Response to Reviewer Comments on Manuscript bg-2020-15:

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

Kathrin Busch, Ulrike Hanz, Furu Mienis, Benjamin Müller, Andre Franke, Emyr Martyn Roberts, Hans Tore Rapp, Ute Hentschel

We thank the reviewers for the overall positive evaluation of our manuscript and for the time and effort taken. We have made considerable effort to address the points raised and also included three additional figures (Supplementary Material S1, Supplementary Material S2A, Supplementary Material S3), elaborated existing figures (Fig.3, Fig.4, Fig.6) and conducted further statistical analyses (i.e. TukeyHSD Posthoc tests, Spearman´s rank correlation). Below please find our responses that are listed in the order raised. We show the referees' comments in black text, while our responses are formatted in red. The new line numbers refer to the revised manuscript (marked-up version). Thank you for your consideration.

Reviewer #1 (Comments for the authors):

Overall comments: This manuscript brings to bear physical oceanographic, biogeochemical, and microbiological data on the question of whether seamounts impact the microbial community composition of the water column and benthic organisms like sponges. I was skeptical of water column impacts, imagining that a given water mass would have a microbial signature irrespective of the seamount. However, the data in this paper convinced me of the unexpected findings that not only do seamounts exert an effect on the bacterial community composition up to 200 meters above their summit, but also a more subtle effect on the bacterial community composition of sponges growing at various depths on the seamount. The scientific methods are clearly described and appropriate for the work. CTD data were collected at stations both on and off the seamount, so there are appropriate mid-water and near-bottom water controls to assess the influence of the seamount. A sufficient number of sponge samples were collected for each species, which is not a small matter for deep-sea work. Moreover, the authors have put a tremendous amount of work into creating excellent visualizations of the data that clearly show how the results support their conclusions (particularly Figures 3 and 6). It takes real effort to combine such large amounts of information into figures and still have them clearly and cleanly illustrate the narrative points you are making in the discussion. The discussion is very concise and logically structured. The conclusions are well sup-ported by the results. The references are appropriate in scope, including very recent findings (2018-2019) as well as citing classic papers from multiple decades (centuries). All of the references cited in the text are listed in the bibliography. I don't often have the pleasure of reviewing a paper that is so articulate and well organized and makes such surprising findings. This manuscript is excellent.
Typographic issues:

Abstract:

Line 17: 'extend' should be 'extent'
DONE

Line 19: ‘which extend’ should be ‘what extent’
DONE

Line 21: amplicon does not need to be capitalized
DONE

Lines 38 and 42: remove the comma after ‘both’
DONE

Lines 40-41: You do not define HMA or LMA prior to usage
The explanation of HMA or LMA as well as the taxonomic status has been removed here as it is explained later (LL79-81).

Introduction:

Lines 65-66: ‘Rix, De Goeij et al. 2016’ should be either Rix et al.2016a or Rix et al. 2016b
DONE

Line 71: ‘Intimate sponge-microbe associations have been observed. . .’
DONE

Line 85: ‘. . .interactivity are still lacking’
DONE

Results:

Line 242: ‘The dominant microbial phylum in S. rosea and L. complicate was Proteobacteria’
DONE

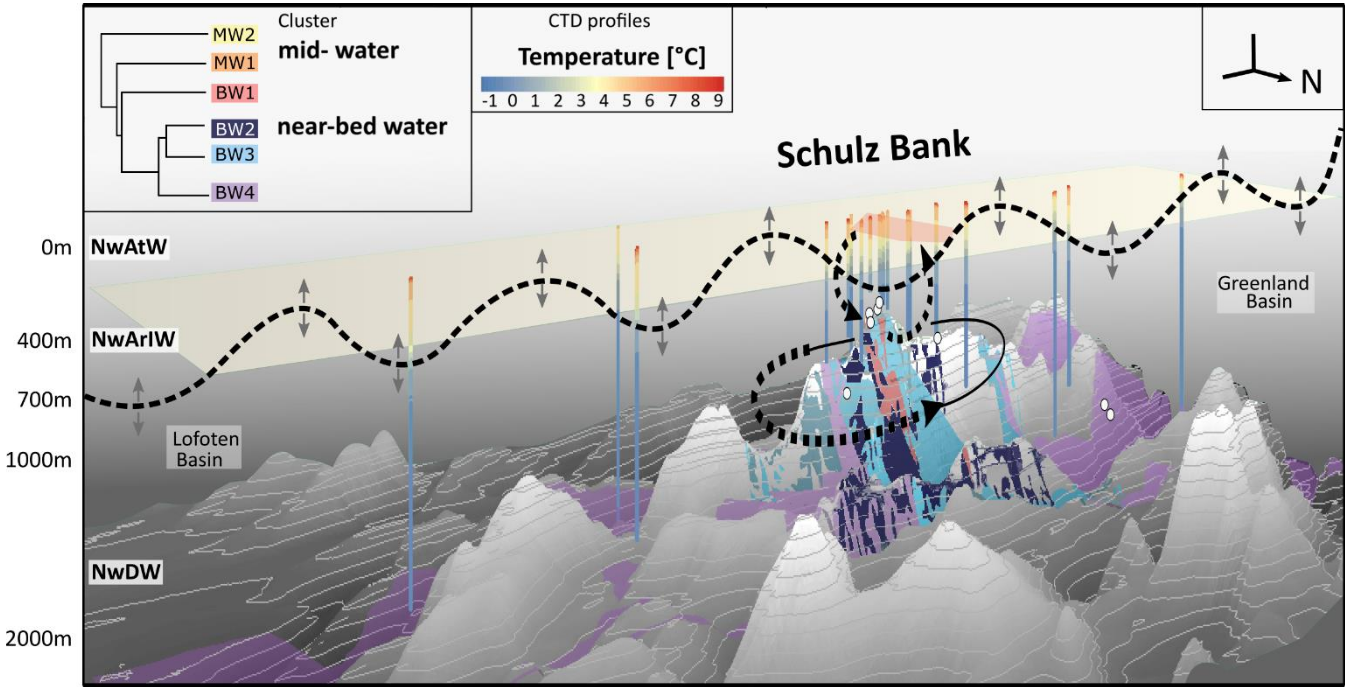
Throughout: There is inconsistency of the in-text citations throughout the manuscript. Some citations italicize ‘et al.’ while others do not. Please check the journal’s preference and then make all of them the same.
DONE

References:

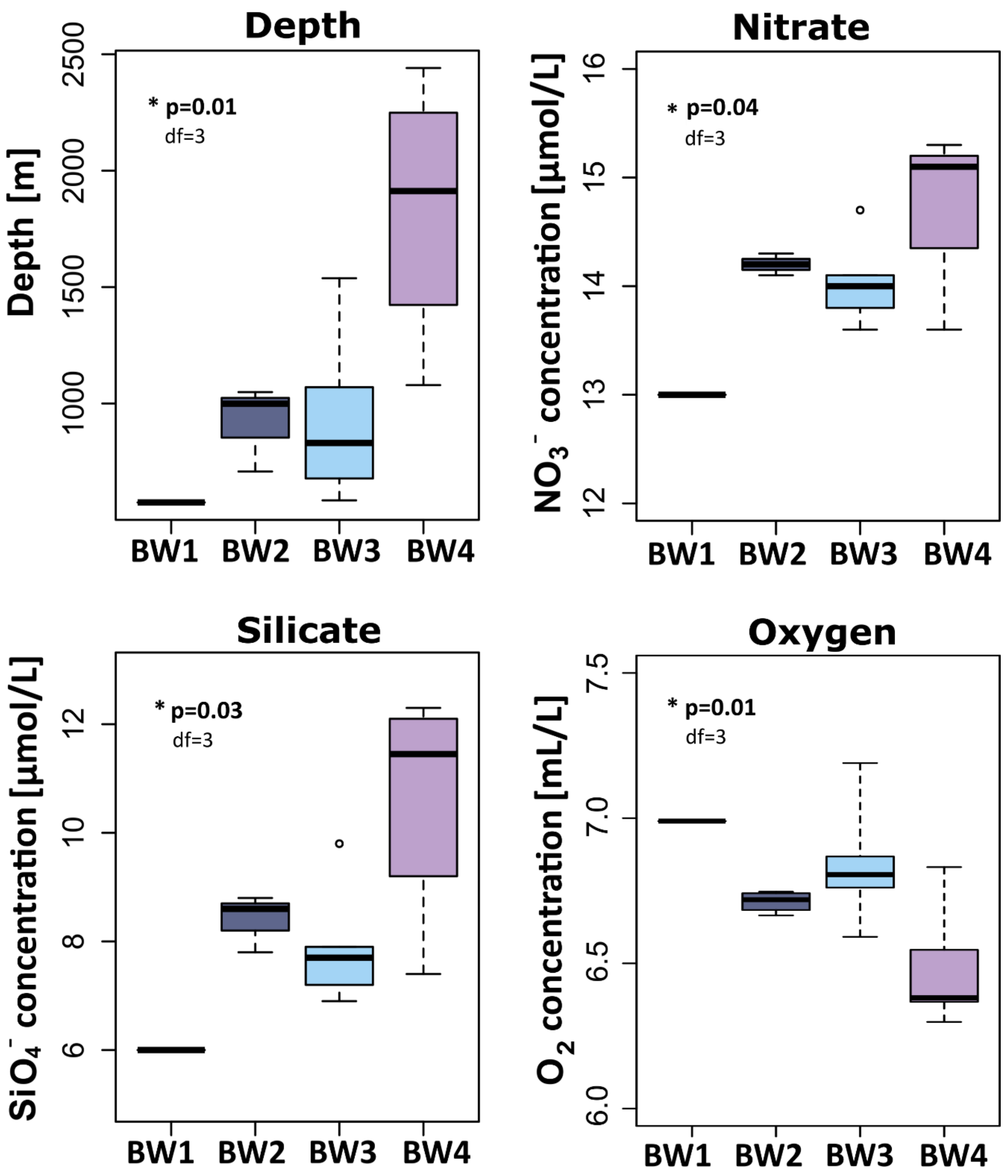
Line 463: Van Haren is listed under ‘H’ instead of ‘V’
DONE

Lines 452-457: two De Goeij references are listed under ‘G’ instead of under ‘D’
DONE

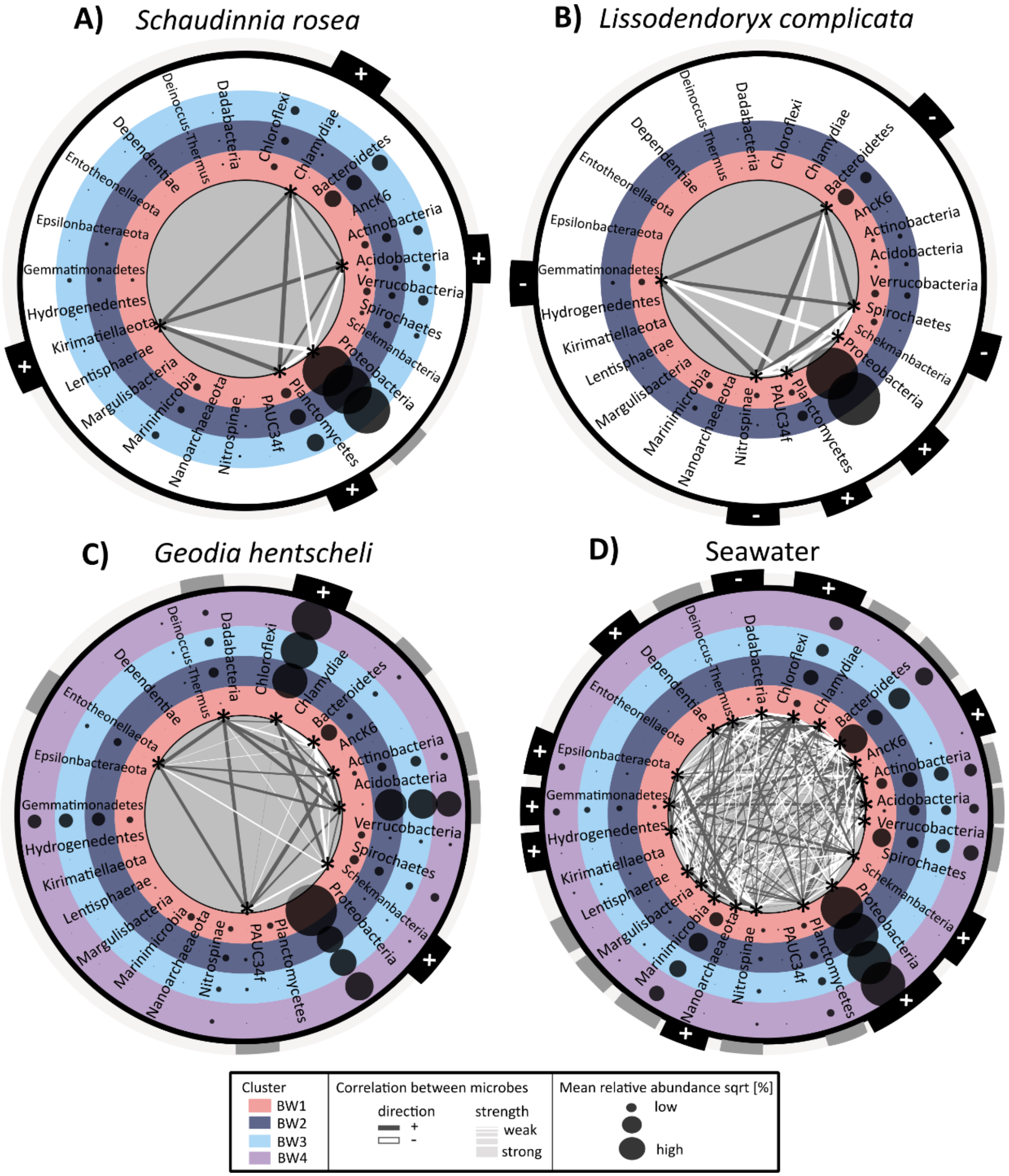
Line 569: Isme should be ISME
DONE



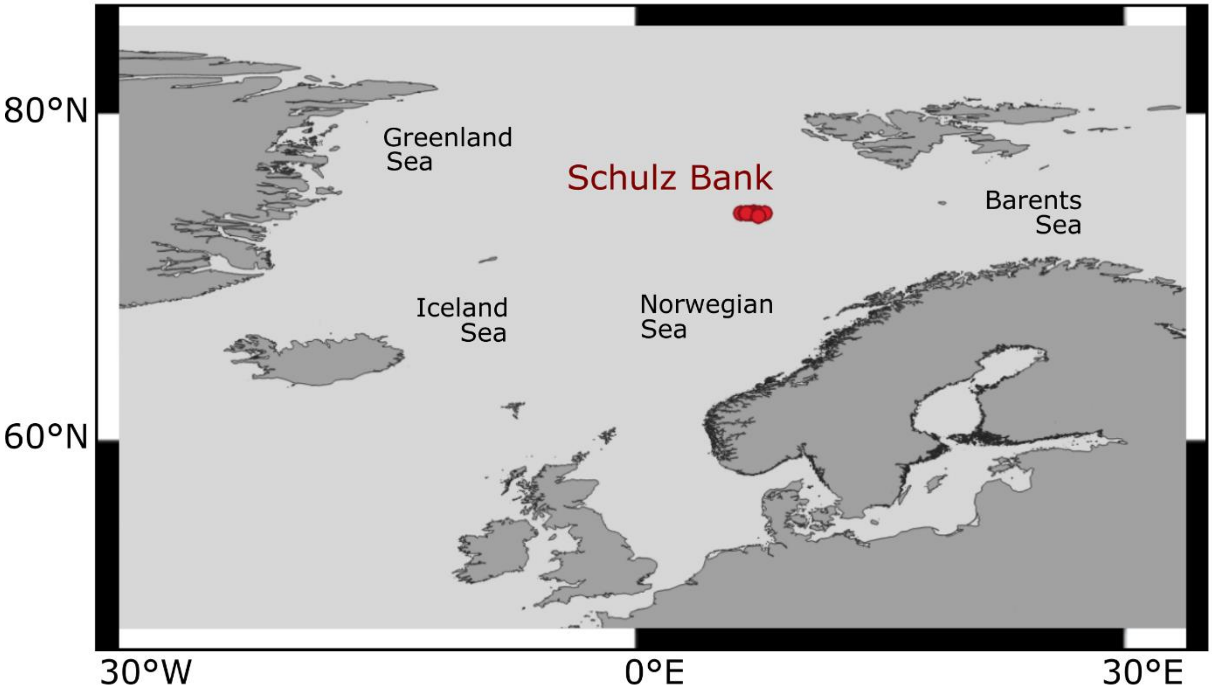
(Revised) Figure 3: Conceptual overview and vertical 3D section showing spatial distribution of microbial clusters and oceanographic patterns on the Schulz Bank seamount. Extrapolated seawater microbial clusters are indicated by colored polygons: mid-water clusters are marked in orange (MW1) and yellow (MW2), while near-bed water clusters are marked in red (BW1), dark blue (BW2), light blue (BW3), and purple (BW4). The degree of cluster similarity can be deduced from the dendrogram in the left corner of the plot. Whole water column CTD profiles are indicated, showing the measured temperature values from surface to bottom at the respective sampling locations. Sponge sampling locations visible on this side of the seamount are indicated by white balls. Vertical positions of major watermasses: Norwegian Atlantic Water (NwAtW), Norwegian Arctic Intermediate Water (NwArIW), and Norwegian Deep Water (NwDW) are indicated. To give a broad orientation in space, a north arrow is depicted, as well as the major geologic features (Lofoten Basin and Greenland Basin). For Schulz Bank, water flows, such as a potential Taylor column circulating around the seamount, mixing between summit and pelagic realm, as well as tidally-driven internal motions (black horizontal line with bidirectional arrows) are indicated by dashed arrows and lines.



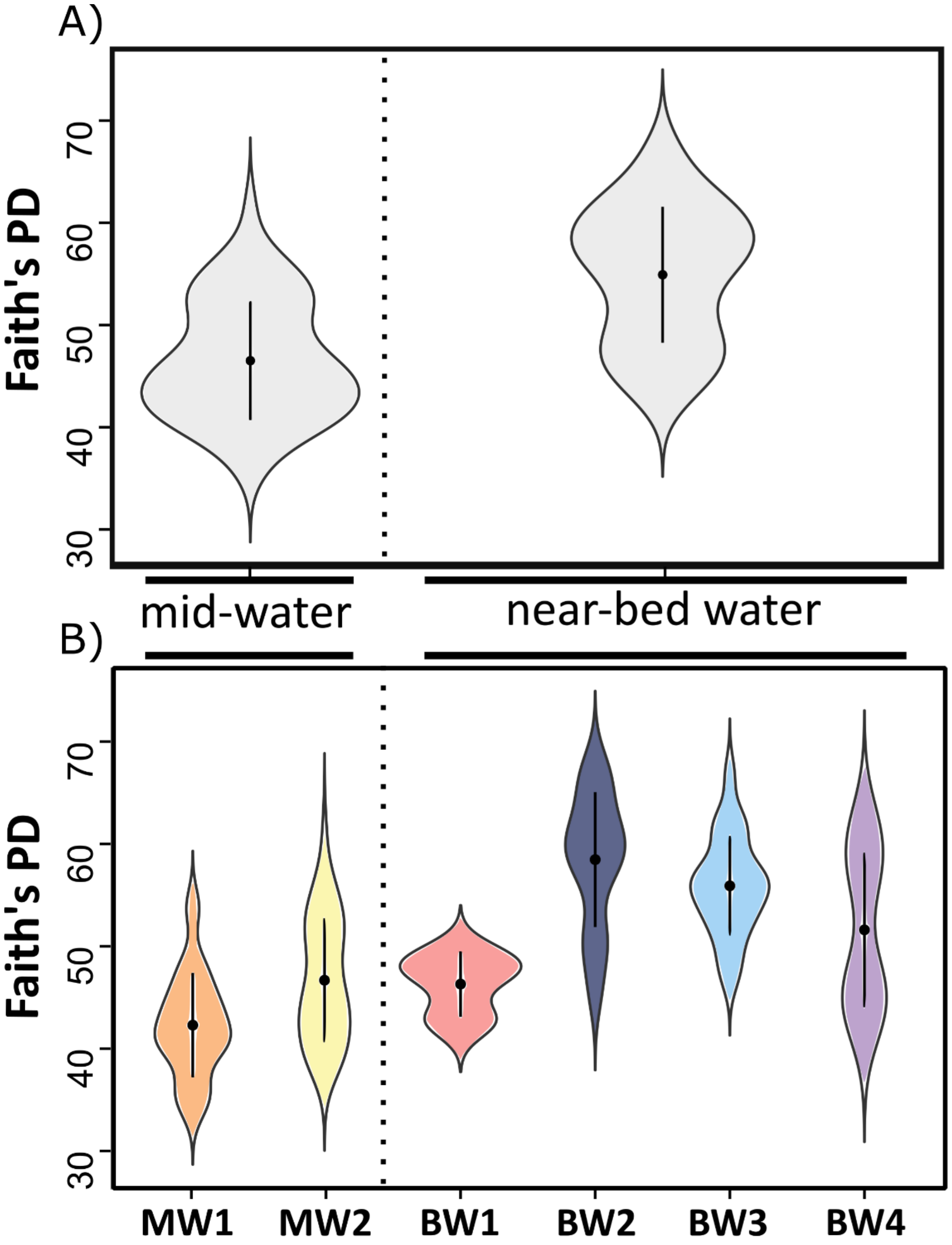
(Revised) Figure 4: Concentrations and measurements of significant (ANOVA, α=0.05) biogeochemical parameters for near-bed water samples, across the determined near-bed water clusters. p-values as well as degrees of freedom (df) for these parameters are written into the respective graphs. Colouring is the same as chosen for Fig. 2 and 3.



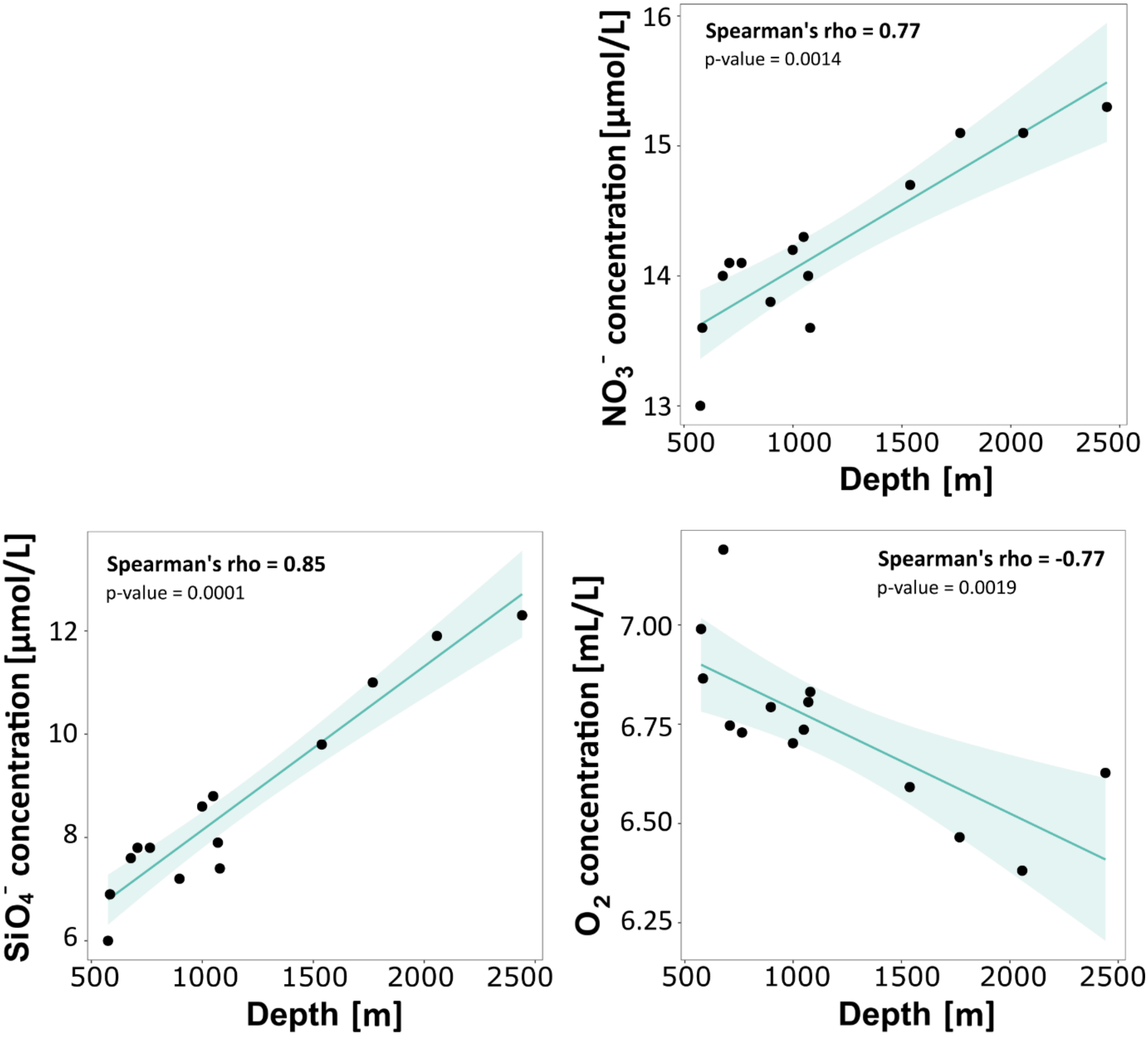
(Revised) Figure 6: Co-occurrence network and differential abundance of microbial phyla across the four determined near-bed water clusters. Sub-plots A-C) show sponge data, with plot A) showing average *Schaudinnia rosea* data, B) presenting average *Lissodendoryx complicata* data and C) illustrating *Geodia hentscheli* data. Sub-plot D) contains seawater data. Near-bed water clusters are represented by differently colored rings. Each ring contains a list with microbial phyla which are alphabetically sorted. Average relative abundances of each of the respective phyla for the samples within a given cluster are indicated by bubble sizes. Those microbial phyla which are statistically significantly enriched or depleted across the four clusters (LEfSe analysis), are marked with an asterisk inside the inner most ring. Only for those taxa where the difference is significant, correlation strength (indicated by size of connecting lines) and direction (represented by color of connecting lines: white = negative correlation, dark grey = positive correlation) with all other significant taxa are plotted. For all microbial phyla relation with depth is indicated in the outer ring of each plot by + (meaning significant positive relation) or - (meaning significant negative relation).



(Newly added) Supplementary Figure S1: Overview map showing the location of the Schulz Bank seamount between the Greenland and Norwegian Seas.



(Newly added) 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).



(Newly added) 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.