

1308 **Arctic phytoplankton microdiversity across the**  
1309 **marginal ice zone: sub-species vulnerability to**  
1310 **sea-ice loss**

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<sup>1337</sup> *cromonas polaris*, *Baffinella frigidus*

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<sub>1339</sub> **Supplementary material**

<sub>1340</sub> Supplementary Data

<sub>1341</sub> Supplementary Data S1: Sample dates and environmental data used in the analyses of this  
<sub>1342</sub> study are available at [https://github.com/catherine-gerikas/GE\\_Amundsen\\_18S\\_metaB\\_supplementary\\_material](https://github.com/catherine-gerikas/GE_Amundsen_18S_metaB_supplementary_material)  
<sub>1343</sub>

<sup>1344</sup> Supplementary Tables

Table S1: List of variables measured during the Green Edge cruise (see Data 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	$\text{ng } \mu\text{L}^{-1}$
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	$\text{cells mL}^{-1}$
nano_ml	nano-phytoplankton abundance	$\text{cells mL}^{-1}$
pico_and_nano_ml	pico- and nano phytoplankton abundance	$\text{cells mL}^{-1}$
crypto_ml	cryptophyceae abundance	$\text{cells mL}^{-1}$
bact	bacteria abundance	$\text{cells mL}^{-1}$
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	$\text{mol photons m}^{-2} \text{ d}^{-1}$
primary_production	primary production	$\mu\text{gC L}^{-1} \text{ day}^{-1}$
primary_production_std_dev	primary production standard deviation	$\mu\text{gC L}^{-1} \text{ day}^{-1}$

Table S1: (*continued*)

<b>Variable</b>	<b>Description</b>	<b>Unit</b>
don_release	dissolved organic nitrogen	nM L <sup>-1</sup> day <sup>-1</sup>
NO3_assimilation	nitrate assimilation	nM L <sup>-1</sup> day <sup>-1</sup>
NH4_assimilation	ammonium assimilation	nM L <sup>-1</sup> day <sup>-1</sup>
urea_assimilation	urea assimilation	nM L <sup>-1</sup> day <sup>-1</sup>
NH4_regeneration	ammonium regeneration	nM L <sup>-1</sup> day <sup>-1</sup>
nitrification	nitrification	nM L <sup>-1</sup> day <sup>-1</sup>
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 <sup>-3</sup>
chlorophyll_b	chlorophyll b concentration	mg m <sup>-3</sup>

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

Size fraction ( $\mu\text{m}$ )	Sectors	ASVs	Class	Species	A	B	Stat	p.value	Sign
0.2–3	MIZ	asv_00049	Bacillariophyta	Navicula_sp.	0.74	0.39	0.54	0.006	**
0.2–3	MIZ	asv_00008	Bacillariophyta	Thalassiosira_antarctica	0.51	0.78	0.63	0.02	*
0.2–3	MIZ+OW	asv_00016	Bacillariophyta	Porosira_glacialis	0.87	0.53	0.68	0.0006	***
0.2–3	MIZ+OW	asv_00136	Bacillariophyta	Chaetoceros_decipiens	0.91	0.88	0.9	0.0001	***
0.2–3	MIZ+OW	asv_00247	Prymnesiophyceae	Prymnesiophyceae_Clade_E_XX_sp.	0.93	0.5	0.68	0.0008	***
0.2–3	MIZ+UI	asv_00041	Cryptophyceae	Baffinella_frigidus	0.95	0.91	0.93	0.0001	***
0.2–3	MIZ+UI	asv_00046	Bacillariophyta	Pseudo-nitzschia_seriata	1	0.59	0.77	0.0002	***
0.2–3	MIZ+UI	asv_00048	Bacillariophyta	Chaetoceros_neogracilis	0.97	0.79	0.88	0.0001	***
0.2–3	MIZ+UI	asv_00055	Cryptophyceae	Baffinella_frigidus	1	0.57	0.75	0.0003	***
0.2–3	MIZ+UI	asv_00061	MOCH-2	MOCH-2_XXX_sp.	1	0.78	0.88	0.0001	***
0.2–3	MIZ+UI	asv_00073	Bolidophyceae	Triparma_laevis_clade	0.97	0.76	0.86	0.0002	***
0.2–3	MIZ+UI	asv_00075	Dictyochophyceae	Dictyocha_speculum	1	0.62	0.79	0.0001	***
0.2–3	MIZ+UI	asv_00081	Mamiellophyceae	Bathycoccus_prasinus	0.96	0.91	0.94	0.0001	***
0.2–3	MIZ+UI	asv_00114	Dictyochophyceae	Florenciellales_X_sp.	0.98	0.66	0.8	0.0003	***
0.2–3	MIZ+UI	asv_00133	Pelagophyceae	Pelagomonas_calceolata	0.98	0.83	0.9	0.0001	***
0.2–3	MIZ+UI	asv_00151	Dictyochophyceae	Florenciella_parvula	0.97	0.83	0.9	0.0001	***
0.2–3	MIZ+UI	asv_00235	Mamiellophyceae	Micromonas_commoda_A2	0.96	0.9	0.93	0.0001	***
0.2–3	MIZ+UI	asv_00236	Dictyochophyceae	Pseudochattonella_sp.	1	0.76	0.87	0.0001	***
0.2–3	MIZ+UI	asv_00105	Prymnesiophyceae	Phaeocystis_cordata	1	0.5	0.71	0.001	**
0.2–3	MIZ+UI	asv_00154	Mamiellophyceae	Micromonas_polaris	1	0.48	0.7	0.001	**
0.2–3	MIZ+UI	asv_00086	Prymnesiophyceae	Chrysochromulina_sp.	1	0.33	0.57	0.03	*
0.2–3	MIZ+UI	asv_00192	Prymnesiophyceae	Haptolina_sp.	0.94	0.45	0.65	0.04	*
0.2–3	MIZ+UI	asv_00267	Mamiellophyceae	Dolichomastigaceae-B_sp.	1	0.29	0.54	0.04	*
0.2–3	OW	asv_00156	Chrysophyceae	Chrysophyceae_Clade_H_X_sp.	0.81	0.88	0.84	0.0001	***
0.2–3	OW	asv_00248	Chrysophyceae	Chrysophyceae_Clade_H_X_sp.	0.86	0.94	0.9	0.0001	***
0.2–3	OW	asv_00421	Mamiellophyceae	Dolichomastigaceae-B_sp.	0.89	0.44	0.62	0.0002	***
0.2–3	OW	asv_00593	Dictyochophyceae	Pedinellales_X_sp.	1	0.5	0.71	0.0001	***
0.2–3	OW	asv_00666	Chrysophyceae	Chrysophyceae_Clade_I_X_sp.	1	0.38	0.61	0.0002	***
0.2–3	OW	asv_00731	Dictyochophyceae	Pedinellales_X_sp.	1	0.31	0.56	0.0002	***

Table S2: (continued)

Size fraction ( $\mu\text{m}$ )	Sectors	ASVs	Class	Species	A	B	Stat	p.value	Sign
0.2–3	OW	asv_00223	Prymnesiophyceae	Prymnesiophyceae_Clade_F_XX_sp.	0.89	0.19	0.41	0.02	*
0.2–3	OW	asv_00949	Mamiellophyceae	Dolichomastigaceae_B_sp.	1	0.13	0.35	0.05	*
0.2–3	UI	asv_00009	Bacillariophyta	Melosira_arctica	0.98	0.7	0.83	0.0003	***
0.2–3	UI	asv_00015	Bacillariophyta	Fragilariopsis_cylindrus	0.93	0.75	0.83	0.0001	***
0.2–3	UI	asv_00104	Mamiellophyceae	Mantoniella_squamata	1	0.48	0.69	0.0002	***
0.2–3	UI	asv_00125	Prymnesiophyceae	Phaeocystis_sp.	0.93	0.75	0.84	0.0001	***
0.2–3	UI	asv_00171	Bacillariophyta	Raphid-pennate_X_sp.	0.97	0.68	0.81	0.0001	***
0.2–3	UI	asv_00244	Pyramimonadophyceae	Pterosperma_sp.	1	0.43	0.65	0.0002	***
0.2–3	UI	asv_00311	Pelagophyceae	Ankylochrysis_sp.	0.96	0.48	0.67	0.0007	***
0.2–3	UI	asv_00381	Haptophyta_Clade_HAP4	Haptophyta_Clade_HAP4_XXX_sp.	1	0.28	0.52	0.008	**
0.2–3	UI	asv_00384	Mamiellophyceae	Dolichomastigaceae_B_sp.	1	0.33	0.57	0.003	**
0.2–3	UI	asv_00239	Prymnesiophyceae	Chrysochromulina_sp.	1	0.23	0.47	0.02	*
0.2–3	UI	asv_00472	Chrysophyceae	Chrysophyceae_Clade_F_X_sp.	1	0.23	0.47	0.02	*
0.2–3	UI	asv_00537	Chrysophyceae	Chrysophyceae_Clade_H_X_sp.	1	0.2	0.45	0.04	*
3–20	MIZ	asv_00049	Bacillariophyta	Navicula_sp.	0.82	0.89	0.85	0.0007	***
3–20	MIZ	asv_00016	Bacillariophyta	Porosira_glacialis	0.82	0.74	0.78	0.004	**
3–20	MIZ	asv_00008	Bacillariophyta	Thalassiosira_antarctica	0.77	0.74	0.76	0.02	*
3–20	MIZ	asv_00064	Bacillariophyta	Fragilaria_sp.	0.89	0.44	0.63	0.02	*
3–20	MIZ	asv_00277	Bacillariophyta	Naviculales_sp.	0.93	0.37	0.59	0.05	*
3–20	MIZ	asv_00164	Chrysophyceae	Paraphysomonas_foraminifera	1	0.44	0.67	0.01	*
3–20	MIZ	asv_00347	MOCH-2	MOCH-2_XXX_sp.	0.89	0.59	0.73	0.01	*
3–20	MIZ+OW	asv_00223	Prymnesiophyceae	Prymnesiophyceae_Clade_F_XX_sp.	0.9	0.5	0.67	0.03	*
3–20	MIZ+OW	asv_00079	Bacillariophyta	Eucampia_sp.	0.93	0.75	0.83	0.001	***
3–20	MIZ+OW	asv_00136	Bacillariophyta	Chaetoceros_decipliens	0.92	0.78	0.85	0.0005	***
3–20	MIZ+OW	asv_00218	Bacillariophyta	Chaetoceros_danicus	0.92	0.69	0.8	0.003	**
3–20	MIZ+OW	asv_00013	Bacillariophyta	Thalassiosira_rotula	0.97	0.31	0.55	0.05	*
3–20	MIZ+OW	asv_00283	Bacillariophyta	Attheya_septentrionalis	0.92	0.34	0.56	0.05	*
3–20	MIZ+OW	asv_00108	Chrysophyceae	Chrysophyceae_XXX_sp.	1	0.34	0.59	0.04	*
3–20	MIZ+OW	asv_00225	Pelagophyceae	Ankylochrysis_sp.	0.96	0.53	0.72	0.01	*
3–20	MIZ+UI	asv_00003	Mamiellophyceae	Micromonas_polaris	1	0.61	0.78	0.02	*
3–20	MIZ+UI	asv_00041	Cryptophyceae	Baffinella_frigidus	1	0.81	0.9	0.0003	***
3–20	MIZ+UI	asv_00149	Cryptophyceae	Plagioselmis_prolonga	0.99	0.56	0.75	0.04	*
3–20	MIZ+UI	asv_00105	Prymnesiophyceae	Phaeocystis_cordata	1	0.58	0.76	0.03	*
3–20	MIZ+UI	asv_00125	Prymnesiophyceae	Phaeocystis_sp.	1	0.65	0.8	0.03	*
3–20	MIZ+UI	asv_00015	Bacillariophyta	Fragilariopsis_cylindrus	1	0.98	0.99	0.0001	***
3–20	MIZ+UI	asv_00046	Bacillariophyta	Pseudo-nitzschia_seriate	1	0.87	0.93	0.0001	***

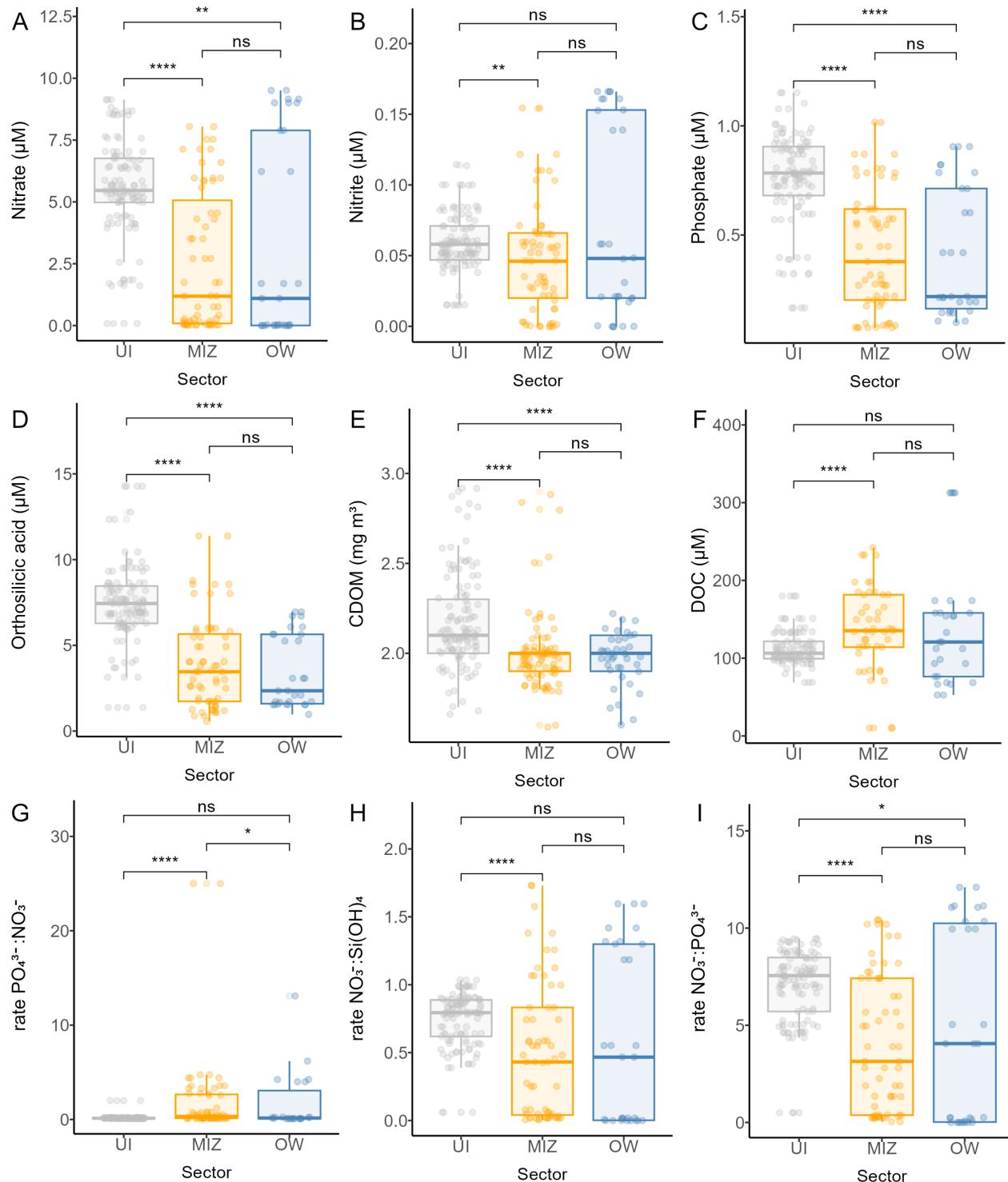
Table S2: (*continued*)

Size fraction ( $\mu\text{m}$ )	Sectors	ASVs	Class	Species	A	B	Stat	p.value	Sign
3–20	MIZ+UI	asv_00048	Bacillariophyta	Chaetoceros_neogracilis	0.99	0.98	0.99	0.0001	***
3–20	MIZ+UI	asv_00009	Bacillariophyta	Melosira_arctica	1	0.69	0.83	0.006	**
3–20	MIZ+UI	asv_00022	Bacillariophyta	Actinocyclus_curvatulus	0.98	0.77	0.87	0.01	*
3–20	MIZ+UI	asv_00099	Bacillariophyta	Cylindrotheca_closterium	1	0.65	0.8	0.02	*
3–20	MIZ+UI	asv_00109	Bacillariophyta	Fragilariopsis_sublineata	1	0.61	0.78	0.02	*
3–20	MIZ+UI	asv_00073	Bolidophyceae	Triparma_laevis_clade	1	0.89	0.94	0.0003	***
3–20	MIZ+UI	asv_00094	Chrysophyceae	Dinobryon_faculiferum	0.98	0.66	0.81	0.01	*
3–20	MIZ+UI	asv_00075	Dictyochophyceae	Dictyocha_speculum	1	0.79	0.89	0.0008	***
3–20	MIZ+UI	asv_00114	Dictyochophyceae	Florenciellales_X_sp.	1	0.73	0.85	0.004	**
3–20	MIZ+UI	asv_00061	MOCH-2	MOCH-2_XXX_sp.	1	0.94	0.97	0.0001	***
3–20	OW	asv_00057	Bacillariophyta	Thalassiosira_sp.	0.92	0.8	0.86	0.0002	***
3–20	OW	asv_00177	Bacillariophyta	Chaetoceros_rostratus	0.83	1	0.91	0.0002	***
3–20	OW	asv_00320	Bacillariophyta	Navicula_sp.	0.55	0.8	0.66	0.01	**
3–20	UI	asv_00104	Mamiellophyceae	Mantoniella_squamata	0.94	0.46	0.66	0.02	*
3–20	UI	asv_00244	Pyramimonadophyceae	Pterosperma_sp.	1	0.49	0.7	0.01	**
3–20	UI	asv_00281	Cryptophyceae	Cryptomonadales_XX_sp.	0.87	0.57	0.71	0.03	*
3–20	UI	asv_00239	Prymnesiophyceae	Chrysochromulina_sp.	0.94	0.4	0.61	0.03	*
3–20	UI	asv_00171	Bacillariophyta	Raphid-pennate_X_sp.	0.94	0.6	0.75	0.005	**
3–20	UI	asv_00311	Pelagophyceae	Ankylochrysis_sp.	0.86	0.46	0.63	0.04	*
>20	MIZ	asv_00259	Bacillariophyta	Entomoneis_ornata	0.83	0.62	0.72	0.0001	***
>20	MIZ	asv_00265	Bacillariophyta	Pauliella_toeniata	0.69	0.68	0.68	0.005	**
>20	MIZ	asv_00164	Chrysophyceae	Paraphysomonas_foraminifera	1	0.41	0.64	0.0001	***
>20	MIZ+OW	asv_00001	Prymnesiophyceae	Phaeocystis_pouchetii	0.91	1	0.96	0.0001	***
>20	MIZ+OW	asv_00013	Bacillariophyta	Thalassiosira_rotula	0.96	0.96	0.96	0.0001	***
>20	MIZ+OW	asv_00028	Bacillariophyta	Thalassiosira_sp.	0.77	0.85	0.81	0.0001	***
>20	MIZ+OW	asv_00057	Bacillariophyta	Thalassiosira_sp.	0.93	0.9	0.92	0.0001	***
>20	MIZ+OW	asv_00071	Bacillariophyta	Thalassiosira_anguste-lineata	0.97	0.71	0.83	0.0001	***
>20	MIZ+OW	asv_00079	Bacillariophyta	Eucampia_sp.	0.94	0.9	0.92	0.0001	***
>20	MIZ+OW	asv_00111	Bacillariophyta	Chaetoceros_cinctus	0.89	0.81	0.85	0.0001	***
>20	MIZ+OW	asv_00136	Bacillariophyta	Chaetoceros_decipliens	0.87	0.79	0.83	0.0001	***
>20	MIZ+OW	asv_00137	Bacillariophyta	Detonula_confervacea	0.9	0.79	0.84	0.0001	***
>20	MIZ+OW	asv_00177	Bacillariophyta	Chaetoceros_rostratus	0.89	0.85	0.87	0.0001	***
>20	MIZ+OW	asv_00218	Bacillariophyta	Chaetoceros_danicus	0.92	0.73	0.82	0.0001	***
>20	MIZ+UI	asv_00038	Cryptophyceae	Teleaulax_gracilis	0.97	0.51	0.71	0.001	***
>20	MIZ+UI	asv_00009	Bacillariophyta	Melosira_arctica	1	1	1	0.0001	***
>20	MIZ+UI	asv_00025	Bacillariophyta	Melosira_arctica	1	0.81	0.9	0.0001	***

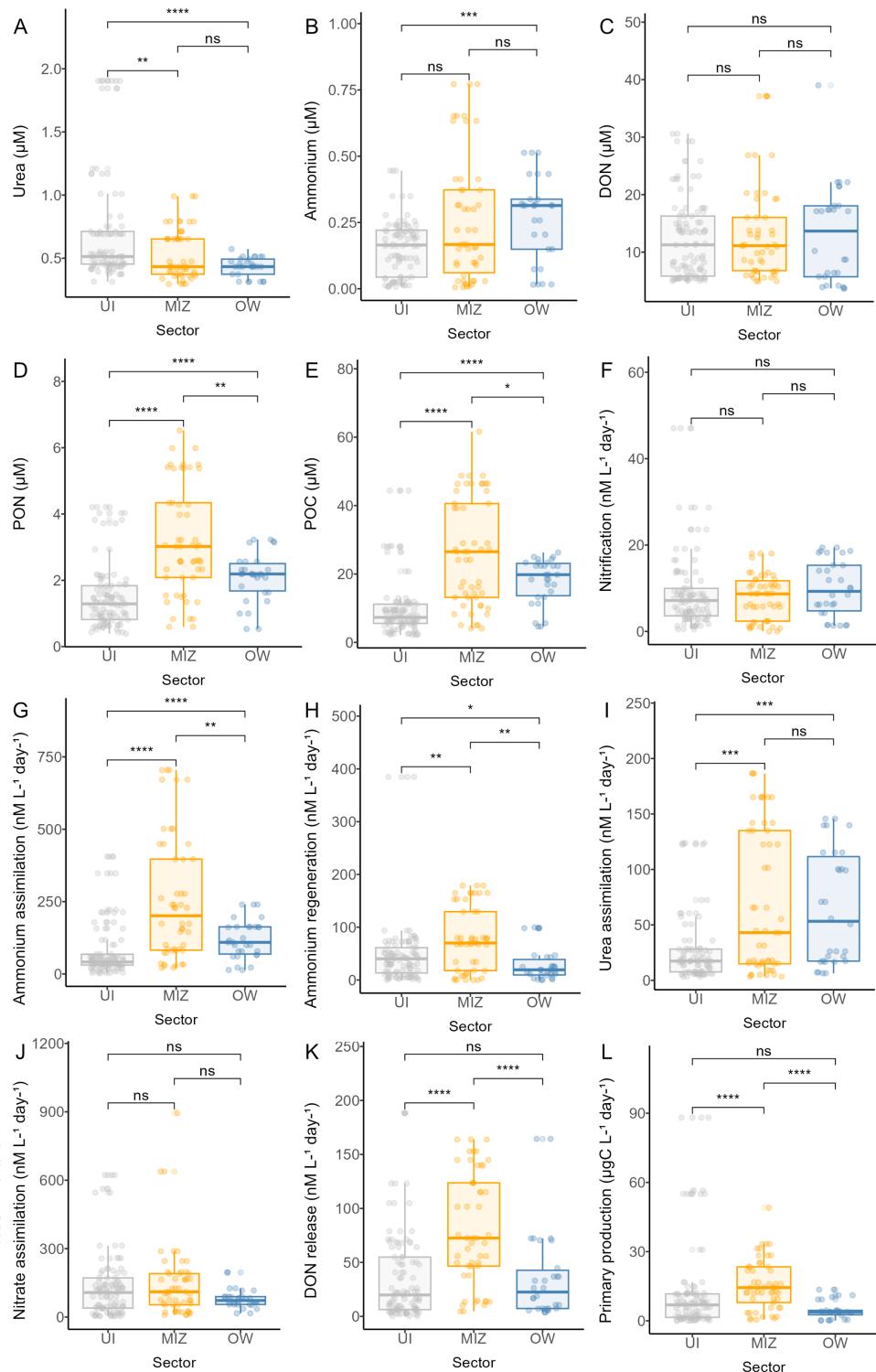
Table S2: (continued)

Size fraction ( $\mu\text{m}$ )	Sectors	ASVs	Class	Species	A	B	Stat	p.value	Sign
>20	MIZ+UI	asv_00049	Bacillariophyta	Navicula_sp.	0.97	0.84	0.9	0.0001	***
>20	MIZ+UI	asv_00064	Bacillariophyta	Fragilaria_sp.	0.98	0.73	0.85	0.0001	***
>20	MIZ+UI	asv_00084	Bacillariophyta	Raphid-pennate_X_sp.	1	0.81	0.9	0.0001	***
>20	MIZ+UI	asv_00099	Bacillariophyta	Cylindrotheca_closterium	1	0.57	0.75	0.0001	***
>20	MIZ+UI	asv_00172	Bacillariophyta	Attheya_septentrionalis	1	0.8	0.89	0.0001	***
>20	MIZ+UI	asv_00184	Bacillariophyta	Pleurosigma_intermedium	1	0.65	0.81	0.0001	***
>20	MIZ+UI	asv_00219	Bacillariophyta	Bacillaria_paxillifer	1	0.5	0.71	0.0002	***
>20	MIZ+UI	asv_00268	Bacillariophyta	Stauroneis_kriegeri	1	0.49	0.7	0.0005	***
>20	MIZ+UI	asv_00277	Bacillariophyta	Naviculales_sp.	0.97	0.61	0.77	0.0002	***
>20	MIZ+UI	asv_00335	Bacillariophyta	Raphid-pennate_X_sp.	1	0.61	0.78	0.0001	***
>20	MIZ+UI	asv_00308	Bacillariophyta	Synedra_hyperborea	1	0.42	0.65	0.002	**
>20	MIZ+UI	asv_00178	Bacillariophyta	Raphid-pennate_X_sp.	1	0.31	0.56	0.01	*
>20	MIZ+UI	asv_00328	Bacillariophyta	Nitzschia_sp.	1	0.34	0.58	0.02	*
>20	MIZ+UI	asv_00073	Bolidophyceae	Triparma_laevis_clade	0.99	0.61	0.78	0.0001	***
>20	MIZ+UI	asv_00075	Dictyochophyceae	Dictyocha_speculum	1	0.8	0.89	0.0001	***
>20	OW	asv_00334	Bacillariophyta	Chaetoceros_contortus	0.72	0.83	0.77	0.0001	***
>20	OW	asv_00407	Bacillariophyta	Chaetoceros_diadema_1	0.82	0.67	0.74	0.0001	***
>20	OW	asv_00156	Chrysophyceae	Chrysophyceae_Claude-H_X_sp.	0.99	0.28	0.53	0.0006	***
>20	UI	asv_00105	Prymnesiophyceae	Phaeocystis_cordata	0.76	0.45	0.58	0.002	**
>20	UI	asv_00086	Prymnesiophyceae	Chrysosochromulina_sp.	0.96	0.18	0.41	0.02	*
>20	UI	asv_00046	Bacillariophyta	Pseudo-nitzschia_seriate	0.79	0.85	0.82	0.0001	***

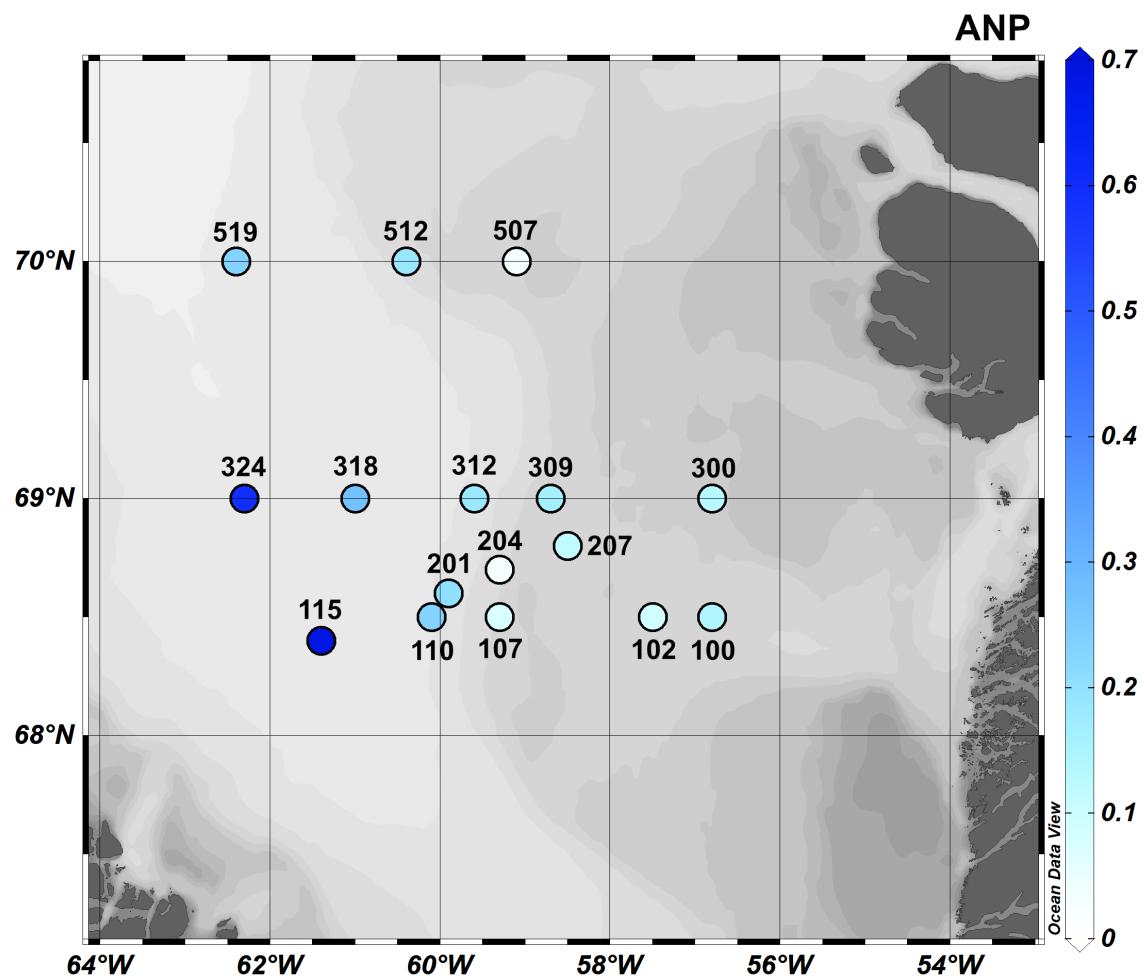
<sup>1345</sup> Supplementary Figures



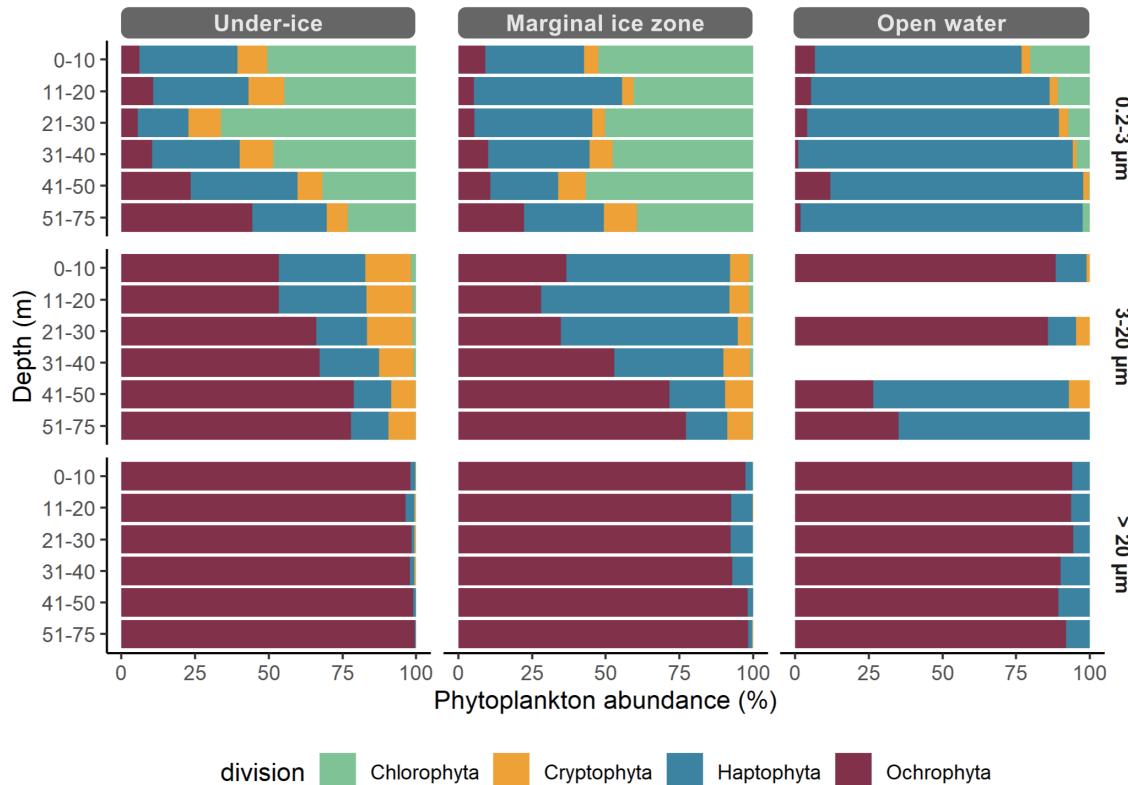
**Figure S1. Nutrients for the three sectors: under ice (UI, grey), marginal ice zone (MIZ, yellow), and open water (OW, blue); (A) nitrates ( $\mu\text{M}$ ); (B) nitrites ( $\mu\text{M}$ ); (C) phosphates ( $\mu\text{M}$ ); (D) orthosilicic acid ( $\mu\text{M}$ ); (E) colored dissolved organic matter ( $\text{mg.m}^{-3}$ ); (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.**



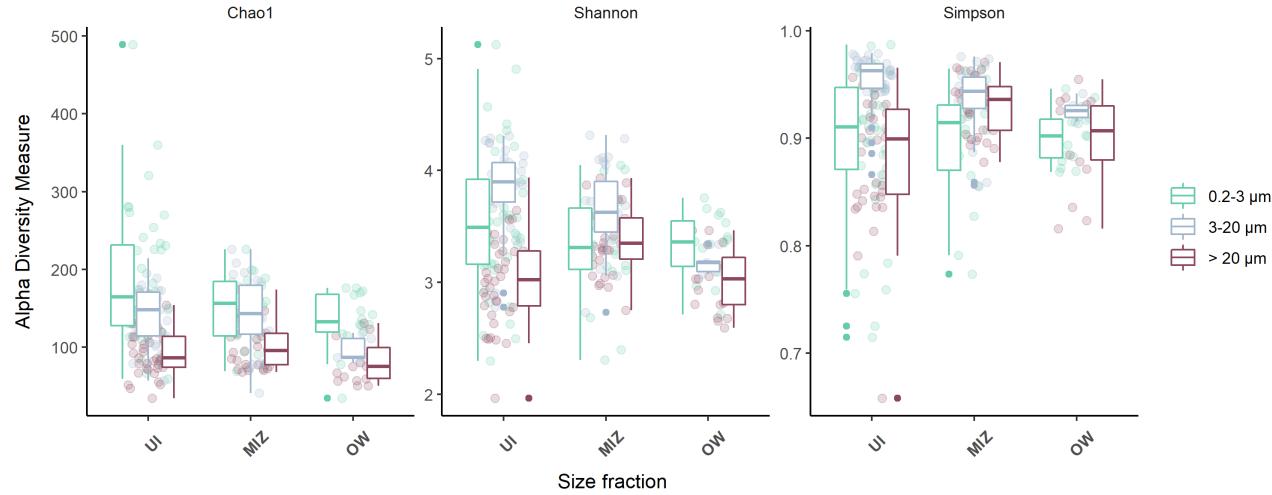
**Figure S2.** Nutrients and metabolic rates for the three sectors: under ice (UI, grey), marginal ice zone (MIZ, yellow), and open water (OW, blue); (A) urea ( $\mu\text{M}$ ); (B) ammonium ( $\mu\text{M}$ ); (C) dissolved organic nitrogen ( $\mu\text{M}$ ); (D) particulate organic nitrogen ( $\mu\text{M}$ ); (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.** Water mass characterization in each station using Arctic N-P relationship (ANP) calculated by Randelhoff et al. (2019) following Newton et al. (2013). ANP values close to one indicate the presence of Pacific-originated waters, whereas close to zero indicate Atlantic Water influence.



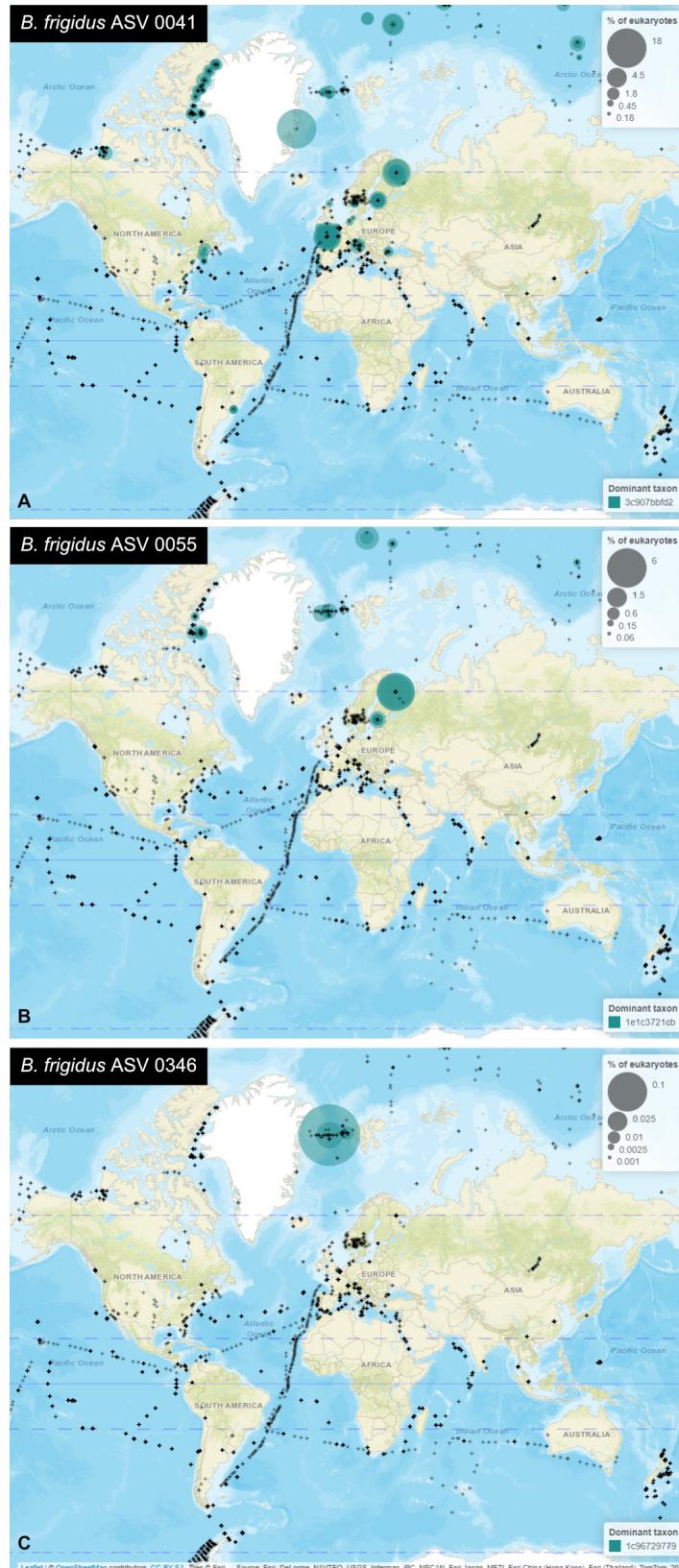
**Figure S4.** Relative abundance of reads at the division level between size fractions across the three sectors: under ice, marginal ice zone, and open water. There are no samples for the depths 11-20 m and 31-40 m in the 3–20  $\mu\text{m}$  size fraction of the open water sector. Note that the deeper interval covers a greater range of depths (from 51 m to 75 m) due to fewer samples in this lower limit.



**Figure S5. Chao1, Shannon and Simpson alpha diversity indices according to size fraction; sectors are represented by the colors grey (UI), yellow (MIZ) and blue (OW).**



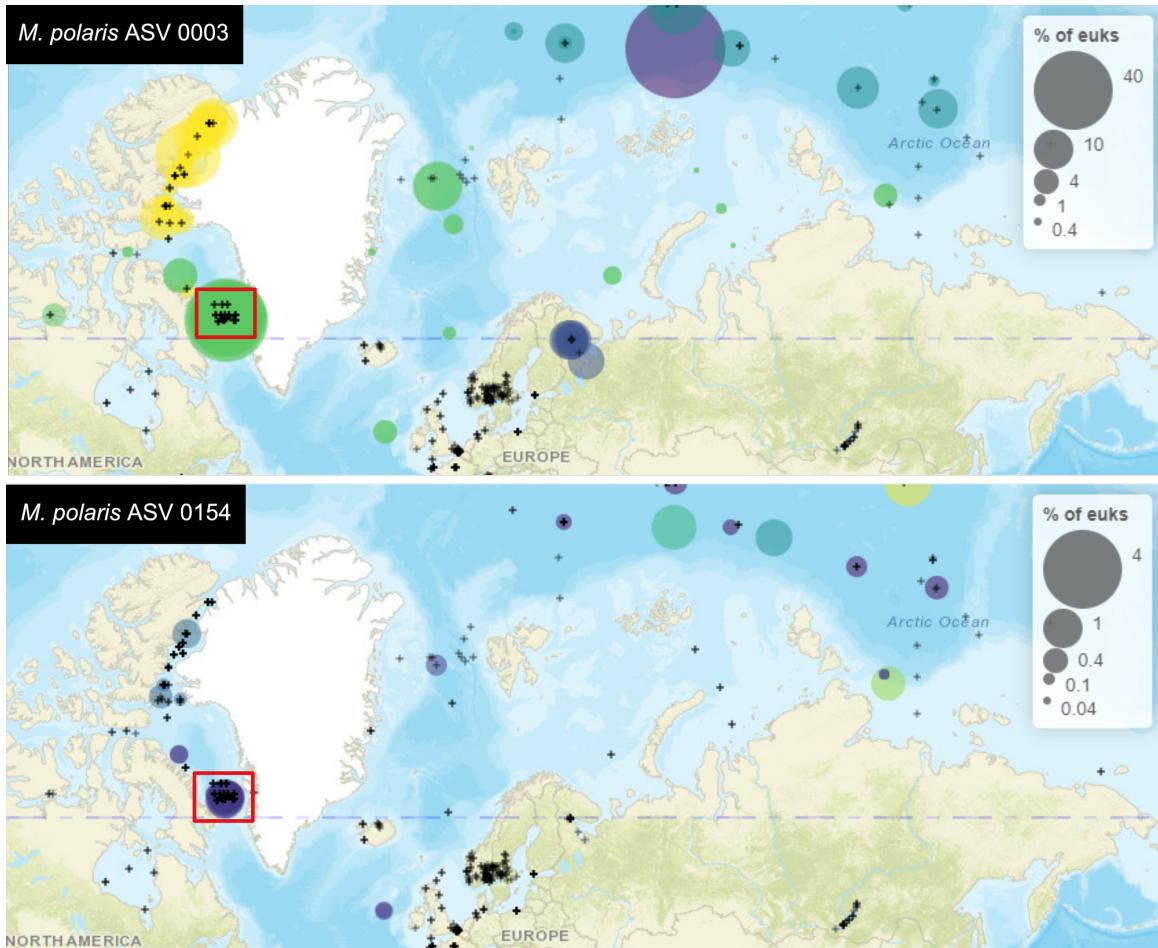
**Figure S6. Sequence alignment of the partial 18S rRNA of *B. frigidus* found in the present study (ASVs 0041/0055/0346) and the type-strain of *B. frigidus* description (CCMP2045)**



**Figure S7.** *B. frigidus* ASV\_0041 (A), ASV\_0055 (B), and ASV\_0346 (C) distribution in the metaPR<sup>2</sup> database showing 100% similar reads from other studies. The size of the bubbles represents the percentage in relation to other eukaryotes within each station. Note that maximum percentages are distinct between panels

Micromonas polaris - CCMP2099 - DQ025753 1 10 19 20 29 30 39 40 50 51 59 60 69 70 79 80 89 90 100  
 Micromonas polaris - asv\_00003 AGCTCCAATAGCGTATATAAAGTTGGCTGGAGTTAAAAAGCTGTGATTGGATTCGGTTGGCTGGTCAACT  
 Micromonas polaris - asv\_00154 AGCTCCAATAGCGTATATAAAGTTGGCTGGAGTTAAAAAGCTGTGATTGGATTCGGTTGGCTGGTCAACT  
 Micromonas commoda A2 - asv\_00235 AGCTCCAATAGCGTATATAAAGTTGGCTGGAGTTAAAAAGCTGTGATTGGATTCGGTTGGCTGGTCAACT  
 Micromonas polaris - CCMP2099 - DQ025753 110 120 130 140 150 160 170 180 190 200 210  
 Micromonas polaris - asv\_00003 TCTCTGAGAGGACGGCGCTCTGG TAAACGCTC GGAGCGCGAGGTCTACGTGGTTACTTTAAA  
 Micromonas polaris - asv\_00154 TCTCTGAGAGGACGGCGCTCTGG TAAACGCTC GGAGCGCGAGGTCTACGTGGTTACTTTAAA  
 Micromonas commoda A2 - asv\_00235 TCTCTGAGAGGACGGCGCTCTGG TAAACGCTC GGAGCGCGAGGTCTACGTGGTTACTTTAAA  
 Micromonas polaris - CCMP2099 - DQ025753 220 230 240 250 260 270 280 290 300 310  
 Micromonas polaris - asv\_00003 CATGGAAATACACTATAGAACCTCTGGCTTATTTCTGGCTGGGAGTAATGTTAAAGGAGAACAGT  
 Micromonas polaris - asv\_00003 CATGGAAATACACTATAGAACCTCTGGCTTATTTCTGGCTGGGAGTAATGTTAAAGGAGAACAGT  
 Micromonas polaris - asv\_00154 CATGGAAATACACTATAGAACCTCTGGCTTATTTCTGGCTGGGAGTAATGTTAAAGGAGAACAGT  
 Micromonas commoda A2 - asv\_00235 CATGGAAATACACTATAGAACCTCTGGCTTATTTCTGGCTGGGAGTAATGTTAAAGGAGAACAGT  
 Micromonas polaris - CCMP2099 - DQ025753 320 330 340 350 360 370 380 390 400  
 Micromonas polaris - asv\_00003 AATTCTTGAGTTTATGAAGAGCAACGACTTCTGGCAAAGGCATTTGCCAAGGATGTTT  
 Micromonas polaris - asv\_00154 AATTCTTGAGTTTATGAAGAGCAACGACTTCTGGCAAAGGCATTTGCCAAGGATGTTT  
 Micromonas commoda A2 - asv\_00235 AATTCTTGAGTTTATGAAGAGCAACGACTTCTGGCAAAGGCATTTGCCAAGGATGTTT

Figure S8. 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).



**Figure S9.** 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>. The size of the bubbles represents 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.