

Arctic phytoplankton microdiversity across the marginal ice zone suggests sub-species vulnerability to sea-ice loss

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1385 **Supplementary material**

1386 **Supplementary Data**

1387 **Supplementary Data S1:** Sample dates and environmental data available.

1388 **Supplementary Data S2:** Indicator ASVs with their taxonomic assignation for each sector or
1389 group of sectors, divided by size fraction. "A" represents the positive predictive power of the
1390 ASV, or the probability of a sampling site being a member of the sector or group of sectors
1391 when the ASV appears in that site. "B" represents how often one ASV is found in sampling
1392 sites of the sector or group of sectors. The value of the correlation (Stat) and the statistical
1393 significance of the association (p -value) are also shown.

1394 Available in: [https://github.com/catherine-gerikas/GE_Amundsen_18S_metaB_](https://github.com/catherine-gerikas/GE_Amundsen_18S_metaB_supplementary_material)
1395 [supplementary_material](https://github.com/catherine-gerikas/GE_Amundsen_18S_metaB_supplementary_material)

1396 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 on each 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. μL^{-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 $^{-1}$
primary_production	primary production	$\mu\text{gC.L}^{-1}$.day $^{-1}$
primary_production_std_dev	primary production standard deviation	$\mu\text{gC.L}^{-1}$.day $^{-1}$

Table S1: *(continued)*

Variable	Description	Unit
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	μM
poc_std_dev	particulate organic carbon standard deviation	μM
pon	particulate organic nitrogen	μM
pon_std_dev	particulate organic nitrogen standard deviation	μM
doc	dissolved organic carbon	μM
don	dissolved organic nitrogen	μM
nitrate	nitrate concentration	μM
nitrite	nitrite concentration	μM
phosphate	phosphate concentration	μM
silica	orthosilicic acid concentration	μM
ammonium	ammonium concentration	μM
urea	urea concentration	μM
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	mg.m^{-3}
chlorophyll_b	chlorophyll b concentration	mg.m^{-3}

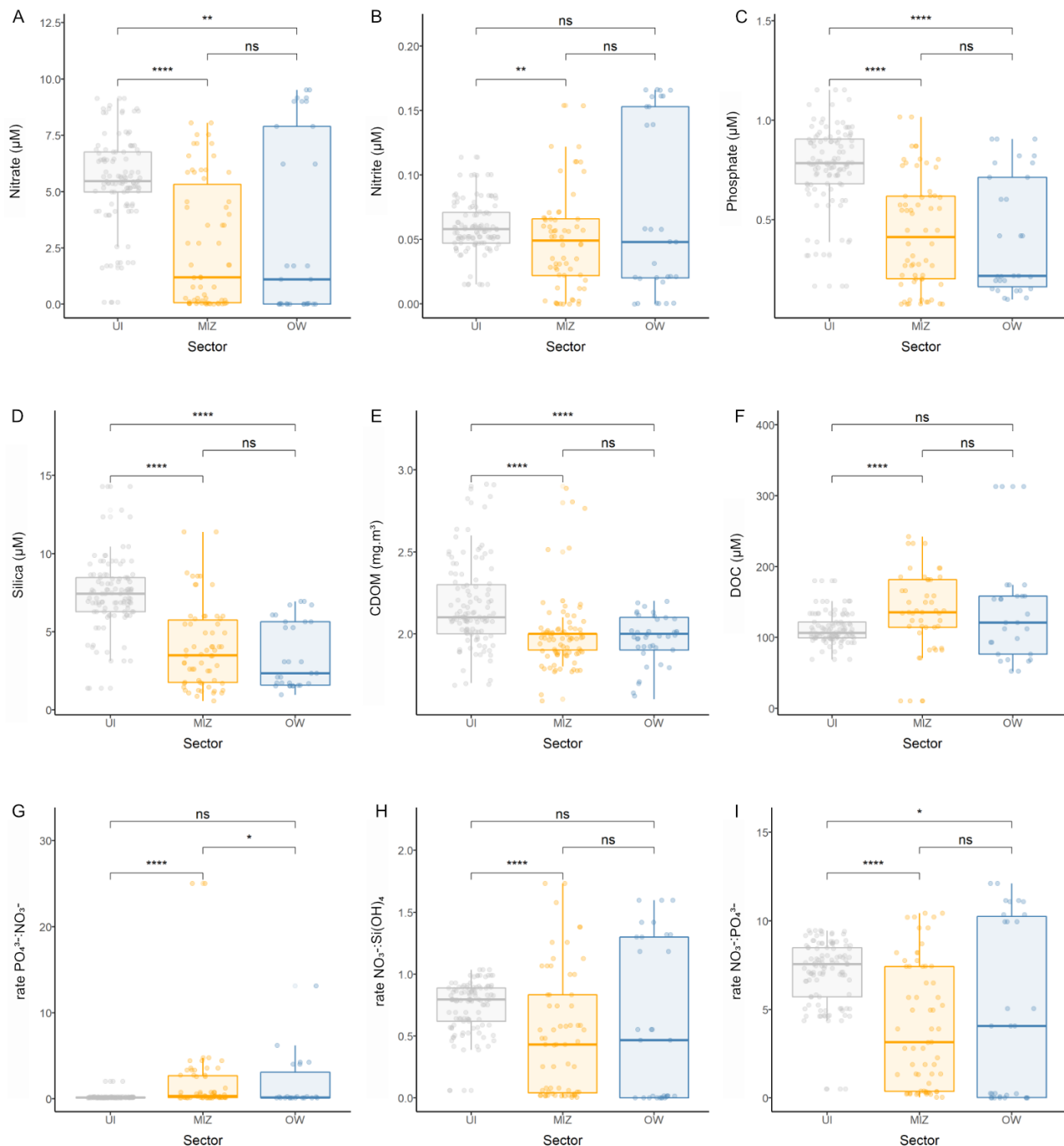


Figure S1. Nutrients for the three sectors: UI (grey), MIZ (yellow) and OW (blue); (A) nitrates (μM); (B) nitrites (μM); (C) phosphates (μM); (D) orthosilicic acid (μM); (E) colored dissolved organic matter (mg.m^{-3}); (F) dissolved organic carbon (μM); (G) phosphate to nitrate ratio; (H) nitrate to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

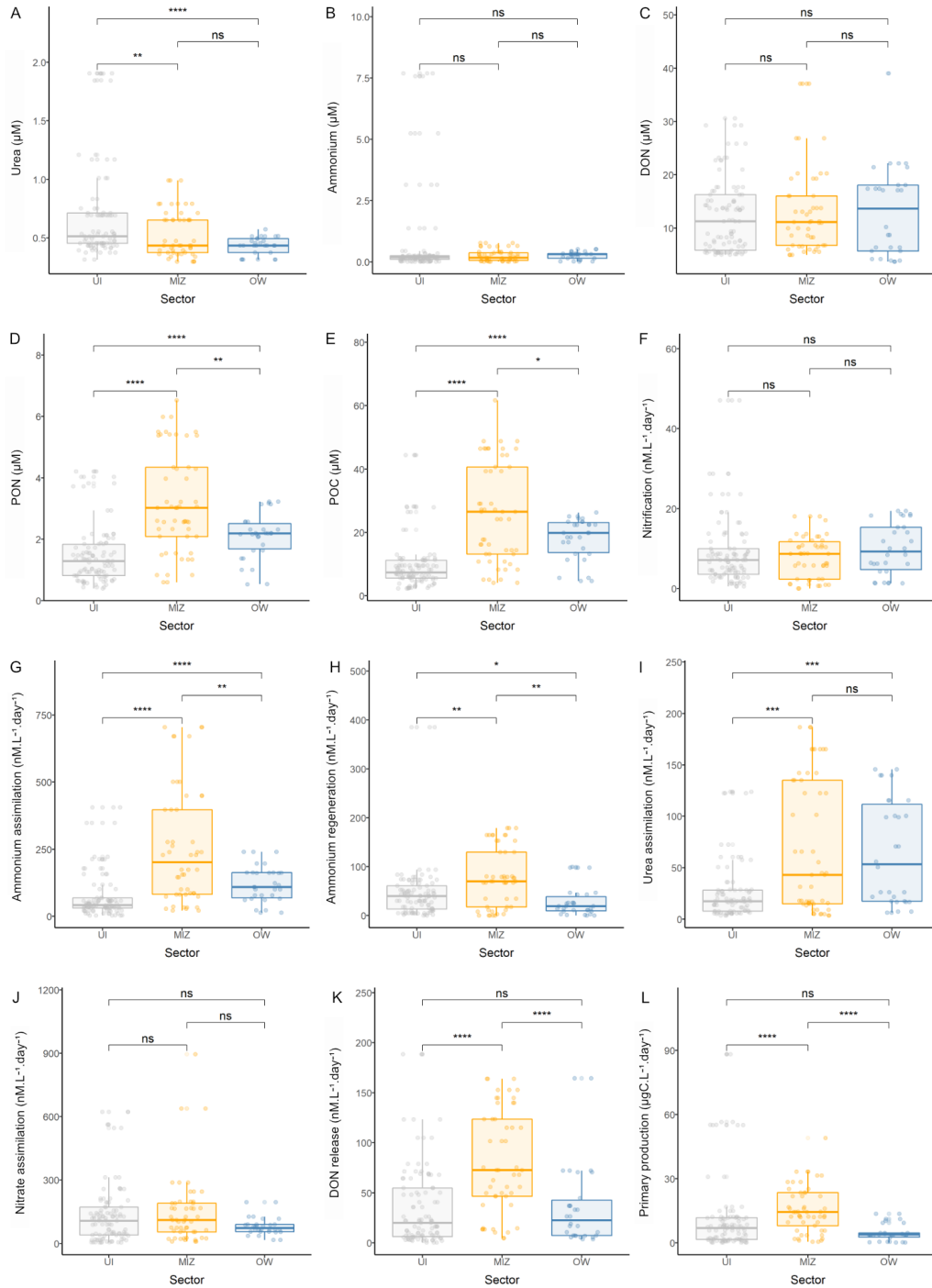


Figure S2. Nutrients and metabolic rates for the three sectors: Under-Ice, UI (grey), Marginal Ice Zone, MIZ (yellow) and Open Water, OW (blue); (A) urea (μM); (B) ammonium (μM); (C) dissolved organic nitrogen (μM); (D) particulate organic nitrogen (μM); (E) particulate organic carbon (mg.m^3); (F) nitrification (μM); (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 (μM); (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.**

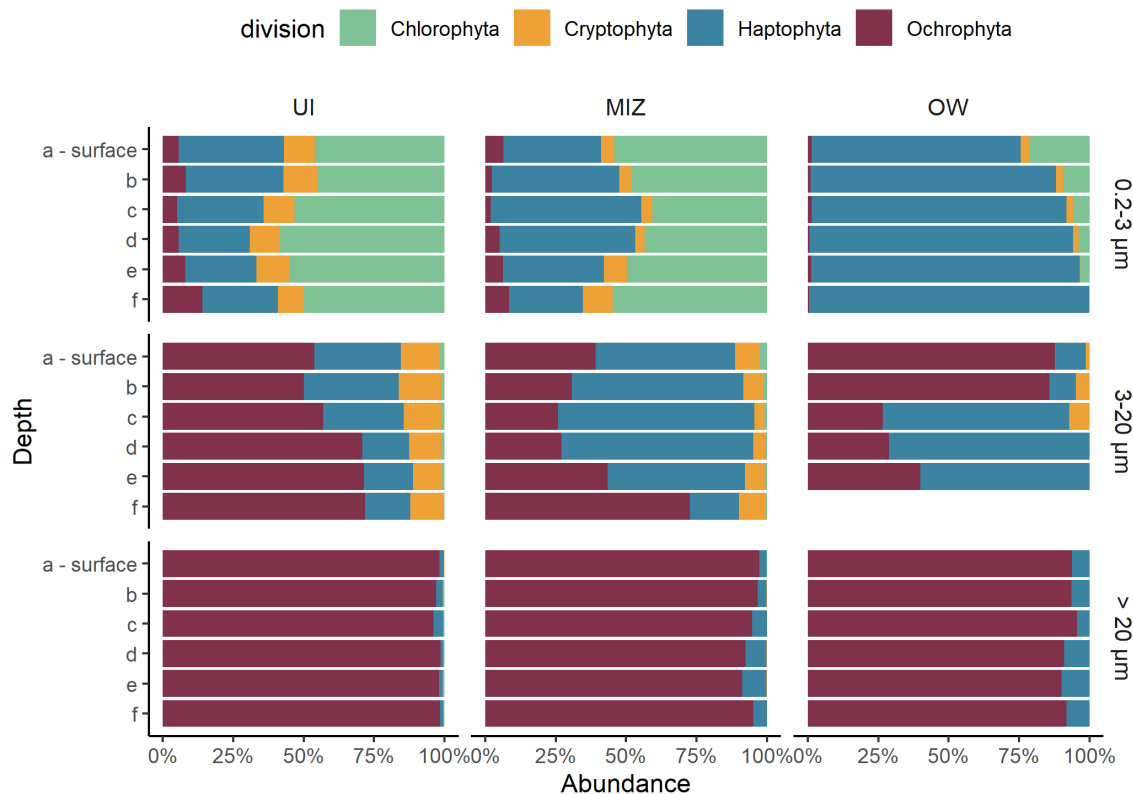


Figure S3. Relative abundance of reads at the division level between sectors and size fractions. UI: Under-Ice; MIZ: Marginal Ice Zone; OW: Open Water; letters on the y-axis refer to the depth level where “a” corresponds to the surface and “f” to the deepest sampled depth, usually between 40m and 60m.

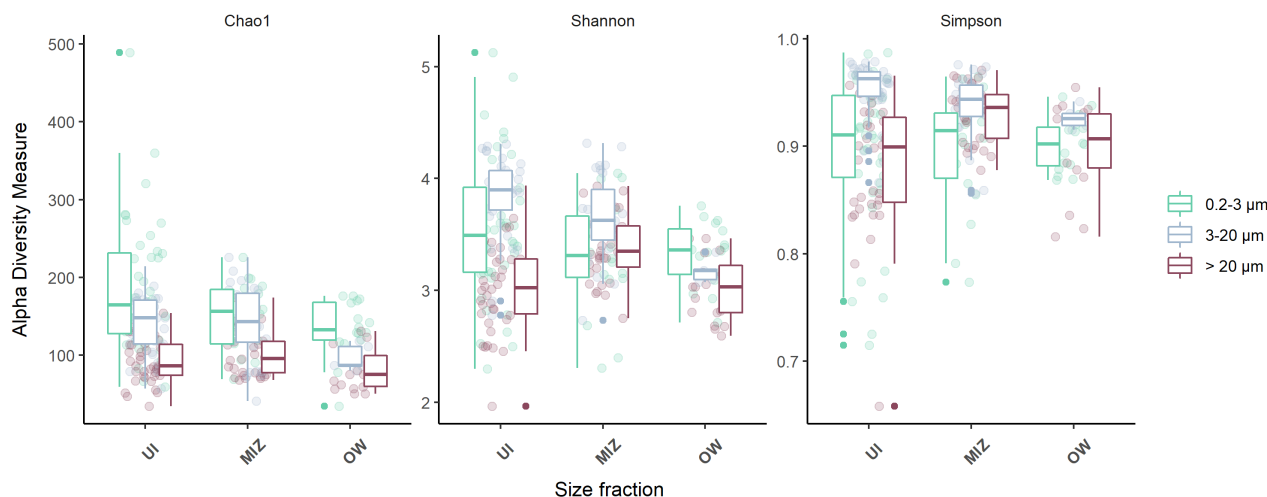


Figure S4. Chao1, Shannon and Simpson alpha diversity indices divided by size fraction; sectors are represented by the colors grey (UI), yellow (MIZ) and blue (OW).

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Micromonas polaris - CCMP2099 - DQ025753 1 AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGTTGAGAACGTCGGTCCGCCGTTTGGTGTGCACCTGGCTGGTCTCAACT
Micromonas polaris - asv_00003 AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGTTGAGAACGTCGGTCCGCCGTTTGGTGTGCACCTGGCTGGTCTCAACT
Micromonas polaris - asv_00154 AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGTTGAGAACGTCGGTCCGCCGTTTGGTGTGCACCTGGCTGGTCTCAACT
Micromonas commoda A2 - asv_00235 AGCTCCAATAGCGTATATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCGGTTGAGAACGTCGGTCCGCCGTTTGGTGTGCACCTGGCTGGTCTCAACT

Micromonas polaris - CCMP2099 - DQ025753 TCCTGTAGAGGACGCGCTCTGGG TTAACGCTC GGACGCGGAGTCTACGTGGTTACTTTGAAAAAATTAGAGTGTTCAAAGCGGGCTTACGCTTGAATATTTTCAG
Micromonas polaris - asv_00003 TCCTGTAGAGGACGCGCTCTGGG TTAACGCTC GGACGCGGAGTCTACGTGGTTACTTTGAAAAAATTAGAGTGTTCAAAGCGGGCTTACGCTTGAATATTTTCAG
Micromonas polaris - asv_00154 TCCTGTAGAGGACGCGCTCTGGG TTAACGCTC GGACGCGGAGTCTACGTGGTTACTTTGAAAAAATTAGAGTGTTCAAAGCGGGCTTACGCTTGAATATTTTCAG
Micromonas commoda A2 - asv_00235 TCCTGTAGAGGACGCGCTCTGGG TTAACGCTC GGACGCGGAGTCTACGTGGTTACTTTGAAAAAATTAGAGTGTTCAAAGCGGGCTTACGCTTGAATATTTTCAG

Micromonas polaris - CCMP2099 - DQ025753 CATGGAATAACACTATAGGACTCCTGTCCTATTTTCGTTGGTCTCGGGACGGGAGTAATGATTAAAGAGGAACAGTTGGGGGCATTTCGTATTTTCATTGTCAGAGGTGA
Micromonas polaris - asv_00003 CATGGAATAACACTATAGGACTCCTGTCCTATTTTCGTTGGTCTCGGGACGGGAGTAATGATTAAAGAGGAACAGTTGGGGGCATTTCGTATTTTCATTGTCAGAGGTGA
Micromonas polaris - asv_00154 CATGGAATAACACTATAGGACTCCTGTCCTATTTTCGTTGGTCTCGGGACGGGAGTAATGATTAAAGAGGAACAGTTGGGGGCATTTCGTATTTTCATTGTCAGAGGTGA
Micromonas commoda A2 - asv_00235 CATGGAATAACACTATAGGACTCCTGTCCTATTTTCGTTGGTCTCGGGACGGGAGTAATGATTAAAGAGGAACAGTTGGGGGCATTTCGTATTTTCATTGTCAGAGGTGA

Micromonas polaris - CCMP2099 - DQ025753 AATTCTTGGATTATGAAAGACGAACCTTCTGCGAAAGCATTTTGCCAAAGGATGTTT
Micromonas polaris - asv_00003 AATTCTTGGATTATGAAAGACGAACCTTCTGCGAAAGCATTTTGCCAAAGGATGTTT
Micromonas polaris - asv_00154 AATTCTTGGATTATGAAAGACGAACCTTCTGCGAAAGCATTTTGCCAAAGGATGTTT
Micromonas commoda A2 - asv_00235 AATTCTTGGATTATGAAAGACGAACCTTCTGCGAAAGCATTTTGCCAAAGGATGTTT

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Figure S5. Sequence alignment of the partial 18S rRNA of *Micromonas* ASVs found in the present study (*M. polaris* ASVs 0003/0154; *M. commoda* A2 0235) and the type-strain of *M. polaris* (CCMP2099).

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Baffinella frigidus - CCMP2045 - GQ375264 1 CGGATTTTCGGGCTCGGGACGCTGTCCGGTCGGTCCGAGCGGACGGCTCGGGCCCTTCTGCCTGGGACCTCCGTCACACTTAACTGTGGGGCGGTTGGACGACGGCCG
Baffinella frigidus - RCC5246 - MH764727 CGGATTTTCGGGCTCGGGACGCTGTCCGGTCGGTCCGAGCGGACGGCTCGGGCCCTTCTGCCTGGGACCTCCGTCACACTTAACTGTGGGGCGGTTGGACGACGGCCG
Baffinella frigidus - asv_00041 CGGATTTTCGGGCTCGGGACGCTGTCCGGTCGGTCCGAGCGGACGGCTCGGGCCCTTCTGCCTGGGACCTCCGTCACACTTAACTGTGGGGCGGTTGGACGACGGCCG
Baffinella frigidus - asv_00055 CGGATTTTCGGGCTCGGGACGCTGTCCGGTCGGTCCGAGCGGACGGCTCGGGCCCTTCTGCCTGGGACCTCCGTCACACTTAACTGTGGGGCGGTTGGACGACGGCCG
Baffinella frigidus - asv_00346 CGGATTTTCGGGCTCGGGACGCTGTCCGGTCGGTCCGAGCGGACGGCTCGGGCCCTTCTGCCTGGGACCTCCGTCACACTTAACTGTGGGGCGGTTGGACGACGGCCG

Baffinella frigidus - CCMP2045 - GQ375264 TTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCCTACGCTTGAATACATTAGCATGGAATAATGGAATAGGACTTTGGTGTCTATTTTGTGGTTTATGGGACCGAA
Baffinella frigidus - RCC5246 - MH764727 TTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCCTACGCTTGAATACATTAGCATGGAATAATGGAATAGGACTTTGGTGTCTATTTTGTGGTTTATGGGACCGAA
Baffinella frigidus - asv_00041 TTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCCTACGCTTGAATACATTAGCATGGAATAATGGAATAGGACTTTGGTGTCTATTTTGTGGTTTATGGGACCGAA
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Baffinella frigidus - CCMP2045 - GQ375264 GTAATGATTAAACAGGGACAGTTGGGGCCGTTTATATTTTCGTTGTGACAGGTTGAAATCTTGGATTACGAAAGATAAACTTCTGCGAAAGCATTTCGGCAAGGATGTTT
Baffinella frigidus - RCC5246 - MH764727 GTAATGATTAAACAGGGACAGTTGGGGCCGTTTATATTTTCGTTGTGACAGGTTGAAATCTTGGATTACGAAAGATAAACTTCTGCGAAAGCATTTCGGCAAGGATGTTT
Baffinella frigidus - asv_00041 GTAATGATTAAACAGGGACAGTTGGGGCCGTTTATATTTTCGTTGTGACAGGTTGAAATCTTGGATTACGAAAGATAAACTTCTGCGAAAGCATTTCGGCAAGGATGTTT
Baffinella frigidus - asv_00055 GTAATGATTAAACAGGGACAGTTGGGGCCGTTTATATTTTCGTTGTGACAGGTTGAAATCTTGGATTACGAAAGATAAACTTCTGCGAAAGCATTTCGGCAAGGATGTTT
Baffinella frigidus - asv_00346 GTAATGATTAAACAGGGACAGTTGGGGCCGTTTATATTTTCGTTGTGACAGGTTGAAATCTTGGATTACGAAAGATAAACTTCTGCGAAAGCATTTCGGCAAGGATGTTT

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Figure S6. Sequence alignment of the partial 18S rRNA of *B. frigidus* found in the present study (ASVs 0041/0055/0346) and the type-strain of *B. frigidus* description (CCMP2045)

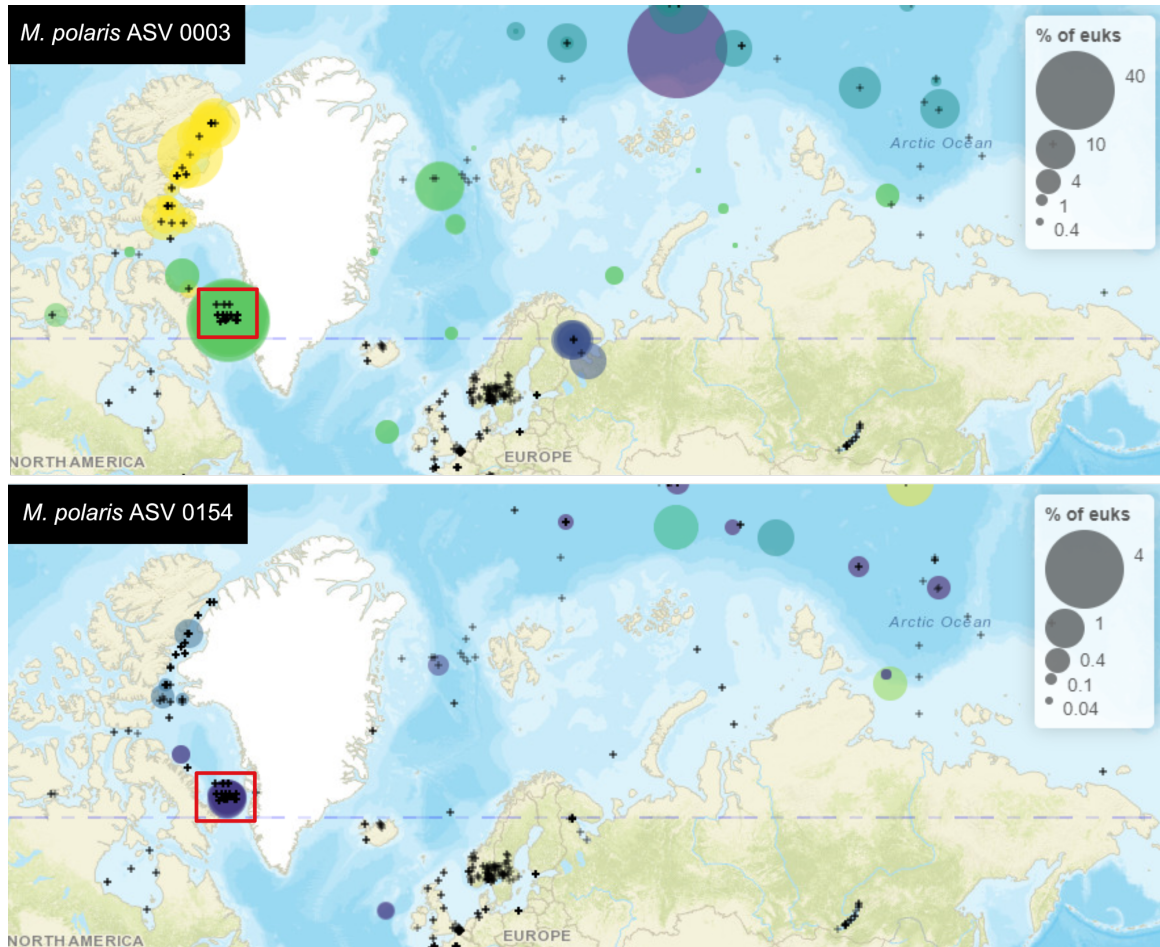


Figure S7. Partial snapshot of *M. polaris* ASV_0003 (top panel) and ASV_0154 (lower panel) distribution in the metaPR² database showing 100% similar reads from other studies. Colors indicate different sampling campaigns within metaPR². Size of bubbles represent the percentage in relation to other eukaryotes within each station. Note that maximum percentages are distinct between panels to compensate for the lower abundance of ASV_0154.

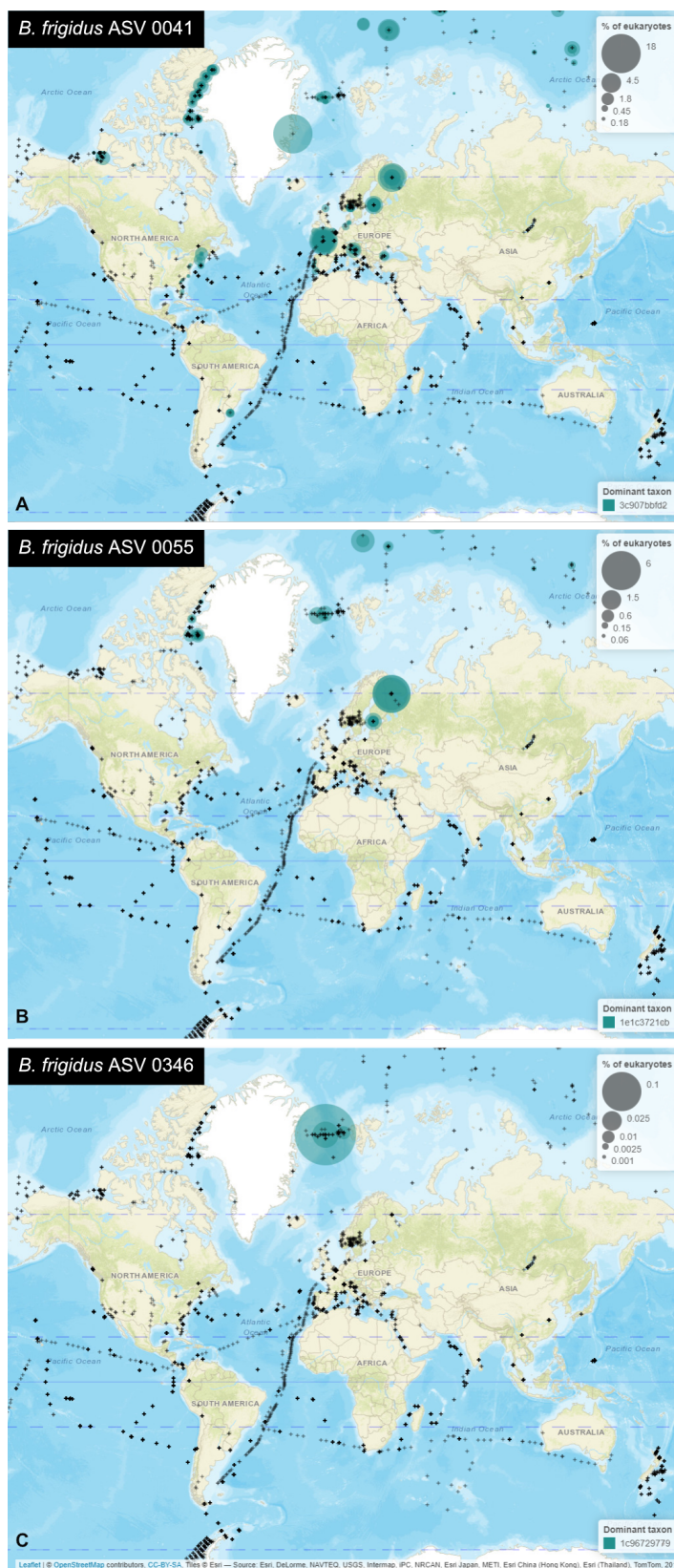


Figure S8. *B. frigidus* ASV_0041 (A), ASV_0055 (B), and ASV_0346 (C) distribution in the metaPR² database showing 100% similar reads from other studies. Size of bubbles represent the percentage in relation to other eukaryotes within each station. Note that maximum percentages are distinct between panels