Analysis of the influence of seasonal water column dynamics on the relationship between marine viruses and microbial food web components using an artificial neural network

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Table S1. Geographical location data and sampling depth at the sampled station

Station	**CJ011**
Geographical location	42°22'0"N; 16°13'12"E
Sampling months	3, 4, 5, 6, 8, 10, 11
Sampling depths (m)	0, 5, 10, 20, 50, 100

Table S2. Spearman's R-rank values from the relationship analysis between virus-like particles (VLPs) and the biotic and abiotic variables observed in this study at CJ011. Statistically significant values are shown in red. Abbreviations of biotic parameters: HB – heterotrophic bacteria, BP – bacterial production, HNF – heterotrophic nanoflagellates, HNA – High Nucleic Acid heterotrophic bacterial group, LNA – Low Nucleic Acid heterotrophic bacterial group, PRO – *Prochlorococcus*, SYN – *Synechococcus*, PE – picoeukaryotes, CHL *a* – Chlorophyll *a*).

n=42	VLP	HB	BP	HNF	HNA	LNA	Pro	Sin	PE	CHL *a*
VLP	1.00	0.12	0.30	**0.36**	0.05	0.16	**-0.42**	0.26	0.11	-0.22
HB	0.12	1.00	0.24	**0.45**	**0.81**	**0.88**	**0.39**	0.02	**0.54**	**0.38**
BP	0.30	0.24	1.00	0.14	0.21	0.17	-0.07	-0.07	0.20	0.09
HNF	**0.36**	**0.45**	0.14	1.00	**0.53**	**0.38**	0.30	0.13	**0.79**	**0.36**
HNA	0.05	**0.81**	0.21	**0.53**	1.00	**0.52**	**0.54**	0.13	**0.67**	**0.52**
LNA	0.16	**0.88**	0.17	**0.38**	**0.52**	1.00	0.13	-0.14	**0.40**	0.25
Pro	**-0.42**	**0.39**	-0.07	0.30	**0.54**	0.13	1.00	0.25	**0.49**	**0.38**
Sin	0.26	0.02	-0.07	0.13	0.13	-0.14	0.25	1.00	0.16	-0.08
PE	0.11	**0.54**	0.20	**0.79**	**0.67**	**0.40**	**0.49**	0.16	1.00	**0.44**
CHL *a*	-0.22	**0.38**	0.09	**0.36**	**0.52**	0.25	**0.38**	-0.08	**0.44**	1.00
T	**0.58**	0.10	0.28	**0.36**	0.02	0.18	**-0.32**	0.20	**0.31**	**-0.34**
S	**-0.56**	-0.04	**-0.35**	-0.29	-0.01	0.00	0.13	-0.22	-0.15	**0.42**
O_2	-0.23	0.30	0.27	0.24	**0.35**	0.21	**0.31**	-0.15	**0.42**	0.26
pH	**0.45**	0.09	0.21	0.24	-0.03	0.26	**-0.48**	-0.17	0.22	-0.28
NO_3	-0.02	**-0.41**	-0.28	-0.17	**-0.41**	**-0.41**	-0.14	0.08	**-0.47**	-0.13
NO_2	**-0.44**	0.09	**-0.39**	0.03	0.25	-0.19	**0.58**	0.22	0.05	**0.34**
NH_4	-0.30	-0.11	**-0.41**	0.16	0.04	-0.22	**0.38**	**0.36**	0.26	0.08
PO_4	0.09	0.02	-0.05	0.12	-0.08	0.06	0.06	-0.14	0.01	-0.07
SiO_4	**-0.44**	-0.28	-0.11	-0.21	-0.21	-0.19	-0.01	-0.26	-0.24	0.21
NO_3/NH_4	0.15	-0.21	0.14	-0.24	**-0.32**	-0.13	**-0.36**	-0.23	**-0.52**	-0.19

Table S3. The biomass of MFW components with a percentage of biomass in parenthesis for the studied area and each BMU. The last column shows the change in biomass with respect to the change in MWC and SWC periods.

MFW components	CJ011	BMU1	BMU2	BMU3	BMU4	biomass change (%)
HB (µg C L^{-1} L^{-1})	6.77 (56.91)	5.87 (63.58)	7.76 (49.94)	7.3 (58.43)	5.75 (56.13)	-15.68
PE (µg C L^{-1} L^{-1})	3.18 (26.73)	1.93 (20.87)	4.5 (28.95)	3.48 (27.87)	2.94 (28.72)	13.72
HNF (µg C L^{-1} L^{-1})	0.81 (6.8)	0.61 (6.65)	1.32 (8.48)	0.65 (5.24)	0.82 (8.03)	29.67
SYN (µg C L^{-1} L^{-1})	0.66 (5.59)	0.41 (4.48)	1.3 (8.38)	0.62 (4.93)	0.33 (3.27)	25.37
VLP (µg C L^{-1} L^{-1})	0.37 (3.1)	0.28 (3.06)	0.54 (3.5)	0.34 (2.68)	0.36 (3.54)	19.15
PRO (µg C L^{-1} L^{-1})	0.1 (0.87)	0.13 (1.36)	0.12 (0.75)	0.11 (0.86)	0.03 (0.31)	-85.60

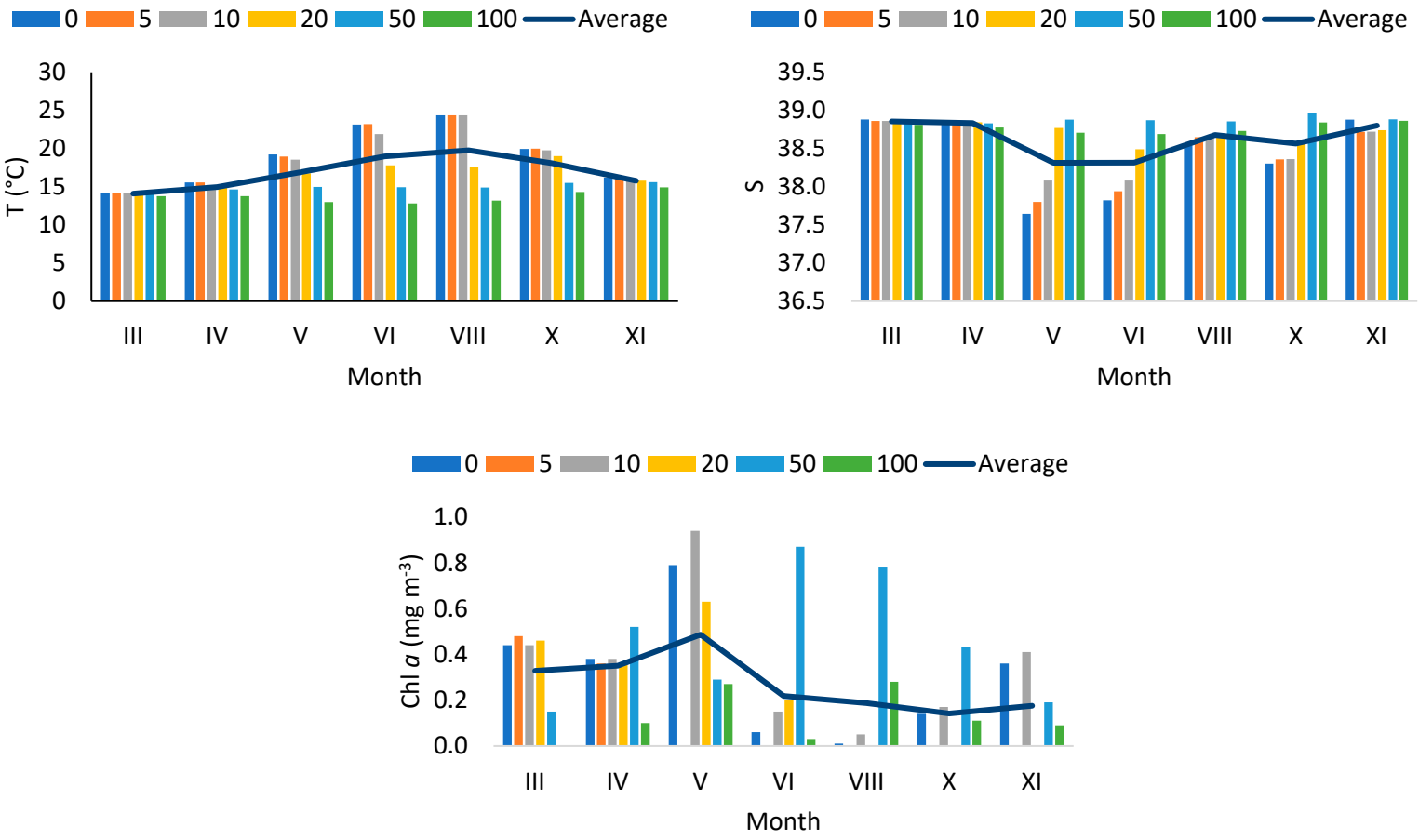

Figure S1. Monthly values of temperature (T), salinity (S), and chlorophyl a concentration (Chl a) with the average value at the sampled depths.

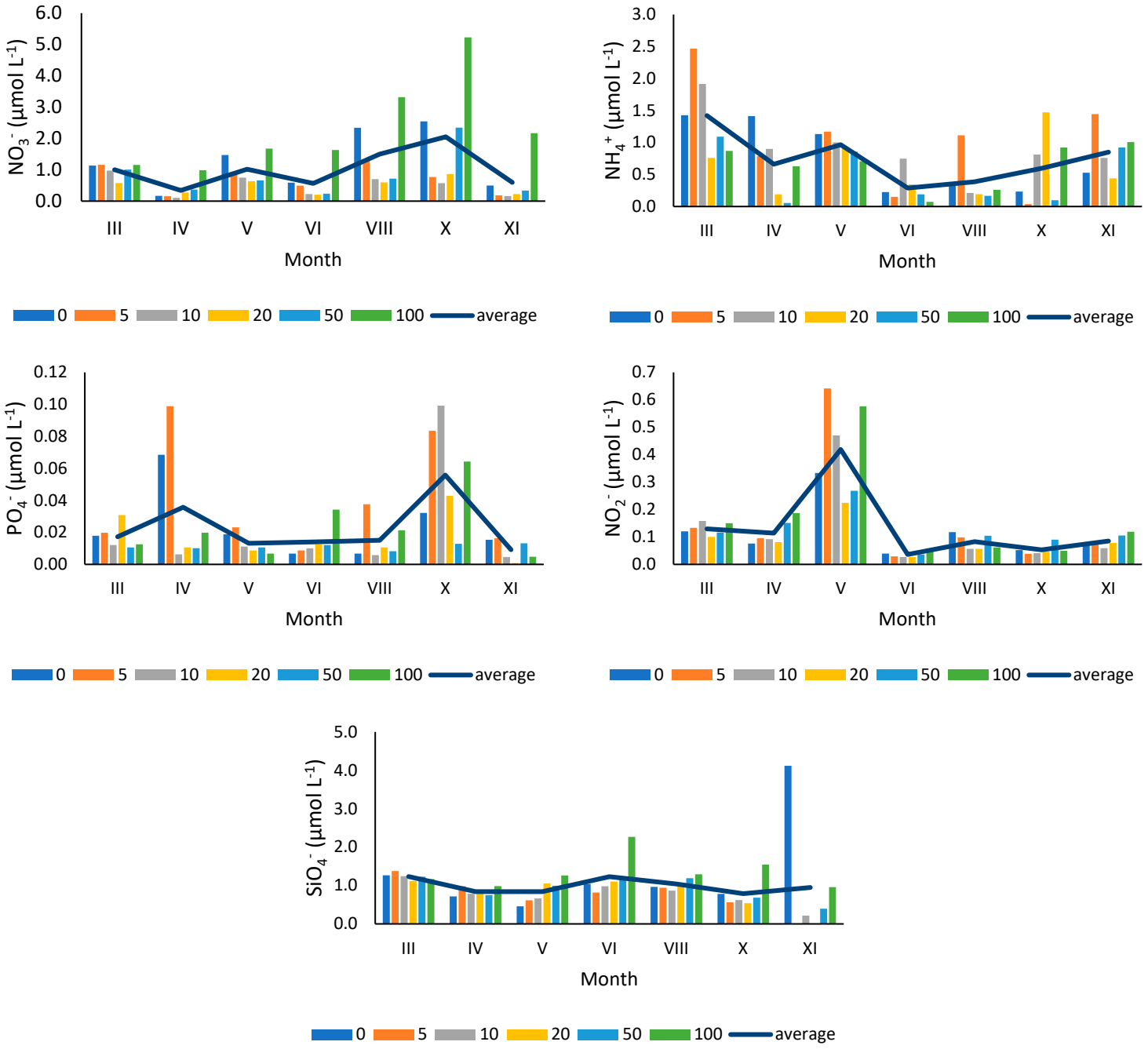

Figure S2. Monthly concentration of nutrients with the average value at the sampled depths.

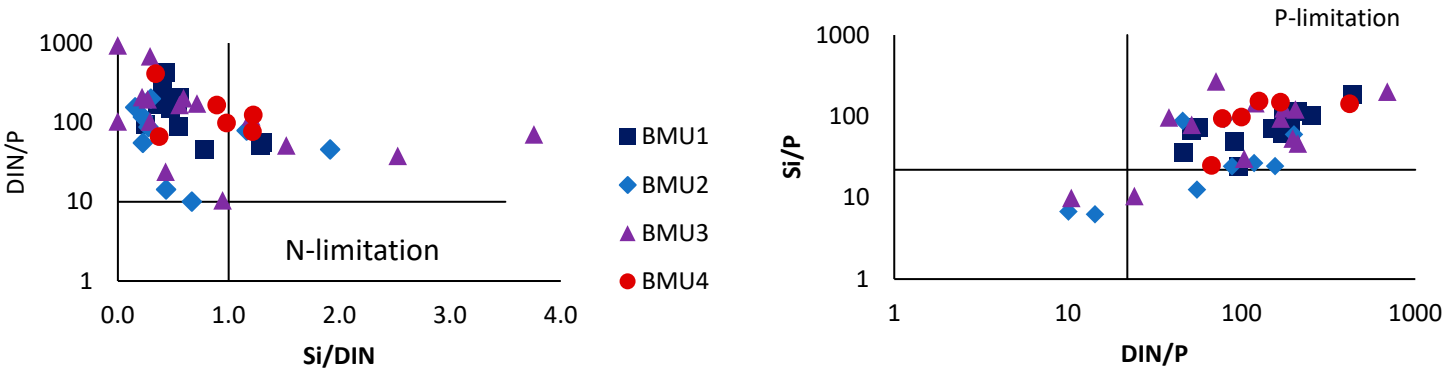

Figure S3. Cluster mapping in the nutrient ratio framework with stoichiometric criteria for potential limitations of phosphorus and nitrogen. Concentrations are in µM.

Table S4. The ratio between HNA and LNA group of bacteria for the sampled months and depths.

depth/month	III	IV	V	VI	VIII	X	XI
0	0.99	0.76	1.51	0.88	0.85	0.80	1.15
5	1.19	0.92	1.75	1.05	0.79	0.72	1.11
10	1.01	1.15	1.69	0.91	0.61	0.80	1.23
20	0.98	0.77	1.12	0.86	0.66	0.78	1.16
50	1.35	1.16	0.66	1.16	0.91	0.95	1.30
100	1.44	1.04	0.92	0.90	0.76	1.21	1.24

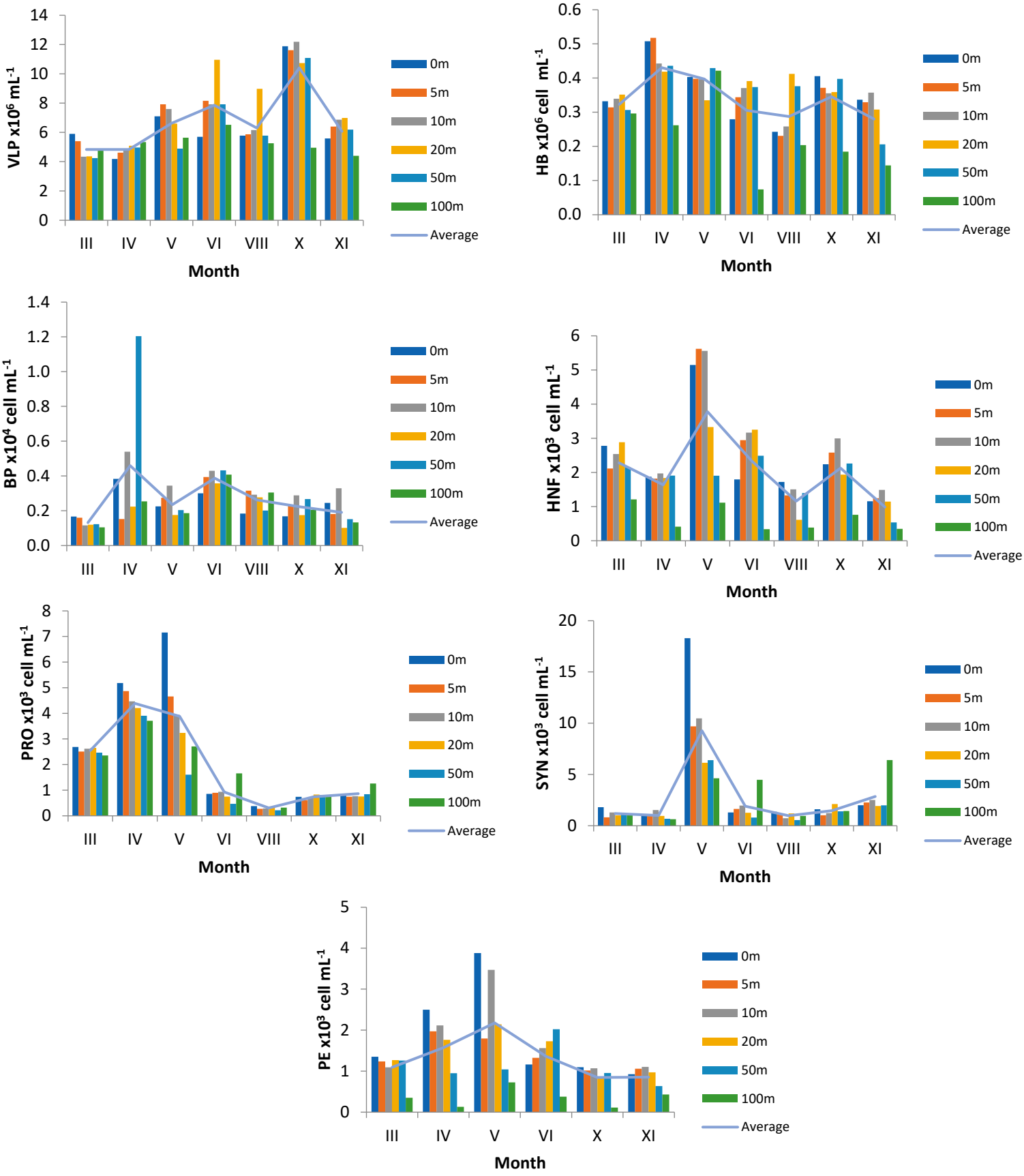

Figure S4. Abundances with average values for viruses (VLP), heterotrophic bacteria (HB), heterotrophic nanoflagellates (HNF), *Prochlorococcus* (PRO), *Synechococcus* (SYN) and picoeukaryotes (PE) at the sampling station.

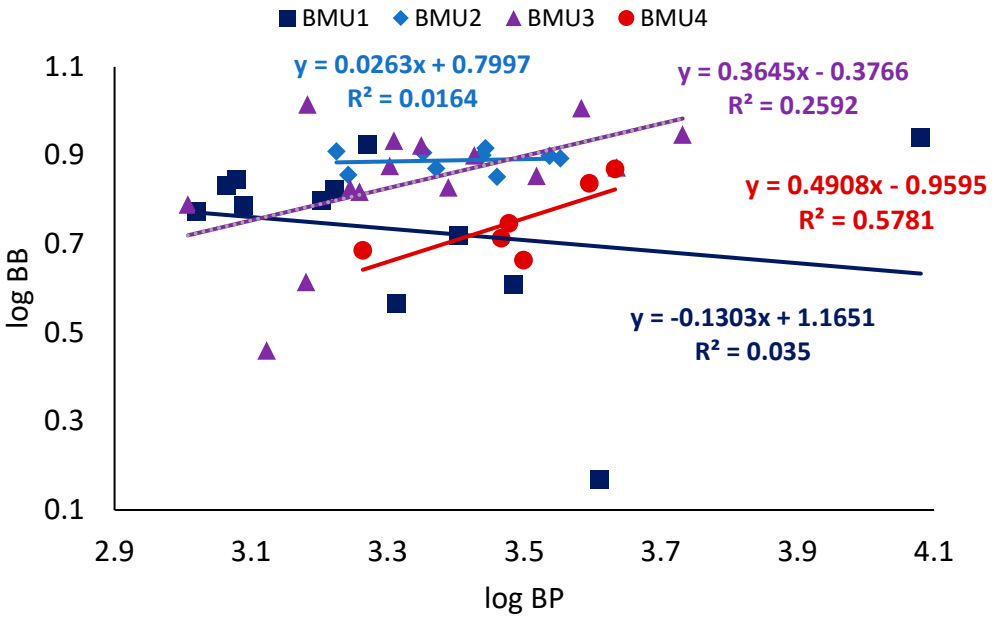

Figure S5. Log-log scatter plot of bacterial biomass (BB) and bacterial production (BP) according to the defined BMUs. The solid line represents the regression line showing the best fit to the data.

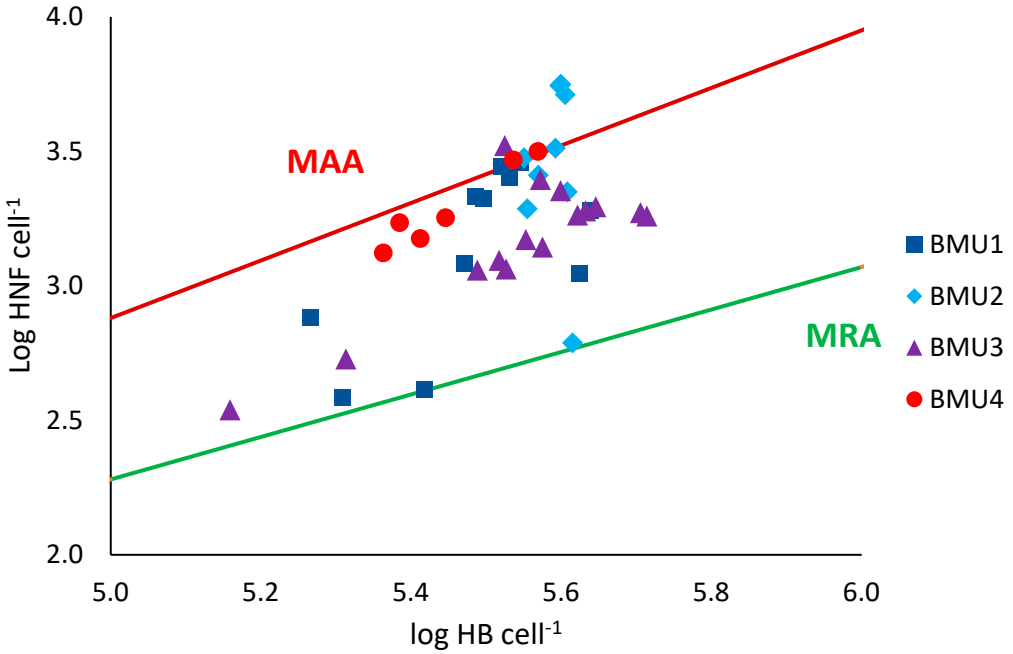

Figure S6. Relationship between the log abundances of heterotrophic nanoflagellates (HNF) and heterotrophic bacteria (HB) compared with the empirical model by Gasol (1994) for the sampling sites and months. MAA is the maximum attainable abundance while MRA is mean realized abundance.