Supplementary

Community composition analysis

DNA was extracted using the DNeasy PowerSoil Pro Kit (Qiagen) from SML and ULW samples collected from leads and concentrated on polycarbonate filters. Quantification of bacterial 16S and eukaryotic 18S rRNA gene copies by qPCR followed Jensen et al. (2022) and Wieber et al. (2025). For library preparation, 16S rRNA amplicons followed Jensen et al. (2022) with 2 µl template and 20 PCR cycles used in the first PCR, while 18S rRNA amplicons followed Wieber et al. (2025) with 2.5 µl template and 30 PCR cycles used in the first PCR. Final PCR products were quantified, diluted, and pooled as described in Wieber et al. (2025). Bioinformatics were performed in R v4.4.1 (R Core Team, 2024) using the same pipeline for both 16S and 18S rRNA reads, following Wieber et al. (2025). Steps included primer/adaptor removal, quality control, chimera removal, error modeling, and taxonomic assignment. Contaminants were removed using the prevalence method (threshold = 0.1) in the *decontam* package (Davis et al., 2018). Amplicon sequence variants (ASVs) were extracted at the genus level. Absolute abundances of selected bacterial genera were estimated by combining ASV relative abundances with 16S qPCR concentrations following (Vandeputte et al., 2017).

$$G = \left(\frac{ASV\ relative\ abundance}{100}\right) \cdot qPCR\ concentration$$

$$N = \frac{G}{mean\ operon\ number\ for\ the\ genus}$$

Where *G* is the absolute gene copy number and *N* the estimated cell count. Operon numbers were obtained from rrnDB (Stoddard et al., 2015).

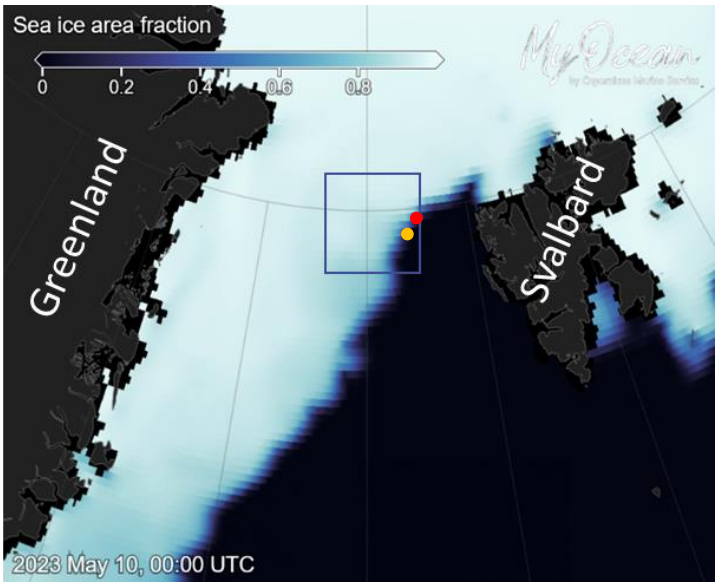

Figure S1: Sea ice area fraction on 10 May in the Fram Strait (E.U.-Copernicus Marine Service, 2020, https://data.marine.copernicus.eu/-/9a661qmlrm). The blue box indicates the study area with the red dot marking the first station (10 May) and the yellow dot marking the last station (11 June).

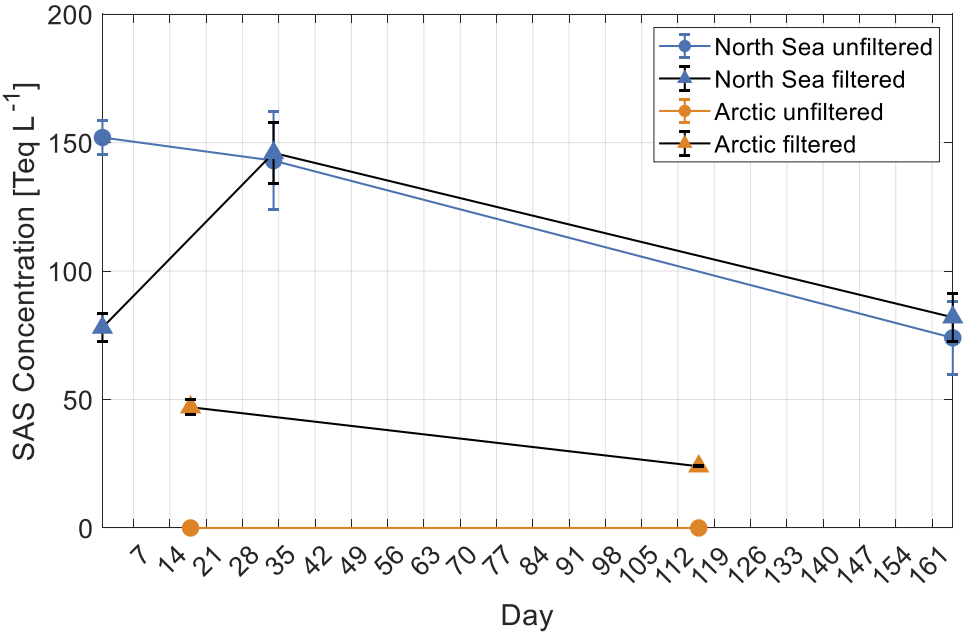

Figure S2: Results from a SAS preservation experiment with seawater from the North Sea and Arctic water from this study. Samples were stored in the dark at 4°C for up to 165 days after sampling (day of sampling = 1). For filtered samples, 0.2 µm Nucleopore syringe filters were used. The last sample collected during the ARTofMELT23 expedition was measured as soon as possible (17 days after sampling). Higher SAS concentrations in filtered samples were likely the result of cell lysis during filtration. For a storage time of 4 to 6 weeks (as in the presented data), a reduction in SAS concentration of 5–13% was observed for unfiltered seawater from the North Sea and 14–21% for filtered Arctic water. Because the concentration of the Arctic unfiltered sample was below the detection limit, no change could be detected. The increase in SAS concentration in the filtered North Sea sample after 35 days was likely the results of microbes remaining after filtration and producing SAS.

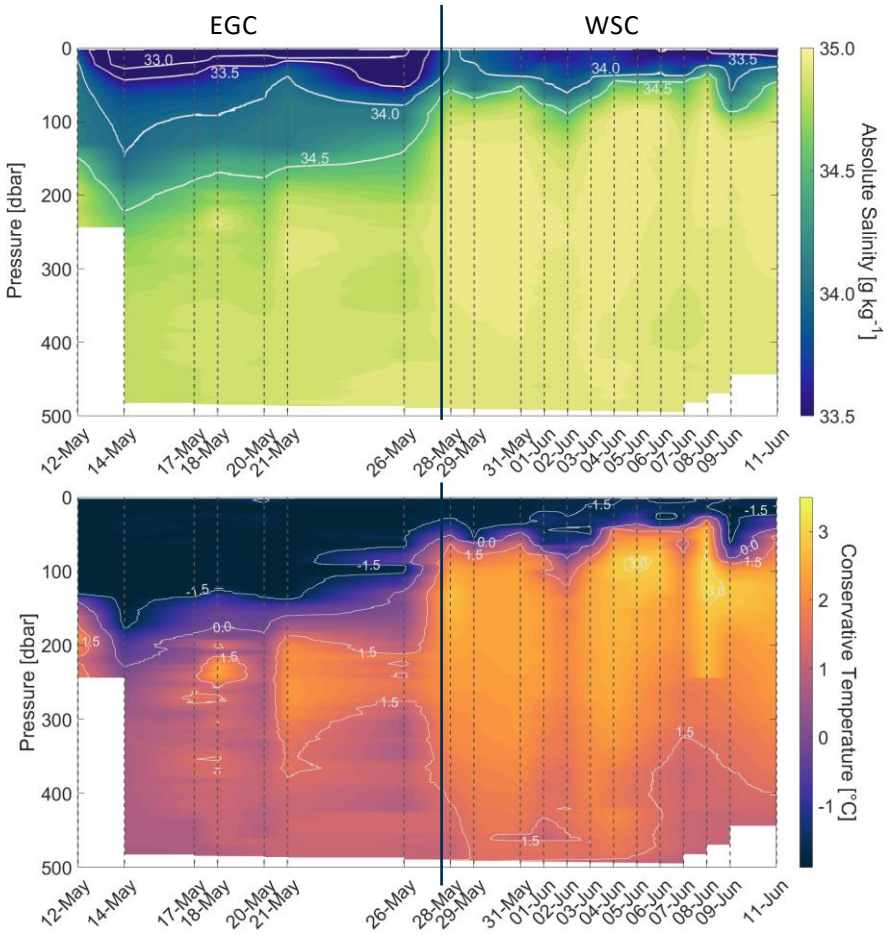

Figure S3: All VMP profiles for Absolute Salinity and Conservative Temperature visualized with linear interpolation. Grey dashed lines indicate the days of measurements. The EGC (all stations west of 0° latitude) exhibited a pronounced cold (<0°C) and fresh layer of Polar Surface Water (Rudels et al., 2005) in the upper 100-200 m of the water column, while this layer only covered the upper 50-100 m in the WSC. Below the Polar Surface Water, warmer (>2°C) and more saline Atlantic Water was present at all stations of the WSC as well as on 12 May and in the EGC on 17, 18, and 21 May. The intermediate waters with temperatures between 0°C and 2°C can be associated with Arctic Atlantic Water(Rudels et al., 2005). The cold (≤0°C) and more saline deep waters were in the range of the Arctic Intermediate Water (Rudels et al., 2005)

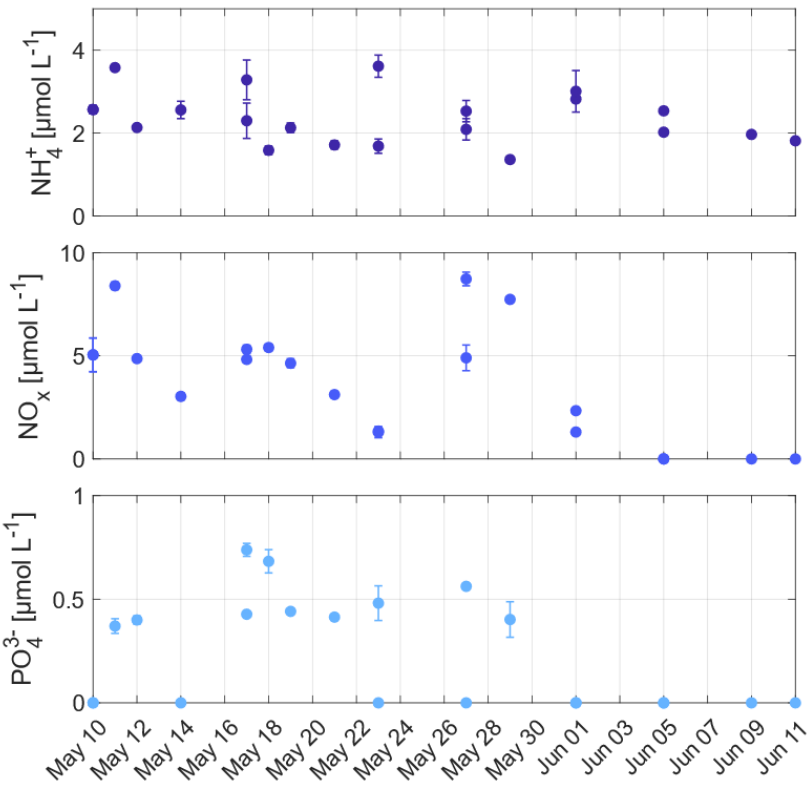

Figure S4: Surface concentrations of NH_4^+, NO_x, and PO_4^{-3} over time. Data are from (Rush and Vlahos, 2025).

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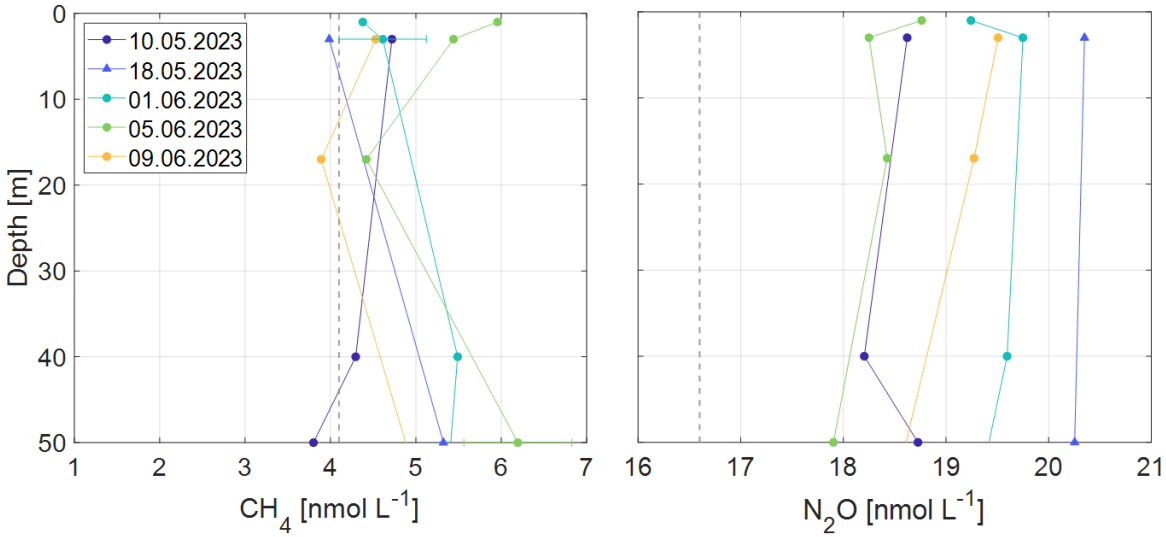

Figure S5: Dissolved CH_4 (left) and N_2O (right) concentrations in the upper 50 m of the water column.

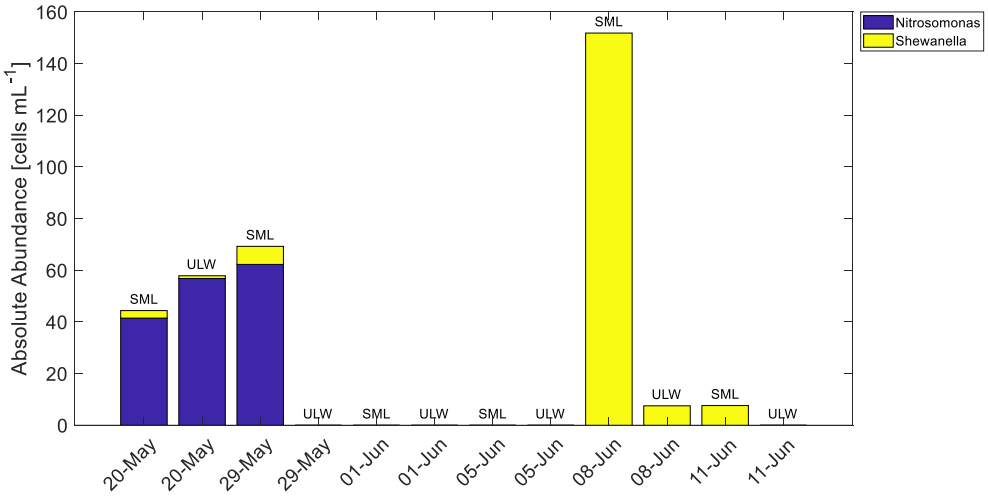

Figure S6: Absolute abundances of selected bacteria with potential influence on N_2O concentrations.

References

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