Supplementary material: Terrestrial runoff is the dominant source of a new type of biological INPs observed in Arctic fjords

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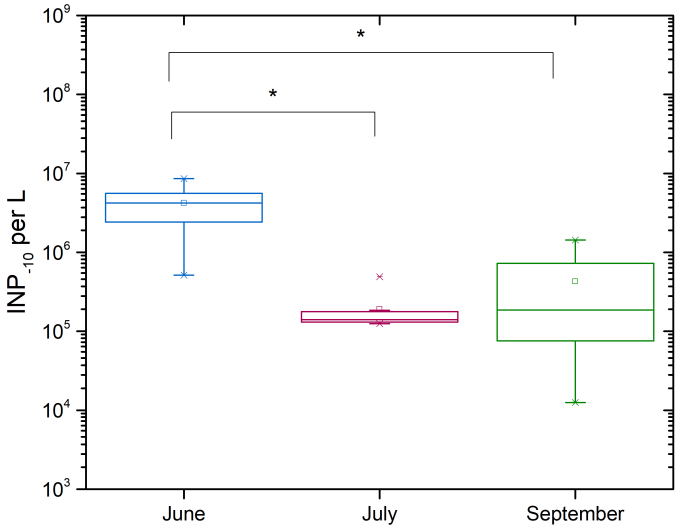

Figure S1: Concentration of INPs active at -10 °C for SBW and SML samples separated by months shown as box plot with 25th and 75th percentiles. INP$_{-10}$ concentrations are significantly higher in June ($p < 0.05$).

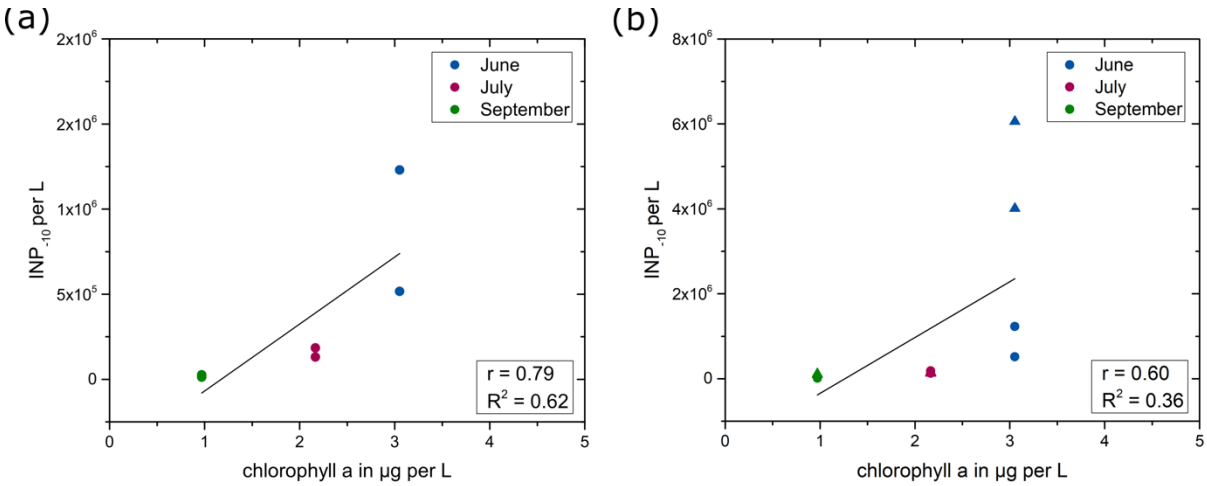

Figure S2: Number of INPs active at -10°C in relation to the chlorophyll concentration measured on the sampling dates at Kobbefjord. (a) only data for SBW samples from Kobbefjord, (b) data from SBW samples in Kobbefjord and Godthåbsfjord.

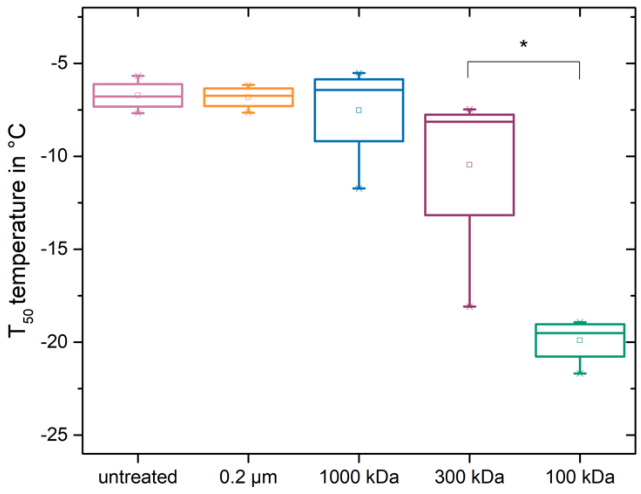

Figure S3: T_{50} temperatures for the June samples (SBW and SML) after filtration treatments shown as box plot with 25th and 75th percentiles. Freezing temperatures after filtration with 300 kDa and 100 kDa are significantly different ($p < 0.05$).

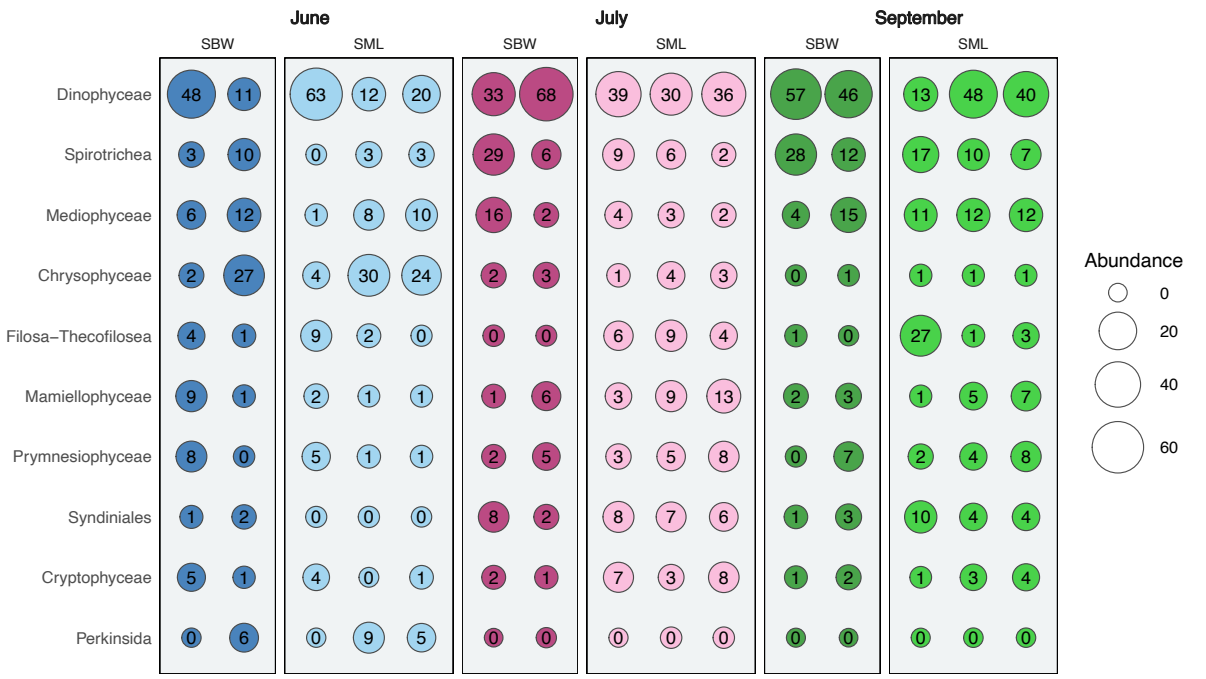

Figure S4: Eukaryotic community composition derived from the 18S rRNA data on the class level. The abundance is indicated by the size of the circle and given in percent rounded to the closest whole number inside the circles.

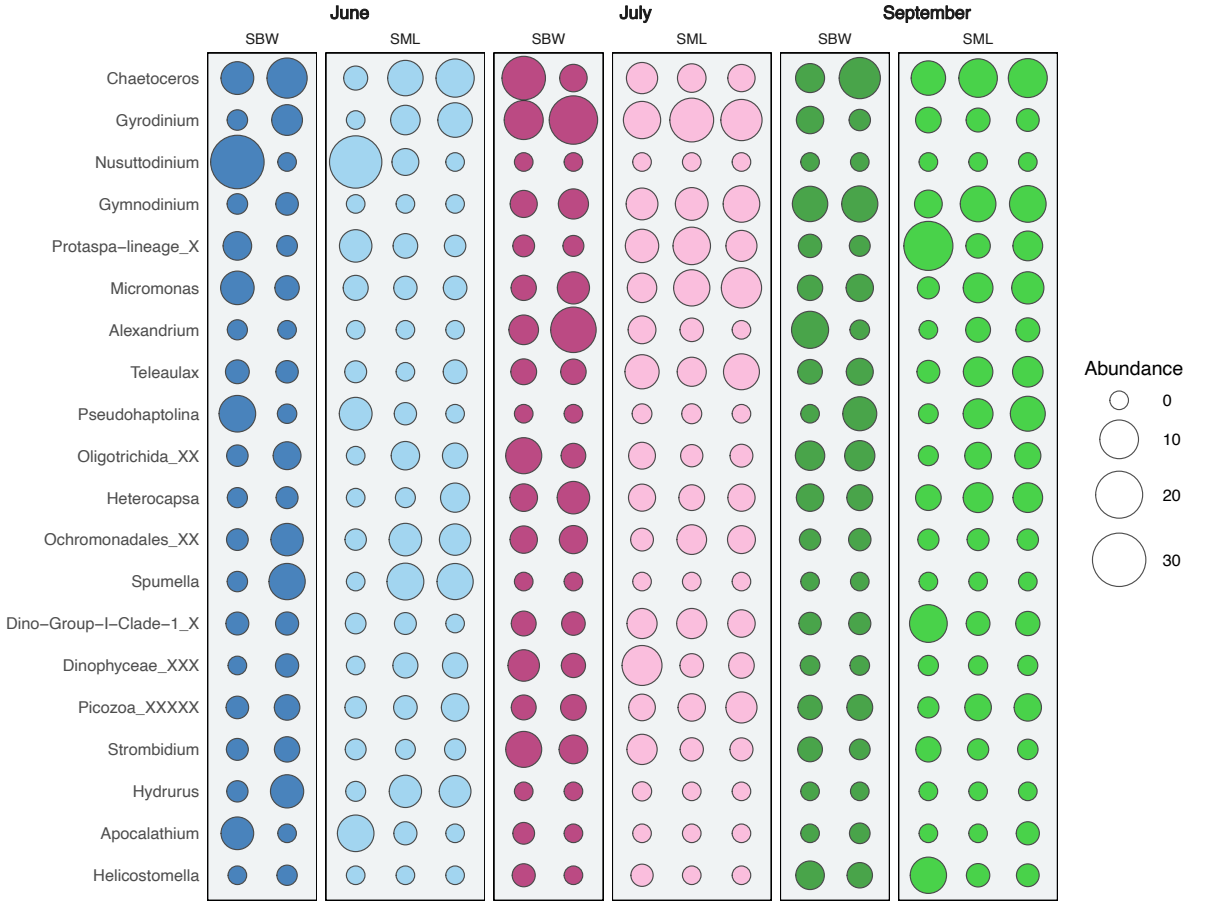

Figure S5: Eukaryotic community composition derived from the 18S rRNA data on the genus level. The abundance is indicated by the size of the circle.

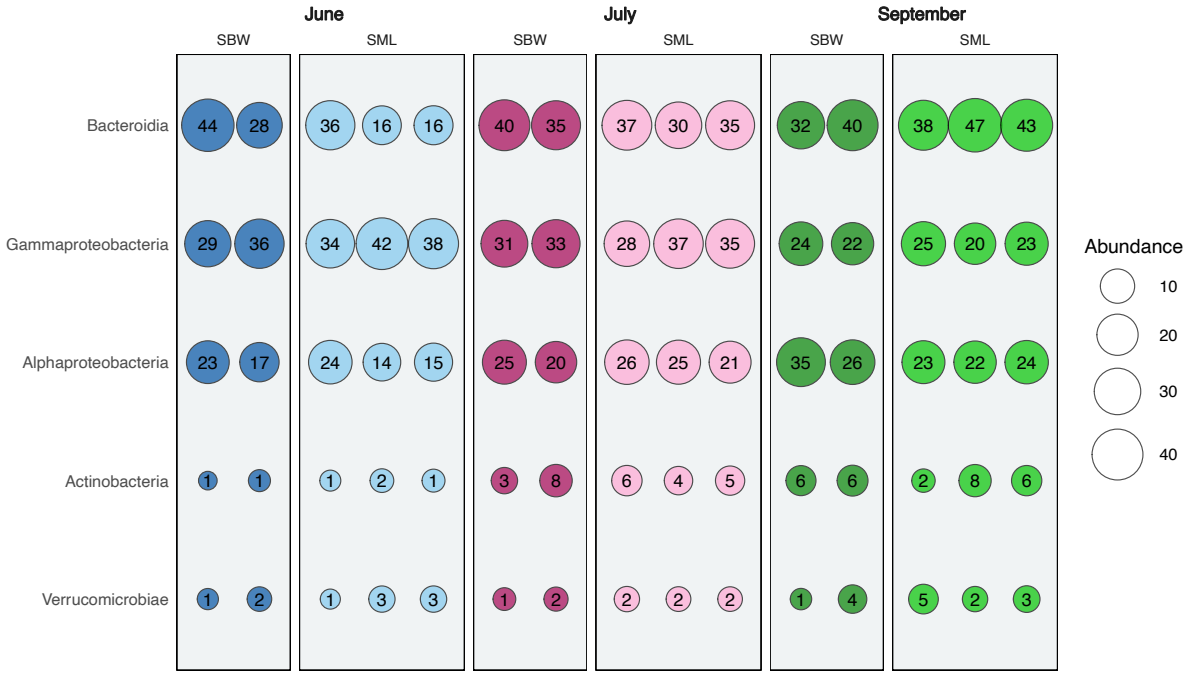

Figure S6: Bacterial community composition derived from the 16S rRNA data on the class level. The abundance is indicated by the size of the circle and given in percent rounded to the closest whole number inside the circles.

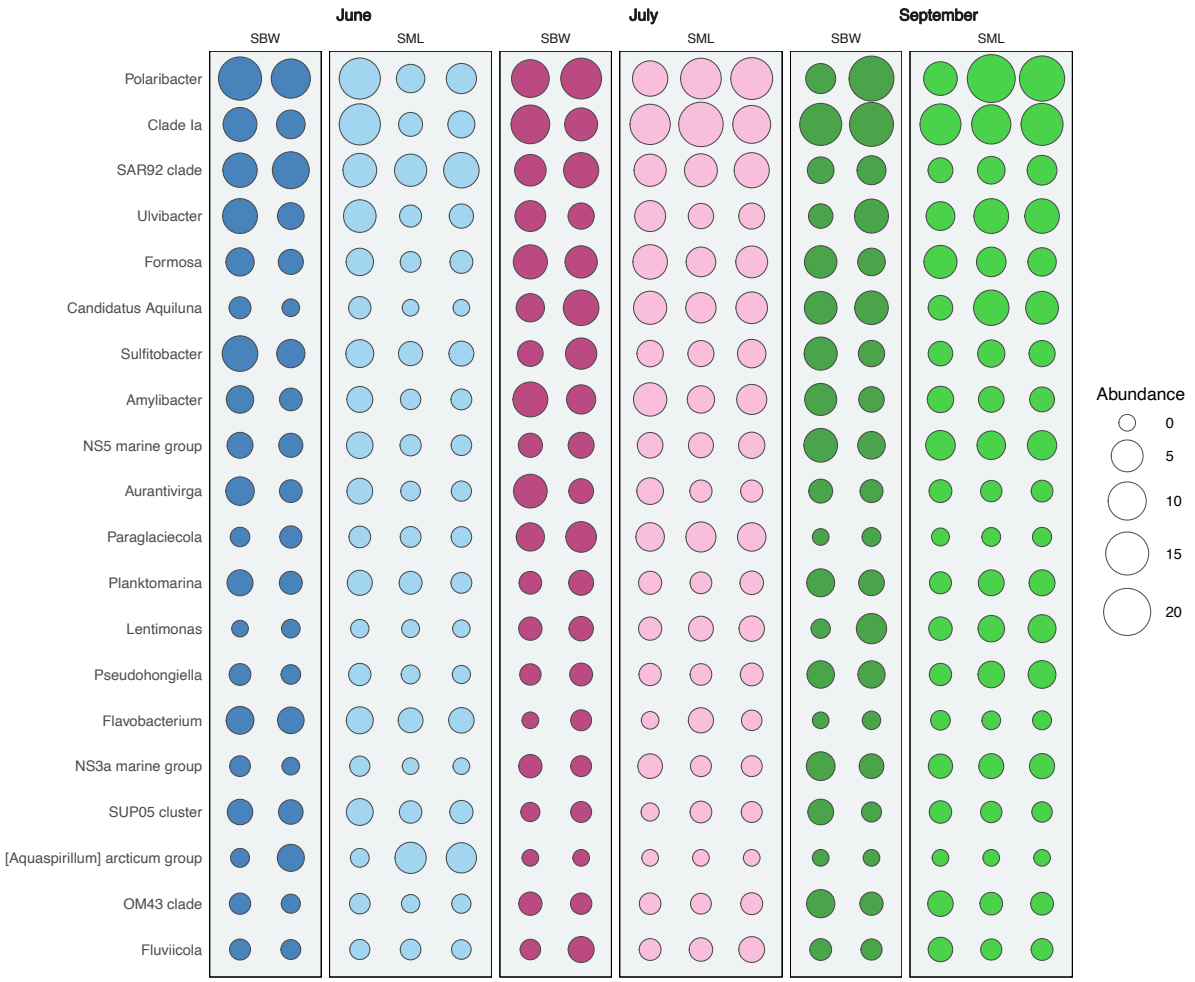

Figure S7: Bacterial community composition derived from the 16S rRNA data on the genus level. The abundance is indicated by the size of the circle.

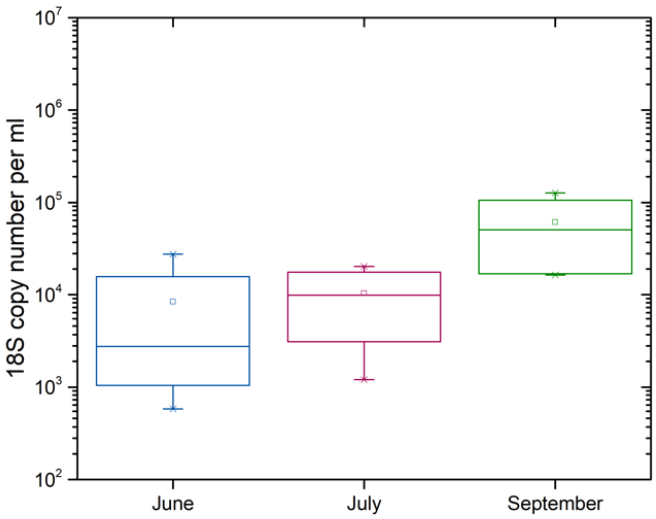

Figure S8: Ribosomal gene copy numbers based on the 18S rRNA data. Differences in copy numbers are not significant on the $p < 0.05$ level.

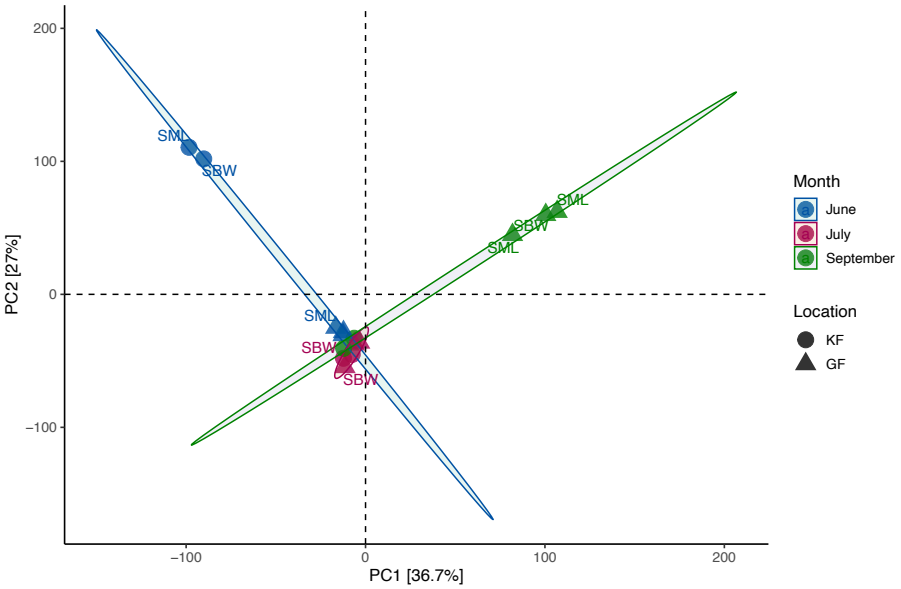

Figure S9: Principal component analysis for the eukaryotic community (18S rRNA). PC1 emerges as the most influential, encapsulating 36.7% of the total variance. Followed by PC2 (27%) collectively representing a significant portion of the compositional diversity.

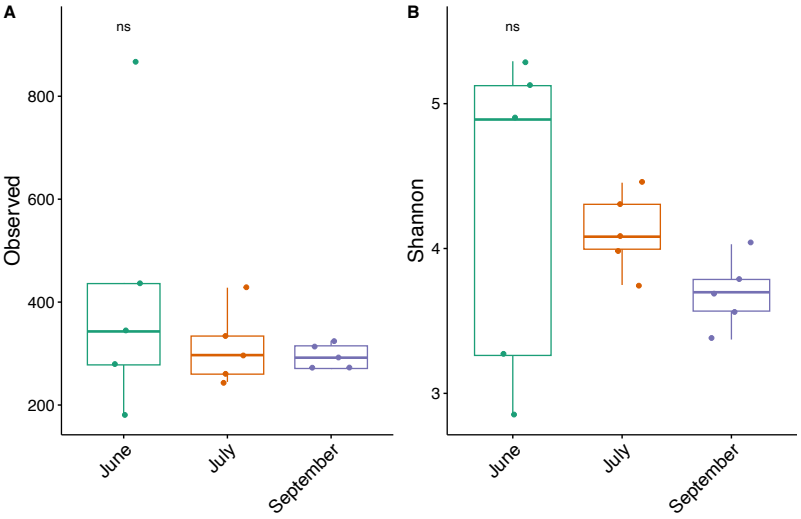

Figure S10: Observed and Shannon diversity for the 18S rRNA data. No significant differences are observed in this dataset.

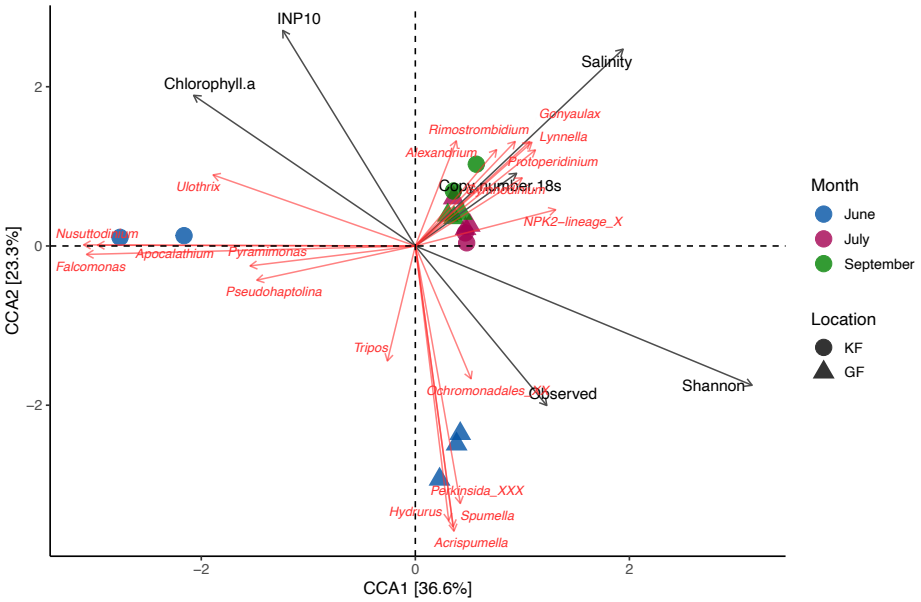

Figure S11: Canonical correspondence analysis for the 18S rRNA data (20 taxa). The total inertia in the dataset was 2.7093, partitioned into constrained and unconstrained inertias. Constrained inertia accounted for a substantial proportion (68.28%) of the total inertia.

Table S1: Mantel test for the 18S rRNA data using the robust Aitchison distance. The results indicated significant correlation for salinity and chlorophyll a and while all other variables showed no correlation ($p > 0.05$).

Variable	Correlation Coefficient	p-value	Significance
18S copy number	0.205	0.130	-
INP_{-10}	0.149	0.137	-
Salinity	0.376	0.018	*
Chlorophyll a	0.388	0.006	**
Observed alpha diversity	0.312	0.057	-
Shannon index	0.293	0.050	-

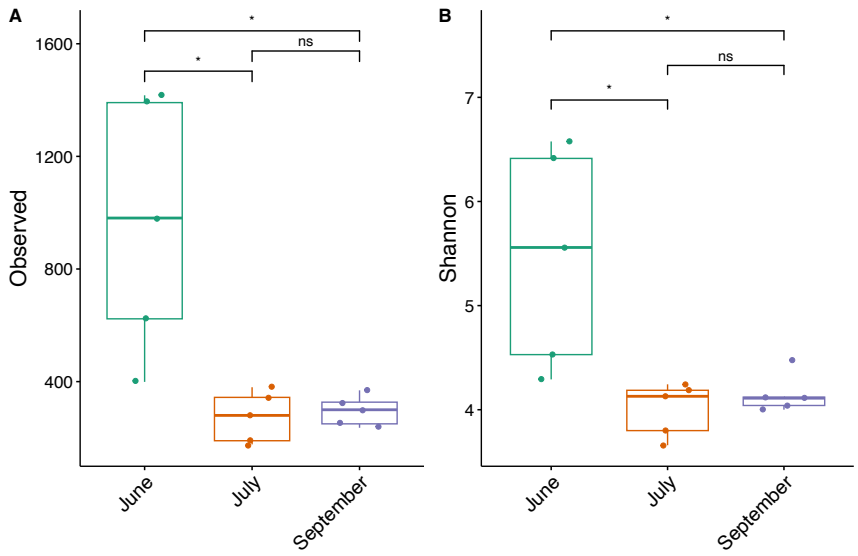

Figure S12: Observed and Shannon diversity for the 16S rRNA data. Significance is indicated by stars, n.s. stands for not significant.

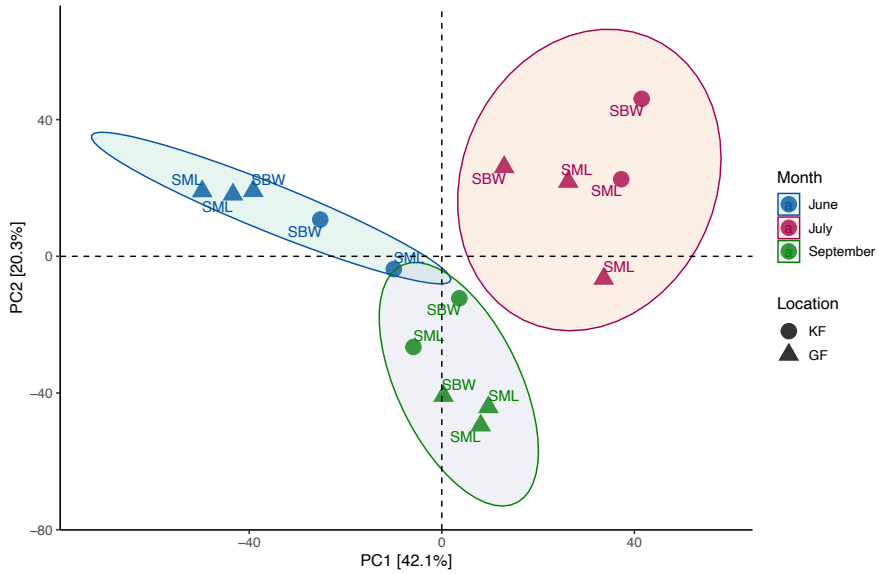

Figure S13: Principal component analysis for the bacterial community. Eigenvalues from PCA revealed that the first few principal components (PC1-PC3) contribute significantly to the variance in the bacterial community composition. PC1 was the most influential, representing 42.1% of the total variance, followed by PC2 (20.3%) and PC3 (12.6%).

Table S2: Mantel test to assess the correlation between bacterial community dissimilarities (measured using robust Aitchison distance) and environmental parameters

Variable	Correlation Coefficient	p-value	Significance
16S copy number	0.1841	0.1300	-
INP_{-10}	0.6495	0.0030	**
Salinity	0.6698	0.0030	**
Chlorophyll a	0.3111	0.0096	**
Observed alpha diversity	0.6397	0.0030	**
Shannon index	0.6493	0.0030	**

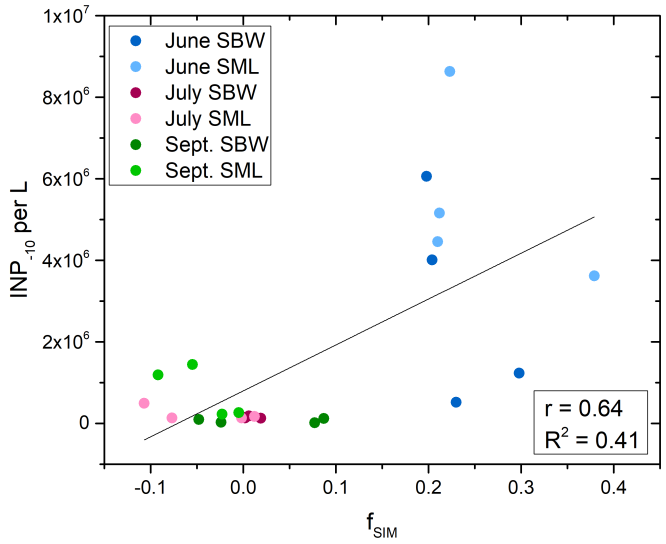

Figure S14: Correlation between the freshwater fraction of sea ice melt and the number of INPs active at -10 °C. The line represents a linear regression for all data points ($p < 0.001$).