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Supplement of

On giant shoulders: how a seamount affects the microbial community composition of seawater and sponges

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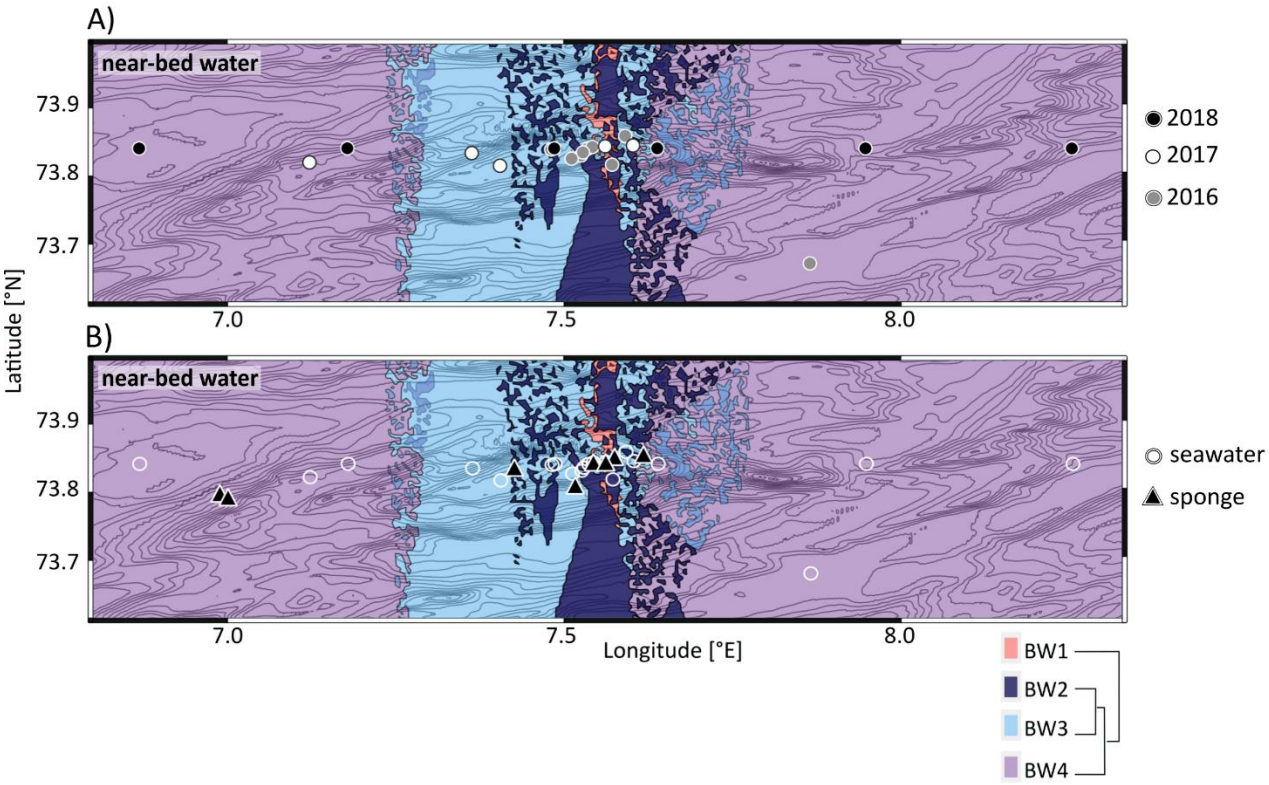
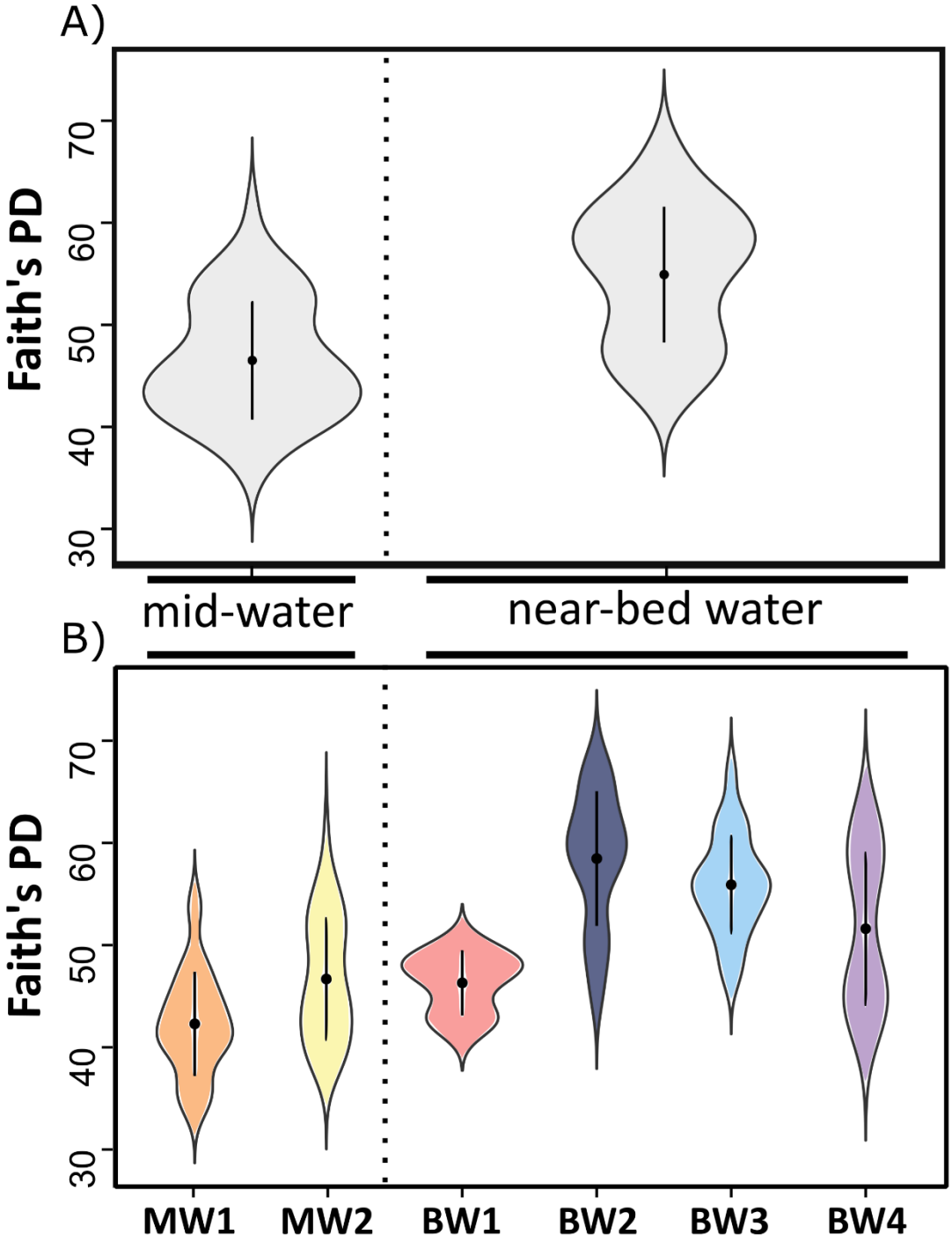
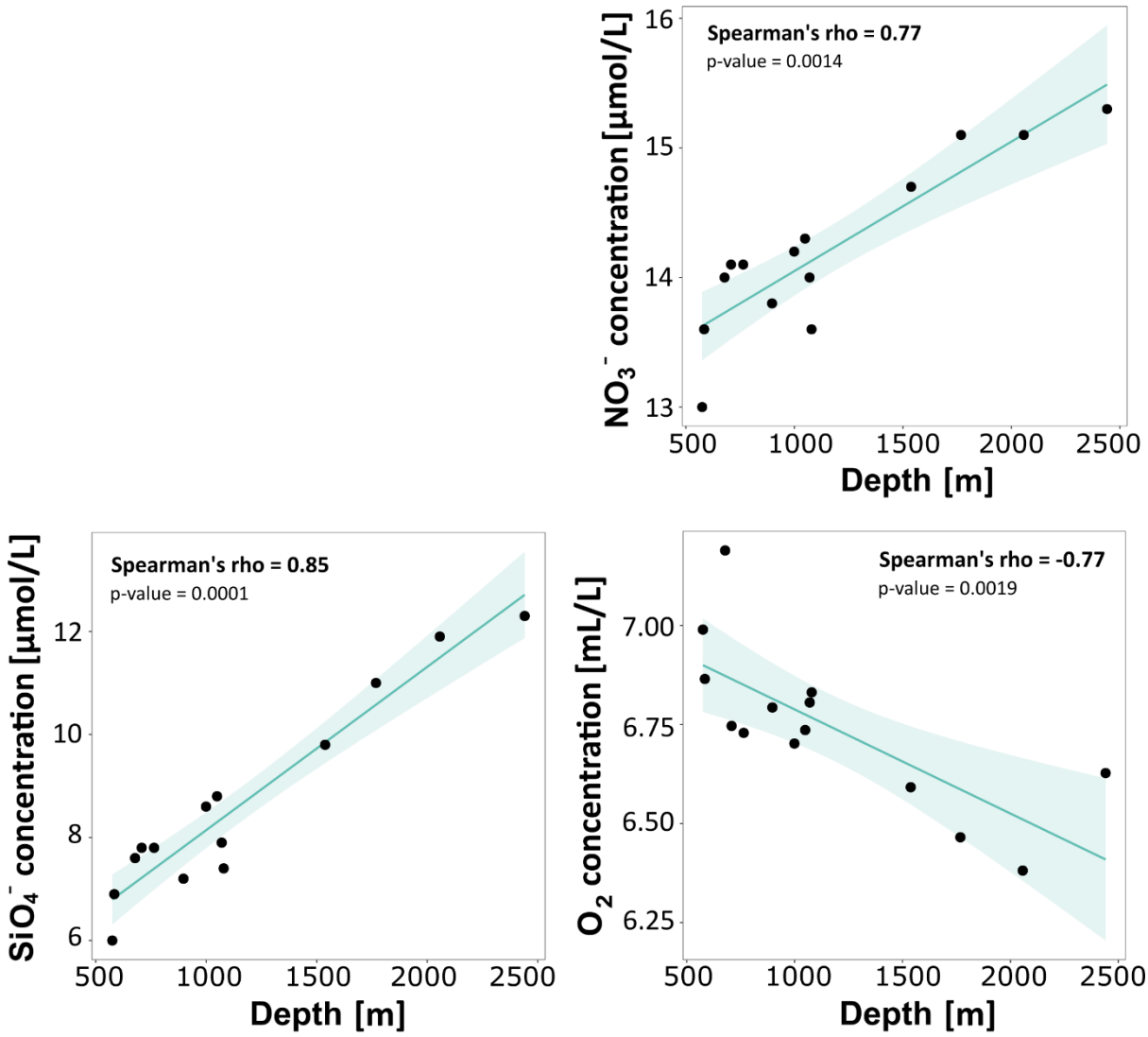


Supplementary Figure S1 Near-bed water microbial community structure across Schulz Bank in combination with either **(A)** information on sampling years of each seawater sampling station or **(B)** information on sampling locations of sponge samples (in relation to seawater sampling locations) across Schulz Bank. Contour lines in all three subplots represent the underlying topography. Colors in all subplots represent clusters based on weighted UniFrac distances, where colored dots indicate stations with in situ sampling and filled areas represent extrapolations based on machine learning. The degree of cluster similarity can be deduced from the dendrogram at the bottom of the plot. **A)** Different sampling years of the 19 CTD stations are indicated by colors of the dots. Samples from the 2018 cruise have a black color, samples from the 2017 cruise have a white color, and samples from the 2016 cruise have a grey color. **B)** Sponge sampling locations are marked by black triangles, while seawater sampling stations are indicated by white circles.



Supplementary Figure S2 A) Overall richness of pooled mid-water microbial communities and pooled near-bed water microbial communities. Faith Phylogenetic Diversity (Faith's PD) is plotted as alpha-diversity measure. **B)** Richness of seawater microbial communities for the mid-water and near-bed water samples, across the determined clusters. Mid-water clusters are coloured in orange (MW1) and yellow (MW2), while near-bed water clusters are marked in red (BW1), dark blue (BW2), light blue (BW3), and purple (BW4).



Supplementary Figure S3 Spearman's rank correlations calculated between depth and the three biogeochemical parameters which differed significantly (ANOVA, α=0.05) across the determined near-bed water clusters.

Supplementary Table S1 Overview of pairwise-comparisons (PERMANOVAs) across pelagic microbial micro-habitats based on weighted UniFrac matrices of microbial communities for both, seawater and the three sponge species. All possible pairwise combinations were tested. *L. complicata* and *S. rosea* were not present in all near-bed water clusters. Four biological replicates per near-bed water cluster were tested for every sponge species.

Group 1	Group 2	pseudo-F	p-value	
MW1	MW2	22.49	0.001	*
BW1	BW2	27.7	0.004	*
BW1	BW3	11.79	0.002	*
BW1	BW4	15.07	0.003	*
BW2	BW3	8.52	0.001	*
BW2	BW4	15.56	0.001	*
BW3	BW4	10.98	0.001	*
G. hentscheli BW1	*G. hentscheli* BW2	5.77	0.032	*
G. hentscheli BW1	*G. hentscheli* BW3	8.07	0.028	*
G. hentscheli BW1	*G. hentscheli* BW4	16.71	0.030	*
G. hentscheli BW2	*G. hentscheli* BW3	4.57	0.039	*
G. hentscheli BW2	*G. hentscheli* BW4	14.41	0.035	*
G. hentscheli BW3	*G. hentscheli* BW4	5.57	0.028	*
L. complicata BW1	*L. complicata* BW2	35.93	0.034	*
S. rosea BW1	*S. rosea* BW2	1.88	0.035	*
S. rosea BW1	*S. rosea* BW3	1.71	0.174	
S. rosea BW2	*S. rosea* BW3	1.18	0.36	
all MW	all BW	46.72	0.001	*

Supplementary Table S2 Averages and standard errors of biogeochemical parameters for each mid-water and near-bed water cluster.

	SPM [mg L^{-1}]	**DIC [µmol L^{-1}]**	**SiO_4^- [µmol L^{-1}]**	**PO_4^{3-} [µmol L^{-1}]**	**NH_4^+ [µmol L^{-1}]**	**NO_3^- [µmol L^{-1}]**	**NO_2^- [µmol L^{-1}]**	**O_2 [mL L^{-1}]**	**Depth [m]**
MW1	NA	2246.00 ± 6.99	5.72 ± 0.10	0.88 ± 0.02	NA	12.84 ± 0.08	0.02 ± 0.02	6.90 ± 0.04	400 ± 0
MW2	2.22 ± 1.39	2292.14 ± 53.64	5.63 ± 0.08	0.84 ± 0.01	0.11 ± 0.03	13.08 ± 0.11	0.02 ± 0.01	6.75 ± 0.03	400 ± 0
significance mid-water								*	
BW1	0.49 ± NA	NA	6.00	0.90	0.10	13.00	0.00	6.99 ± NA	575
BW2	NA	2265.67 ± 7.69	8.40 ± 0.31	0.97 ± 0.03	NA	14.20 ± 0.06	0.00 ± 0.00	6.71 ± 0.02	919 ± 106
BW3	1.87 ± 1.08	2260.40 ± 12.35	7.87 ± 0.42	0.95 ± 0.02	0.17 ± 0.03	14.03 ± 0.15	0.03 ± 0.02	6.84 ± 0.07	922 ± 142
BW4	0.95 ± 0.33	2248.00	10.65 ± 1.42	0.95 ± 0.03	0.10 ± 0.00	14.78 ± 0.52	0.05 ± 0.03	6.48 ± 0.10	1836 ± 376
significance near-bed water			*			*		*	*