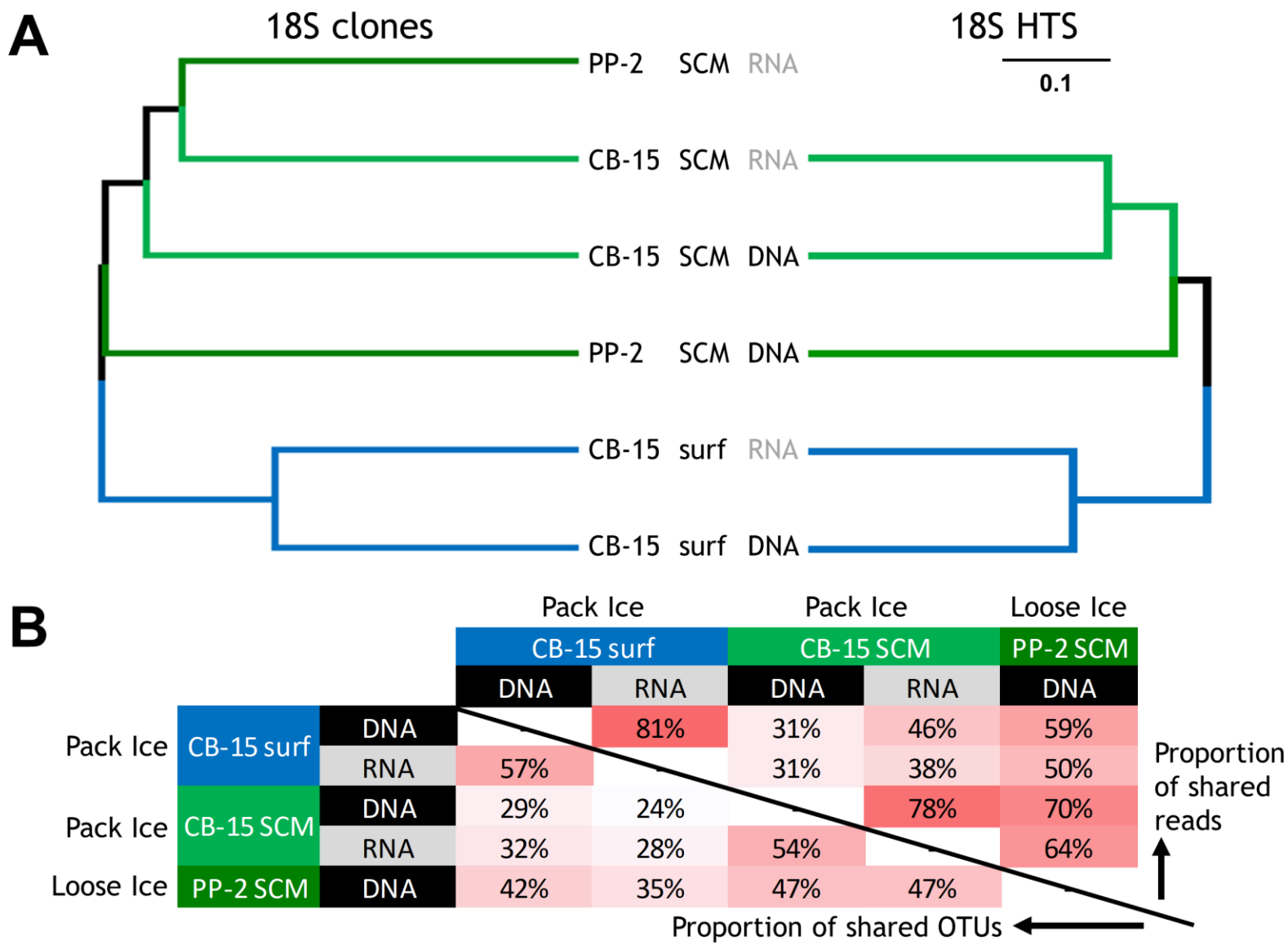

Fig. S1. (**A**) Community similarity between samples and between DNA and RNA, comparing 18S cloning vs. high-throughput sequencing (HTS). Bray-Curtis tree of the 18S cloning (99% OTUs) and HTS (98% OTUs) diversity (i.e.: richness + evenness) by sample. DNA (black text) or RNA (grey text), as well as surface (surf; blue) or SCM samples (shades of green), are indicated. Note that no RNA remained for HTS analysis of PP-2. The scale bar equals 10% dissimilarity. (**B**) Proportions of shared HTS OTUs (lower triangle) and reads (upper triangle) between each pairwise sample combination.

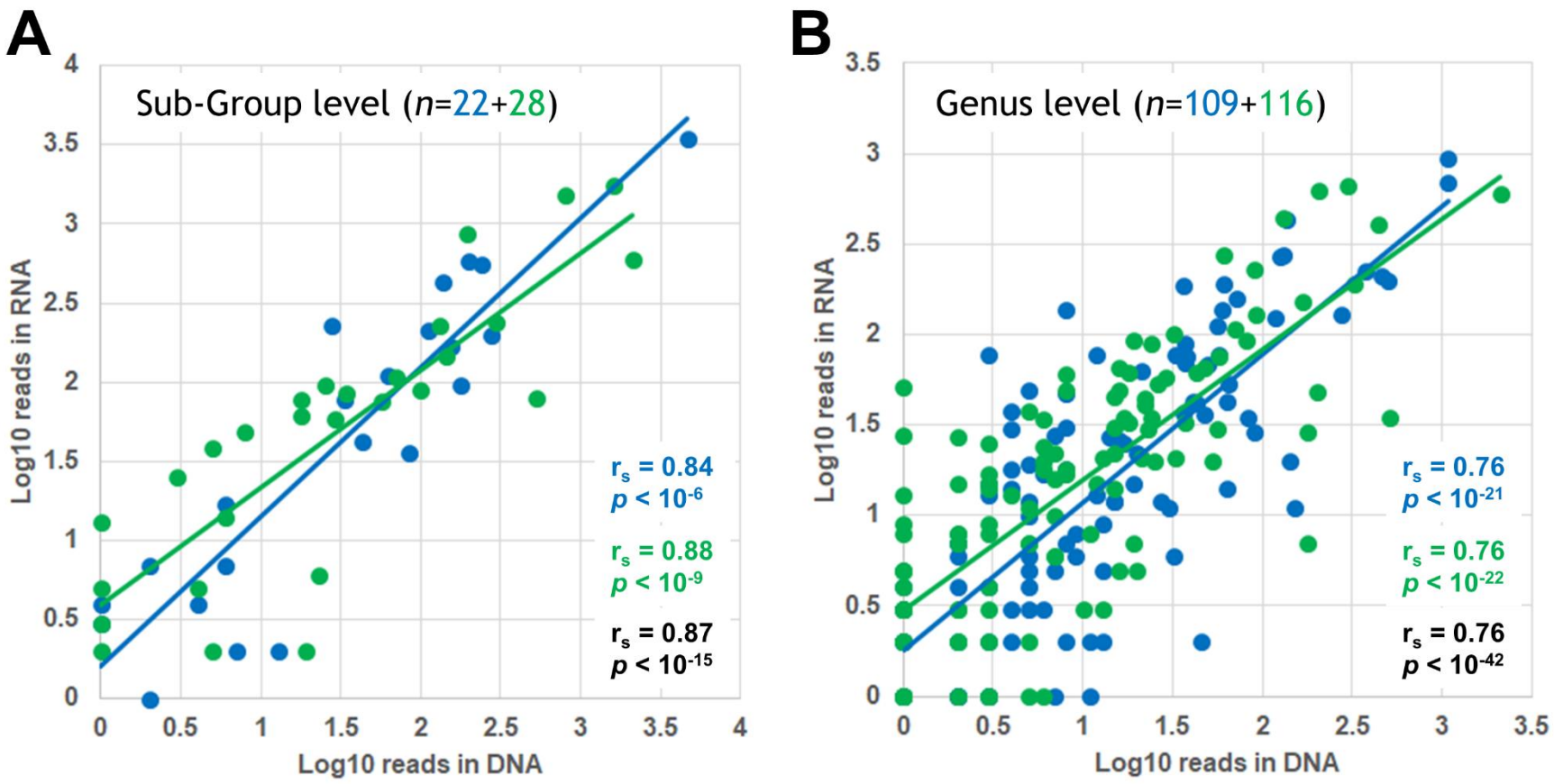

Fig. S2. Correlations of log-scale taxa high-throughput sequencing (HTS) reads between DNA and RNA samples at the coarser Sub-Group level (**A**) and at the finer genus level (**B**). Only CB-15 surface (blue) and CB-15 SCM (green) samples are presented as no RNA remained for HTS analysis of station PP-2. Listed are the Spearman r_s and *p*-values for the correlations of each individual sample (in matching colors) and for the overall trend with both samples combined (in black).

Table S1. Sample and station characteristics ("-" indicates missing data) of screened public Arctic metagenome studies.

	AGulf	JGI Sea of Change	JGI W. Arctic Ocean	UAF GEOTRACES
Region(s)	AGulf	NS+GS	CB	CB+AO
# of samples	1	6	8	17
# of stations	1	6	4	9
Dates of sampling	Dec.2007	Jun.-Jul.2012	Oct.2015	Aug.-Oct.2015
Range of latitudes (°N)	71.62	69.23 to 79.02	73.22 to 79.25	72.80 to 89.99
Range of longitudes (°E)	-126.07	-9.52 to 9.86	-150.23 to -150.06	-180.00 to -89.25
Depths of sampling (m)	10	10-20	5-79	1-100
Size fraction	0.2-50 µm	1.2-100 µm	0.2-3.0 µm	>0.22 µm
Accession #	PRJNA337945	JGI Proposal 532	JGI Proposal 2011	PRJEB14154
Reference	(1)	(2)	(3)	(4)
Ranges of physicochemical characteristics				
Salinity (psu)	30.56	31.03-35.15	25.70-31.48	27.41-36.68
Temperature (°C)	-1.60	-1.03 to +9.10	-1.46 to +0.02	-1.67 to +1.64
Nitrate (µM)	-	bd-6.6	bd-4.7	bd-17.5
Phosphate (µM)	-	0.46-0.88	0.52-1.11	-
Silicate (µM)	-	1.5-5.5	2.4-10.8	-
Sequence characteristics				
Average # reads screened/sample (M)	314	372	200	5.5
Range # reads screened/sample (M)	314	327-450	161-219	2.0-11.1
Total # reads screened (M)	314	2,234	1,599	93
Total # assembled GenSeed-HMM contigs	1	87	64	96
Total # of target plankton NR contigs	1	55	40	15
Total # of non-target eukaryote contigs	0	23	7	22
Total # of non-target prokaryote contigs	0	5	16	53
Average % identity of target NR matches	100%	82%	85%	79%
Range % identity of target NR matches	100%	45-100%	53-100%	51-99%

AGulf, Amundsen Gulf; AO, Arctic Ocean; bd, below detection; CB, Canada Basin; GS, Greenland Sea; JGI, Joint Genome Institute; NR, nitrate reductase; NS, Norwegian Sea; UAF, University of Alaska - Fairbanks.

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2. Mock T. 2014. Sea of Change: Eukaryotic phytoplankton communities in the Arctic Ocean. JGI: https://genome.jgi.doe.gov/portal/SeaofArctiOcean/SeaofArctiOcean.info.html
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Table S3. Primers used for cloning and (pyro)sequencing of 18S rRNA and nitrate reductase (NR) genes

Assay/use	Primer[a]	Product size	Sequence (5'-3')[a]	Source
18S V4 pyrosequencing	A#-E572F B-E1009R	508 bp	(RocheA+MID#)CYGCGGTAATTCCAGCTC (RocheB)AYGGTATCTRATCRTCTTYG	(1)
18S cloning – PCR	NSF4/18 EukR	~1800 bp	CTG GTT GAT YCT GCC AGT TGA TCC TTC TGC AGG TTC ACC TAC	(2) (3)
18S cloning – sequencing	Euk528f	n/a	GCG GTA ATT CCA GCT CCA A	(4)
NR cloning – 1st round	NRPt907F NRPt2325R	1419 bp	GGY GGN MGN ATG RTB AAG TGG CT GGG VGT GAT RCC HGT VCC DCC VGC	(5)
NR cloning – 2nd round	NRPt1000F NRPt1389R	390 bp	GRD GGH TGG TGG TAC AAG CC GTT GTT YMY CAT BCC CAT	(5)

[a] Pyrosequencing forward primers exist in 12 numbered versions (#), differing only by the 12 individual multiplex identifiers (MID = bar-codes). Also incorporated into the primers were the Roche A (forward) and B (reverse) adaptors.

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