Organic matter from Arctic sea ice loss alters bacterial community structure and function. Underwood et al. *Nature Climate Change*
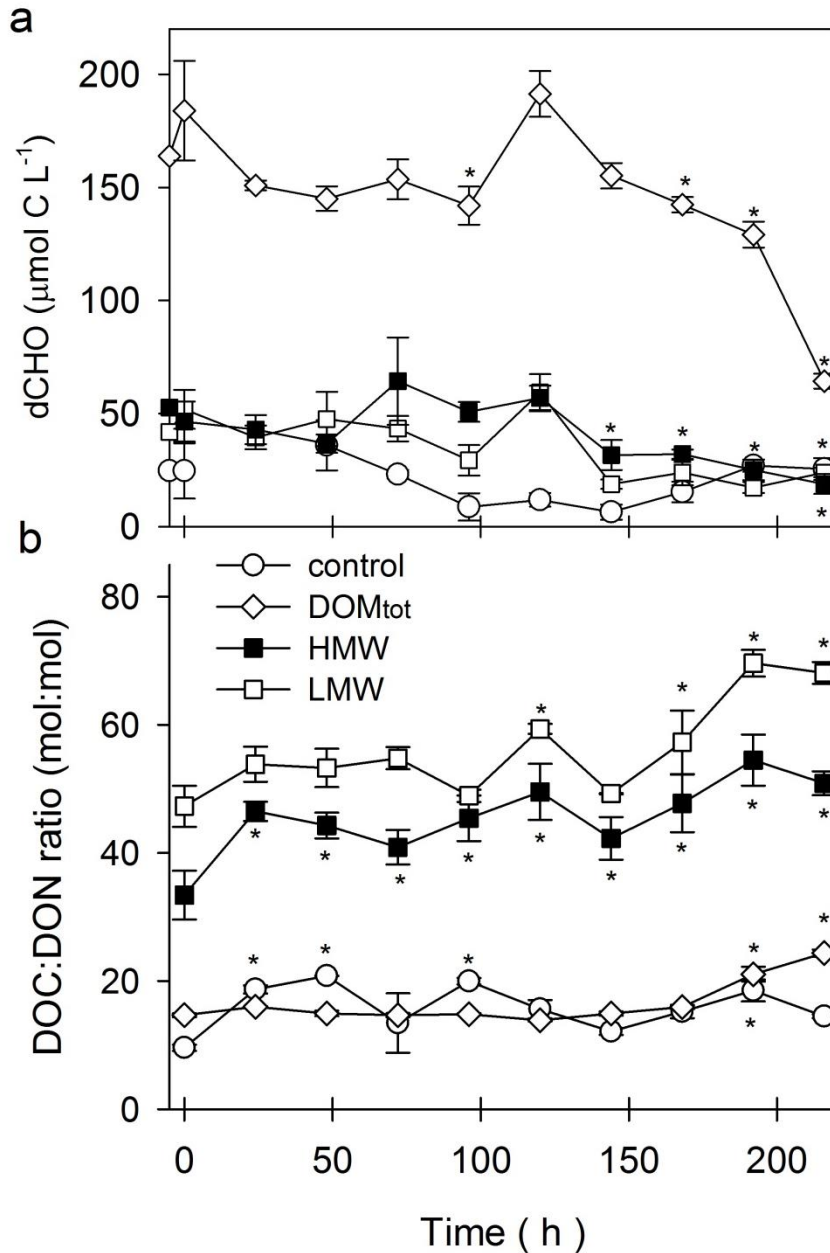
Supplementary Materials:

Fig. S1. Changes in carbohydrates and organic carbon: nitrogen ratios during experiments on Arctic under-ice surface water enriched with three sea ice derived organic matter fractions over a 216 h experimental period. (a) dissolved carbohydrate (dCHO), and (b) DOC:DON ratio. Symbols mean ± standard error, n = 3. * indicate samples significantly different (ANOVA P < 0.001 or less) from T0 value.
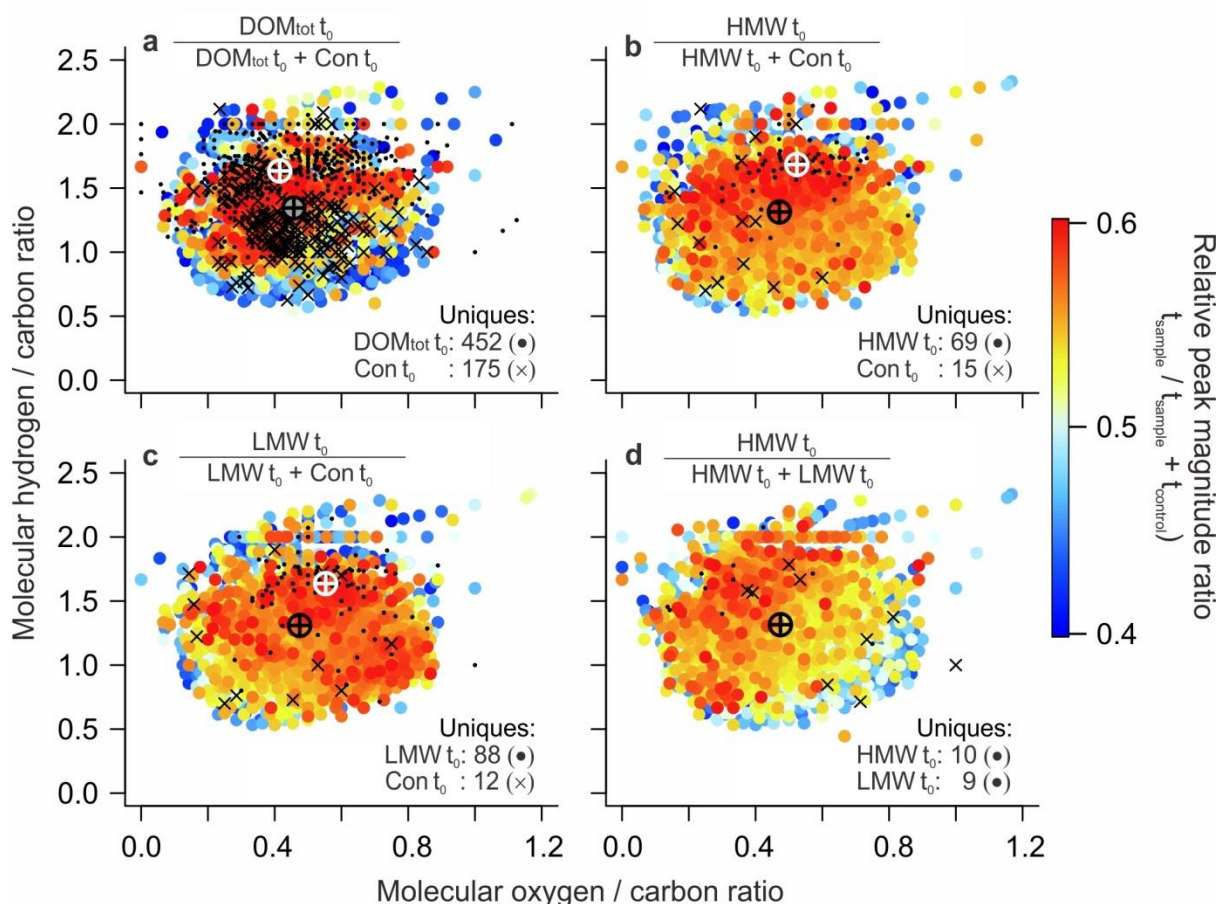
Fig. S2. Molecular formulas (for the mass range 200-600 Da) determined by FT-ICR-MS represented in van Krevelen plots (a-d). Each dot represents at least one detected molecular formula represented as the molecular oxygen/carbon and hydrogen/carbon ratio. Colours represent compositional differences (changes in relative peak magnitude ratios) due to the addition of substrate (panel a-c) and comparison of different molecular size fractions (panel d). Higher values (in red) and unique formulas (dots) are represented for the added substrate (panel a-c), and between $HMW_{>100kDa}$ and $LMW_{10-100kDa}$ fraction of DOM (panel d). The average elemental compositions for all (black marker) and unique molecular formulas in the substrate (white marker) are also shown.
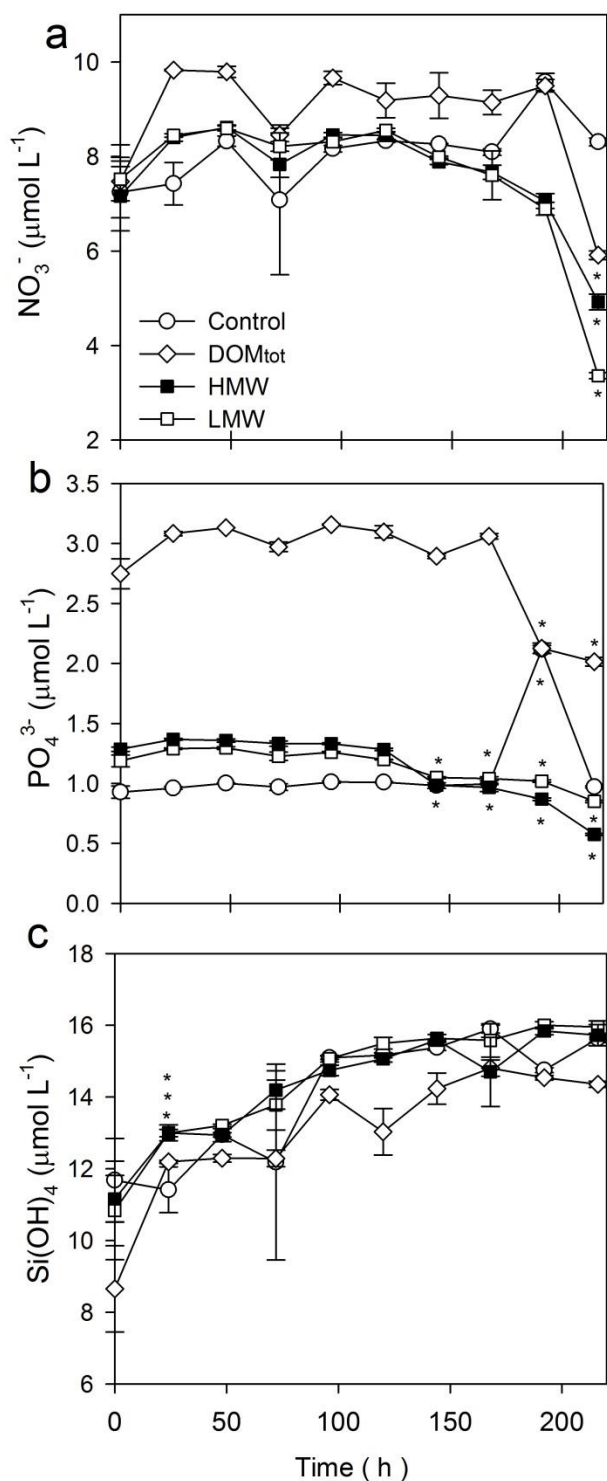
Fig. S3. Changes in (a) nitrate, (b) phosphate and (c) silicate (μmol L^{-1}) in Arctic under-ice surface water enriched with three sea-ice derived organic matter and controls, over a 216 h experimental period. Symbols and vertical lines represent mean $\pm$ standard error for triplicate experiments. * indicate samples significantly different (ANOVA $P < 0.05$ or less) from T0 value. Note in S3c all treatment silicate concentrations significantly greater than T0 values from T24 onwards
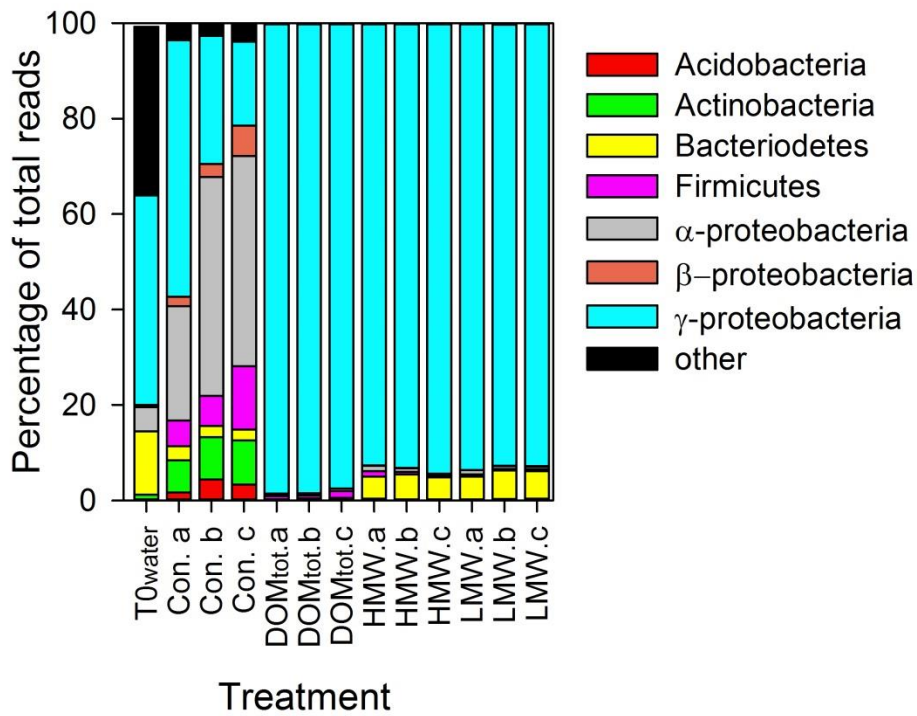
Fig. S4. Differences in community composition (at phylum/class level) of under-ice bacterial assemblages in three different sea-ice derived organic carbon fractions compared to controls. T0 underlying water (T0water), and after 216 hours incubation enriched with three organic matter amendments, or with no amendment (controls), from 16S rRNA operational taxonomic units (OTU) counts, "other" category includes minor classes as well as unidentified OTUs assigned as "Bacteria".

Table S1. Initial (T0) conditions during enrichment experiments of Arctic under-ice surface water with three sea-ice derived organic matter fractions. Concentrations and enrichment factors for dissolved organic carbon (DOC), dissolved carbohydrates (dCHO) and dissolved nitrogen (DN), relative contribution of dCHO to total DOC, and relative contribution of extracellular polymeric substances (EPS) to dCHO, salinity (Sal), intensity-weighted average elemental H:C, C:N and C:S ratios in the <600 Da molecular fraction determined by FT-ICR-MS, and number of unique compounds (NUC) in enhanced organic matter treatments compared to controls (FT-ICR-MS). Values represent the mean and, in italics, standard error, from triplicate experiments.

Variable / Treatment	Concentration (μmol C or N L^{-1})			Enrichment factor (no unit)			Relative contribution (%)		Sal	Elemental ratio in < 600 Da fraction			NUC
	DOC	dCHO	DN	DOC	dCHO	DN	dCHO	EPS		H:C	C:N	C:S	
Control	60 *3.1*	24.63 *12.2*	14 *0.5*	–	–	–	42	14.4	33.67 *0.33*	1.306 *0.027*	50 *3*	196 *40*	
DOMtot	451 *5.6*	183.9 *22*	38 *0.6*	7.5	7.5	2.8	41	9.9	29 *1.0*	1.382 *0.001*	69 *1*	135 *11*	452
HMW	304 *12.2*	51.8 *8.6*	16 *0.7*	5.1	2.1	1.2	17.3	24.4	34 *0.0*	1.319 *0.004*	56 *3*	163 *22*	69
LMW	562 *31.6*	46.4 *8.8*	20 *1*	9.4	1.9	1.5	8.2	16.1	33.3 *0.33*	1.311 *0.008*	54 *3*	187 *19*	88

Table S2. Average data of the molecular characterization via FT-ICR MS: number of formulas assigned (n), peak magnitude weighted averages of the molecular mass ($Mass_{wa}$), number of atoms per element (C, O, N, S), oxygen to carbon ratio (O/C), hydrogen to carbon ratio (H/C), carbon to nitrogen ratio (C/N), and carbon to sulfur ratio (C/S).

Treatment	n	$Mass_{wa}$	C	O	N	S	O/C	H/C	C/N	C/S
Con T_0	3913 ± 374	406 ± 11	19.2 ± 0.3	25.1 ± 0.2	9.0 ± 0.5	0.35 ± 0.02	0.473 ± 0.022	1.306 ± 0.027	50 ± 3	196 ± 40
Con T_{216}	3826 ± 485	409 ± 11	19.2 ± 0.4	25.1 ± 0.6	9.2 ± 0.5	0.35 ± 0.01	0.488 ± 0.016	1.311 ± 0.058	50 ± 2	208 ± 29
DOMtot T_0	4226 ± 56	399 ± 0	19.3 ± 0.1	26.6 ± 0.1	8.4 ± 0.0	0.24 ± 0.01	0.443 ± 0.001	1.382 ± 0.001	69 ± 1	135 ± 11
DOMtot T_{216}	3961 ± 527	403 ± 6	19.6 ± 0.3	26.9 ± 0.5	8.5 ± 0.2	0.21 ± 0.03	0.439 ± 0.010	1.374 ± 0.009	81 ± 12	176 ± 15
HMW T_0	4185 ± 131	406 ± 5	19.2 ± 0.1	25.3 ± 0.1	8.9 ± 0.3	0.32 ± 0.01	0.471 ± 0.013	1.319 ± 0.004	56 ± 3	163 ± 22
HMW T_{216}	3733 ± 265	412 ± 10	19.4 ± 0.6	25.1 ± 0.8	9.3 ± 0.3	0.32 ± 0.02	0.484 ± 0.010	1.298 ± 0.008	56 ± 5	211 ± 61
LMW T_0	4148 ± 177	407 ± 10	19.2 ± 0.3	25.2 ± 0.3	9.1 ± 0.4	0.33 ± 0.01	0.478 ± 0.014	1.311 ± 0.008	54 ± 3	187 ± 19
LMW T_{216}	3820 ± 69	406 ± 10	19.2 ± 0.5	25.1 ± 0.7	9 ± 0.3	0.31 ± 0.02	0.473 ± 0.012	1.304 ± 0.009	55 ± 4	199 ± 36

Table S3. OTU identity codes for the bacteria taxa given in Fig 4c, and significant differences in % relative abundance (ANOVA, P < 0.05 or less, adjusted for multiple testing) for individual OTUs between the 4 treatments after 216 h. Treatments coded **a** had significantly higher RA than those coded **b**, which was higher than **c**, which was higher than **d**. ns, no significant difference between the treatments.

Taxon	OTU code	Control	DOM^{tot}	HWM	LMW
Acidobacteria					
Acidobacteria_Gp6	denovo231	a	b	b	b
Actinobacteria	*				
Cellulomonadaceae; *Cellulomonas*	denovo16999	a	b	b	b
Bacteroidetes					
Flavobacteriaceae; *Polaribacter* [1]	denovo12822	ns	ns	ns	ns
Flavobacteriaceae; *Polaribacter* [2]	denovo14078	b	b	a	a
Flavobacteriaceae; *Tenacibaculum* [1]	denovo22616	b	b	a	a
Flavobacteriaceae; *Tenacibaculum* [2]	denovo7458	b	b	a	a
Cytophagaceae; *Adhaeribacter*	denovo2035	a	b	b	b
Firmicutes					
Bacillaceae 1; *Bacillus*	denovo8856	ns	ns	ns	ns
Alphaproteobacteria	*				
Rickettsiales; Pelagibacteraceae	denovo18897	a	b	b	b
	denovo5224	a	b	b	b
Rhizobiales; Hyphomicrobiaceae; *Devosia*	denovo17594	ns	ns	ns	ns
Rhizobiales; Methylobacteriaceae	denovo4830	a	b	b	b
Rhodospirillales; *Roseomonas*	denovo14103	ns	ns	ns	ns
Rhodobacterales; Rhodobacteraceae	*	ns	ns	ns	ns
Betaproteobacteria; Burkholderiales;	*				
Oxalicibacterium	denovo753	ns	ns	ns	ns
Gammaproteobacteria; Alteromonadales	*				
denovo15318	denovo15318	ns	ns	ns	ns
Psychorium	denovo16333	d	a	c	b
Colwellia [1]	denovo1506	d	a	c	b
Colwellia [2]	denovo16444	a	b	a	a
Colwellia [3]	denovo17722	b	b	a	ns
Colwellia [4]	denovo18019	ns	ns	ns	ns
Colwellia [5]	denovo6146	b	b	a	a
Thalassomonas	denovo7640	ns	ns	ns	ns
Moritellaceae; *Moritella*	denovo12074	c	a	b	b
Psychromonadaceae; *Psychromonas*	denovo23606	b	a	b	b
Gammaproteobacteria; Oceanospirillales	*				
denovo19004	denovo19004	a	b	a	a
denovo22973	denovo22973	ns	ns	ns	ns
Oleispira	denovo264	ns	ns	ns	ns