

# 1045 Arctic phytoplankton spring bloom diversity 1046 across the marginal ice zone in Baffin Bay

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## 1066 Supplementary material

1067 All supplementary material is available at

<sup>1068</sup> **Supplementary Data**

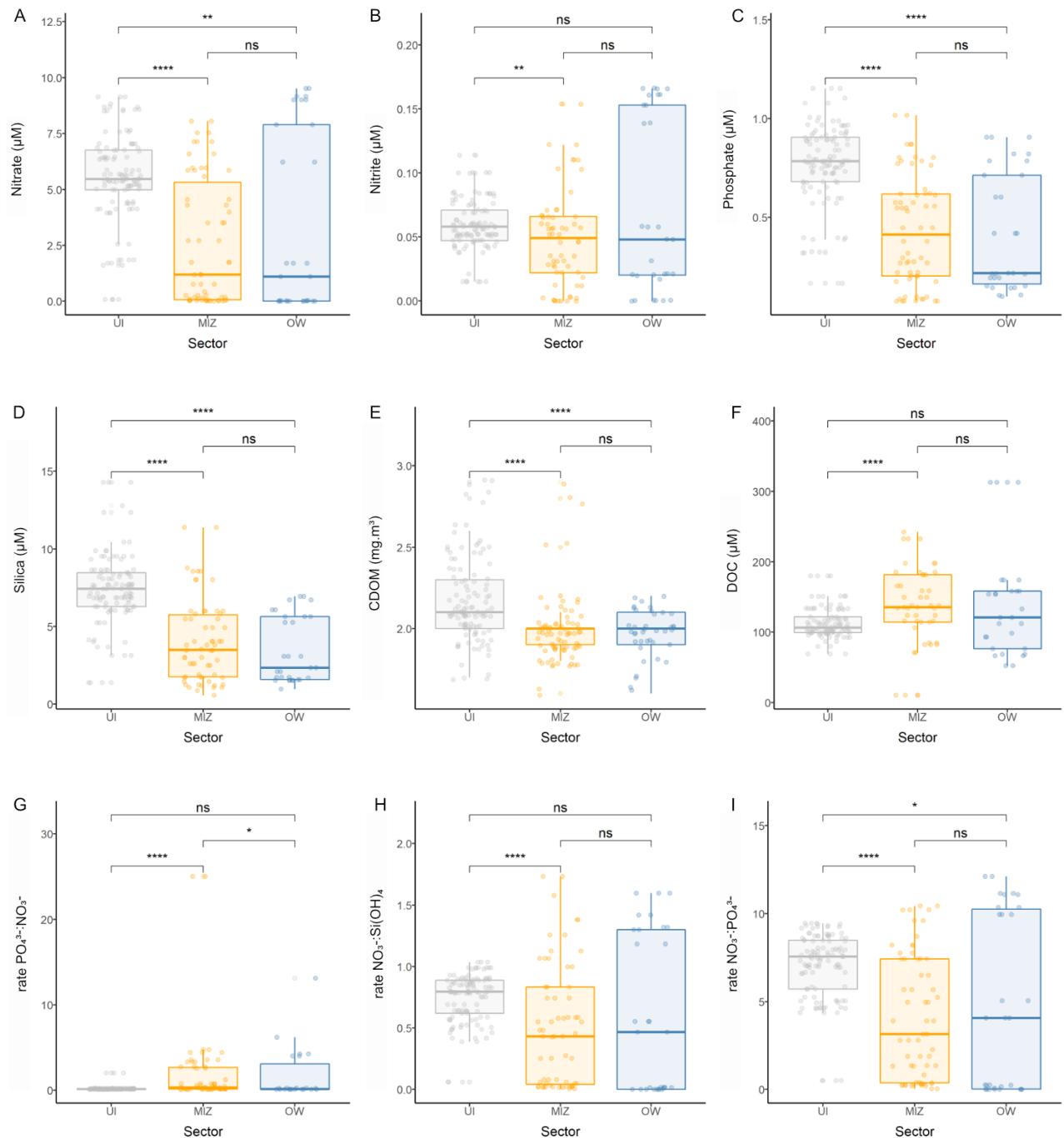
<sup>1069</sup> Supplementary Data S1: Sample dates and environmental data available.

1070 **Supplementary Tables****Table S1:** List of variables measured during the Green Edge cruise (see Data Set S1).

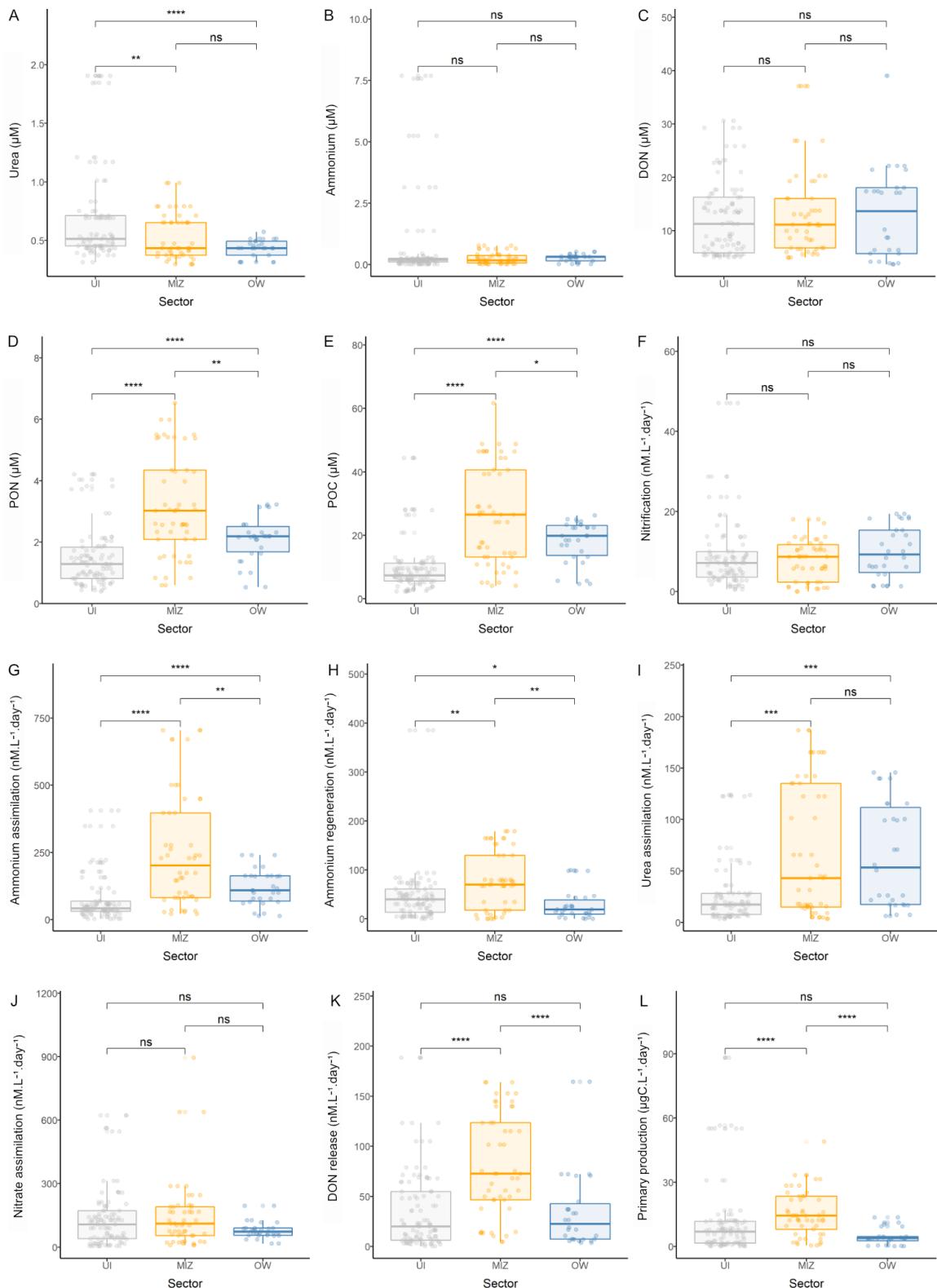
Variable	Description	Unit
sample_code	sample code	
fraction_name	size fraction	
station_id	station ID	
CTD	ID of CTD cast	
transect	cruise transect ID	
bot_depth	bottom depth at a given station	m
depth	depth at which the sample was taken	m
depth_rank	rank of sampling depth in the water column	
sampling_date	sampling date	
julian_day	julian day	
longitude	longitude coordinates	degrees east
latitude	latitude coordinates	degrees north
OWD	days a given station was ice-free	days
by_OW_minus10_10	classification of sectors based in OWD	sector
ice_concentration_percent	ice concentration cover	%
dna_concentration	dna concentration	ng. $\mu$ L $^{-1}$
dna_extraction_kit	dna extraction kit	
n_reads	number of reads after filtering	
reads_total	number of reads obtained from sequencing	
pico_ml	pico-phytoplankton abundance	cells.mL $^{-1}$
nano_ml	nano-phytoplankton abundance	cells.mL $^{-1}$
pico_and_nano_ml	pico- and nano phytoplankton abundance	cells.mL $^{-1}$
crypto_ml	cryptophyceae abundance	cells.mL $^{-1}$
bact	bacteria abundance	cells.mL $^{-1}$
temperature	temperature	degrees Celsius
fluo	fluorescence	
cdom	colored dissolved organic matter	(ppb)
salinity	salinity	
mixed_layer_depth	mixed layer depth	m
nitracline_depth	nitracline depth	m
PAR_irradiance	photosynthetically available radiation at 3 m depth	mol photons.m $^{-2}$ .d $^{-1}$

**Table S1:** (*continued*)

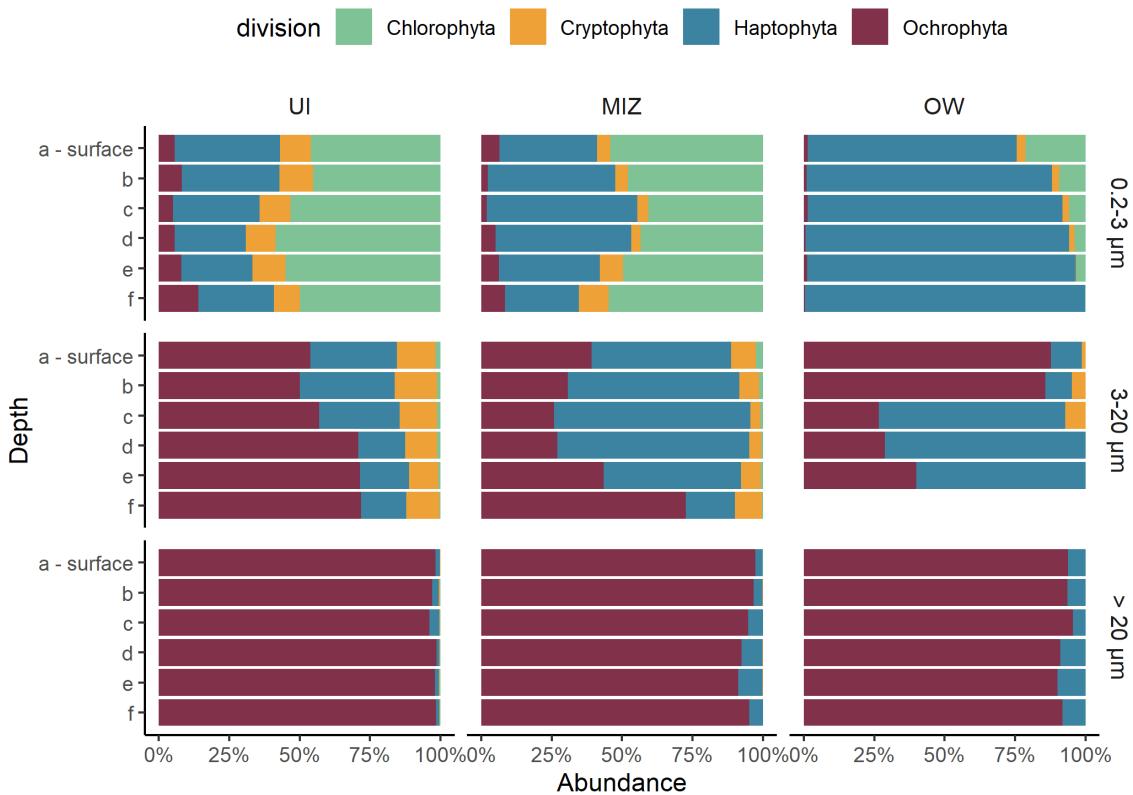
Variable	Description	Unit
primary_production	primary production	$\mu\text{gC.L}^{-1}.\text{day}^{-1}$
primary production_std_dev	primary production standard deviation	$\mu\text{gC.L}^{-1}.\text{day}^{-1}$
don_release	dissolved organic nitrogen	$\text{nM.L}^{-1}.\text{day}^{-1}$
NO3_assimilation	nitrate assimilation	$\text{nM.L}^{-1}.\text{day}^{-1}$
NH4_assimilation	ammonium assimilation	$\text{nM.L}^{-1}.\text{day}^{-1}$
urea_assimilation	urea assimilation	$\text{nM.L}^{-1}.\text{day}^{-1}$
NH4_regeneration	ammonium regeneration	$\text{nM.L}^{-1}.\text{day}^{-1}$
nitrification	nitrification	$\text{nM.L}^{-1}.\text{day}^{-1}$
poc	particulate organic carbon	$\mu\text{M}$
poc_std_dev	particulate organic carbon standard deviation	$\mu\text{M}$
pon	particulate organic nitrogen	$\mu\text{M}$
pon_std_dev	particulate organic nitrogen standard deviation	$\mu\text{M}$
doc	dissolved organic carbon	$\mu\text{M}$
don	dissolved organic nitrogen	$\mu\text{M}$
nitrate	nitrate concentration	$\mu\text{M}$
nitrite	nitrite concentration	$\mu\text{M}$
phosphate	phosphate concentration	$\mu\text{M}$
silica	orthosilicic acid concentration	$\mu\text{M}$
ammonium	ammonium concentration	$\mu\text{M}$
urea	urea concentration	$\mu\text{M}$
ratio_NO3_SiOH4	ratio nitrate to silica	
ratio_PO4_NO3	ratio phosphate to nitrate	
ratio_NO3_PO4	ratio nitrate to phosphate	
chlorophyll_a	chlorophyll a concentration	$\text{mg.m}^{-3}$
chlorophyll_b	chlorophyll b concentration	$\text{mg.m}^{-3}$



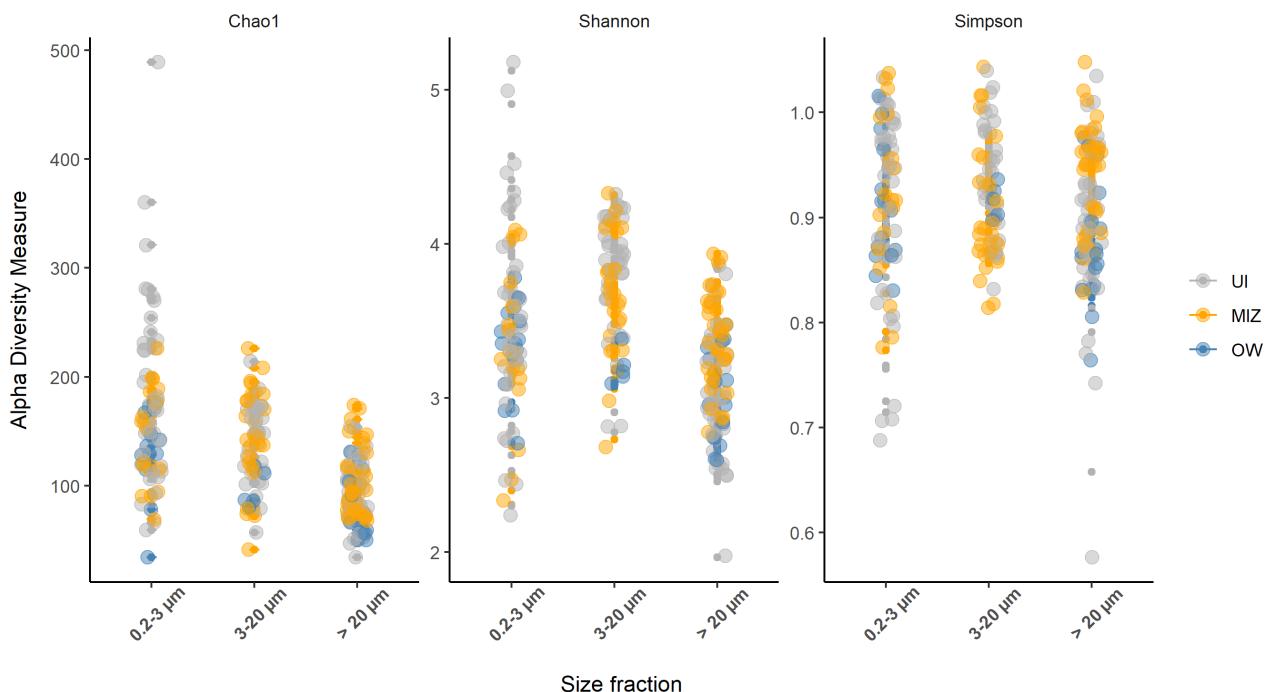
**Figure S1:** Nutrients for the three sectors: UI (grey), MIZ (yellow) and OW (blue); (A) nitrates ( $\mu\text{M}$ ); (B) nitrites ( $\mu\text{M}$ ); (C) phosphates ( $\mu\text{M}$ ); (D) orthosilicic acid ( $\mu\text{M}$ ); (E) colored dissolved organic matter ( $\text{mg.m}^{-3}$ ); (F) dissolved organic carbon ( $\mu\text{M}$ ); (G) phosphate to nitrate ratio; (H) nitrate to orthosilicic acid ratio; (I) nitrate to phosphate ratio. Number of asterisks represent  $p$ -value obtained with the Wilcoxon test as follows: (\*)  $p \leq 0.05$ ; (\*\*)  $p \leq 0.01$ ; (\*\*\*)  $p \leq 0.001$ ; (\*\*\*\*)  $p \leq 0.0001$ ; "ns" = not significant.



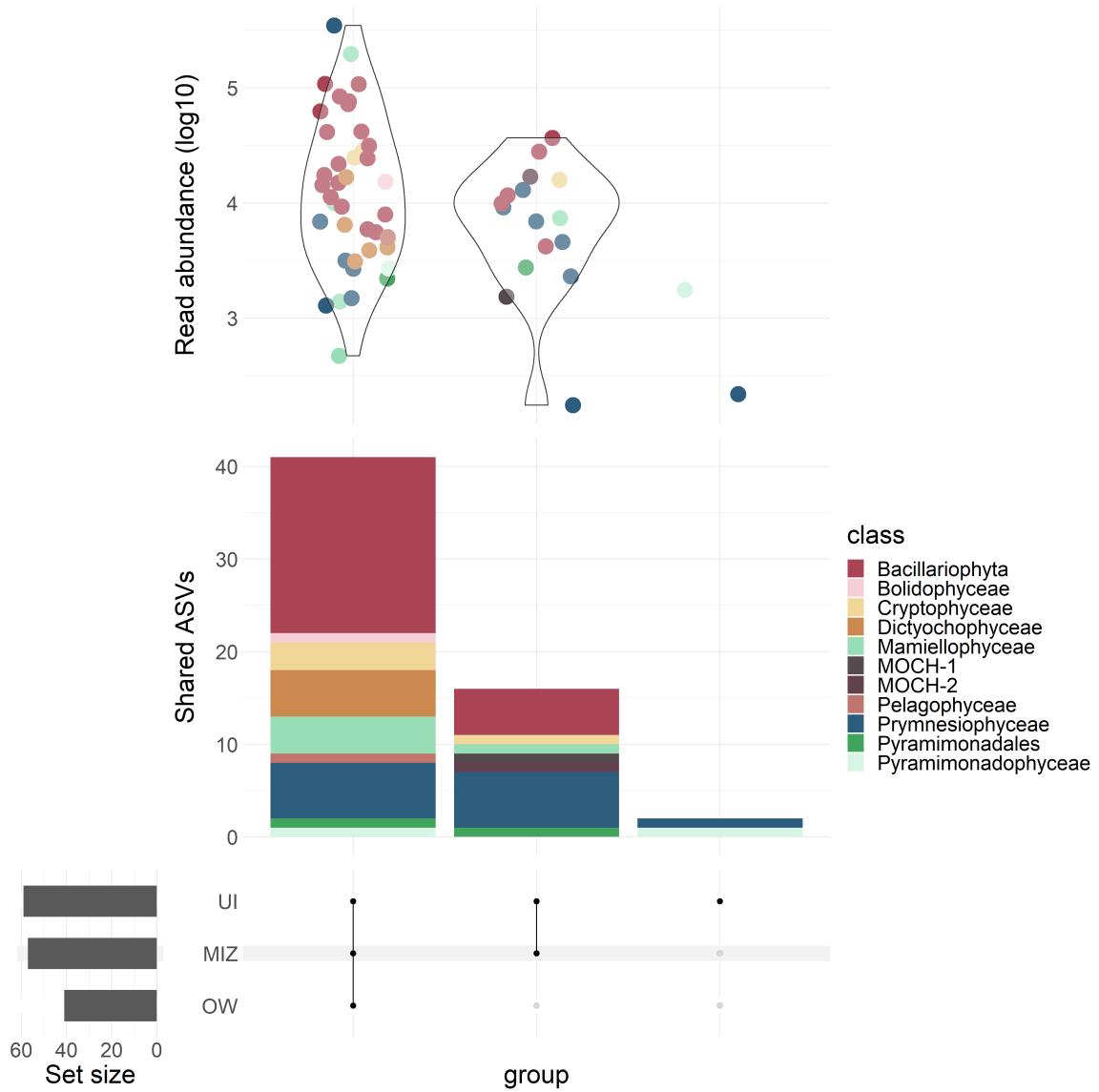
**Figure S2:** Nutrients and metabolic rates for the three sectors: UI (grey), MIZ (yellow) and OW (blue); (A) urea ( $\mu\text{M}$ ); (B) ammonium ( $\mu\text{M}$ ); (C) dissolved organic nitrogen ( $\mu\text{M}$ ); (D) particulate organic nitrogen ( $\mu\text{M}$ ); (E) particulate organic carbon ( $\text{mg.m}^{-3}$ ); (F) nitrification ( $\mu\text{M}$ ); (G) ammonium assimilation ( $\text{nM.L}^{-1}\text{day}^{-1}$ ); (H) ammonium regeneration ( $\text{nM.L}^{-1}\text{day}^{-1}$ ); (I) urea assimilation ( $\text{nM.L}^{-1}\text{day}^{-1}$ ); (J) nitrate assimilation; (K) dissolved organic nitrogen ( $\mu\text{M}$ ); (L) primary production ( $\mu\text{gC.L}^{-1}\text{day}^{-1}$ ). Number of asterisks represent  $p$ -value obtained with the Wilcoxon test as follows: (\*)  $p \leq 0.05$ ; (\*\*)  $p \leq 0.01$ ; (\*\*\*)  $p \leq 0.001$ ; (\*\*\*\*)  $p \leq 0.0001$ ; “ns” = not significant.



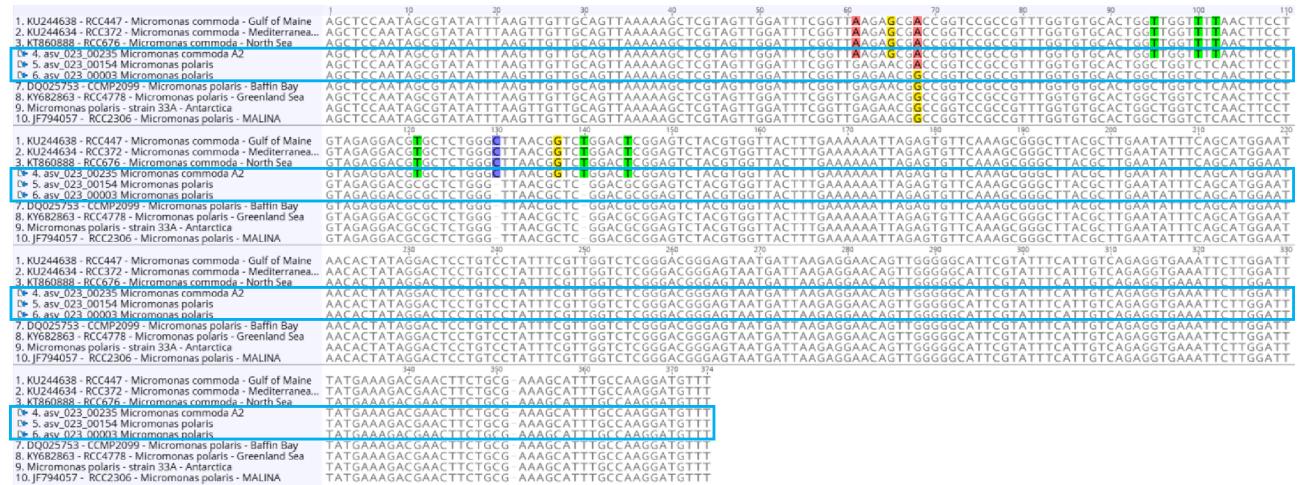
**Figure S3:** Relative abundance of reads at the division level between sectors and size fractions. UI: Under Ice; MIZ: Marginal Ice Zone; OW: Open Water; letters on the y-axis refer to the depth level where “a” corresponds to the surface and “f” to the deepest sampled depth, usually between 40 m and 60 m.



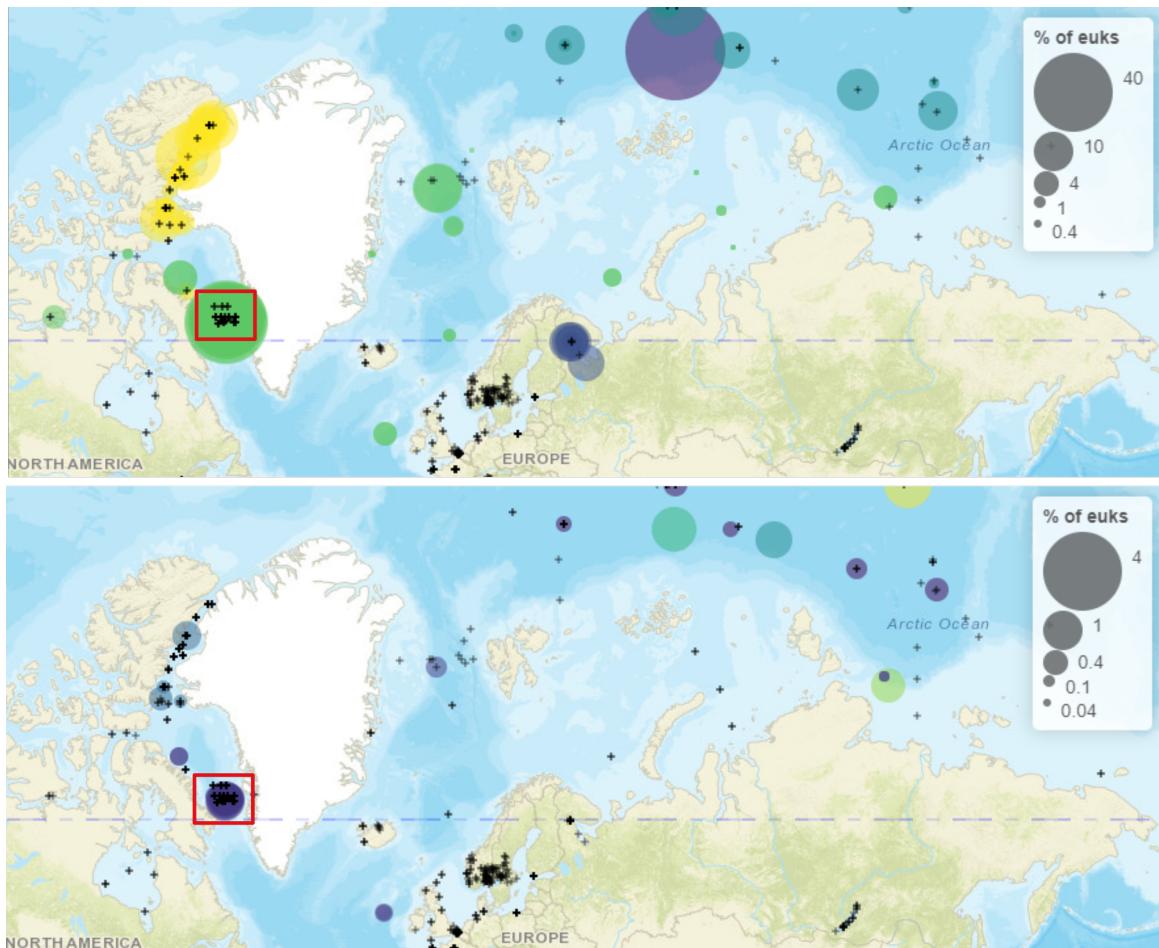
**Figure S4:** Chao1, Shannon and Simpson alpha diversity indices divided by size fraction; sectors are represented by the colors grey (UI), yellow (MIZ) and blue (OW).



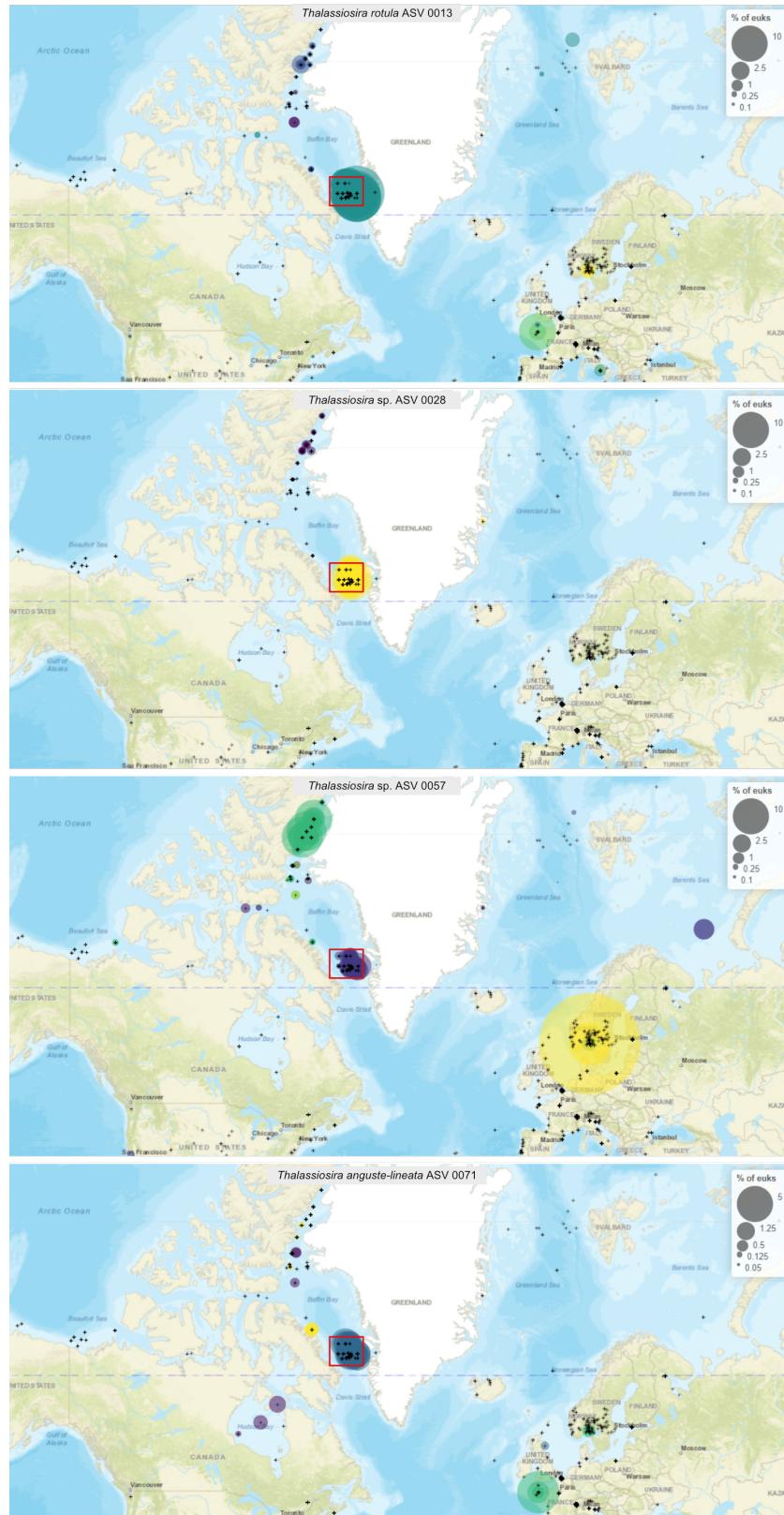
**Figure S5:** Number of ASVs from the abundant community exclusive from or shared between the sectors UI (under ice), MIZ (marginal ice-zone), and OW (open water); colors represent the class from each ASV; read abundance (in log10) is displayed at the top of each intersection; the names and assignations of the ASVs exclusive from ice-associated sectors are shown in grey panels.



**Figure S6:** Sequence alignment of the 18S rRNA of *Micromonas* ASVs showing two *M. polaris* ASVs with a single nucleotide difference, and a *M. commoda* A2 ASV.



**Figure S7:** Partial snapshot of *M. polaris* ASV\_0003 (top panel) and ASV\_0154 (lower panel) distribution in the metaPR<sup>2</sup> database showing 100% similar reads from other studies. Colors indicate different sampling campaigns within metaPR<sup>2</sup>. Size of bubbles represent the percentage in relation to other eukaryotes within each station. Note that maximum percentages are distinct between panels to compensate for the lower abundance of ASV\_0154.



**Figure S8:** Partial snapshot of *Thalassiosira* ASV\_0013 (top panel), ASV\_0057 (middle panel), and ASV\_0071 (lower panel) distribution in the metaPR<sup>2</sup> database showing 100% similar reads from other studies. Colors indicate different sampling campaigns within metaPR<sup>2</sup>. Size of bubbles represent the percentage in relation to other eukaryotes within each station. Note that maximum percentages are distinct between panels. The approximate region of sampling from the present study is marked by a red square.