77	2.97	2.90	*Bacteroidetes*	*Flavobacteriaceae bacterium* LE20	97
OTU99_000059	0.07	0	1.43	1.61	3.04	3.66	1.01	*Bacteroidetes*	*Lacinutrix* sp. KLE1229	99
OTU99_000054	0.21	1.76	0	0.57	1.11	0.61	0.59	*Bacteroidetes*	*Bacteroidetes bacterium* SCGC AAA160-F08	90
OTU99_000079	0.43	2.57	1.74	0.95	0.09	0	0	*Chloroflexi*	*Litorilinea aerophila* strain PRI-4131	91
OTU99_000013	0.85	0.73	5.13	7.56	0	0	0	*Cyanobacteria*	*Synechococcus* sp. MW73B4	99
OTU99_000057	1.14	0.29	1.74	1.80	0	0	0	*Cyanobacteria*	*Synechococcus* sp. MV1218D	100
OTU99_000076	0	0	0	0	4.15	5.26	0	*Cyanobacteria*	*Synechococcus rubescens* strain SAG 3.81	99
OTU99_000064	0.64	1.40	0.45	2.74	8.39	0	0	*Cyanobacteria*	*Aphanizomenon flos-aquae* CH-1	100
OTU99_000133	0	0.73	2.11	0.66	0.83	0.38	0	*Planctomycetes*	*Planctomycete* MS3054	87
OTU99_000016	4.06	5.95	3.70	3.59	4.80	4.72	4.44	*Alphaproteobacteria*	*Pseudorhodobacter ferrugineus* strain M63032	99
OTU99_000180	0	1.10	1.36	0	1.20	1.45	0	*Alphaproteobacteria*	*Roseovarius* sp. S708	99
OTU99_000071	0	0	0	0	0.09	0	5.04	*Alphaproteobacteria*	*Alpha proteobacterium* SF44	99
OTU99_000014	6.13	5.00	3.40	3.69	1.66	1.75	1.24	*Alphaproteobacteria*	*Pelagibacterales bacterium* LSUCC0261	99
OTU99_000027	0	0	0	3.69	2.03	1.60	3.02	*Alphaproteobacteria*	*Candidatus* Pelagibacter sp. AAA795-O19	99
OTU99_000200	0.36	2.57	2.72	0.76	0	0	0	*Alphaproteobacteria*	*Candidatus* Pelagibacter sp. AAA795-O20	99
OTU99_000156	3.42	1.98	1.36	2.93	0	0	0	*Alphaproteobacteria*	*Candidatus* Pelagibacter sp. AAA795-N17	99
OTU99_000363	0	0	0	0	0	0	3.32	*Gammaproteobacteria*	*Gamma proteobacterium* HTCC6124	99
OTU99_000019	1.57	1.76	0.60	0.85	1.29	0.46	4.80	unclassified	*Gamma proteobacterium* SCGC AAA158-L15	99
OTU99_000029	3.92	0.59	0.91	0	0.92	0.91	0.65	unclassified	*Actinobacterium* SCGC AAA278-P20	94
OTU99_000005	0	0	0	0	2.68	4.49	0	*Verrucomicrobia*	*Verrucomicrobia bacterium* SCGC AAA278-E15	98
OTU99_000101	0.21	0.81	4.60	4.54	0	0	0	*Verrucomicrobia*	*Verrucomicrobia bacterium* SCGC AAA278-E15	97

Table S2. Biomass of the phytoplankton taxa and ciliates at the different stations 1-8 (in µg C L^{-1}). No data were obtained for station 4.

Species name	***Phylum***	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
ciliate (mainly Lohmaniella)	Ciliophora	11.67	3.83	6.36		80.46	49.64	37.97	29.61
ciliate (mainly Mesodinium & Strombidium)	Ciliophora		1.63	2.93		2.21	2.26	1.57	1.55
Peridiniella catenata	Dinophyta	6.32	0.72	0.02		1.57	0.19		0.17
Scrippsiella sp.	Dinophyta	30.98	9.73	0.20		1.61	4.65	4.83	1.92
Aphanizomenon flos-aquae	Cyanobacteria	1.37	0.01						0.05
Skeletonema costatum	Heterokontophyta	0.44	0.13	0.07		12.54	127.21	76.25	321.64
Plagioselmis prolonga	Cryptophyta	0.14	0.12	0.23		0.12	0.25	0.42	0.15
Teleaulax ampioxeia	Cryptophyta		0.08	0.61		0.41	0.19	0.21	0.11
Heterocapsa rotundata	Dinophyta		0.13			1.19	1.13	3.41	1.26
Gyrodinium spirale	Dinophyta		0.09	0.05			0.09	0.19	0.28
Gymnodinium ostenfeldii	Dinophyta		0.03				0.05	0.06	0.22
Gymnodinium (probably simplex)	Dinophyta		0.43	0.20		0.76	1.01	0.41	
Gymnodinium sp.	Dinophyta			0.77		1.90		8.75	2.98
Gymnodinium sp.	Dinophyta							10.80	6.57
Ceratium tripos	Dinophyta			0.12					
Ebria tripartita	Protozoa incertae sedis			2.79					
Dinobryon sp.	Heterokontophyta			0.00					0.00
Pyramimonas sp.	Chlorophyta					0.83	0.72	5.16	0.80
Eutreptiella gymnastica	Euglenophyta					0.36		0.31	0.02
Thalassiosira rotula	Heterokontophyta						2.35	0.48	1.91
Chaetoceros spp.	Heterokontophyta						1.60	6.86	6.11
Chrysochromulina sp.	Haptophyta						4.44	6.93	
Tetraselmis sp.	Chlorophyta						2.76	5.21	
Rhizosolenia setigera	Heterokontophyta								1.09
Protoperidinium sp.	Dinophyta								0.46
Thalassionema nitzschioides	Heterokontophyta								0.14
Prymnesium parvum	Haptophyta						2.61		1.00
Ochromonas sp.	Heterokontophyta								0.08