Supplementary on line Table and Figures for:

Biodiversity and species change in the Arctic Ocean: A view through the lens of Nares Strait

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Table S1: Sample ID is Station from Figure 1 main text and depth in meters (m), salinity (Sal) nitrate, phosphate and silicate in μ M, Oxygen as percent saturation at depth and photosynthetically available radiation (PAR) as % attenuation relative to first surface reading, values less the 0.01% are not shown.

Table S2. Additional contextual data. Trip Depth is the actual depth (m) recorded as the sample bottle closed on the upward cast. The *f*CDOM (ppb) units refer to factory calibrations and Chl *a* concentrations (mg m⁻³) estimated from relative fluorescence. Cell counts from FCM for Bacteria (×10⁵ cells ml⁻¹), both picophytoplankton (PPP and nanophytoplankton(NPP) in cells ml⁻¹.

Supplementary Figure Legends

Figure S1: Bray Curtis cluster analysis grouping the water masses based on the temperature, the salinity and the Pacific Water contribution (see text). The dot colors show a normalized representation of each of the 3 parameters, with blue for the minimum value through to red for the maximum value. The warmed and fresh Surface Water clustered apart.

Figure S2: Depth profiles of temperature (Black), Chl *a* (green), nitrate concentration (red I) and Density (Blue) at the 7 stations sampled.

Figure S3: Decision tree applied to each OTUs present in the Ken1 station to categorize them into of the eight categories used in source tracking from the rarified data set (see text). Below each category is the number of sequences and OTUs in the category.

Figure S4: Depth profiles of the rDNA and rRNA fractions showing the relative proportion of sequences belonging to the categories defined from station Kennedy 1 following Fig. S3.

Figure S5: Taxonomic contribution to the categories displayed in Figure S4, for the rDNA and rRNA fraction. a) "Ken1 All Depths rDNA" and "Ken1 All Depths rDNA & rRNA" categories. b) "Ken1 aphotic rDNA" and "Ken1 aphotic rDNA & rRNA" categories. c) "Ken1 photic rDNA" and "Ken1 photic rDNA & rRNA" categories. d) "Ken1 rRNA only" category, e) "Rare in Ken1" category and f) "Not detected in Ken1" category.

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Table S1: Sample ID is Station from Figure 1 main text and depth in meters (m), salinity (Sal) nitrate, phosphate and silicate in μ M, Oxygen as percent saturation at depth and photosynthetically available radiation (PAR) as % attenuation relative to first surface reading, values less the 0.01% are not shown.

Sample_ID Depth	Sal	NO ₃	PO ₄ ³⁻	SiO ₂	O_2	PAR %
Ken1-2m	30.73	1.40	0.51	5.56	89%	100
Ken1-30m	30.95	1.98	0.58	7.06	89%	0.98
Ken1-47m	31.19	3.05	0.70	9.10	87%	0.12
Ken1-80m	32.52	7.66	1.09	17.07	74%	
Ken1-121m	33.98	10.29	0.93	11.23	69%	
Ken1-253m	34.68	11.77	0.90	8.13	67%	
Ken1-303m	34.71	11.84	0.89	8.03	67%	
Ken1-542m	34.78	12.05	0.91	7.87	69%	
Ken3-1m	30.26	0.23	0.38	3.34	94%	100
Ken3-24m	30.66	0.87	0.48	5.20	93%	1.07
Ken3-40m	31.13	2.47	0.63	7.93	89%	0.12
Ken3-101m	33.63	10.37	1.10	17.11	69%	
Kane1-1m	29.96	0.19	0.34	-	94%	100
Kane1-30m	31.93	1.01	0.46	2.78	94%	0.20
Kane1-50m	32.67	8.01	0.94	12.92	77%	0.02
Kane1-126m	34.28	10.98	0.91	10.13	69%	
Kane3-1m	30.45	0.17	0.28	0.99	93%	100
Kane3-12m	31.17	0.39	0.34	1.51	100%	9.58
Kane3-50m	33.13	9.52	1.10	15.99	73%	0.06
Kane3-127m	33.98	11.57	1.02	13.13	67%	
Kane3-162m	34.63	11.97	0.91	8.99	69%	
Kane4-1m	29.98	0.17	0.29	2.25	94%	100
Kane4-35m	31.52	2.60	0.63	8.48	90%	0.43
Kane4-50m	32.05	5.00	0.76	9.83	89%	0.10
Kane4-126m	33.61	10.85	1.03	13.97	70%	
Kane4-228m	34.00	12.38	1.09	15.47	66%	
Kane5-1m	30.29	0.26	0.31	0.96	99%	100
Kane5-10m	30.69	0.40	0.37	2.07	100%	12.2
Kane5-26m	31.75	3.06	0.65	7.57	90%	0.20

Kane5-51m	32.71	7.75	0.94	12.95	79%	0.01
Kane5-91m	33.56	9.55	1.02	13.92	73%	
Kane5-142m	33.84	11.15	-	-	70%	
Kane5-162m	33.95	11.52	1.04	13.66	69%	
Kane5-238m	34.60	11.54	0.91	9.20	70%	
120-2m	28.89	0.25	0.31	0.76	90%	100
120-20m	31.76	0.58	0.53	2.58	93%	5.32
120-40m	32.29	1.63	0.57	4.61	89%	0.73
120-71m	32.71	5.82	0.93	11.04	83%	0.07
120-101m	33.10	7.89	0.99	12.94	81%	0.01
120-304m	34.17	11.06	0.98	12.02	71%	
120-404m	34.29	11.28	0.96	11.16	71%	
120-549m	34.38	11.47	0.96	11.24	71%	

Table S2. Additional contextual data. Trip Depth is the actual depth (m) recorded as the sample bottle closed on the upward cast. The *f*CDOM (ppb) units refer to factory calibrations and Chl *a* concentrations (mg m⁻³) estimated from relative fluorescence. Cell counts from FCM for Bacteria (×10⁵ cells ml⁻¹), both picophytoplankton (PPP and nanophytoplankton(NPP) in cells ml⁻¹.

Sample	Trip Depth	fCDOM	Chl a	Bacteria	PPP	NPP
Ken1-2m	2.11	11.1	0.42	1.66	720	220
Ken1-30m	30.21	10.91	0.55	1.55	430	160
Ken1-47m	47.45	10.46	0.59	1.52	3830	610
Ken1-80m	80.99	9.41	0.12	0.84	120	30
Ken1-121m	121.4	7.22	0.02	0.69	310	30
Ken1-253m	253.1	4.58	0.01	0.67	670	290
Ken1-303m	303.5	4.57	0.01	0.47	310	140
Ken1-542m	542.3	4.4	0.01	0.45	460	210
Ken3-1m	1.86	10.09	1.24	1.87	190	60
Ken3-24m	24.12	10.34	1.96	1.51	5820	1170
Ken3-40m	40.87	11.25	0.29	1.15	1520	2000
Ken3-101m	101.6	7.47	0.02	0.62	350	90
Kane1-1m	1.82	9.35	0.38	2.17	90	20
Kane1-30m	30.24	9.25	4.26	1.59	2640	3730
Kane1-50m	50.57	8.55	0.81	1.02	180	30
Kane1-126m	126.2	5.66	0.02	0.69	1540	2120
Kane3-1m	1.71	8.25	0.90	2.07	240	70
Kane3-12m	12.78	8.66	1.07	2.17	340	40
Kane3-50m	50.69	7.83	0.13	1.37	750	1450
Kane3-127m	127.3	5.53	0.02	1.40	110	30
Kane3-162m	162.4	4.99	0.02	0.94	650	300
Kane4-1m	1.94	8.6	0.22	2.05	1210	410
Kane4-35m	35.51	10.4	3.23	1.08	1280	700
Kane4-50m	50.67	10	0.60	1.88	160	30
Kane4-126m	126.9	6.07	0.03	2.05	220	40
Kane4-228m	228.1	5.35	0.03	1.66	1460	2650

Kane5-1m	1.72	8.67	1.21	2.02	130	10
Kane5-10m	10.84	9.04	1.42	0.94	1090	410
Kane5-26m	26.05	10.33	5.59	1.05	270	100
Kane5-51m	51.12	8.61	0.21	1.12	180	40
Kane5-91m	91.83	6.78	0.04	1.44	300	70
Kane5-142m	142.6	5.98	0.02	1.46	220	160
Kane5-162m	162.5	5.78	0.02	1.60	1950	620
Kane5-238m	238.6	4.89	0.02	0.97	350	80
120-2m	2.07	6.46	0.19	5.54	1750	640
120-20m	20.21	9.03	0.07	2.95	1150	350
120-40m	40.76	7.66	0.13	5.00	290	40
120-71m	71.32	7.79	0.05	1.67	130	80
120-101m	101.4	7.02	0.03	1.80	40	20
120-304m	304.3	5.69	0.02	1.09	4110	1310
120-404m	405	5.55	0.02	1.08	2380	730
120-549	549.8	5.34	0.01	1.19	920	290



Fig. S2





Fig. S4



Proportion of sequences belonging to each Ken1 categories (%)



Proportion of sequences belonging to each Ken1 categories (%)

Fig. S5

