Supplementary Information

Linking microbial diversity and functionality of Arctic glacial surface habitats

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Material and Methods

Samples representing the 7 different habitats (clean snow, red snow, green snow, biofilm, clean ice, dirty ice, and cryoconite hole sediments; see full definition below) were collected on 6 glaciers in Svalbard and 6 glaciers and snow fields in Arctic Sweden (for location details see Figure 1 main text and Table S1 below).

Field measurements

At each sampling point prior to collecting any sample, the snow temperature (upper few cm), pH and conductivity were measured *in-situ* using a multi-meter (Hanna instruments, HI 98129). For all snow and cryoconite hole samples, pH and conductivity were measured after allowing the multi-meter to equilibrate in the upper 2-3 cm of the sampling site. For ice samples this was achieved by melting a few ice chips prior to measurements. Furthermore, at each site, irradiation was measured using a radiometer with specific PAR (PMA2132), UV-A (PMA2110) and UV-B (PMA2106) sensors. Albedo was calculated by taking the ratio of reflected to incident radiation (400-700 nm range) and measuring the values always in the same position to the sun. The reading of the sensor was not affected by shading by the observer. Measurements were carried out with the sensors held at 30 cm above the snow surface (field of view 160º). At first, the sensor was pointed upwards (incident radiation) and then towards the snow surface (reflected radiation). Five measurements for incident and reflected radiation were acquired each, and the average was taken to avoid measuring bias. The standard deviations for each measurement set was below 10%.

Field sampling strategy

Based on visual observations 7 distinct microbial snow and ice surface habitats that were considered to be highly representative of the whole glacial surface were defined as follows: clean snow (white snow with no visual presence of particles), green snow (light to dark green colouration, often deep penetration of the snowpack), red snow (red colouration with all shades from orange to pink with variable densities of particles and only within the surface layer), biofilms (wet snow at snow-ice melting interfaces), clean ice (white ice with no visual presence of particles), dirty ice (light grey to dark grey colouration and variable densities of particles), and cryoconite holes (1-50 cm large rounded or elongated and variably deep holes filled with sediment). In each of these habitats samples were collected for various complementary microbial, mineralogical and geochemical analyses.

Field sample preservation and handling

For inorganic aqueous analyses samples were collected either in sterile 50 mL centrifuge tubes or sterile sample bags. The snow/ice samples were melted at room temperature over a ~ 6 hour period and all samples were filtered through single use 0.2 uM cellulose-acetate syringe filters. For cation analyses by inductively coupled plasma mass spectrometry (ICP-MS), samples were directly filtered into acid-washed (HCl) and pre-acidified (Aristar grade HNO_3) Nalgene HDPE bottles, while for anion analyses by ion chromatography (IC), solutions were filtered into un-acidified 15 mL centrifuge tubes.

For dissolved organic carbon (DOC) and organic particulate analysis, samples were collected in 250 mL glass jars that had been ashed at 450 °C. for > 4 h. After melting at room temperature these samples were filtered through ashed 0.7 μm glass fibre filters (GFF) directly into pre-acidified (100μl Aristar grade HNO_3) 40 mL, amber glass vials with Teflon® seals (Supelco). The GFF filters with the retained particulates were folded into quarters and preserved cold and in ashed aluminium foil for pigment and fatty acid analyses.

From these samples in addition to the organic particulates, particulates for X-ray diffraction (XRD) and Fourier transform infrared spectroscopy (FTIR) were also collected by filtering through 0.2 μm polycarbonate filters. Samples were returned to Leeds either frozen in liquid nitrogen in a cryo-shipper or in an ice-box at ~ 4 ˚C.

Aqueous organic (DOC) and inorganic analyses

Nutrients (NO_3^-, Cl^-, SO_4^{2-}) were analysed by ion chromatography (IC) on a Dionex DX 600 system with an autosampler, an IonPac AS16 analytical column with an AG16 guard column, an eluent gradient of 0-15 mM KOH and an ED50 conductivity detector. Injection volume was 25 μL and flow rate was set to 0.35 mL min^{-1}. The precision of the analysis was 5% and the limits of detection (LOD) were the following: NO_3^- = 96 ppb, Cl^- = 72 ppb, SO_4^{2-} = 121 ppb.

Major, minor and trace elements were measured by inductively coupled plasma mass spectrometry (ICP-MS) on an Agilent 7500ce with collision cell Octopole Reaction System (ORS) technology (ICP-MS facility, University of Portsmouth). The precision of the analysis was 3% and LODs were the following: Al, Ba, Co, Cr, Cu, Fe, Mg, Ni, Si, Sr, Zn = 0.1 ppb; Bi, Cd, Mn, Pb = 0.01 ppb; Ca, Na = 1 ppb; K,P,S = 10 ppb.

Dissolved organic carbon (DOC) was analysed on a Shimadzu TOC analyser (University of Plymouth). PO_4 was analysed by segmented flow-injection analyses (AutoAnalyser3, Seal Analytical).

Particulate total carbon, total nitrogen, total sulphur, total phosphate as well as particulate carbon and nitrogen isotope analyses

Particulates in the samples were analysed for $\delta^{15}N$ and $\delta^{13}C$ by a Vario Pyro Cube elemental analyser (Elementar Inc) coupled to an Isoprime mass spectrometer. Samples were combusted in tin capsules at 1150 °C and gases were separated using temperature controlled adsorption/desorption columns. Carbon analyses were calibrated with in-house C4-sucrose and urea standards assigned values of -11.93‰ and -46.83‰ respectively via calibration with the international standards LSVEC (-46.479‰), CH7 (-31.83‰), CH6 (-10.45‰), and CO-1 (+2.48‰). Nitrogen isotope values were calibrated using the international standards USGS-25 and USGS-26 with assigned values of -30.4‰ and +53.7‰ respectively. Total carbon (TC), total nitrogen (TN), and total sulphur (TS) were derived from the thermal conductivity detector in the elemental analyser and calibrated using a sulphanilamide standard. Particulate phosphorus was extracted by ashing of the samples at 550°C for 2 h and incubating in 1 M HCl for 16 h according to extraction step V in Ruttenberg et al.(2009).

Mineralogy

The mineralogical composition of each sample was determined by X-ray diffraction (XRD) with dried and ground samples analysed on a Bruker D8 Advance diffractometer. XRD spectra were recorded from 2-75°2Θ using a copper diffraction source and a run time of 12 min per sample. Spectra were analysed in DIFFRAC.EVA (Bruker, V.3.0).

Fourier transform infrared spectroscopy

Functional groups distributions were determined on bulk, dried samples by Fourier transform infrared (FTIR) using an A2 Technology Microlab Portable mid-IR spectrometer with a Diamond internal reflection cell (DATR), with spectra acquired in the mid-infrared range (650-4000 cm-1). From the bulk spectra, the peak area ratios of the main functional groups representing the lipids (CH_2 and CH_3 stretching modes between 3050 and 2800 cm^{-1}), and proteins (amide I and II bands at 1700-1500 cm^{-1}) to those of the carbohydrates (C-O-C, C-O-

P, P-O-P ring vibrations between 1204-815 cm^{-1}) were evaluated in Omnic (Thermos Scientific, V.5.1).

Pigment analysis

To determine the carotenoid and chlorophyll contents in the samples, high pressure liquid chromatography (HPLC) and a modified carotenoid/chlorophyll specific extraction protocol (Remias and Lutz 2007) were used. Cells were disrupted by shock freezing in liquid nitrogen for 10 min followed by grinding using a Teflon® mortar and pestle. The resulting powder was re-suspended in 1 mL of dimethylformamide (DMF) and 1.0 mm glass beads and horizontally shaken on a laboratory shaker (MoBio Vortex Genie 2) at maximum speed (3000 rpm) for 10 min followed by centrifugation for 5 min at 10 000 rpm. The supernatant was separated from the debris by filtering through a 0.45 µm Teflon® filter and the filtrate was mixed with methanol (25 vol %). Extracted samples were analysed immediately on an Agilent Technologies 1200 Infinity HPLC instrument with a gradient pump, an autosampler, a variable wavelength detector and ODS Hypersil column (250x4.6 mm; 5 um particle size). Two solvents were used: solvent A consisted of a mixture of acetonitrile/water/methanol/hexane/tris buffer at ratios of 80:7:3:1:1 while solvent B was a mix of methanol and hexane at a ratio of 5:1. The HPLC was run at a flow rate of 1 mL min^{-1} and with an injection volume of 25 µL. Spectra were recorded from 200 to 800 nm and chromatograms were quantified at 450 nm for carotenoids and 660 nm for chlorophyll a and b. Run time was 60 min and the protocol required a 15 minute run with 100% of solvent A followed by a linear gradient from 100 % solvent A to 100% solvent B between 32 and 45 min and finally with 15 minutes of column re-equilibration through a 5 min linear gradient from solvent B back to 100% solvent to A, followed by a further column conditioning with 100 % solvent A for 10 min. The following commercially available standards were used for peak identification: chlorophyll a, chlorophyll b (Sigma), violaxanthin, neoxanthin, antheraxanthin, lutein, β-carotene, trans-astaxanthin, and cis-astaxanthin (Carotenature). Chromatogram peak areas were calculated and the carotenoid data is reported as normalized to the peak area of chlorophyll a. The precision of the analysis was 5%.

Fatty acids analysis

Fatty acids were extracted according to the method described by Wacker & Martin-Creuzberg (2007). Briefly, 20 ng of internal standard (tricosanoic acid methyl ester) were added to each sample, before ultrasonic extraction using dichloromethane:methanol (2:1 v:v), followed by centrifugation to remove particulates and evaporation of solvent from the supernatant. Fatty acids were transesterified by adding methanolic HCl to the dried extract and heating at 60˚ C for 20 minutes. After cooling, fatty acid methyl esters were extracted in isohexane, solvent was removed under nitrogen and the sample resuspended in isohexane for analysis

Analysis of fatty acid methyl esters was carried out using a Trace 1300 gas chromatograph with flame ionisation detector (Thermo Scientific, Hemel Hempstead, UK), equipped with a non-polar-fused silica capillary column (CPSil-5CB, 50m x 0.32mm x 0.12 mm, Agilent Technologies, USA). Samples (1µl) were injected in splitless mode, with the injector maintained at 200˚C. Carrier gas was helium, with a constant flow rate of 1.5 ml/min. The following temperature programme was used: initial temperature 40 °C, rising to 140 °C at 20 °C min^{-1}, then rising to 240 °C at 4 ° min^{-1}, holding at 240 °C for 5 min. Fatty acid methyl esters were identified by comparison of retention time with those of reference compounds (Supelco, USA) and by gas chromatography/mass spectrometry. Gas chromatography/mass spectrometry was carried out using the gas chromatograph and column previously described, with identical operating conditions, coupled to an ISQ mass spectrometer (Thermo Scientific, Hemel Hempstead, UK). The transfer line and the ion source were maintained at 300˚C. The emission current was set to 50mA and the electron energy to 70 eV. The analyser was set to scan at m/z 50–650 with a scan cycle time of 0.6 s. The precision of the analysis was 5%.

DNA analysis

Total DNA was extracted using the PowerSoil® DNA Isolation kit (MoBio Laboratories). 16S rRNA genes were amplified using bacterial primers 27F (5’-AGAGTTTGATCMTGGCTCAG) and 357R (5’-CTGCTGCCTYCCGTA) (tagged with the Ion Torrent adapter sequences and MID barcode) spanning the V1-V2 hypervariable regions. 18S rRNA genes were amplified using the eukaryotic primers 528F (5′-GCGGTAATTCCAGCTCCAA) and 706R (5’-AATCCRAGAATTTCACCTCT) (Cheung et al., 2010) (tagged with the Ion Torrent adapter sequences and MID barcode) spanning the V4-V5 hypervariable region. Polymerase chain reactions (PCR) were performed using Platinum® PCR SuperMix High Fidelity according to manufacturer’s protocols. Initial denaturation at 95 ºC for 5 min was followed by 30 cycles of denaturation at 95 ºC for 30 s, annealing at 60 ºC for 30 s and elongation at 72 ºC for 30 s. Final elongation was at 72 ºC for 7 min. Archaeal 16S rRNA genes were amplified following a nested PCR approach. The first PCR reaction was carried out using primers 20F and 915R. Initial denaturation at 95 ºC for 5 min was followed by 35 cycles of denaturation at 95 ºC for 30 s, annealing at 62 ºC for 30 s and elongation at 72 ºC for 180 s. Final elongation was at 72 ºC for 10 min. The PCR product was used as template for the second PCR reaction with primers 21F (5'-TCCGGTTGATCCYGCCGG) and 519R (5'- GWATTACCGCGGCKGCTG) (tagged with the Ion Torrent adapter sequences and MID barcode) spanning the V1-V2 hypervariable region. Initial denaturation at 95 ºC for 5 min was followed by 30 cycles of denaturation at 95 ºC for 30 s, annealing at 60 ºC for 30 s and elongation at 72 ºC for 30 s. Final elongation was at 72 ºC for 7 min. All PCRs were carried out in triplicates to reduce amplification bias and in reaction volumes of 1 x 25 µl and 2 x 12.5 µl. All pre-amplification steps were done in a laminar flow hood with DNA-free certified plastic ware and filter tips. The pooled amplicons were purified with AMPure XP beads (Agencourt©) with a bead to DNA ratio of 0.6 to remove nucleotides, salts and primers and analyzed on the Agilent 2100 Bioanalyser (Agilent Technologies) with the High Sensitivity DNA kit (Agilent Technologies) and quality, size and concentration were determined. Sequencing was performed on an Ion Torrent Personal Genome Machine using the Ion Xpress™ Template Kit and the Ion 314™ or Ion 316™ chips following manufacturer's protocols. The raw sequence data was processed in QIIME (Caporaso et al., 2010). Barcodes and adapter sequences were removed from each sequence. Filtering of sequences was performed using an average cutoff of Q20 over a 350 bp range. Reads shorter than 200 bp were removed. OTUs were picked *de novo* using a threshold of 99%, 97% and 95% identity. Taxonomic identities were assigned for representative sequences of each OTU using the reference databases Greengenes for bacteria and archaea. The Silva database (DeSantis et al., 2006; extended with additional 223 sequences of cryophilic algae kindly provided by Dr. Thomas Leya from the CCCryo - Culture Collection of Cryophilic Algae, Fraunhofer IZI-BB) was used for eukaryotes. Data were aligned using PyNAST and a 0.80 confidence threshold. Singletons were excluded from the analysis. For bacterial sequence matching, plant plastids were removed from the data set prior to further analysis. For eukaryotic sequence matching *Chloroplastida* were pulled out of the data set and stored in a separate OTU table. In order to focus upon algal diversity, sequences matching *Embryophyta* (e.g., moss, fern) were removed from the data set. For archaea, sequences matching bacteria were removed. Finally, for diversity analyses samples were rarefied to the smallest sequence number and Shannon indices were calculated in QIIME. A matrix of each OTU table representing relative abundance was imported into Past3 (Hammer et al., 2012) for multivariate statistical analyses (principal component analysis, PCA). Representative sequences of the major algal species found in all samples were imported into Geneious (7.1.3., Biomatters) for phylogenetic tree building based on neighbour-joining.

References

Remias D, Lutz C (2007). Characterisation of esterified secondary carotenoids and of their isomers in green algae: a HPLC approach. *Algological Studies* 124: 85-94.

Ruttenberg K, Ogawa N, Tamburini F, Briggs R, Colasacco N, Joyce E (2009). Improved, high-throughput approach for phosphorus speciation in natural sediments via the SEDEX sequential extraction method. *Limnology and Oceanography: Methods* 7: 319-333.

Wacker A, Martin-Creuzburg D (2007). Allocation of essential lipids in Daphnia magna during exposure to poor food quality. *Functional Ecology* 21: 738-747.

Table S1: Overview of sample numbers, locations, coordinates and field measurements.

Sample ID	Glacier	Habitat	Collection date	GPS location [UTM]	Elevation [m a.s.l.]	pH	Snow temp. [°C]	PAR [W/m²]	UV-A [W/m²]	UV-B [W/m²]	Albedo [%]
Svalbard, Norway (SVA)											
SVA-13_1	Vestre Brøggerbreen	Green snow	20/07/2013	33H 0433185 E, 8759758 N	257	7.00	0.0	36	6.8	3.37	31
SVA-13_2	Vestre Brøggerbreen	Red snow	20/07/2013	33H 0433169 E, 8759838 N	265	7.03	0.0	48			63
SVA-13_3	Vestre Brøggerbreen	Clean snow	20/07/2013	33H 0433169 E, 8759838 N	265	7.32	0.0	43			72
SVA-13_4	Vestre Brøggerbreen	Red snow	20/07/2013	33H 0432976 E, 8760004 N	254	6.10	0.0	39			67
SVA-13_5	Vestre Brøggerbreen	Cryoconite hole	20/07/2013	33H 0432098 E, 8760034 N	196			35			24
SVA-13_6	Vestre Brøggerbreen	Clean ice	20/07/2013	33H 0432098 E, 8760034 N	196			41			59
SVA-13_7	Vestre Brøggerbreen	Dirty ice	20/07/2013	33H 0432098 E, 8760034 N	196			41			42
SVA-13_8	Vestre Brøggerbreen	Dirty ice	20/07/2013	33H 0432098 E, 8760034 N	196			31			48
SVA-13_10	Midre Lovénbreen	Red snow	21/07/2013	33H 0436410 E, 8757512 N	299	6.65	0.0	54	7.5	3.99	76
SVA-13_12	Midre Lovénbreen	Clean snow	21/07/2013	33H 0436410 E, 8757512 N	299	7.30	0.0	61			76
SVA-13_16	Midre Lovénbreen	Cryoconite hole	21/07/2013	33H 0436414 E, 8758244 N	267			50			36
SVA-13_17	Midre Lovénbreen	Clean ice	21/07/2013	33H 0436414 E, 8758244 N	267			54			61
SVA-13_18	Midre Lovénbreen	Dirty ice	21/07/2013	33H 0436402 E, 8758208 N	276			80			41
SVA-13_19	Midre Lovénbreen	Dirty ice	21/07/2013	33X 0436467 E, 8759176 N	172			81			35
SVA-13_20	Austre Brøggerbreen	Red snow	24/07/2013	33X 0429286 E, 8761458 N	209	6.38		91			60
SVA-13_21	Austre Brøggerbreen	Green snow	24/07/2013	33X 0429228 E, 8761426 N	232	6.56		86	12.5	3.25	26
SVA-13_22	Austre Brøggerbreen	Clean snow	24/07/2013	33X 0429286 E, 8761458 N	209	6.29		77			76
SVA-13_23	Austre Brøggerbreen	Red snow	24/07/2013	33X 0429448 E, 8761568 N	227	6.27		75			63
SVA-13_24	Austre Brøggerbreen	Green snow	24/07/2013	33X 0429448 E, 8761568 N	227			75			45
SVA-13_25	Austre Brøggerbreen	Dirty ice	24/07/2013	33X 0430467 E, 8762386 N	91			64			37
SVA-13_26	Austre Brøggerbreen	Dirty ice	24/07/2013	33X 0430087 E, 8761810 N	144			79			39
SVA-13_27	Austre Brøggerbreen	Cryoconite hole	24/07/2013	33X 0430087 E, 8761810 N	144	6.36		83			22
SVA-13_29	Austre Brøggerbreen	Clean ice	24/07/2013	33X 0430087 E, 8761810 N	144			82			59
SVA-13_31	Austre Brøggerbreen	Red snow	24/07/2013	33X 0430139 E, 8761706 N	146	8.07		70			62
SVA-13_33	Pedersenbreen	Red snow	27/07/2013	33X 0441747 E, 8756068 N	320			22	24.7	1.07	55
SVA-13_35	Pedersenbreen	Clean snow	27/07/2013	33X 0441747 E, 8756068 N	320			25			64
SVA-13_36	Pedersenbreen	Red snow	27/07/2013	33X 0441609 E, 8756682 N	262			115			55
SVA-13_37	Pedersenbreen	Cryoconite hole	27/07/2013	33X 0441593 E, 8756844 N	237			94			26
SVA-13_38	Pedersenbreen	Dirty ice	27/07/2013	33X 0441593 E, 8756844 N	237			147			44
SVA-13_39	Pedersenbreen	Clean ice	27/07/2013	33X 0441593 E, 8756844 N	237			273			61
SVA-13_40	Pedersenbreen	Dirty ice	27/07/2013	33X 0441898 E, 8757712 N	115			48			37
SVA-13_43	Austre Lovénbreen	Red snow	03/08/2013	33X 0439635 E, 8756676 N	413	6.3	0.1	182	19.6	0.66	66
SVA-13_44	Austre Lovénbreen	Green snow	03/08/2013	33X 0439635 E, 8756676 N	413			212			26
SVA-13_45	Austre Lovénbreen	Clean snow	03/08/2013	33X 0439635 E, 8756676 N	413			224			71

SVA-13_47	Austre Lovénbreen	Dirty ice	03/08/2013	33X 0439077 E, 8756528 N	383	5.17		170			55
SVA-13_48	Austre Lovénbreen	Red snow	03/08/2013	33X 0438286 E, 8756948 N	345			36			60
SVA-13_49	Austre Lovénbreen	Clean ice	03/08/2013	33X 0438640 E, 8757616 N	287			73			56
SVA-13_50	Austre Lovénbreen	Dirty ice	03/08/2013	33X 0438640 E, 8757616 N	287			107			37
SVA-13_51	Austre Lovénbreen	Cryoconite hole	03/08/2013	33X 0438658 E, 8757902 N	252	5.94	0.0	191			37
SVA-13_54	Feiringbreen	Red snow	05/08/2013	33X 0446691 E, 8773282 N	401	5.68		88	11.8	0.35	51
SVA-13_55	Feiringbreen	Clean snow	05/08/2013	33X 0446691 E, 8773282 N	401			66			74
SVA-13_56	Feiringbreen	Biofilm	05/08/2013	33X 0446574 E, 8772968 N	367						
SVA-13_60	Feiringbreen	Clean ice	05/08/2013	33X 0445766 E, 8772392 N	262			62			55
SVA-13_61	Feiringbreen	Cryoconite hole	05/08/2013	33X 0445766 E, 8772392 N	262	5.23		47			43
SVA-13_62	Feiringbreen	Dirty ice	05/08/2013	33X 0445766 E, 8772392 N	262	5.14		47			45
SVA-13_63	Feiringbreen	Dirty ice	05/08/2013	33X 0445766 E, 8772392 N	262			63			47
SVA-13_65	Midre Lovénbreen	Red snow	05/08/2013	33X 0436693 E, 8759332 N	151			108			49
Tarfala, Sweden (TAR)											
TAR-13_1	Storglaciären	Red snow	01/07/2013	34W 0398931 E, 7533637 N	1268	6.98	0.0	52	8.1	0.08	56
TAR-13_2	Storglaciären	Green snow	01/07/2013	34W 0399035 E, 7533630 N	1258	5.81	0.0	32	6.3	0.15	32
TAR-13_3	Storglaciären	Green snow	01/07/2013	34W 0399035 E, 7533630 N	1258	4.85	0.0	26.5			18
TAR-13_4	Storglaciären	Green snow	01/07/2013	34W 0398948 E, 7534177 N	1291	5.78	0.0	61.1			34
TAR-13_5	Storglaciären	Red snow	01/07/2013	34W 0399260 E, 7534131 N	1221	5.56	0.0	29.8			66
TAR-13_8	Storglaciären	Red snow	03/07/2013	34W 0397551 E, 7534187 N	1412	7.23	0.1	97			72
TAR-13_9	Storglaciären	Clean snow	03/07/2013	34W 0397551 E, 7534187 N	1412	7.55	0.0	83.9			78
TAR-13_10	Storglaciären	Biofilm	03/07/2013	34W 0397494 E, 7534083 N	1419			142			30
TAR-13_11	Storglaciären	Biofilm	03/07/2013	34W 0397705 E, 7533762 N	1383	5.87	0.0	81			34
TAR-13_12	Storglaciären	Clean ice	03/07/2013	34W 0397705 E, 7533762 N	1383	5.93	0.0	84			56
TAR-13_13	Storglaciären	Dirty ice	03/07/2013	34W 0398556 E, 7534166 N	1436	5.55	0.0	55			42
TAR-13_14	Storglaciären	Dirty ice	03/07/2013	34W 0398727 E, 7533953 N	1320	5.34	0.0	72			33
TAR-13_16	Storglaciären	Green snow	03/07/2013	34W 0399301 E, 7534133 N	1203	5.48	0.0	80			31
TAR-13_17	Rabot	Red snow	05/07/2013	34W 0394929 E, 7534801 N	1350	6.13	0.0	112	16.5	1.05	75
TAR-13_18	Rabot	Clean snow	05/07/2013	34W 0394929 E, 7534801 N	1350	6.38	0.0	114			84
TAR-13_19	Rabot	Biofilm	05/07/2013	34W 0394909 E, 7534939 N	1357	6.34	0.0	124			33
TAR-13_21	Rabot	Red snow	05/07/2013	34W 0394160 E, 7535197 N	1282	5.45	0.0	122			73
TAR-13_22	Rabot	Dirty ice	05/07/2013	34W 0392291 E, 7534683 N	1193	5.69	0.0	80			37
TAR-13_24	Rabot	Red snow	05/07/2013	34W 0393074 E, 7534485 N	1165			95			54
TAR-13_27	Liljetopsrännan	Red snow	06/07/2013	34W 0398423 E, 7533989 N	1119	5.41	0.2	54	11.1	0.40	65
TAR-13_28	Liljetopsrännan	Red snow	06/07/2013	34W 0398656 E, 7536883 N	1209	6.35	0.0	51			56
TAR-13_30	SE-Kasskasatjåkkå	Red snow	07/07/2013	34W 0399446 E, 7537111 N	1374	0.45	0.3	123	19.4	2.78	77
TAR-13_31	SE-Kasskasatjåkkå	Clean snow	07/07/2013	34W 0399446 E, 7537111 N	1374	5.80	0.0	178			64
TAR-13_32	SE-Kasskasatjåkkå	Red snow	07/07/2013	34W 0399458 E, 7536982 N	1318	5.78	0.0	108			57

TAR-13_33	SE-Kasskasatjåkkå	Green snow	07/07/2013	34W 0399820 E, 7536730 N	1247	5.83	0.0	113			28
TAR-13_34	Storglaciären	Cryoconite hole	09/07/2013	34W 0398607 E, 7534297 N	1338	5.6	0.4				
TAR-13_35	Storglaciären	Red snow	09/07/2013	34W 0398849 E, 7534337 N	1308	5.41	0.0	88			76
TAR-13_36	Permanent snow field	Red snow	09/07/2013	34W 0399453 E, 7534692 N	1167	5.68	0.0	85			65
TAR-13_37	Permanent snow field	Red snow	09/07/2013	34W 0399376 E, 7534942 N	1163	5.73	0.4	82			62
TAR-13_39	Permanent snow field	Red snow	10/07/2013	34W 0400256 E, 7535905 N	1318			199	18.4	3.86	66
TAR-13_40	Permanent snow field	Clean snow	10/07/2013	34W 0400256 E, 7535905 N	1318	6.28		158			77
TAR-13_41	Björling	Red snow	11/07/2013	34W 0395764 E, 7532198 N	1295	5.44	0.0	127	20.3	4.49	66
TAR-13_42	Björling	Red snow	11/07/2013	34W 0396623 E, 7531127 N	1156	6.1	0.3	100			57
TAR-14_1	Storglaciären	Red snow	04/07/2014	34W 0398031 E, 7533618 N	1268	7.4	0.1				
TAR-14_2	Storglaciären	Green snow	04/07/2014	34W 0399302 E, 7534091 N	1216		0.1				
TAR-14_3	SE-Kasskasatjåkkå	Green snow	05/07/2014	34W 0399093 E, 7534138 N	1249	7.3	0.1				
TAR-14_4	Storglaciären	Green snow	07/07/2014	34W 0398886 E, 7533623 N	1277	7.35	0.1				
TAR-14_5	Storglaciären	Red snow	07/07/2014	34H 0399085 E, 7533632 N	1247	7.78	0.3				
TAR-14_6	Storglaciären	Red snow	07/07/2014	34H 0393734 E, 7535101 N	1226	6.17	0.1				
TAR-14_7	Rabot	Green snow	09/07/2014	34W 0394036 E, 7535053 N	1326	8.13	0.1				
TAR-14_8	Rabot	Green snow	09/07/2014	34W 0392829 E, 7534726 N	1088		0.1				
TAR-14_9	Rabot	Green snow	09/07/2014	34W 0399578 E, 7536800 N	1249						
TAR-14_10	Liljetopsrännan	Red snow	10/07/2014	34W 0398650 E, 7536880 N	1215	7.51	0.1				
TAR-14_11	SE-Kasskasatjåkkå	Red snow	10/07/2014	34W 0399438 E, 7537029 N	1340	7.14	0.1				
TAR-14_12	Permanent snow field	Red snow	10/07/2014	34W 0400194 E, 7535878 N	1318	8.16	0.1				

- Temperature was also measured at each site and in most cases it was 0.0 ^{o}C; only in a few snow samples did we measure 0.1 or 0.2 ^{o}C.

Table S2: Distribution of 97% clustered OTUs aligned and assigned to *Archaeplastida* (green algae) taxa separated by habitat and locations. Values are the relative abundance of the taxa in percentage of total sequences and table shows taxa with OTUs of a minimum total observation count of 0.1%. It is important to note that values are rounded to one digit; therefore, the abundance of a taxon with a value of 0 in one sample can range between 0 and 0.04%. The clean snow and clean ice habitats did not contain enough particulates for analyses and thus these habitats are not listed in this or the following tables listing particulate analyses. In this and all subsequent tables, samples ID's labelled as *SVA* denote samples from Svalbard and those marked *TAR* are samples from the Tarfala Valley in Arctic Sweden.

pecies **ample ID**	***Ancylonema nordenskiöldii***	***Chloromonas cf. alpina*** **AF514403**	***Chlamydomonas cf. proboscigera***	***Chloromonas polyptera*** **JQ790556**	***Chloromonas sp.*** **CCCryo 273-06**	***Chloromonas nivalis*** **AF514409**	***Chloromonas tughillensis***	***Microglena sp.*** **EF537906**	***Prototheca cutis***	***Trebouxia usneae***	***Raphidonema sempervirens*** **AJ309939**	**Uncultured *Chlamydo-monadaceae*** **(1) GU117577**	**Uncultured *Chlamydo-monadaceae*** **(2)**	**Uncultu *Chlamy monada*** **(3)**
reen snow														
VA-13_1	0	0.1	1.6	0.4	0.1	0	0	0.6	0	0	93.4	3.4	0.5	
VA-13_21	0	1.2	0.1	1	31.4	0	0.1	60.1	0	0	2.7	3	0.3	
VA-13_44	0	4.7	0	8.8	0	0.7	0	0	0	0	68.9	16.3	0.8	
verage SVA	**0**	**2.0 ± 2.4**	**0.6± 0.9**	**3.4 ± 4.7**	**10.5 ± 18.1**	**0.2 ± 0.4**	**0.0 ± 0.1**	**20.2 ± 34.5**	**0**	**0**	**55.0± 46.9**	**7.6 ± 7.6**	**0.5 ± 0.3**	
AR-13_2	0	8.6	0	21.5	0	0.4	0	0	0	0	11.9	53.2	4.5	
AR-13_3	8.5	16.5	0.2	17	0	0.3	0	0	8.3	0	35.7	8.5	0.2	
AR-13_4	0.2	22.3	0.1	18	0.9	0.8	0.1	0	37.8	0	6.1	4.1	0.2	
AR-13_16	0	5.1	0	30.1	0	32	6.5	0	0	0.2	1.4	23.1	1.4	
AR-13_33	0	3.7	0	52.5	0	14.9	4.1	0	12	0	0	11.6	0	
AR-14_2	0	0.2	0	45	0	20.5	2.1	0	2.1	0.1	1.7	27.6	0.7	
AR-14_3	0.1	0.6	0.1	35.2	0	20.1	1	0	0.8	0	3.6	37.7	0.9	
AR-14_4	0	1	0	10.1	0	3.3	0.4	0	0.5	12.2	1	68.9	2.4	
AR-14_7	0	22.7	0	53.1	0	0	0	0	1.5	10	0.4	7.9	0.4	
AR-14_8	0	0.3	0	90.6	0	0	0	0	1.5	0.8	0.3	5.4	0.5	
AR-14_9	0	1.9	0	38.1	0	1.9	0.1	0	8.4	0.2	0.1	47.1	1.9	
verage TAR	**0.8 ± 2.6**	**7.5 ± 8.8**	**0.0 ± 0.1**	**37.4 ± 22.8**	**0.1 ± 0.3**	**8.6 ± 11.3**	**1.3 ± 2.1**	**0**	**6.6 ± 11.1**	**2.1 ± 4.5**	**5.7** ± 10.6	**26.8 ± 22.2**	**1.2 ± 1.3**	**2.0 ±**
ed snow														
VA-13_2	0	0.1	0	22.5	0	1.8	0	0	0	0.2	0	72.3	3	
VA-13_4	0	0.8	0	0.9	0	0.8	0.9	0.1	0	0	0	87.8	8.8	
VA-13_10	0	0	0	5.3	0	0.2	0	0	0	0	0	83.8	10.7	
VA-13_20	0	0	0	8.8	0	14	0.4	0	0	0	1.7	65.0	10.1	
VA-13_23	0	0	0	6.6	0	0.6	0	0	0	0	0.2	89.9	2.6	

VA-13_31	0	0	0	5.8	0	2.7	0	0	0.3	0	0.5	88.9	1.8	
VA-13_33	0	1.9	0	10.8	0.3	9.3	0	0	0	0	5.1	65.2	7.6	
VA-13_36	8.6	0.3	0.1	16.5	0	1.3	0.1	0	0.3	0	3.6	65.9	3.2	
VA-13_43	0	0.9	0	10.3	0	2.8	0.3	0.1	0	0	35.5	45.8	4.2	
VA-13_48	0	1.4	0	12.4	0	2.8	0	0	0.1	0	21.3	59.3	2.1	
VA-13_54	0	0	0	1.5	0.1	0.6	0	0	0	0	2.3	93.3	2.1	
VA-13_65	0.1	0.2	1.2	14.3	0	0	0	0	0.1	0	0.5	81.8	1.8	
verage SVA	**0.7 ± 2.5**	**0.5 ± 0.6**	**0.1 ± 0.3**	**9.6 ± 6.3**	**0.0 ± 0.1**	**3.1 ± 4.2**	**0.1 ± 0.3**	**0**	**0.1± 0.1**	**0.0 ± 0.1**	**5.9 ± 11.1**	**74.9 ± 14.8**	**4.8 ± 3.4**	**0.1 ±**
AR-13_1	0	0.1	0	12.3	0	1.2	1.3	0	0	0.1	0	76.2	8.9	
AR-13_8	0	5.7	0	52.6	0	4.6	0.1	0	0.1	0	0.1	33.5	3.3	
AR-13_17	0	0.2	0	9	0	0.4	0	0	0	0	14.2	67.7	8.6	
AR-13_21	0	0.1	0	6.1	0	12.6	1.3	0	0	0.1	0.1	72.1	7.6	
AR-13_27	0	0	0	17	0	8.8	0.1	0	0.1	0.1	1.7	69	3.2	
AR-13_28	0	0	0	17.6	0	1.1	0	0	0	0	0.3	74.5	6.5	
AR-13_30	0	0	0	1	0	2	0.3	0.6	0	0.1	1.9	87.7	6.4	
AR-13_35	0	12.9	0	26.9	0	7.2	0.9	0	0.4	0.1	0	32.1	0.7	1
AR-13_39	0	0	0	6.4	0	5.2	0.1	0	0	0	0	75.3	13	
AR-13_41	0	0	0	5.4	0	8.4	2.7	0	0	0	0.1	71.8	11.6	
AR-14_1	0	0.3	0	23.2	0	0.7	0.1	0	16.8	0.2	0.7	54.8	1.9	
AR-14_5	0	0.1	0	4.9	0	2.7	0.2	0	0.2	5.1	0.1	84.1	2.7	
AR-14_6	0	0	0	8.1	0	0	0	0	4.4	0	0.5	85.1	2	
AR-14_10	0.2	0	0	14.4	0	9.4	0.1	0	0.3	0.9	1.2	71.1	2.4	
AR-14_11	0.2	0	0	21.1	0	5.1	0	0	0.2	8.5	3.6	59.8	1.5	
AR-14_12	0	0	0	5.7	0	3.8	0	0	0	1.2	20.5	67.3	1.3	
verage TAR	**0.0 ± 0.1**	**1.2 ± 3.4**	**0**	**14.5 ± 12.6**	**0**	**4.6 ± 3.8**	**0.5 ± 0.7**	**0.0 ± 0.2**	**1.4 ± 4.2**	**1.0 ± 2.4**	**2.8 ± 5.9**	**67.6 ± 16.0**	**5.1 ± 3.9**	**1.3 ±**
iofilms														
VA-13_56	0	8.3	0	33.9	0.5	15.1	0.1	0	0	0.1	2.2	38.2	1.5	
AR-13_10	0	6.2	0	53.2	0	5.5	0.1	0	0	0	0	31.7	3.3	
AR-13_11	0	11.9	0	41.1	0	0.2	0	0	4.4	0	27.5	3.9	0.3	1
AR-13_19	0	6.6	0	72.5	0	6.9	5.4	0	0	0	0.3	7.5	0.9	
verage TAR	**0**	**8.2 ± 3.2**	**0**	**55.6 ± 15.8**	**0**	**4.2 ± 3.5**	**1.8 ± 3.1**	**0**	**1.5 ± 2.5**	**0**	**9.3 ± 15.8**	**14.4 ± 15.1**	**1.5 ± 1.6**	**3.6 ±**
irty ice														
VA-13_7	0	0	0	7.5	0	0	0.2	0	0	0	62	28.1	2.2	

VA-13_8	9.4	0.1	0.1	31.5	0	0.1	0	0.1	0	0.1	49.2	7.1	0.1	
VA-13_18	0	1.6	0	4.6	0	0	0	0.3	0	0	31.3	58.7	3.3	
VA-13_19	65.1	0.8	0	0.8	0	0	0	0	0	0	7.9	20.6	0	
VA-13_26	0	0	0.6	15.4	0	0	0	0	0	0	40.1	42	1.9	
VA-13_38	0	0.4	31.3	5.9	0	0	0.4	0.8	0	0	18.8	38.3	3.9	
VA-13_47	0	0.4	0	3.6	0.2	0.4	0	0.4	0	0	78.3	14.1	2.4	
VA-13_50	41.6	0.9	1.8	4.9	0.1	0.1	0	0	0	0	37.7	12.7	0.3	
VA-13_62	30.1	1.4	0	6.9	0	0	0	1.4	0	0	12.3	42.5	0	
verage SVA	**16.2 ± 23.9**	**0.6 ± 0.6**	**3.8 ± 10.3**	**9.0 ± 9.3**	**0.0 ± 0.1**	**0.1 ± 0.1**	**0.1 ± 0.1**	**0.3 ± 0.5**	**0**	**0**	**37.5 ± 23.2**	**29.3 ± 17.2**	**1.6 ± 1.5**	**1.5 ±**
AR-13_13	0	0.9	0	6.1	0	0.3	0	0.9	0	0	87.5	4.3	0	
ryoconite holes														
VA-13_5	1.3	0	0	3.8	0	2.1	0	0	0	0.2	52	38.4	2.3	
VA-13_16	3.8	0	0	1	0	0	0	0	0	0	41.2	54.1	0	
VA-13_27	2.1	0	0	1.1	0	0	0	0	0	0	35.3	60.7	0.8	
VA-13_37	4.1	0	0	3.7	0	2.3	0	0	0.2	0.2	16.3	71.7	1.6	
VA-13_51	54.1	0.1	0.3	0.6	0	0.2	0	0	0	0	18	26.1	0.2	
VA-13_61	3.8	0	0	1.3	0.3	0	0	0	0	0	3.3	91	0.5	
verage SVA	**11.5 ± 20.9**	**0**	**0.1 ± 0.1**	**1.9 ± 1.4**	**0.1 ± 0.1**	**0.8 ± 1.1**	**0**	**0**	**0.0 ± 0.1**	**0.1 ± 0.1**	**27.7 ± 18.2**	**57.0 ± 23.2**	**0.9 ± 0.9**	**0.1 ±**
AR-13_34	6.2	1.5	0.2	1.5	1.9	0.2	0	0	0.1	0	83.6	4.6	0	

Table S3: Distribution of 97% clustered OTUs aligned and assigned to eukaryote taxa separated by habitat and locations. Values are the relative abundance of the taxa in percentage of total sequences. It is important to note that values are rounded to one digit; therefore, the abundance of a taxon with a value of 0 in one sample can range between 0 and 0.04%.

Sample ID	Amoebozoa	Archaeplastida	Centrohelida	Kathablepharidae	Opisthokonta	RT5iin25	SAR	Zeuk77
Green snow								
SVA-13_1	0	64.8	0	0	1.2	0	33.9	0.1
SVA-13_21	0	87.6	0	0	0.7	0	11.3	0.4
SVA-13_44	0	44.7	0	0	38.3	0	15.7	1.3
Average SVA	**0**	**65.7 ± 21.5**	**0**	**0**	**21.6 ± 22.4**	**0**	**20.3 ± 12.0**	**0.6 ± 0.6**
TAR-13_2	0	21.6	0	0	22.4	0	34.9	21.1
TAR-13_3	0	53	0	0	30.7	0	15.9	0
TAR-13_4	0.2	57.1	0	0	37	0	5	0
TAR-13_16	0	37.2	0	0	25.1	0	36.1	1.6
TAR-13_33	0.2	51.4	0	0	19.2	0	24.2	2.4
TAR-14_2	0	56.4	0	0	25.3	0	14	2.8
TAR-14_3	0	46.3	0	0	31.9	0	18.7	1.6
TAR-14_4	0	14.2	0	0	69.9	0	15.3	0
TAR-14_7	0	47.6	0	0	48.4	0	1.4	0
TAR-14_8	0	47.4	0	0	49.9	0	2.3	0
TAR-14_9	0	42	0	0	42.6	0	13.1	2.3
Average TAR	**0.0 ± 0.1**	**43.1 ± 13.9**	**0**	**0**	**36.6 ± 15.1**	**0**	**16.4 ± 11.7**	**2.9 ± 6.1**
Red snow								
SVA-13_2	0	68.0	0	0	31.5	0	0.5	0
SVA-13_4	0	83.3	0	0	4.0	0	12.7	0
SVA-13_10	0	74.5	0	0	24.7	0	0.7	0
SVA-13_20	0	81.8	0	0	12.9	0	5.3	0
SVA-13_23	0	63.3	0	0	32.5	0	2.9	0
SVA-13_31	0	82.4	0	0	9.1	0	7.9	0
SVA-13_33	0	58.0	0	0	26.8	0	14.2	1
SVA-13_36	0	42.0	0	0	38.4	0	19	0.1
SVA-13_43	0	56.6	0	0	24.4	0	17.5	1.5

SVA-13_48	0.1	82.5	0	0	12.9	0	4.2	0
SVA-13_54	0	62.3	0	0	33.8	0	3.8	0
SVA-13_65	0	67.8	0	0	20.8	0	9.3	0
Average SVA	**0**	**68.5 ± 12.9**	**0**	**0**	**22.7 ± 10.9**	**0**	**8.2 ± 6.4**	**0.2 ± 0.5**
TAR-13_1	0	64.1	0	0	32.1	0	3.8	0
TAR-13_8	0	44.7	0	0	47.9	0	7.4	0
TAR-13_17	0	27.1	0	0	72.6	0	0.3	0
TAR-13_21	0	68.0	0	0	23.4	0	8.5	0.1
TAR-13_27	0	29.5	0	0	68.3	0	1.8	0
TAR-13_28	0	76.4	0	0	23.2	0	0.4	0
TAR-13_30	0	38.1	0	0	61.0	0	1.0	0
TAR-13_35	0	72.8	0	0	19.6	0	6.7	0
TAR-13_39	0	88	0	0	11.0	0	1.0	0
TAR-13_41	0	75	0	0	19.8	0	5.2	0
TAR-14_1	0.2	38.1	0	0	50.9	0	10.4	0
TAR-14_5	0	32.6	0	0	58.5	0	8.6	0
TAR-14_6	0.1	37.2	0	0	51.1	0	9.7	0
TAR-14_10	0	26	0	0	71.8	0	1.4	0
TAR-14_11	0	18.2	0	0	77.2	0	3.8	0
TAR-14_12	0	68.8	0	0	21.1	0	9.5	0.2
Average TAR	**0.0 ± 0.1**	**50.3 ± 22.3**	**0**	**0**	**44.3 ± 22.6**	**0**	**5.0 ± 3.7**	**0.0 ± 0.1**
Biofilms								
SVA-13_56	0	48.9	0	0	27.5	0	20.6	1.8
TAR-13_10	0	46.1	0	0	50	0	3.9	0
TAR-13_11	0	56.1	0	0	25.2	0	18.0	0
TAR-13_19	0	36.8	0	0	60.4	0	2.7	0
Average TAR	**0**	**46.3 ± 9.7**	**0**	**0**	**45.2 ± 18.1**	**0**	**8.2 ± 8.5**	**0**
Dirty ice								
SVA-13_7	0.2	47.5	0	0	14.6	4.6	32.0	1.1
SVA-13_8	0	34.9	0	0	17.1	0	47.3	0.1
SVA-13_18	0	60.7	0	0	30.7	0	8.6	0
SVA-13_26	0	53.2	0	0	18.1	0	28.7	0
SVA-13_38	0.1	53.2	0	0	9.0	0	36.9	0.9

SVA-13_47	0	33.8	0	0	33.9	0	32	0.3
SVA-13_50	0	68.4	0	0	20.1	0	8.4	0
SVA-13_62	0	35.6	0	0	50.8	0	13.1	0.5
Average SVA	**0.0 ± 0.1**	**48.4 ± 12.9**	**0**	**0**	**24.3 ± 13.5**	**0.6 ± 1.6**	**25.9 ± 14.3**	**0.4 ± 0.4**
TAR-13_13	0	57.7	0	0	38	0	4.3	0
Cryoconite holes								
SVA-13_5	0.1	48.2	0	0	23.2	0	24	0.4
SVA-13_16	0.3	10.7	0	0	66.4	0	20.3	0
SVA-13_27	0.1	13.5	0	0	75.6	0	7.8	0.1
SVA-13_37	0.1	38	0	0	39.6	0	17.9	0.2
SVA-13_51	0.1	22.9	0	0	47.8	0	26.4	0
SVA-13_61	0.2	9.7	0	0.1	79.9	0	7.9	0
Average SVA	**0.2 ± 0.1**	**23.8 ± 16.0**	**0**	**0**	**55.4 ± 22.2**	**0**	**17.4 ± 7.9**	**0.1 ± 0.2**
TAR-13_34	0	47.6	0	0	10.9	0	41.2	0

Table S4: Distribution of 97% clustered OTUs aligned and assigned to known bacterial taxa separated by habitat and locations. Values are the relative abundance of the taxa in percentage of total sequences and figure shows taxa with >0.01% abundance. It is important to note that values are rounded to one digit; therefore, the abundance of a taxon with a value of 0.0 in one sample can range between 0 and 0.04%.

Phyla	***Acidobacteria***		***Actinobacteria***		***Bacteriodetes***				***Chlorobi***	***Chloroflexi***		
Class	*Acidobacteriia*	*Solibacteres*	*Acidimicrobiia*	*Actinobacteria*	*Cytophagia*	*Flavobacteriia*	*Sphingobacteriia*	*Saprospirae*	*Ignavibacteria*	*Anaerolineae*	*C0119*	*Ktedonobacteria*
Green snow												
SVA-13_1	9	0	0	0	8	0.1	12.3	6.2	0	0	0	0
SVA-13_21	0	0	0	0	3.2	10.7	7.2	1.4	0	0	0	0
SVA-13_44	0.1	0	0	1.7	2.2	5.8	0.2	39.6	0	0	0	0
Average SVA	**3.0 ± 5.2**	**0**	**0**	**0.6 ± 0.1**	**4.5 ± 3.1**	**5.5 ± 5.3**	**6.6 ± 6.1**	**15.7 ± 20.8**	**0**	**0**	**0**	**0**
TAR-13_2	0	0	0	0.1	0.4	0	18.1	42.1	0	0	0	0
TAR-13_3	0.3	0.3	0	1.8	0.2	0.3	47.3	4.3	0	0	0	0
TAR-13_4	0.8	0.1	0	0.1	0.8	0	33.6	1.6	0	0	0	0
TAR-13_16	0	0	0	0.3	0.9	0	23.7	26.9	0.1	0	0	0
TAR-13_33	0	0	0	1.7	1.3	0.1	31.4	14	0	0	0	0
TAR-14_2	0.1	0	0	1.2	6.9	0.1	4.6	18.9	0	0	0	0
TAR-14_3	0.3	0.2	0	2.2	1.6	0.2	12.3	15.5	0	0	0	0
TAR-14_4	10.7	0.3	0	0	0	0	0.2	0	0	0.1	0	0
TAR-14_7	17.2	0.3	0	0	0	0.1	1.7	0	0	0	0	0
TAR-14_8	4.8	0	0	1.4	1.3	0	48.5	0.3	0	0	0	0
TAR-14_9	1.7	0	0	0	1.7	0	6.7	10	0	0	0	0
Average TAR	**3.3 ± 5.7**	**0.1 ± 0.1**	**0**	**0.8 ± 0.9**	**1.4 ± 1.9**	**0.1 ± 0.1**	**20.7 ± 17.6**	**12.1 ± 13.4**	**0**	**0**	**0**	**0**
Red snow												
SVA-13_4	0	0	0	0.5	37.4	0	0.3	51.2	0	0	0	0
SVA-13_10	17	0	0	0	9	0	0	3	0	0	0	0
SVA-13_20	0	0	0	0	10.6	0	1.5	45.2	1.8	0	0	0
SVA-13_23	0	0	0	0.3	6.3	4.6	0	1	0	0	0	0
SVA-13_31	0	0	0	4.2	11.6	0.4	0	44.9	0	0	0	0
SVA-13_33	0.4	0	0	2.1	3.9	0	2.8	26.8	0	0	0	0
SVA-13_36	3.4	0	0	8.4	39	0.5	0.8	1.6	0	0	0	0
SVA-13_43	0.8	0	0	0.8	12.5	0	0.4	67.3	0	0	0	0
SVA-13_48	0	0	0	0.6	44.5	0.6	0	19.1	0	0	0	0

SVA-13_54	0.2	0	0	15.7	3.4	0.5	34.6	3.6	0	0	0	0
SVA-13_65	0.4	0	0	0.2	5.9	1	0.3	3.7	0	0.1	0	0
Average SVA	**2.0 ± 5.1**	**0**	**0**	**3.0 ± 4.9**	**16.7 ±** 15.5	**0.7 ± 1.3**	**3.7 ± 10.3**	**24.3 ± 24.1**	**0.2 ± 0.5**	**0**	**0**	**0**
TAR-13_1	0	0	0	0.1	3.6	0	91.1	1.9	0	0	0	0
TAR-13_8	0.4	0	0	0	0	0	89.3	0	0.4	0	0	0
TAR-13_17	0.2	0	0	0	0.8	0	90.7	0.1	0	0	0	0
TAR-13_21	0	0	0	0	1	0	75.7	22.3	0	0	0	0
TAR-13_27	0	0	0	0	0.5	0	71.4	0.5	5.1	0	0	0
TAR-13_28	4.7	0	0	0	0	0	12.5	0	0	0	0	0
TAR-13_30	0.2	0	0	0	3.8	0	81.6	3.2	0.2	0	0	0
TAR-13_35	0.8	0	0	0.1	4.1	0.9	63	4.3	0	0	0	0
TAR-13_41	0	0	0	0.1	0.5	0	82.1	15.8	0.3	0	0	0
TAR-14_1	1.1	0	0	4.3	1.2	0	46.3	11.2	0	0	0	0
TAR-14_5	16.7	0.2	0	0	15	0	1.3	0	0	0	0	0
TAR-14_6	0.1	0	0	0.1	1.9	0.1	81.3	2.4	0	0	0	0
TAR-14_10	17.1	0.7	0	0.1	7.3	0	45.8	1	0	0	0	0
TAR-14_11	4.6	0.5	0	0.4	13.6	0	51.8	6.3	0	0	0	0
TAR-14_12	3.1	0	0	0.3	2.2	0	59.3	0	0	0	0	0
Average TAR	**3.3 ± 5.8**	**0.1 ± 0.2**	**0**	**0.4 ± 1.1**	**3.7 ± 4.7**	**0.1 ± 0.2**	**62.9 ± 27.5**	**4.6 ± 6.7**	**0.4 ± 1.3**	**0**	**0**	**0**
Biofilms												
SVA-13_56	0	0	0	7.6	9.5	5.4	2.8	14.2	0	0	0	0
TAR-13_10	0	0	0	0	0.2	0	92.1	1.9	0	0	0	0
TAR-13_11	0.1	0	0	3.8	0.7	0	66.8	2.8	0	0	0	0
TAR-13_19	0	0	0	0	1	0	97.8	0.8	0	0	0	0
Average TAR	**0.0 ± 0.1**	**0**	**0**	**1.3 ± 2.2**	**0.6 ± 0.4**	**0**	**85.6 ± 16.5**	**1.8 ± 1.0**	**0**	**0**	**0**	**0**
Dirty ice												
SVA-13_7	0.2	0	0	0.4	2.9	30.8	4.4	0.5	0	0	0	0
SVA-13_8	1.6	0.2	0.1	7	0.2	0	1.7	2.6	0	1.1	0	0.2
SVA-13_18	8.7	0	0	2.1	37.6	0.2	2.1	1.1	0	0	0	0
SVA-13_19	5	0.2	0	8	0.5	0	4.2	0.3	0	0.3	0	0
SVA-13_26	0.2	0.2	0	5.1	1.3	0.2	4.2	5.9	0	0	0	0
SVA-13_38	2.9	0.4	0	3.6	1	0.2	7.1	8.9	0	0.1	0	0
SVA-13_47	22.8	0.1	0	1.9	4.1	0.2	9.5	1.7	0	0	0	0

SVA-13_50	3.2	0	0	15.9	4.7	0	2.9	2.7	0	0	0	0
SVA-13_62	1	0.1	0	1.6	8.3	0.4	8.3	1.7	0	0	0	0
Average SVA	**5.1 ± 7.2**	**0.1 ± 0.1**	**0**	**5.1 ± 4.8**	**6.7 ± 11.9**	**3.6 ± 10.2**	**4.9 ± 2.8**	**2.8 ± 2.8**	**0**	**0.2 ± 0.4**	**0**	**0.0 ± 0.1**
TAR-13_13	7.3	0	0	0.3	8.1	0.2	10.4	18.5	0	0	0	0
TAR-13_14	38.9	0	0	0	0	0	11.1	0	0	0	0	0
Average TAR	**23.1 ± 22.3**	**0**	**0**	**0.2 ± 0.2**	**4.1 ± 5.7**	**0.1 ± 0.1**	**10.8 ± 0.5**	**9.3 ±13.1**	**0**	**0**	**0**	**0**
Cryoconite holes												
SVA-13_5	1.3	0.4	0.3	0.7	0.3	0.5	0.5	4.8	0	7.4	0	0.5
SVA-13_16	0.5	0.2	0	1.4	0.1	0	0.7	6.2	0	4.7	0	0.1
SVA-13_27	0.2	0.6	0	1.6	0.1	0.1	1.3	5.5	0	3.7	0	0
SVA-13_37	1.1	0.1	0	1.3	0	0	1.1	0.9	0	4.3	0	0
SVA-13_51	0.6	0.1	0	1.1	0	0	0.8	2.7	0	3.4	0	0
SVA-13_61	1.3	0.4	0	2.4	0.3	0	2.7	29.4	0	13.4	1.5	0
Average SVA	**0.8 ± 0.5**	**0.3 ± 0.2**	**0.1 ± 0.1**	**1.4 ± 0.6**	**0.1 ±0.1**	**0.1 ± 0.2**	**1.2 ± 0.8**	**8.3 ± 10.5**	**0**	**6.2 ± 3.8**	**0.3 ±0.6**	**0.1 ± 0.2**
TAR-13_34	7	0.2	0.1	2.3	0.6	0	2.5	0	0	0	0	0

Table S4: continued

Phyla	***Cyanobacteria***				***Fibrobacteres***	***Firmicutes***	***Gemmatimonadetes***	***Proteobacteria***				***TM7-3***	***WPS-2***	***Thermi***
Class	*Cyanobacteria*	*Nostocophycideae*	*Oscillatoriophycideae*	*Synechococcophycideae*	*Fibrobacteria*	*Clostridia*	*Gemmatimonadetes*	*Alphaproteobacteria*	*Betaproteobacteria*	*Deltaproteobacteria*	*Gammaproteobacteria*	*TM7-3*	*WPS-2*	*Deinococci*
Green snow														
SVA-13_1	0	0	0	0.3	0	0	0	57.1	5	0.1	0.1	0.1	1.8	0
SVA-13_21	0	0	0	0.2	0	0	0	0.6	76.5	0.1	0.1	0	0	0
SVA-13_44	0	0	0	0.1	0	0	0	0.8	49.4	0	0	0	0	0
Average SVA	**0**	**0**	**0**	**0.2 ± 0.1**	**0**	**0**	**0**	**19.5 ± 32.6**	**43.6 ± 36.1**	**0.1 ± 0.1**	**0.1 ± 0.1**	**0.0 ± 0.1**	**0.6 ±1.0**	**0**
TAR-13_2	0	0	0	0	0	0	0	0.8	38.5	0	0	0	0	0
TAR-13_3	0	0.8	0	1.8	0	0	0	7.8	34.7	0	0.5	0	0.1	0
TAR-13_4	0	0.1	0	0	0	0	0	14.1	48.6	0	0.3	0	0	0
TAR-13_16	0	0	0	0	0	0	0	2	46.2	0	0	0	0	0
TAR-13_33	0	0	0	0.3	0	0	0	10.1	41	0	0	0	0	0
TAR-14_2	0	0.4	0.1	3	0	0	0	3	61.2	0	0.5	0	0	0
TAR-14_3	0	0.1	0	3.5	0	0.1	0.1	4.4	59.1	0	0.4	0	0.1	0

TAR-14_4	0.6	38.6	30	5	0	0	0	13.9	0.5	0	0	0	0	0
TAR-14_7	3.1	42.8	2.5	1.8	0	0	0	26.1	4.4	0	0	0	0.1	0
TAR-14_8	0.2	0	0.9	0.7	0	0	0	1.6	31.2	0	9	0	0.1	0
TAR-14_9	0	1.7	0	1.7	0	0	0	0	76.7	0	0	0	0	0
Average TAR	**0.4 ± 0.9**	**7.7 ± 16.4**	**3.0 ± 9.0**	**1.6 ± 1.7**	**0**	**0**	**0**	**7.6 ± 8.0**	**40.2 ± 22.8**	**0**	**1.0 ± 2.7**	**0**	**0.0 ± 0.1**	**0**
Red snow														
SVA-13_4	0	0.3	0	0.5	0	0	0	0	9.5	0	0.3	0	0	0
SVA-13_10	0	1	17	20	0	2	0	8	22	0	0	0	1	0
SVA-13_20	0	0.6	1.2	1.5	0	0	0	0	30.2	0	7.6	0	0	0
SVA-13_23	0.3	2.9	0.1	77.3	0	1.3	0	0.7	4.9	0	0.3	0	0	0
SVA-13_31	0	1.8	0.4	10.2	0	0	0	1.1	25.6	0	0	0	0	0
SVA-13_33	0	0.2	0	0.6	0	0.2	0	2.1	60.8	0	0	0	0	0
SVA-13_36	0	0	0	8.2	0	0	0	12	24.3	0.1	0	0.1	0	1.4
SVA-13_43	0	0	0	0	0	0	0	0.8	17.5	0	0	0	0	0
SVA-13_48	0	0	0	4.2	0	0	0	0.6	30.4	0	0	0	0	0
SVA-13_54	0	0.2	0	18.5	0	0	0	4.8	18.4	0	0.2	0	0	0
SVA-13_65	0	0.2	0	24.2	0	0.1	0	0.9	62.6	0	0.4	0	0.1	0
Average SVA	**0.0 ± 0.1**	**0.7 ± 0.9**	**1.7 ± 5.1**	**15.0 ± 22.4**	**0**	**0.3 ± 0.7**	**0**	**2.8 ± 3.9**	**27.8 ± 18.5**	**01**	**0.8 ± 2.3**	**0**	**0.1 ± 0.3**	**0.1 ± 0.4**
TAR-13_1	0.1	0	0	0.1	0	0	0	0.1	2.1	0	1	0	0	0
TAR-13_8	0.8	3.1	3.3	0	0	0	0	2.3	0.4	0	0	0	0.1	0
TAR-13_17	0.2	4.8	1.4	0.1	0	0	0	1.3	0.4	0	0	0	0	0
TAR-13_21	0.1	0	0	0.1	0	0	0	0.1	0.3	0	0.2	0	0	0
TAR-13_27	0	4.3	0.8	0.5	0	0	0	6.6	0.3	0	10	0	0	0
TAR-13_28	1.6	20.3	4.7	6.3	0	0	0	50	0	0	0	0	0	0
TAR-13_30	0.7	1.1	0.9	0.1	0	0	0	1.1	7	0	0.2	0	0	0
TAR-13_35	0	3	0.4	20.6	0	0.2	0	1	1.3	0	0.4	0	0	0
TAR-13_41	0	0.2	0.2	0.2	0	0	0	0.5	0.1	0	0	0	0	0
TAR-14_1	0	0.4	0.4	1.8	0	0	0	18.7	14.4	0	0.2	0	0	0
TAR-14_5	3	12.7	15.5	1.9	0	0	0	32.2	1.3	0	0	0	0.2	0
TAR-14_6	0	0.1	0.1	10.2	0	0	0	2.1	1.1	0	0.5	0	0	0
TAR-14_10	0.2	0.7	0.3	0.5	0	0	0	8.8	16.9	0	0.4	0	0.2	0
TAR-14_11	0	0.1	0.2	0.1	0	0	0	4.4	4.2	0	13.8	0	0.2	0
TAR-14_12	0	0.6	0	16.7	0	0	0	17	0.3	0	0.6	0	0	0
Average TAR	**0.4 ± 0.8**	**3.4 ± 5.7**	**1.9 ± 4.0**	**3.9 ± 6.7**	**0**	**0.0 ± 0.1**	**0**	**9.7 ± 14.4**	**3.3 ± 5.4**	**0**	**1.8 ± 4.2**	**0**	**0.0 ± 0.1**	**0**

Biofilms														
SVA-13_56	0	0	0	6.4	0	0	0	6.2	47.8	0	0	0	0	0
TAR-13_10	0	0.1	0.1	0	0	0	0	1.5	4.1	0	0	0	0	0
TAR-13_11	0	0.1	0.1	0.9	0	0	0	9.1	15	0	0.4	0	0	0
TAR-13_19	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0
Average TAR	**0**	**0.1 ± 0.1**	**0.1 ± 0.1**	**0.3 ± 0.5**	**0**	**0**	**0**	**3.7 ± 4.7**	**6.4 ± 7.8**	**0**	**0.1 ± 0.2**	**0**	**0**	**0**
Dirty ice														
SVA-13_7	0	0	0.5	12.6	0	0	0	3.7	17.7	0.1	26.2	0.1	0.1	0
SVA-13_8	0	0	0	75.5	0	0	0.1	6.4	0.6	0.1	0	0.1	2.3	0
SVA-13_18	0	0	0	2.8	0	0	0	43.8	1.4	0.2	0	0	0	0
SVA-13_19	0	0	0	68.7	0	0.1	0	11.3	0.2	0.1	0	0.1	0.7	0.1
SVA-13_26	0	2.3	0	29.7	0	0	0.1	34.8	11.9	1.8	0	2.1	0	0
SVA-13_38	0	0.1	0.1	22	0	0	0.4	17.9	28.7	1.5	0	3	2.1	0
SVA-13_47	0	0	0	43.6	0	0	0.1	11.3	0.6	0.2	0	0.3	3.3	0
SVA-13_50	0	0	0	42.4	0	0	0	19.5	7.3	0.2	0	1.1	0	0.1
SVA-13_62	0	0.5	0	11.5	0	0	0	44.1	20.8	0.7	0.3	0.3	0.5	0
Average SVA	**0**	**0.3 ± 0.8**	**0.1 ± 0.2**	**34.3 ± 25.5**	**0**	**0**	**0.1 ± 0.1**	**21.4 ± 15.6**	**9.9 ± 10.5**	**0.5 ± 0.7**	**2.9 ± 8.7**	**0.8 ± 1.1**	**1.0 ± 1.2**	**0**
TAR-13_13	0	0	0	0.6	0	0	0	35.7	17.4	0.2	0	0	1.4	0
TAR-13_14	0	0	0	5.6	0	0	0	38.9	5.6	0	0	0	0	0
Average TAR	**0**	**0**	**0**	**3.1± 3.5**	**0**	**0**	**0**	**37.3 ± 2.3**	**11.5 ± 8.3**	**0.1 ± 0.1**	**0**	**0**	**0.7 ± 1.0**	**0**
Cryoconite holes														
SVA-13_5	0	0	0.1	69.2	6.7	0	0.5	3.8	0.5	0.3	0	0	2.3	0
SVA-13_16	0	0	0.3	79.8	0.3	0	0	2.9	0.7	0.7	0	0	1.5	0
SVA-13_27	0	0.2	0.3	71.9	0.5	0	1	5.2	7.4	0.2	0	0	0.2	0
SVA-13_37	0	0	0.2	88.2	0	0	0	2.1	0.1	0	0	0	0.4	0
SVA-13_51	0	0	0	88.5	0	0	0	1.9	0.1	0	0	0	0.4	0
SVA-13_61	0	0.1	0	31.4	0	0	0	10.2	3.5	0.2	0	0.1	3	0
Average SVA	**0**	**0.1 ± 0.1**	**0.2 ± 0.1**	**71.5 ± 21.2**	**1.3 ± 2.7**	**0**	**0.3 ± 0.4**	**4.4 ± 3.1**	**2.1 ±2.9**	**0.2 ±0.3**	**0**	**0**	**1.3 ± 1.2**	**0**
TAR-13_34	0	0	0	0.2	0	7.4	0	8.1	18.7	0	51.5	0.1	1.4	0

Table S5: Distribution of 97% clustered OTUs aligned and assigned to archaea separated by habitat and locations. It is important to note that values are rounded to one digit; therefore, the abundance of a taxon with a value of 0 in one sample can range between 0 and 0.04%.

	Crenarchaeota					***Euryarchaeota***			
	MBGA	*MBGA; NRP-J*	*MCG; pGrfC26*	*Thaumarchaeota; Cenarchaeales*	*Thaumarchaeota; Nitrososphaerales*	*Methanobacteria; Methanobacteriales*	*Methanomicrobia; Methanomicrobiales*	*Methanomicrobia; Methanosarcinales*	*Thermoplasmata; E2*
Green snow									
SVA-13_1	0	0	0	1.7	98.3	**0**	**0**	**0**	**0**
SVA-13_21	0	0	0	1.9	97.8	0.2	0	0	0.1
Average SVA	**0**	**0**	**0**	**1.8 ± 0.1**	**98.1 ± 0.4**	**0.1 ± 0.1**	**0**	**0**	**0.1 0.1**
TAR-13_4	0	0.2	0	0.2	3.4	76	0	9.3	11
TAR-13_33	2.8	0.1	0	83	7	0.1	0.1	0	6.9
TAR-14_2	0	0	0	0.1	0.6	0	0	99.3	0
TAR-14_3	0	0	0	99.7	0.1	0	0	0	0.2
TAR-14_4	0	0	0	0.6	99.4	0	0	0	0
TAR-14_8	0	0	0	98.9	1.1	0	0	0	0
TAR-14_9	0	0	1.9	87.7	9	0	0	0.1	1.2
Average TAR	**0.4 ± 1.1**	**0.0 ± 0.1**	**0.3 ±0.7**	**52.9 ± 49.5**	**17.2 ± 36.4**	**10.9 ± 28.7**	**0**	**15.5 ± 37.1**	**2.8 ± 4.4**
Red snow									
SVA-13_2	0	0	0	0.3	99.7	0	0	0	0
SVA-13_23	0	0	0	0.5	99.4	0.2	0	0	0
SVA-13_31	0	0	0	0	99.4	0.6	0	0	0
SVA-13_36	0	0	0	3.6	92.9	2.4	0	0	1.2
SVA-13_48	0	0	0	5	16.8	78.2	0	0	0
SVA-13_54	0	0	0	13.2	74.5	8.5	0	0	3.8
SVA-13_65	0	0	0	14.3	42.9	28.6	14.3	0	0
Average SVA	**0**	**0**	**0**	**5.3 ± 6.1**	**75.1 ± 33.0**	**16.9 ± 28.9**	**2.0 ± 5.4**	**0**	**0.7 ± 1.4**
TAR-13_8	0	0	0	4.9	86.2	2	1.2	0	5.7
TAR-14_1	0	0	0	0.1	100	0	0	0	0
TAR-14_5	0	0	0	2.2	97.8	0	0	0	0

TAR-14_6	0	0	0	0	0	0	0	90	10
Average TAR	**0**	**0**	**0**	**1.8 ± 2.3**	**71.0 ± 47.7**	**0.5 ± 1.0**	**0.3 ± 0.6**	**22.5 ± 45.0**	**3.9 ± 4.9**
Biofilms									
SVA-13_56	0	0	0	48.7	51.3	0	0	0	0
TAR-13_10	0	0	0	3.2	91.6	5.3	0	0	0
TAR-13_11	0	0.1	0	99.1	0.2	0	0	0	0.6
Average TAR	**0**	**0.1 ± 0.1**	**0**	**51.2 ± 67.8**	**45.9 ± 64.6**	**2.7 ± 3.7**	**0**	**0**	**0.3 ± 0.4**
Dirty ice									
SVA-13_8	0	0	0	0	100	0	0	0	0
SVA-13_19	0	0	3.1	0	53.1	0	0	0	43.9
SVA-13_50	0	0	0	6.3	40.5	46.8	0	0	6.3
Average SVA	**0**	**0**	**1.0 ± 1.8**	**2.1 ± 3.6**	**64.5 ± 31.4**	**15.6 ± 27.0**	**0**	**0**	**16.7 ± 23.7**
TAR-13_14	0	0	0	4.9	80.6	12.6	0	0	1.9
Cryoconite holes									
SVA-13_5	0	0	3.5	1.8	36.8	7	0	5.3	45.6
SVA-13_16	0	0	0	0	99.9	0.1	0	0	0
SVA-13_27	2.2	0	0	28.1	64.5	4.2	0.3	0	0.6
SVA-13_37	0	0	0	2.8	97.2	0	0	0	0
SVA-13_51	0	0	0	0	0	0	26.9	0	73
SVA-13_61	1.5	0	0	30.9	47.1	16.2	0	0	4.4
Average SVA	**0.6 ± 1.0**	**0**	**0.6 ± 1.4**	**10.6 ± 14.7**	**57.6 ± 38.1**	**4.6 ± 6.4**	**4.5 ± 11.0**	**0.9 ± 2.2**	**20.6 ± 31.2**

Table S6: Number of sequences before and after quality control, assigned to taxa and with respective diversity indices (Shannon, Simpson).

	Eukaryotes				Algae			Bacteria					Archaea	
Sample ID	**Raw seqs**	**Seqs after QC**	**Shannon**	**Simpson**	**Seqs assigned to algae**	**Shannon**	**Simpson**	**Raw seqs**	**Seqs after QC**	**Seqs assigned to bacteria**	**Shannon**	**Simpson**	**Raw seqs**	**Seqs after QC**
Green snow														
SVA-13_1	2912	2634	6.09	0.94	1078	4.45	0.85	15036	3013	1841	5.23	0.92	85586	71255
SVA-13_21	14590	6238	5.53	0.9	5460	4.68	0.87	16095	4621	3092	5.69	0.93	55972	45789
SVA-13_44	7775	2900	6.04	0.95	1295	4.86	0.9	11369	2817	1838	6.83	0.98		
TAR-13_2	10765	2454	6.87	0.98	743	4.88	0.9	14136	5417	4010	6.25	0.97		
TAR-13_3	17796	11388	6.04	0.96	6031	4.15	0.88	3595	2040	1458	4.34	0.84		
TAR-13_4	19323	13597	5.34	0.93	7765	3.32	0.81	4654	2514	2258	4.44	0.89	4528	1396
TAR-13_16	8022	2183	7.17	0.98	809	5.22	0.94	7453	3842	2097	4.21	0.97	5229	265
TAR-13_33	1389	947	5.8	0.95	487	5.1	0.92	3095	1576	1282	4.71	0.9	72767	64246
TAR-14_2	6064	4332	5.43	0.94	2441	3.52	0.82	5513	2976	2253	5.57	0.94	30663	19720
TAR-14_3	6799	5052	5.28	0.94	2341	3.35	0.8	6142	3215	2506	5.25	0.92	127172	114214
TAR-14_4	10393	7341	5.4	0.93	1013	2.93	0.7	8647	5419	3922	5.55	0.94	1023027	886676
TAR-14_7	2038	1265	5.71	0.95	586	3.76	0.85	6318	3729	2055	6.04	0.96		
TAR-14_8	22201	16264	3.86	0.82	7700	2.08	0.47	7456	3602	1426	3.42	0.78	1548	530
TAR-14_9	7479	5575	4.92	0.9	2336	3.55	0.8	263	107	80	6.34	0.92	94145	82445
Red snow														
SVA-13_2	6135	5148	3.34	0.76	3500	2.34	0.57	98*	4*	1*			60965	54688
SVA-13_4	6979	3937	4.56	0.8	3280	3.41	0.7	7509	1421	770	6.16	0.97		40
SVA-13_10	13448	6583	4.24	0.81	4904	3.52	0.73	29728	3511	334	6.69	0.99		
SVA-13_20	7130	3952	5.2	0.88	3226	4.08	0.81	12881	2344	987	7.00	0.99		
SVA-13_23	5373	4485	2.93	0.68	2832	1.74	0.39	8352	4008	1850	5.36	0.94	1695	732
SVA-13_31	12752	10621	3.07	0.6	8743	1.79	0.4	5040	2341	598	5.52	0.95		43331
SVA-13_33	7678	3008	6.22	0.94	1727	4.4	0.84	9129	1911	1041	6.86	0.98		
SVA-13_36	23283	16789	5.28	0.91	7056	2.93	0.67	11503	6109	2573	4.26	0.86	2318	921
SVA-13_43	16457	5447	7.24	0.98	3059	5.43	0.93	5473	988	627	6.60	0.98		

SVA-13_48	6294	5123	3.96	0.8	4184	2.93	0.7	2838	1183	556	4.83	0.91	2665	722
SVA-13_54	23068	16698	3.89	0.73	10391	1.68	0.36	3777	1519	812	4.84	0.9	39830	34942
SVA-13_65	7362	5408	4.17	0.77	3667	2.42	0.55	13545	7349	4245	4.25	0.8	1267	295
TAR-13_1	9632	4770	5.29	0.91	3058	4.23	0.81	21581	6431	5087	4.39	0.85		
TAR-13_8	77757	26947	5.85	0.96	12012	4.64	0.9	12368	3661	1051	4.39	0.84	2059	926
TAR-13_17		4863	4.85	0.88	1318	4.68	0.86	16240	5850	3632	4.36	0.83		
TAR-13_21	9330	4354	5.25	0.89	2920	3.89	0.79	10946	3997	3169	5.45	0.92		
TAR-13_27	19416	15725	2.55	0.59	4639	3.04	0.68	16105	2297	630	5.87	0.96		
TAR-13_28	9402	5344	4.39	0.84	4082	3.56	0.73	15312	2525	227	6.28	0.94		
TAR-13_30	6493	3042	4.56	0.86	1133	2.91	0.61	10571	2327	1558	5.27	0.98	1871	371
TAR-13_35	7274	5474	4.91	0.92	3987	3.61	0.85	4562	2424	1437	4.04	0.77		
TAR-13_39	11667	6810	4.25	0.79	5992	3.41	0.72	15247	3447					
TAR-13_41	7606	3715	4.83	0.86	2785	3.73	0.77	17534	5305	3651	4.99	0.91		
TAR-14_1	12436	9069	5.12	0.92	3454	3.34	0.76	3009	1705	1356	4.00	0.83	148712	146362
TAR-14_5	4251	3254	3.99	0.8	1059	1.86	0.42	1974	1064	724	5.86	0.97	1020	590
TAR-14_6	7573	5312	3.93	0.8	1976	2.03	0.46	9112	4794	3868	2.25	0.48	587	414
TAR-14_10	6037	4720	3.68	0.75	1218	2.5	0.6	5809	3158	2412	5.32	0.91		
TAR-14_11	4899	3453	5.47	0.93	614	3.42	0.77	4453	2404	1893	4.76	0.87		
TAR-14_12	7387	5701	4.29	0.83	3909	2.54	0.65	1892	979	425	4.30	0.82		
Biofilms														
SVA-13_56	8929	6986	4.88	0.92	3412	3.78	0.84	9055	5154	3570	6.04	0.97	177818	150612
TAR-13_10	14460	5679	5.63	0.95	2604	4.54	0.9	26266	10369	8418	4.25	0.83	2852	473
TAR-13_11	24975	16236	5.52	0.94	9112	3.75	0.85	10536	6442	1893	3.62	0.71	558037	467198
TAR-13_19	9524	4315	5.18	0.93	1585	4.97	0.91	4408	2502	1621	6.63	0.84		
Dirty ice														
SVA-13_7	2201	1790	6.73	0.97	931	5.12	0.92	18431	5685	3999	6.36	0.97		
SVA-13_8	9012	6619	4.96	0.92	2313	4.03	0.85	5506	3193	2738	3.59	0.71	2481	716

SVA-13_18	2833	938	5.59	0.93	569	4.37	0.85	7824	1468	671	5.28	0.94		
SVA-13_19	1980	1189	4.08	0.8	152			137044	74279	60321	3.36	0.72	2214	562
SVA-13_26	3340	536	6.77	0.97	285	5.03	0.92	16847	2833	1750	6.92	0.99		
SVA-13_38	4410	1205	6.61	0.97	634	5.3	0.94	13137	2866	1676	6.88	0.99		
SVA-13_47	7694	2784	7.28	0.98	942	4.71	0.87	13273	6486	3359	6.16	0.97		
SVA-13_50	3912	2525	5.11	0.94	1726	3.84	0.88	9188	5116	1736	4.85	0.91	761	385
SVA-13_62	7900	970	6.87	0.97	344	6.07	0.97	16249	2635	1658	6.24	0.97		
TAR-13_13	15845	1228	6.3	0.95	706	5	0.89	20891	3256	1126	6.25	0.98		
TAR-13_14	280	93			3*			14006	6574	24*			2924	596
Cryoconite holes														
SVA-13_5	2450	1707	5.08	0.93	823	3.04	0.78	9897	5263	5087	3.99	0.78	2307	1102
SVA-13_16	6223	3874	5.5	0.92	416	2.57	0.74	9096	5195	4670	2.96	0.62	19551	13644
SVA-13_27	5344	3445	4.23	0.85	461	2.52	0.66	11963	6675	5846	3.85	0.75	3869	1185
SVA-13_37	3158	2075	5.65	0.93	788	2.92	0.67	10262	6041	5692	2.33	0.51	36724	28732
SVA-13_51	9796	7221	5.53	0.95	1653	2.53	0.71	18289	11166	10434	2.28	0.49	66266	78352
SVA-13_61	8588	5913	4.18	0.79	583	2.58	0.6	19110	10769	9207	4.53	0.9	3133	1055
TAR-13_34	18043	13464	3.9	0.8	6405	1.87	0.44	5001	2983	2531	4.35	0.85		

* removed from analysis due to low sequence numbers (sequences < 100)

Table S7: Dissolved organic carbon (DOC), nutrients and other inorganic aqueous chemical data for all samples separated into the 7 habitats.

Sample ID	**DOC [µM]**	PO$_4^{3-}$ **[µM]**	**NO$_3^-$**	**SO$_4^{2-}$**	**Cl$^-$**	**Al**	**Ba**	**Bi**	**Ca**	**Cd**	**Co**	**Cr**	**Cu**	**Fe**	**K**	**Mg**	**Mn**	**Na**	**Ni**	**P**	**Pb**	**S**	**Si**	**Sr**	**Zn**
Clean snow																									
SVA-13-3	24	0.31	<	<	678	0.5	0.3	<	26	<	<	<	<	0.3	12	5	2.2	494	<	<	<	<	<	<	1.3
SVA-13_12	42	0.27	6026	<	191	0.7	<	<	15	<	<	<	<	0.5	<	5	0.1	129	<	<	<	16	<	<	1.3
SVA-13_22	125	0.05	263	<	494	1.1	<	<	23	<	<	0.2	<	1.4	39	12	0.2	370	<	<	<	12	<	0.1	2
SVA-13_35	19	0.08	1040	<	449																				
SVA-13_45	18	1.29	<	<	139	0.2	5.5	<	3	<	<	<	<	0.1	<	2	0.4	94	<	<	<	22	<	0.2	1.8
SVA-13_55	15	5.73	<	<	269	0.2	6.1	<	14	<	<	<	<	<	<	4	0.1	182	<	<	<	62	<	0.2	0.7
TAR-13_9	129	0.07	573	<	<	0.5	<	<	6	<	<	<	<	0.3	18	2	<	27	<	<	<	<	<	<	1.4
TAR-13_18	56	0.05	<	<	<	0.5	<	<	<	<	<	<	<	0.3	<	1	<	12	<	<	<	<	11	<	1
TAR-13_31			<	167	<	0.4	6.3	<	<	<	<	<	<	1.3	<	1	<	43	<	<	<	<	11	0.2	0.6
TAR-13_40			<	<	123	0.4	5.7	<	14	<	<	<	<	<	24	1	<	86	<	<	<	<	<	0.2	1.4
Green snow																									
SVA-13-1	35	0.07	<	152	478	1.8	1.4	<	166	<	<	<	<	1.4	77	52	6.2	328	<	<	<	<	35	0.4	0.6
SVA-13_21	99	0.55	<	103	302	7.5	0.7	<	410	<	<	0.2	0.2	4.6	97	176	1.3	251	0.3	<	<	32	32	0.7	1.2
SVA-13_24	92	0.12	<	169	492	1	0.3	<	1260	<	<	<	<	0.4	130	341	0.5	353	<	28.2	<	74	<	1.4	1.8
SVA-13_44	45	1.29	<	<	126	1.8	7.3	<	317	<	0.5	<	0.3	1.7	92	78	40.9	93	0.6	<	0.1	44	11	0.7	0.5
TAR-13_2	210	0.11	<	<	148	3.5	0.5	<	10	<	0.2	<	1.4	1.8	56	3	1.8	271	0.2	<	<	25	22	0.1	0.6
TAR-13_3	87	0.41	<	<	<	2.5	0.5	<	79	<	0.2	<	0.7	3	37	13	1.3	9	0.2	<	<	<	32	0.4	0.9
TAR-13_4	154	0.24	<	<	<	2.8	0.4	<	47	<	<	<	0.5	4.3	66	7	0.6	20	0.1	<	<	<	48	0.2	1.2
TAR-13_16	93	0.5	230		74	1.8	0.3	<	26	<	0.2	<	0.5	5.3	36	4	1.1	40	<	<	<	<	18	0.2	0.8
TAR-13_33			<	<	<	1	5.7	<	24	<	0.4	<	0.3	10.5	<	4	2.8	46	<	<	<	<	16	0.4	0.2
Red snow																									
SVA-13-2	31	0.19	1043	<	344	0.4	<	<	100	<	<	<	<	0.5	14	44	1.7	228	<	<	<	12	<	0.2	0.9
SVA-13-4	39	0.14	288	<	381	0.9	0.3	<	94	<	<	<	<	0.9	59	46	1.7	248	<	<	0	14	<	0.3	1.3
SVA-13_10	17	0.05	1862	<	242	1.1	0.3	<	64	<	<	0.1	<	2.1	19	12	1.3	139	<	<	0	17	<	0.2	1.2
SVA-13_20	41	0.04	7010	160	545	2.1	0.2	<	180	0	<	<	<	2.8	56	70	2	376	<	<	0	34	<	0.7	0.7
SVA-13_23	36	0.08	<	<	332	1.7	0.8	<	955	<	<	0.1	0.2	1.6	65	396	3.1	250	0.1	<	0	48	16	0.9	4.5
SVA-13_31	51	0.14	<	<	321	2	0.5	<	2020	<	<	<	<	2	68	687	3.4	244	0.1	<	0	17	<	2.1	0.6

SVA-13_33	18	0.02	895	<	342	1.1	0.5	<	69	<	0.2	<	0.3	1.1	27	12	9.5	243	0.1	<	0	<	15	0.4	0.4
SVA-13_36	20	0.05	999	<	354	2.1	0.2	<	34	<	<	<	0.2	4.3	45	15	1.9	259	<	<	0.2	<	<	0.2	0.7
SVA-13_43	60	1.21	<	<	136	1.4	5.6	<	212	<	0.2	<	0.2	2.1	27	65	13	90	0.3	<	0.1	50	<	0.6	0.9
SVA-13_48	40	6.08	<	<	297	2.3	6.3	<	639	<	0.1	<	0.1	2.9	64	94	6.1	172	0.2	<	0	30	17	0.9	0.4
SVA-13_54	38	0.51	<	<	158	1.3	6	<	188	<	<	<	<	1.3	31	53	0.7	97	<	<	0	61	<	0.4	1
SVA-13_65	39	0.71	<	<	254	0.2	6.7	<	22	<	<	<	<	1.6	20	7	0.5	179	<	<	0.1	20	<	0.4	0.5
TAR-13_1	107	0.26	<	<	102	1	<	<	2	<	<	<	<	0.4	47	2	0.1	75	<	<	<	12	11	<	0.4
TAR-13_5	170	0.08	<	<	<	1.1	<	<	2	<	<	<	<	0.3	31	1	0	40	<	<	<	15	12	<	0.2
TAR-13_8	198	0.05	<	<	<	1.6	<	<	<	<	<	<	<	2.1	97	4	0.2	42	<	<	0	<	24	<	0.9
TAR-13_17	75	0.08	<	<	48	1.3	<	<	5	<	<	<	<	0.9	34	2	0.1	16	<	<	0	<	31	<	0.8
TAR-13_21	246	0.1	<	<	173	3.4	0.1	<	14	<	<	<	0.1	3.3	28	3	0.2	132	<	<	0	<	<	<	0.5
TAR-13_24			<	<	75																				
TAR-13_27			157	<	<	0.8	5.4	<	6	<	<	<	<	2.1	12	1	0.1	45	<	<	0	<	29	0.2	0.7
TAR-13_28			<	<	<																				
TAR-13_30			<	<	90	2.6	5.9	<	127	0.2	<	<	0.5	2.7	66	5	0.2	298	0.5	74.5	0.1	<	11	0.4	6.8
TAR-13_32			<	<	<	0.4	5.6	<	4	<	<	<	<	0.9	18	2	0.1	22	<	<	<	<	<	0.2	0.5
TAR-13_35			256	<	<	1.1	6.1	<	12	<	<	<	<	0.3	32	3	0.2	45	<	<	0	<	<	0.2	1
TAR-13_36			<	<	<	1.1	6	<	7	<	<	<	<	1.2	38	3	0.1	31	<	<	0	<	<	0.3	0.4
TAR-13_37	303	0.07	17	147	310	2.6	1.1	<	55	<	<	<	0.4	2.1	52	10	0.3	190	0.2	<	0.1	<	13	0.2	2.7
TAR-13_39			<	<	83	0.8	7.1	<	2	<	<	<	<	0.5	20	1	0	76	<	<	0	<	<	0.2	0.2
TAR-13_41	305	3.18	2351	149	554	7.6	1.8	<	191	<	0.1	<	1.3	2.7	303	11	0.9	414	0.7	<	0.2	67	16	0.5	12.9
TAR-13_42	107	0.48	1240	<	<	3.5	0.2	<	43	<	<	<	0.2	1.9	94	5	0.4	44	<	<	0	<	<	0.2	4.8
Biofilms																									
SVA-13_56	73	2.22	<	<	275	4.3	7	<	647	0	<	<	0.2	4.4	120	96	0.6	157	<	14.7	0.1	125	<	1	0.9
TAR-13_10	166	0.06	<	<	76	3.1	<	<	15	<	<	<	<	2	148	8	0.2	44	<	<	0.1	12	25	0.2	0.9
TAR-13_11	1142	2.13	133	<	<	24.2	1.1	<	266	0.1	0.6	0.5	3.9	23.8	1030	62	2.9	62	1.6	332	0.8	134	273	1.7	4.1
TAR-13_19	760	1.28	<	<	<	4.3	<	<	18	<	<	<	0.1	4.3	478	12	0.4	35	<	<	0.1	37	31	0.4	1.9
Clean ice																									
SVA-13-6	29	0.27	430	<	115	1	<	<	41	<	<	0.2	<	0.5	31	10	0.8	75	0.3	<	0	20	<	0.1	2.6
SVA-13_17	22	0.18	444	<	<	1.1	<	<	25	0	<	<	0.1	1.5	36	3	0.3	11	0.2	<	0	12	<	<	1.7
SVA-13_29	46	0.12	99	<	<	1.2	0.2	0.1	99	<	<	<	<	0.7	24	7	0.2	53	0.5	<	0.1	32	<	0.2	3.7

SVA-13_39	23	0.04	<	<	211	0.4	5.8	<	7	<	<	<	<	1.9	<	3	0.3	53	<	<	0.1	69	<	0.2	0.8
SVA-13_49	13	1.17	115	<	125	0.2	5.8	<	4	<	<	<	<	8.1	<	3	0.3	47	0.1	<	0	<	<	0.2	1
SVA-13_60	66	0.72	<	<	<	5.4	5.8	0	10	<	<	<	<	2.4	<	3	0.3	8	0.2	<	<	41	<	0.2	3.1
TAR-13_12	51	0.15	<	<	<	1.2	0.2	<	44	<	<	<	0.5	5.3	<	4	0.7	17	<	<	<	<	32	0.2	1.1
Dirty ice																									
SVA-13-7	32	1.8	<	<	127	19.2	1.7	<	1540	0	<	0.1	0.2	22.7	52	804	7.8	96	0.1	<	0	22	22	0.9	0.5
SVA-13-8	22	0.11	1363	<	263	2.5	0.5	<	34	<	<	<	<	2.3	11	18	4.2	171	0.2	<	<	<	<	0.2	0.9
SVA-13_18	25	0.09	928	<	164	1.7	0.1	<	18	<	<	0.2	<	6.2	33	9	1.1	106	<	<	0.3	<	<	0.1	1.7
SVA-13_19	34	0.09	<	<	<	5.3	0.3	<	15	<	<	<	<	7.5	29	6	1.5	24	<	<	1.3	16	12	0.2	1.8
SVA-13_25	33	0.05	5883	<	<	2.4	0.2	<	188	<	<	<	<	8	69	75	1	77	0.2	<	0.4	13	<	0.3	1.3
SVA-13_26	48	0.05	<	<	109	7.7	0.4	<	558	<	<	<	<	4.1	18	246	2.9	108	0.2	<	0.3	33	31	1.1	1.6
SVA-13_38	33	0.08	<	<	89	2.7	0.2	<	23	<	<	<	<	14.4	24	14	0.9	50	<	<	1.1	<	<	0.2	0.5
SVA-13_40	29	0.12	<	<	<	2	5.7	<	52	<	<	<	<	6	26	11	1.4	14	<	<	0	<	17	0.3	0.6
SVA-13_47	30	3.4	<	<	417	0.5	6.8	<	8	<	<	<	<	2.1	12	11	0.6	230	<	<	0.1	170	11	0.3	0.8
SVA-13_50	37	1.2	<	178	512	5.7	6.9	<	165	<	0.2	<	0.2	7.9	64	84	8.5	334	0.2	<	0.2	32	19	0.8	1.2
SVA-13_62	116	1.43	<	<	<	1.4	5.8	<	62	<	<	<	<	4.4	<	20	0.8	19	<	<	0.2	49	<	0.3	0.3
SVA-13_63	40	0.94	<	158	80	3	7.8	<	114	<	<	<	<	8.3	86	17	0.6	54	<	<	0.4	132	<	0.5	2.8
TAR-13_13	194	0.05	<	<	149	16.1	0.2	<	43	<	<	<	<	169	57	18	0.8	159	<	<	4.7	15	24	0.3	1.8
TAR-13_14	103	0.04	4048	<	76	7.1	0.7	<	30	<	<	<	<	149	73	11	0.6	74	<	<	2.7	<	<	0.2	7.6
TAR-13_22	190	0.08	<	<	<	12.9	<	<	8	<	<	<	0.1	44.2	<	1	0.2	15	<	<	2.1	<	30	<	0.4
Cryoconite holes																									
SVA-13-5	63	0.06	<	131	247	11.8	1	<	448	0	0.3	0.1	0.4	13.4	146	282	13	282	0.2	24.2	0.2	79	130	1.7	3.5
SVA-13_16	22	0.07	<	140	95	5.6	0.7	<	209	<	0.1	0.2	0.1	5.6	41	107	6.1	65	0.1	<	0.4	47	56	0.8	2.4
SVA-13_27	42	0.05	<	127	99	1.1	<	<	100	<	<	<	<	0.4	<	43	0.4	162	<	<	0.1	48	<	0.3	1.1
SVA-13_37	20	0.05	5005	152	261	2.2	0.6	<	96	<	<	<	0.2	4.2	87	71	2.6	226	<	<	0.5	45	42	0.9	1.7
SVA-13_51	27	1.24	<	139	271	4.5	7.8	<	56	0	0.1	<	0.2	5	58	34	4.6	229	0.1	<	0.4	43	50	0.8	1.9
SVA-13_61	37	0.99	<	155	<	1.2	5.8	<	119	<	<	<	<	1.4	20	45	1.2	27	<	<	0.4	70	25	0.8	0.7
TAR-13_34	54	0.09	<	141	<	4.9	1.6	0	3	0	<	<	0.6	8.4	33	4	0.5	40	0.2	15.1	0.8	32	25	0.2	0.5

All values except DOC and PO_4^{3-} are given in ppb; NO^{3-}, SO_4^{2-} and Cl^- all determined by IC, all others analysed by ICP-MS; limit of detection (LOD) for IC: NO_3^- = 96 ppb, Cl^- = 72 ppb, SO_4^{2-} = 121 ppb, LOD's for ICP-MS: Al, Ba, Co, Cr, Cu, Fe, Mg, Ni, Si, Sr, Zn = 0.1 ppb; Bi, Cd, Mn, Pb = 0.01 ppb; Ca, Na = 1 ppb; K,P,S = 10 ppb; no value indicates no measurement available for the respective sample.

Table S8: Particulate total carbon (TC), total nitrogen (TN), total phosphorus (TP) and total sulphur (TS) values reported as % of dry weight of sample with the corresponding C/N, C/P and N/P ratios as well as δ^{15}N and δ^{13}C isotope values; samples are separated by habitat and location and the averages for each habitat and location are also shown. Samples that did not contain enough particulate material for analyses are shown as n.s. (no sample). For Arctic Sweden (TAR) samples, pollen counts are also included since they have likely contributed to the higher TC and therefore C/N and C/P values.

Sample ID	**Total C [%]**	**Total N [%]**	**Total P [%]**	**Total S [%]**	**C/N**	**C/P**	**N/P**	**d^{15}N [‰]**	**d^{13}C [‰]**	**Pollen [ml^{-1}]**
Green snow										
SVA-13_1	1.5	0.21	0.05	0.06	7	32	4	-4.98	-29.28	
SVA-13_21	1	0.14	0.07	0.07	7	15	2	-2.10	-38.97	
SVA-13_44	2.8	0.13	0.09	0.09	21	32	2	-2.81	-27.14	
Average SVA	**1.8 ± 0.9**	**0.16 ± 0.04**	**0.07 ± 0.02**	**0.07 ± 0.02**	**12 ± 8**	**26 ± 10**	**3 ± 1**	**-3.30 ± 1.50**	**-31.80 ± 6.30**	
TAR-13_2	2.2	0.27	0.05	0.02	8	40	5	-5.74	-26.71	n.s.
TAR-13_3	1.8	0.2	0.1	0.02	9	19	2	-1.66	-26.55	7813
TAR-13_4	0.5	0.08	n.s.	0.02	6	n.s.	n.s.	2.32	-28.95	n.s.
TAR-13_16	1.5	0.14	0.06	0.03	11	26	2	-6.19	-26.8	3125
TAR-13_33	1.2	0.09	0.07	0.04	13	16	1	-4.6	-25.94	2604
Average TAR	**1.4 ± 0.6**	**0.16 ± 0.08**	**0.07 ± 0.02**	**0.03 ± 0.01**	**9 ± 3**	**25 ± 11**	**3 ± 2**	**-3.17 ± 3.54**	**-26.99 ± 1.15**	
Red snow										
SVA-13_2	3.7	0.26	0.06	0.16	14	59	4	-8.86	n.s.	
SVA-13_4	3.1	0.21	0.06	0.11	15	51	3	-6.37	n.s.	
SVA-13_10	1.5	0.11	0.06	0.18	13	24	2	-6.92	n.s.	
SVA-13_20	1.9	0.19	0.15	0.07	10	12	1	0.27	-26.06	
SVA-13_31	8.9	0.50	0.08	0.14	18	111	6	-2.35	-27.8	
SVA-13_33	3	0.21	0.06	0.06	14	47	3	-5.18	-25	
SVA-13_36	6.3	0.36	0.06	0.1	18	107	6	-5.37	n.s.	
SVA-13_43	2.7	0.15	0.04	0.1	19	63	3	-2.6	-27.95	
SVA-13_48	4.9	0.23	0.06	0.12	21	80	4	-6.13	-28.18	
SVA-13_54	17.4	1.02	n.s.	0.12	17			-4.66	-29.43	
SVA-13_65	4.5	0.27	0.06	0.1	17	75	5	-5.52	-29.23	
Average SVA	**5.3 ± 4.5**	**0.32 ± 0.26**	**0.07 ± 0.03**	**0.11 ± 0.04**	**16 ± 3**	**63 ± 32**	**4 ± 2**	**-4.88 ± 2.50**	**-27.66 ± 1.61**	
TAR-13_1	4.1	0.25	0.05	0.02	17	84	5	-4.94	-25.01	7813
TAR-13_5	30.0	1.84	n.s.	0.11	16	n.s.	n.s.	n.s.	-28.73	0

TAR-13_8	12.9	0.78	n.s.	0.06	17	n.s.	n.s.	-1.1	n.s.	1250
TAR-13_17	19.7	1.11	n.s.	0.1	18			0.37	-26.59	893
TAR-13_21	8.8	0.41	0.04	0.07	22	220	10	-4.19	-21.8	422
TAR-13_24	8.6	0.47	0.05	0.08	18	166	9	-5.11	-25.32	n.s.
TAR-13_27	8.4	0.33	0.08	0.06	26	112	4	-4.76	-27.74	16667
TAR-13_28	12.9	0.57	0.07	0.07	23	176	8	-5.49	-24.63	521
TAR-13_30	11.0	0.28	0.04	0.06	39	287	7	-3.29	-24.86	1339
TAR-13_32	5.1	0.34	0.07	0.05	15	75	5	-5.96	-26.61	4395
TAR-13_35	9.7	0.46	0.07	0.08	21	149	7	-4.54	n.s.	1042
TAR-13_36	25.3	0.9	0.07	0.09	28	370	13	-4.95	n.s.	0
TAR-13_37	9.0	0.39	0.07	0.06	23	130	6	-5.4	n.s.	0
TAR-13_41	9.6	0.5	0.03	0.07	19	276	14	-6.15	n.s.	7292
TAR-13_42	11.5	0.55	0.06	0.09	21	192	9	-4.73	n.s.	446
Average TAR	**12.4 ± 7.2**	**0.61 ± 0.42**	**0.06 ± 0.02**	**0.07 ± 0.02**	**22 ± 6**	**186 ± 89**	**8 ± 3**	**-4.30 ± 1.84**	**-25.70 ± 2.02**	
Biofilms										
SVA-13_56	7.8	0.81	0.13	0.09	10	60	6	4.24	-27.38	
TAR-13_10	26.1	1.56	0.13	0.12	17	205	12	-3.77	-27.42	29688
TAR-13_11	17.3	1.69	n.s.	0.18	10	n.s.	n.s.	-4.07	-30.03	156
TAR-13_19	27.7	1.9	n.s.	0.17	15	n.s.	n.s.	-5.02	-29.5	21875
Average TAR	**23.7 ± 5.6**	**1.72 ± 0.17**	**0.13**	**0.16 ± 0.03**	**14 ± 4**	**205**	**12**	**-4.29 ± 0.65**	**-28.98 ± 1.38**	
Dirty ice										
SVA-13_7	0.9	0.09	0.06	0.05	10	17	2	-2.14		
SVA-13_8	1.4	0.13	0.03	0.06	11	42	4	-2.78	-25.21	
SVA-13_18	1.3	0.14	0.06	0.05	9	24	3	-5.54	-26.88	
SVA-13_19	2.1	0.17	0.05	0.06	13	45	4	-4.01	-25.93	
SVA-13_25	7.4	0.03	0.03	0.06	217	277	1	9.84	-25.9	
SVA-13_26	2.5	0.22	0.07	0.07	12	36	3	-1.49	-25.41	
SVA-13_38	1.9	0.18	0.05	0.07	10	40	4	-2.89	-26.46	
SVA-13_40	1.3	0.09	0.05	0.06	14	26	2	-2.5	-26.21	
SVA-13_47	2.5	0.25	0.05	0.1	10	54	5	-5.51	-27.37	
SVA-13_50	0.9	0.06	0.05	0.08	14	19	1	-0.29	-26.27	
SVA-13_62	2.3	0.21	0.04	0.05	11	65	6	-1.31	-26.33	

SVA-13_63	3.2	0.27	n.s.	0.06	12	n.s.	n.s.	-1.46	-26.7	
Average SVA	**2.3 ± 1.8**	**0.15 ± 0.08**	**0.05 ± 0.01**	**0.06 ± 0.01**	**29 ± 56**	**59 ± 74**	**3 ± 2**	**-1.67 ± 3.97**	**-26.24 ± 0.63**	
TAR-13_13	16.3	1.49	n.s.	0.12	11	n.s.	n.s.	-1.47	n.s.	1250
TAR-13_14	8.7	0.77	0.08	0.07	11	115	10	-2.62	-25.8	0
TAR-13_22	3.8	0.29	0.06	0.04	13	58	4	-2.45	-25.88	1875
Average TAR	**9.6 ± 6.3**	**0.85 ± 0.60**	**0.07 ± 0.01**	**0.08 ± 0.04**	**12 ± 1**	**87 ± 40**	**7 ± 4**	**-2.18 ± 0.62**	**-25.84 ± 0.06**	
Cryoconite holes										
SVA-13_5	1.0	0.11	0.04	0.06	9	27	3	-2.92	-25.14	
SVA-13_16	1.5	0.16	0.03	0.06	10	44	4	-3.47	-25.53	
SVA-13_27	2.2	0.2	0.04	0.06	11	50	5	-0.92	-25.54	
SVA-13_61	3.2	0.31	0.04	0.06	10	81	8	-1.27	-25.74	
Average SVA	**2.0 ± 1.0**	**0.20 ± 0.09**	**0.04 ± 0.01**	**0.06 ± 0.00**	**10 ± 1**	**51 ± 23**	**5 ± 2**	**-2.15 ± 1.24**	**-25.49 ± 0.25**	
TAR-13_34	10.4	0.65	0.06	0.12	16	168	10	-3.49	-25.96	n.s.

Table S9: Bulk functional group distribution from the FTIR analyses of samples that contained enough particulate material, again separated by habitat and location and reported with averages. Main functional groups representing the lipids (CH_2 and CH_3 stretching modes between 3050 and 2800 cm^{-1}), proteins (amide I and II bands between 1700-1500 cm^{-1}) and carbohydrates (C-O-C, C-O-P, P-O-P ring vibrations between 1204-815 cm^{-1}) are reported as percentage of total functional groups.

Sample ID	**lipids [%]**	**proteins [%]**	**carbohydrates [%]**
Green snow			
SVA-13_1	0.2	3.3	96.4
SVA-13_21	0.2	1.5	98.3
SVA-13_44	0.2	2.1	97.7
Average SVA	**0.2 ± 0.0**	**2.3 ± 0.9**	**97.5 ± 1.0**
TAR-13_3	1.1	5.1	93.8
TAR-13_4	12.4	23.3	64.3
TAR-13_16	0.2	5.3	94.5
Average TAR	**4.6 ± 6.8**	**11.2 ± 10.5**	**84.2 ± 17.2**
Red snow			
SVA-13_2	1.8	4.2	94.1
SVA-13_4	1.1	3	95.9
SVA-13_10	0.9	2.1	97
SVA-13_20	3.2	5.3	91.5
SVA-13_31	4.7	6	89.3
SVA-13_33	0.9	3.7	95.4
SVA-13_36	3	5.6	91.4
SVA-13_43	1.7	10.7	87.5
SVA-13_48	3.7	6.5	89.8
SVA-13_54	7.9	12.6	79.5
SVA-13_65	1.3	3.3	95.4
Average SVA	**2.7 ± 2.1**	**5.7 ± 3.3**	**91.5 ± 5.0**
TAR-13_1	6	11.4	82.6
TAR-13_8	7.9	17	75.2
TAR-13_17	7.1	13.7	79.2
TAR-13_21	5.4	19.5	75.1
TAR-13_24	3.7	10.2	86.1
TAR-13_27	4.8	8.9	86.3
TAR-13_28	11.4	19.3	69.2
TAR-13_30	4.5	8.8	86.6
TAR-13_35	9.3	17.6	73.1
TAR-13_36	12.8	17.5	69.7

TAR-13_37	9.7	13	77.2
TAR-13_41	10.2	15	74.7
TAR-13_42	12.4	19.8	67.8
Average TAR	**8.1 ± 3.1**	**14.7 ± 4.0**	**77.1 ± 6.6**
Biofilms			
SVA-13_56	3.9	15.3	80.8
TAR-13_10	9.8	15	75.3
TAR-13_11	3.8	10.4	85.8
TAR-13_19	8.9	16	75.1
Average TAR	**6.6 ± 3.2**	**14.2 ± 2.6**	**79.3 ± 5.1**
Dirty ice			
SVA-13_7	0	0.3	99.6
SVA-13_8	0.2	1.8	98
SVA-13_18	0.3	1.8	97.9
SVA-13_19	0.5	2.2	97.3
SVA-13_26	0.2	1.6	98.2
SVA-13_38	0.7	3.4	95.9
SVA-13_40	0.3	1.5	98.2
SVA-13_47	0.8	7.6	91.6
SVA-13_50	0.2	6.7	93.1
SVA-13_62	0.7	5.8	93.5
SVA-13_63	1.0	4.2	94.7
Average SVA	**0.4 ± 0.3**	**3.4 ± 2.4**	**96.2 ± 2.6**
TAR-13_13	3.3	9.8	86.8
TAR-13_14	4	9.7	86.4
TAR-13_22	0.9	5.3	93.8
Average TAR	**2.7 ± 1.6**	**8.3 ± 2.6**	**89.0 ± 4.2**

Table S10: Dominant fatty acid compounds present in the samples separated by habitats and locations and reported as % of total fatty acid content with **B** designating the **B**ranched and **A** the **A**lkane compounds. Total saturated (SFA), total monounsaturated (MUFA) and total polyunsaturated (PUFA) fatty acids are also reported in grey columns.

Sample ID	C14:0	C15:0	C15 B	C16:0	C16:1	C16:3	C16:4	C17 B	C18:0	C18:1	C18:2	C18:3	C18:4	C20:0	C21:0	C21 A	C22:0	C23 A	C24:0	C27 A	SFA	MUFA	PUFA
Green snow																							
SVA-13_1	10	0	0	17	18	0	5	0	2	21	4	0	5	0	1	0	0	0	0	0	30	39	14
SVA-13_21	3	0	0	17	15	2	13	0	0	14	6	21	5	0	0	0	0	0	0	0	21	29	47
SVA-13_24	14	0	0	7	1	0	2	0	5	5	5	4	17	0	9	0	0	0	0	0	34	6	28
SVA-13_44	0	0	0	19	7	2	4	0	4	16	9	14	4	4	0	2	2	1	1	2	30	23	32
Average SVA																					**29 ± 6**	**24 ± 14**	**30 ± 14**
TAR-13_2	0	0	0	23	23	0	7	0	4	13	4	11	6	2	0	0	2	1	1	2	32	36	28
TAR-13_3	2	0	0	32	10	1	6	0	4	26	0	5	4	2	0	0	2	1	0	2	42	36	17
TAR-13_4	10	0	0	24	27	2	7	0	4	12	9	0	3	2	0	0	2	0	0	0	41	39	20
TAR-13_16	0	0	0	24	13	1	6	0	7	20	5	13	4	2	0	0	0	0	0	0	34	33	29
TAR-13_33	2	0	0	30	13	0	5	0	6	16	4	13	2	3	0	0	3	0	0	0	44	29	25
Average TAR																					**39 ± 5**	**35 ± 4**	**24 ± 5**
Red snow																							
SVA-13_2	0	0	0	25	0	2	12	0	5	16	9	15	10	3	0	0	2	0	0	0	34	16	49
SVA-13_4	2	0	0	25	1	2	13	0	3	15	5	20	9	3	0	0	1	0	0	0	35	16	50
SVA-13_10	0	0	0	28	0	0	12	0	8	2	7	31	9	1	0	0	0	0	0	0	37	2	59
SVA-13_20	0	0	0	23	2	2	15	0	4	13	7	27	7	0	0	0	0	0	0	0	27	14	59
SVA-13_23	3	0	0	23	2	2	15	0	3	12	6	27	7	0	0	0	0	0	0	0	29	14	57
SVA-13_31	0	0	0	24	4	2	12	0	4	15	9	22	9	0	0	0	0	0	0	0	27	19	53
SVA-13_33	0	0	0	23	7	1	6	0	6	15	10	18	5	2	0	0	1	1	0	0	32	23	40
SVA-13_36	1	0	0	30	2	1	7	0	5	15	8	14	6	2	0	1	2	0	0	2	40	17	37
SVA-13_43	1	0	0	20	3	2	8	0	4	17	8	14	3	4	0	1	2	0	1	0	32	20	36
SVA-13_48	0	0	0	20	3	2	12	0	3	13	10	21	9	0	0	0	0	0	0	0	24	16	54
SVA-13_54	2	0	0	27	1	4	14	0	2	14	8	18	8	1	0	0	0	0	0	0	32	15	52
Average SVA																					**32 ± 5**	**16 ± 5**	**50 ± 8**
TAR-13_1	2	0	1	45	4	5	35	0	0	0	0	0	0	2	0	0	1	0	0	0	50	4	40
TAR-13_5	3	0	0	26	0	0	19	0	3	15	1	31	0	0	0	0	0	0	0	0	32	15	52

TAR-13_8	3	0	0	0	3	4	0	0	6	19	3	37	7	4	0	0	3	2	2	4	18	22	51
TAR-13_21	0	1	0	31	2	2	8	0	2	13	4	20	13	0	0	0	1	0	1	0	37	15	48
TAR-13_27	0	0	0	42	0	1	7	0	5	12	4	11	3	4	0	0	3	1	2	2	56	12	26
TAR-13_28	0	0	0	25	1	2	13	0	5	12	10	16	15	1	0	0	0	0	0	0	32	13	56
TAR-13_30	0	0	0	39	0	0	4	0	14	8	6	6	4	5	0	1	3	1	2	2	62	8	19
TAR-13_32	0	0	0	22	2	2	16	0	4	13	7	21	12	0	0	0	0	0	0	0	26	15	58
TAR-13_35	0	0	0	34	0	2	9	0	17	10	5	14	3	2	0	0	2	0	0	0	55	10	31
TAR-13_37	0	0	0	21	0	2	15	0	6	12	0	28	14	0	0	0	0	0	0	0	26	12	60
TAR-13_39	0	0	0	26	1	2	13	0	3	12	7	20	10	1	0	0	1	0	0	1	31	13	53
TAR-13_41	0	0	0	24	2	2	9	0	7	13	9	18	8	2	0	0	2	0	0	2	34	16	46
TAR-13_42	0	0	0	21	1	3	17	0	4	13	5	22	12	1	0	0	0	0	0	0	26	15	58
Average TAR																					**37 ± 14**	**13 ± 4**	**46 ± 13**
Biofilms																							
SVA-13_56	3	1	1	15	16	2	8	0	2	20	5	17	4	0	0	0	0	0	0	0	22	37	37
TAR-13_10	2	0	0	30	3	2	6	0	5	15	5	13	5	3	0	0	3	2	2	4	45	18	30
TAR-13_11	13	0	0	26	4	2	5	0	3	16	4	0	11	1	2	0	1	0	0	0	46	20	22
TAR-13_19	3	0	0	36	2	2	8	0	5	18	0	20	3	3	0	0	1	0	0	0	47	20	33
Average TAR																					**46 ± 1**	**19 ± 1**	**28 ± 6**
Dirty ice																							
SVA-13_7	3	2	5	20	9	5	2	1	8	16	7	15	0	2	3	0	1	1	0	0	38	25	29
SVA-13_8	2	3	8	23	9	2	1	3	3	15	6	12	2	1	0	2	2	3	0	2	34	24	23
SVA-13_18	2	3	8	36	4	0	0	0	14	13	6	10	4	0	0	0	0	0	0	0	55	17	20
SVA-13_19	3	6	19	39	14	3	4	4	0	0	0	0	7	0	0	0	0	0	0	0	48	14	15
SVA-13_25	2	0	2	30	7	3	2	0	21	10	8	13	2	0	0	0	0	0	0	0	53	17	28
SVA-13_26	1	2	10	24	7	0	2	2	4	14	8	20	3	0	0	0	1	0	1	0	33	22	33
SVA-13_38	2	2	10	26	5	2	3	2	2	10	8	17	6	0	0	1	1	2	0	0	34	15	36
SVA-13_40	2	2	4	34	6	2	3	2	8	16	8	8	5	1	0	0	0	0	0	0	47	22	24
SVA-13_47	3	7	7	22	8	2	2	5	3	11	4	12	0	2	0	2	2	3	1	1	40	19	20
SVA-13_50	3	2	3	33	7	1	3	2	4	15	4	13	4	2	0	0	2	0	1	0	47	22	25
SVA-13_62	2	3	6	22	8	2	0	3	2	13	7	11	2	1	0	3	2	4	3	2	35	21	23
SVA-13_63	2	2	3	27	6	2	3	2	2	12	9	17	8	0	0	0	1	2	1	0	36	18	39
Average SVA																					**42 ± 8**	**20 ± 4**	**26 ± 7**
TAR-13_13	0	1	0	30	3	3	9	0	2	11	2	25	14	0	0	0	0	0	0	0	33	13	52

TAR-13_22	0	1	0	30	2	2	7	0	2	11	7	23	13	0	0	0	1	0	0	0	34	13	53
Average TAR																					**34 ± 1**	**13 ± 0**	**53 ± 1**
Cryoconite holes																							
SVA-13_5	2	3	6	20	11	3	1	2	3	12	6	17	3	2	1	2	2	2	1	0	34	23	30
SVA-13_16	2	3	15	19	10	1	0	2	4	8	8	13	0	2	0	2	2	3	2	2	34	18	23
SVA-13_27	2	2	20	19	8	0	0	2	3	11	19	12	0	0	0	0	0	2	2	0	26	18	31
SVA-13_37	1	3	20	19	7	2	0	3	3	9	13	16	0	1	0	1	1	1	0	0	28	16	31
SVA-13_51	0	3	16	24	6	0	0	2	5	11	8	18	2	0	0	0	2	2	0	0	34	17	28
SVA-13_61	5	3	8	23	12	2	0	2	6	10	5	16	0	0	0	2	2	2	1	0	40	22	23
Average SVA																					**33 ± 5**	**19 ± 3**	**28 ± 4**
TAR-13_34	3	3	0	24	4	0	0	2	7	6	0	1	0	5	2	5	9	10	7	10	60	10	1

Table S11: Pigment composition of samples that contained enough particulate material for analysis and separated by habitats and locations. Individual pigments were quantified in ug/L and grey columns show total chlorophylls, total primary carotenoids and total secondary carotenoids in % of total pigments. Chl a = chlorophyll a, Chl b = chlorophyll b, Neo = Neoxanthin, Vio = Violaxanthin, Ant = Antheraxanthin, Lut = Lutein, Zea = Zeaxanthin, β-car = β-carotene, Ast=Astaxanthin.

Sample ID	**Chl a**	**Chl b**	**Neo**	**Vio**	**Ant**	**Lut**	**Zea**	**β-car**	**trans-Ast**	**cis-Ast**	**trans- Ast mono esters**	**cis-Ast mono esters**	**total Ast di esters**	**total chlorophylls [%]**	**total primary carotenoids [%]**	**total secondary carotenoids [%]**
Clean snow																
SVA-13_3	159	60									305	0	0	42	0	58
SVA-13_12	361	141						24	144		3733	164	164	11	1	89
SVA-13_22	279	114									412	0	0	49	0	51
SVA-13_35	88										0	0	0	100	0	0
Average SVA														**51 ± 37**	**0 ± 1**	**50 ± 37**
TAR-13_9	911	828		12		212		3	70		2077	92	33	27	4	69
TAR-13_18	410	176				40			27		614	59	0	29	2	69
TAR-13_40	2985	2230	162	105	90	997		2274	2574	160	34045	4424	9802	5	4	91
Average TAR														**20 ± 13**	**3 ± 1**	**76 ± 13**
Green snow																
SVA-13_1	489	391				32			64		181	0	0	76	3	21
SVA-13_21	495	730				223					58	0	0	81	15	4
SVA-13_24	4254	158		1236	133	4	58	62	2079		936	17	0	49	17	34
SVA-13_44	88			62		329			242		0	0	0	12	54	34
Average SVA														**55 ± 32**	**22 ± 22**	**23 ± 14**
TAR-13_2		60							23		0	0	0	72	0	28
TAR-13_3	890	766	449	1490	356	2766	102		325		247	0	113	21	67	12
TAR-13_4	305	301	23	130		428			162		6	0	0	45	43	13
TAR-13_16	1105	837		45		245			140		1509	45	0	35	5	59
TAR-13_33	723	560				137			124		87	0	0	75	8	17
TAR-14_2	2280	1391	14	77		506			902		17713	2336	0	12	22	67
TAR-14_3	444	408							33		2284	205	52	20	19	60
TAR-14_4	369								76		693	0	0	32	0	68
TAR-14_7	4458	2533	59		29	963	6		330		4565	391	0	52	9	39
TAR-14_8	15518	15150	913	2649	1200	6747	534		11752	791	155232	23059	3208	13	5	82
TAR-14_9	7644	5221	283	274	357	1513			4383	448	118162	13976	3038	8	3	89
Average TAR														**35 ± 24**	**16 ± 21**	**49 ± 28**

Red snow																
SVA-13_2	3682	3132	215	147		1155		15	2976	115	62922	6457	1523	8	3	89
SVA-13_4	3359	2873	114	175		1133		81	2664	116	38758	4397	1776	11	4	85
SVA-13_10	882	748	25	10		351		853	1002	15	5164	362	76	17	14	69
SVA-13_20	1200	980	100	36	6	573		3193	3090	194	17661	1906	2316	7	13	80
SVA-13_31	327	266	308	468		1116		51	3927	164	1448	21	178	7	23	69
SVA-13_33	534	426	33	26		355		237	1251	64	3248	201	540	14	10	77
SVA-13_36	376	230	93	98		155		501	1456	86	9142	877	1318	4	6	90
SVA-13_43	672	757	56	113		577		298	868	9	4332	432	1873	14	11	75
SVA-13_54	450	507	472	624		1525		240	9272	904	5640	546	745	5	14	82
Average SVA														**10 ± 5**	**11 ± 6**	**80 ± 8**
TAR-13_1	3253	2712	117	328		1499	9	1025	1867	101	28521	3562	4005	8	4	88
TAR-13_5	6068	5167	354	670	351	2449	88	957	3546	266	48066	6860	6299	8	4	88
TAR-13_8	3084	3212	315	1149	73	2574	14	728	3658	225	21286	2508	6384	9	7	84
TAR-13_17	2153	1605	402	721		1637		1136	3292	122	16014	3063	3949	7	8	85
TAR-13_21	1323	1266	315	374		1384		390	2386	158	13318	1449	2447	7	6	87
TAR-13_27	478	373				241		50	398		3145	286	404	10	3	87
TAR-13_28	672	417	597	381		563		88	1886	115	11182	1113	959	4	5	91
TAR-13_30	495	328		-31		89			243		3035	164	202	11	1	89
TAR-13_32	2490	2203	304	823	69	2021	7	459	2078	59	20966	2608	2913	8	6	86
TAR-13_35	2319	1578	50	162		691		402	963	14	10994	1557	2416	11	5	84
TAR-13_36	492	310	157	154		628		107	1599	92	6407	551	981	4	6	90
TAR-13_37	1655	1328	47	59		638		102	1351	57	5628	749	1229	15	5	79
TAR-13_41	541	426	747	565	48	1180		640	2764	222	8401	884	1766	4	12	85
TAR-13_42	7724	8730	1007	1391	111	5052	8	778	5032	205	29339	3554	4411	16	9	75
TAR-14_1	1414	632				318			938		21910	2344	639	6	24	71
TAR-14_5	2864	1391				528	22		207		2418	304	47	55	7	38
TAR-14_6	14924	10007	822	752	312	4414			17256	662	141903	13779	3548	12	4	84
TAR-14_10	594					49			238		6358	663	133	7	2	90
TAR-14_11	332										102	0	0	76	0	24
TAR-14_12	4238	2694	16	25		1013	4		1751	170	45152	5915	1015	11	2	86
Average TAR														**14 ± 18**	**6 ± 5**	**80 ±17**
Biofilms																
SVA-13_56	311	87		10		69			62		991	50	313	21	4	75
TAR-13_10	436	230	97	102		34		97	124		3023	224	0	9	4	87
TAR-13_11	1541	417		69		98					1103	0	0	45	4	51
TAR-13_19	473	292				3			28		942	47	0	28	0	72
Average TAR														**27 ± 18**	**3 ± 2**	**70 ± 18**

Clean ice															
SVA-13_6	117									0	0	0	100	0	0
SVA-13_17	145				218					6	0	0	39	59	2
SVA-13_29	88									0	0	0	100	0	0
Average SVA													**80 ± 35**	**20 ± 34**	**1 ± 1**
TAR-13_12	339	167								162	0	0	61	0	39
Dirty ice															
SVA-13_7	264	42				10				0	0	0	97	3	0
SVA-13_18	655	346		14	221	131			6	386	0	372	47	17	36
SVA-13_25	159									0	0	0	100	0	0
SVA-13_38	1763	301		1119		171				341	0	0	56	35	9
SVA-13_47	230	19		296						3	0	0	45	54	1
SVA-13_62	681	257		91		198				146	0	550	49	15	36
Average SVA													**66 ±26**	**21 ± 21**	**14 ± 18**
TAR-13_13	1056	882	231	1252	63	2259	21	89		189	0	0	31	63	6
TAR-13_22	1094	721		502		1046		55	82	279	0	0	45	40	16
Average TAR													**38 ± 10**	**51 ± 16**	**11 ± 7**
Cryoconite holes															
SVA-13_5	654	596	148	114		874			71	64	0	0	50	45	5
SVA-13_16	119			498						0	0	0	19	81	0
SVA-13_27	707	87		713		28			151	131	0	0	44	41	15
SVA-13_37	298	31		187						2	0	0	64	36	0
SVA-13_51	657	275		33		107			13	-3	0	0	86	13	1
Average SVA													**53 ± 25**	**43 ± 24**	**4 ± 6**
TAR-13_34										0	0	0			

Table S12: Carbohydrate compound contents in habitat samples from Svalbard reported as ug of whole compound per L of filtered sample.

Sample ID	Fucose	Rhamnose	Arabinose	Galactose	Glucose	Xylose-Mannose	Fructose-Sucrose	Ribose	Lactose	Total carbohydrates
Clean snow										
SVA-13_3	<	<	<	<	<	<	<	<	<	<
SVA-13_9	<	1.4	<	<	4.4	0.7	3.6	<	11.8	21.9
SVA-13_12	<	<	<	<	7.3	<	7.3	<	13.9	28.5
SVA-13_35	<	<	<	<	<	<	<	<	<	<
SVA-13_39	<	<	<	<	4.1	<	<	<	<	4.1
SVA-13_45	<	<	<	1.1	<	<	<	<	<	1.1
SVA-13_49	<	<	<	0.7	<	<	<	<	<	0.7
SVA-13_55	<	<	<	<	<	<	<	<	<	0
Green snow										
SVA-13_1	<	1.1	<	<	1	<	<	<	<	2.1
SVA-13_21	<	1.4	2.2	<	7.5	<	6.7	<	<	17.8
SVA-13_24	<	1.4	<	1.5	3.9	<	<	<	<	6.8
SVA-13_44	<	1.2	<	2.5	0.8	<	<	<	<	4.5
Red snow										
SVA-13_2	<	0.9	<	<	1.4	<	3.3	<	<	5.6
SVA-13_4	<	1.3	2.3	4	2.3	0.7	25.2	1.6	17.8	55.2
SVA-13_10	<	<	0.9	1.6	10.5	<	8.2	<	8.8	30
SVA-13_11	<	1	<	1.3	6.3	<	9.6	<	<	18.2
SVA-13_20	<	1	<	3.4	10.4	<	13.5	<	<	28.3
SVA-13_23	<	<	<	7.5	6.9	<	11.1	<	<	25.5
SVA-13_31	<	<	1.4	<	8.4	<	9.5	1.1	<	20.4
SVA-13_33	<	<	0.5	<	<	<	<	1.1	<	1.6
SVA-13_36	<	<	0.7	<	14.9	<	<	<	<	15.6
SVA-13_43	<	<	<	2.8	9.2	<	11.5	<	<	23.5

SVA-13_48	<	<	<	3	<	<	16.5	<	15.1	34.6
SVA-13_54	<	<	<	<	<	<	5.9	<	<	5.9
SVA-13_65	<	<	<	<	14.4	<	5.6	<	<	20
Biofilms										
SVA-13_56	<	1.4	<	2.8	<	<	3.2	1.7	<	9.1
Clean ice										
SVA-13_6	<	<	<	<	<	<	<	<	<	<
SVA-13_17	<	<	<	<	<	<	<	<	<	<
SVA-13_29	<	1.1	0.6	<	<	<	4.4	<	10.3	16.4
SVA-13_60	<	<	<	1	1.7	<	<	<	<	2.7
Dirty ice										
SVA-13_7	<	<	<	<	<	<	<	<	<	<
SVA-13_8	<	0.9	<	<	<	<	<	<	10.3	11.2
SVA-13_18	<	1.3	<	<	0.3	<	<	<	20	21.6
SVA-13_19	<	<	<	<	<	<	<	<	11.2	11.2
SVA-13_25	<	<	<	1	4.8	<	2.2	<	<	8.0
SVA-13_26	<	<	<	1.2	21.1	<	6	<	<	28.3
SVA-13_38	<	<	<	<	40.4	<	8.6	<	<	49.0
SVA-13_40	<	<	<	<	<	<	2.4	<	<	2.4
SVA-13_47	<	<	<	<	<	<	<	<	<	<
SVA-13_50	<	<	<	1.1	<	<	3.9	<	<	5.0
SVA-13_62	1.3	<	<	<	14.7	<	<	<	<	16.0
SVA-13_63	<	<	<	1.2	<	<	<	<	<	1.2
Cryoconite holes										
SVA-13_5	<	<	<	<	<	<	<	<	46.6	46.6
SVA-13_16	<	<	<	<	<	<	<	<	<	<

SVA-13_27	<	<	1.3	<	<	<	<	<	<	1.3
SVA-13_37	<	<	0.3	<	0.6	<	<	<	<	0.9
SVA-13_51	<	1	<	1.1	<	<	<	<	<	2.1
SVA-13_61	<	<	<	0.8	6.3	<	3.7	<	24.5	35.3

Detection limits: Fucose < 0.6 ug L^{-1}, Rhamnose < 0.5 ug L^{-1}, Arabinose < 0.4 ug L^{-1}, Glucose < 0.3 ug L^{-1}, Xylose-Mannose < 0.4 ug L^{-1}, Fructose-Sucrose < 2.4 ug L^{-1}, Ribose < 0.9 ug L^{-1}, Lactose < 6.8 ug L^{-1}.

Table 13: Average values, standard deviations and statistical analysis of all biological and geochemical compounds (in % of total), analysed by one-way ANOVA to reveal significant differences between the habitats within one location. Results with p-values of <0.05 were considered to be significant and are in bold, results with p-values <0.01 were considered to be highly significant and are also underlined. n.s. = no sample

	Svalbard p	Green snow	Red snow	Biofilms	Dirty ice	Cryoconite holes	Sweden p	Green snow	Red snow	Biofilms	Dirty ice	Cryoconite holes
Algae												
Ancylonema nordenskiöldii	0.153	0	0.7 ± 2.5	0	16.2 ± 23.9	11.5 ± 20.9	0.429	0.8 ± 2.6	0.0 ± 0.1	0	0	6.2
Chloromonas alpina	**0.024**	2.0 ± 2.4	0.5 ± 0.6	8.3	0.6 ± 0.6	0	**0.023**	7.5 ± 8.8	1.2 ± 3.4	8.2 ± 3.2	0.9	1.5
Chloromonas nivalis	0.093	0.2 ± 0.4	3.1 ± 4.2	15.1	0.1 ± 0.1	0.8 ± 1.1	0.375	8.6 ± 11.3	4.6 ± 3.8	4.2 ± 3.5	0.3	0.2
Chloromonas polyptera	0.169	3.4 ± 4.7	9.6 ± 6.3	33.9	9.0 ± 9.3	1.9 ± 1.4	**<0.001**	37.4 ± 22.8	14.5 ± 12.6	55.6 ± 15.8	6.1	1.5
Microglena sp.	**0.019**	20.2 ± 34.5	0	0	0.3 ± 0.5	0	0.661	0	0.0 ± 0.2	0	0.9	0
Raphidonema sempervirens	**0.002**	55.0± 46.9	5.9 ± 11.1	2.2	37.5 ± 23.2	27.7 ± 18.2	0.455	5.7 ± 10.6	2.8 ± 5.9	9.3 ± 15.8	87.5	83.6
Uncult. *Chlamydomonadaceae* (1)	**<0.001**	7.6 ± 7.6	74.9 ± 14.8	38.2	29.3 ± 17.2	57.0 ± 23.2	**<0.001**	26.8 ± 22.2	67.6 ± 16.0	14.4 ± 15.1	4.3	4.6
Uncult. *Chlamydomonadaceae* (2)	**0.004**	0.5 ± 0.3	4.8 ± 3.4	1.5	1.6 ± 1.5	0.9 ± 0.9	**0.007**	1.2 ± 1.3	5.1 ± 3.9	1.5 ± 1.6	0	0
Bacteria												
Bacteriodetes		32.3 ± 13.6	45.4 ± 27.1	31.9	18.0 ± 13.3	9.7 ± 11.3		34.3 ± 20.5	71.2 ± 27.3	88.0 ± 15.6	24.2 ± 18.5	3.1
Sphingobacteria	0.668	6.6 ± 6.1	3.7 ± 10.3	2.8	4.9 ± 2.8	1.2 ± 0.8	**<0.001**	20.7 ± 17.6	62.9 ± 27.5	85.6 ± 16.5	10.8 ± 0.5	2.5
Saprospirae	**0.058**	15.7 ± 20.8	24.3 ± 24.1	14.2	2.8 ± 2.8	8.3 ± 10.5	0.106	12.1 ± 13.4	4.6 ± 6.7	1.8 ± 1.0	9.3 ±13.1	0
Cytophagia	**0.054**	4.5 ± 3.1	16.7 ± 15.5	9.5	6.7 ± 11.9	0.1 ±0.1	0.202	1.4 ± 1.9	3.7 ± 4.7	0.6 ± 0.4	4.1 ± 5.7	0.6
Cyanobacteria		0.2 ± 0.1	17.4 ± 24.1	6.4	34.7 ± 25.3	71.7 ± 21.2		12.7 ± 25.1	9.7 ± 11.6	0.4 ± 0.6	3.1 ± 3.5	0.2
Nostocophycideae	0.322	0	0.7 ± 0.9	0	0.3 ± 0.8	0.1 ± 0.1	0.472	0.4 ± 0.9	3.4 ± 5.7	0.1 ± 0.1	0	0
Oscillatoriophycideae	0.636	0	1.7 ± 5.1	0	0.1 ± 0.2	0.2 ± 0.1	0.751	3.0 ± 9.0	1.9 ± 4.0	0.1 ± 0.1	0	0
Synechococco-phycideae	**<0.001**	0.2 ± 0.1	15.0 ± 22.4	6.4	34.3 ± 25.5	71.5 ± 21.2	0.357	1.6 ± 1.7	3.9 ± 6.7	0.3 ± 0.5	3.1± 3.5	0.2
Proteobacteria		43.8 ± 36.1	28.6 ± 18.7	47.8	13.4 ± 15.6	2.3 ± 2.9		41.2 ± 22.7	5.2 ± 6.6	6.5 ± 8.0	11.6 ± 8.5	70.2
Alphaproteobacteria	**0.014**	19.5 ± 32.6	2.8 ± 3.9	6.2	21.4 ± 15.6	4.4 ± 3.1	0.697	7.6 ± 8.0	9.7 ± 14.4	3.7 ± 4.7	37.3 ± 2.3	8.1
Betaproteobacteria	**0.003**	43.6 ± 36.1	27.8 ± 18.5	47.8	9.9 ± 10.5	2.1 ±2.9	**0.003**	40.2 ± 22.8	3.3 ± 5.4	6.4 ± 7.8	11.5 ± 8.3	18.7
Fungi [% of total eukaryotes]	**0.001**	21.6 ± 22.4	22.7 ± 10.9	27.5	24.3 ± 13.5	55.4 ± 22.	0.390	36.6 ± 15.1	44.3 ± 22.6	45.2 ± 18.1	38	10.9
Solids (C,N,P,S)												
Total C	0.084	1.8 ± 0.9	5.3 ± 4.5	7.8	2.3 ± 1.8	2.0 ± 1.0	**0.001**	1.4 ± 0.6	12.4 ± 7.2	23.7 ± 5.6	9.6 ± 6.3	10.4
Total N	0.081	0.16 ± 0.04	0.32 ± 0.26	0.81	0.15 ± 0.08	0.20 ± 0.09	**<0.001**	0.16 ± 0.08	0.61 ± 0.42	1.72 ± 0.17	0.85 ± 0.60	0.65
Total P	**0.025**	0.07 ± 0.02	0.07 ± 0.03	0.13	0.05 ± 0.01	0.04 ± 0.01	**0.009**	0.07 ± 0.02	0.06 ± 0.02		0.07 ± 0.01	0.06
Total S	**<0.001**	0.07 ± 0.02	0.11 ± 0.04	0.09	0.06 ± 0.01	0.06 ± 0.00	**<0.001**	0.03 ± 0.01	0.07 ± 0.02	0.16 ± 0.03	0.08 ± 0.04	0.12
C/N	0.764	12 ± 8	16 ± 3	10	29 ± 56	10 ± 1	**<0.001**	9 ± 3	22 ± 6	14 ± 4	12 ± 1	16
C/P	0.705	26 ± 10	63 ± 32	60	59 ± 74	51 ± 23	**0.013**	25 ± 11	186 ± 89		87 ± 40	168
N/P	0.219	3 ± 1	4 ± 2	6	3 ± 2	5 ± 2	**0.019**	3 ± 2	8 ± 3		7 ± 4	10

δ^{15}N	0.106	-3.30 ± 1.50	-4.88 ± 2.50	4.24	-1.67 ± 3.97	-2.15 ± 1.24	0.400	-3.17 ± 3.54	-4.30 ± 1.84	-4.29 ± 0.65	-2.18 ± 0.62	-3.4
δ^{13}C	**0.004**	-31.80 ± 6.30	-27.66 ± 1.61	-27.38	-26.24 ± 0.63	-25.49 ± 0.25	0.056	-26.99 ± 1.15	-25.70 ± 2.02	-28.98 ± 1.38	-25.84 ± 0.06	-25.9
Functional groups												
Carbohydrates	**0.008**	97.5 ± 1.0	91.5 ± 5.0	80.8	96.2 ± 2.6	n.s.	0.146	84.2 ± 17.2	77.1 ± 6.6	79.3 ± 5.1	89.0 ± 4.2	n.s
Lipids	**0.001**	0.2 ± 0.0	2.7 ± 2.1	3.9	0.4 ± 0.3	n.s.	0.134	4.6 ± 6.8	8.1 ± 3.1	6.6 ± 3.2	2.7 ± 1.6	n.s
Proteins	0.056	2.3 ± 0.9	5.7 ± 3.3	15.3	3.4 ± 2.4	n.s.	0.207	11.2 ± 10.5	14.7 ± 4.0	14.2 ± 2.6	8.3 ± 2.6	n.s
Pigments												
Chlorophylls	**0.001**	55 ± 32	10 ± 5	21	66 ±26	53 ± 25	0.310	35 ± 24	14 ± 18	27 ± 18	38 ± 10	n.s
Primary carotenoids	**0.014**	22 ± 22	11 ± 6	4	21 ± 21	43 ± 24	0.209	16 ± 21	6 ± 5	3 ± 2	51 ± 16	n.s
Secondary carotenoids	**<0.001**	23 ± 14	80 ± 8	75	14 ± 18	4 ± 6	0.380	49 ± 28	80 ±17	70 ± 18	11 ± 7	n.s
Fatty acids												
SFA	**0.003**	29 ± 6	32 ± 5	22	42 ± 8	33 ± 5	0.217	39 ± 5	37 ± 14	46 ± 1	34 ± 1	6
MUFA	**0.001**	24 ± 14	16 ± 5	37	20 ± 4	19 ± 3	**<0.001**	35 ± 4	13 ± 4	19 ± 1	13 ± 0	1
PUFA	**<0.001**	30 ± 14	50 ± 8	37	26 ± 7	28 ± 4	**<0.001**	24 ± 5	46 ± 13	28 ± 6	53 ± 1	1
Aqueous geochemistry												
SO4	**0.002**	106.0 ± 76.0	13.3 ± 46.2	0	28.0 ± 65.5	140.7 ± 11.1	0.752	0	18.5 ± 50.6	0	0	141.
Fe	**0.009**	2.0 ± 1.8	1.9 ± 1.0	4.4	7.8 ± 5.7	5.0 ± 4.6	**<0.001**	5.0 ± 3.4	1.5 ± 1.0	10.0 ± 12.0	120.7 ± 67.0	8.4
K	**0.008**	99.0 ± 22.3	41.3 ± 20.3	120.0	38.5 ± 25.3	70.4 ± 48.9	**<0.001**	48.8 ± 14.7	62.3 ± 74.0	552.0 ± 445.6	43.3 ±38.4	33.

Table 14: Average values and standard deviations for all geochemical compounds that revealed significant ($p<0.05$) differences between Svalbard and Arctic Sweden regardless of the habitats.

	Between locations
DOC [µM]	0.001
Cl [ppb]	<0.001
Ca [ppb]	0.096
Mn [ppb]	0.015
Mn [ppb]	0.027
Na [ppb]	0.001

Figure S1: Principal component analysis of fatty acids in the Svalbard and Arctic Sweden samples revealing distance between samples and showing the main fatty acid compounds causing the separations. Samples cluster according to habitats in all locations.

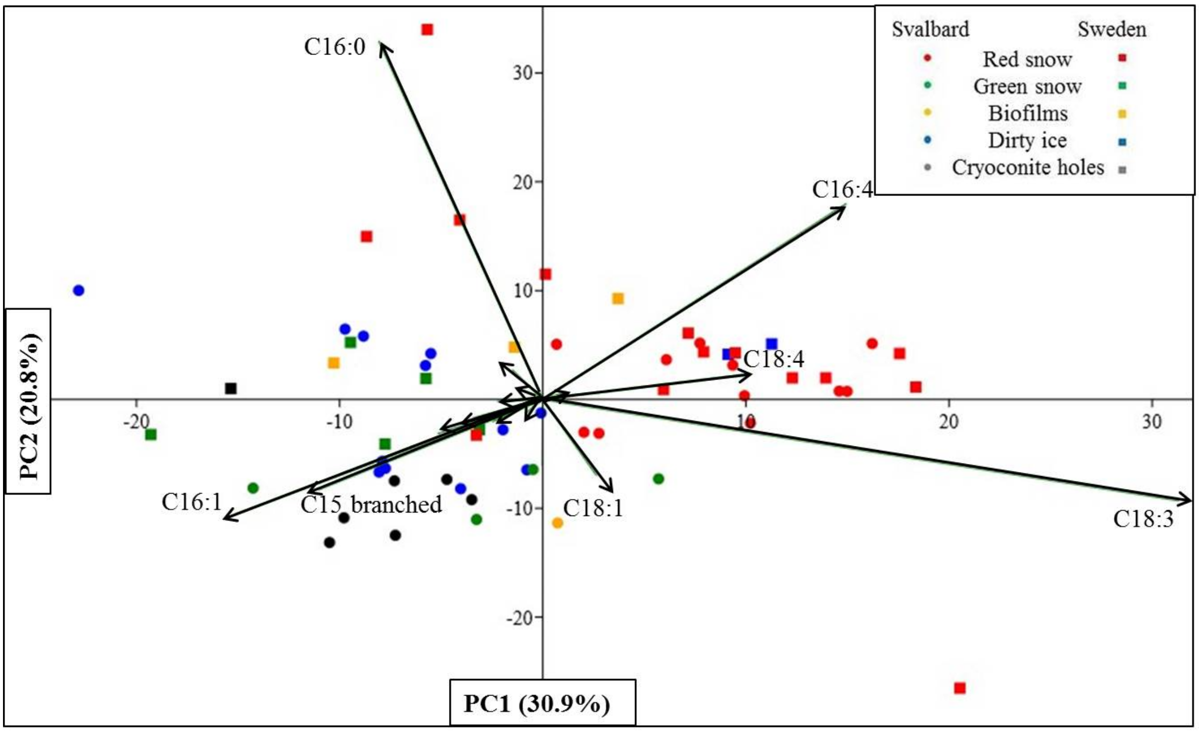

Figure S2: CCA analysis showing the links between algal species and various relevant geochemical parameters. The two uncultured *Chlamydomonadaceae* (1) and (2) positively correlated with increasing C/N ratios, *Chloromonas polyptera* with DOC and K, *Raphidonema sempervirens* with Fe and Mn, and *Chloromonas cf. alpina* with DOC.

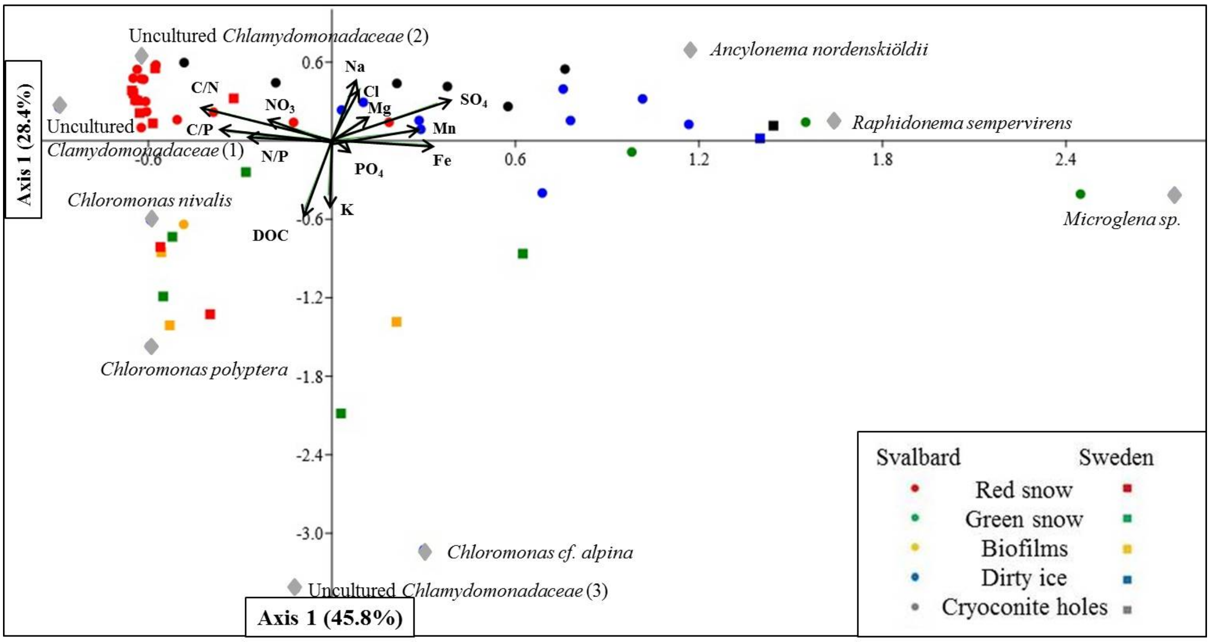

Figure S3: CCA analysis showing the links between bacterial classes and various relevant geochemical parameters. *Sphingobacteria* positively correlated with DOC, C/N, C/P, N/P and K, and *Synechococcophycideae* with SO_4.

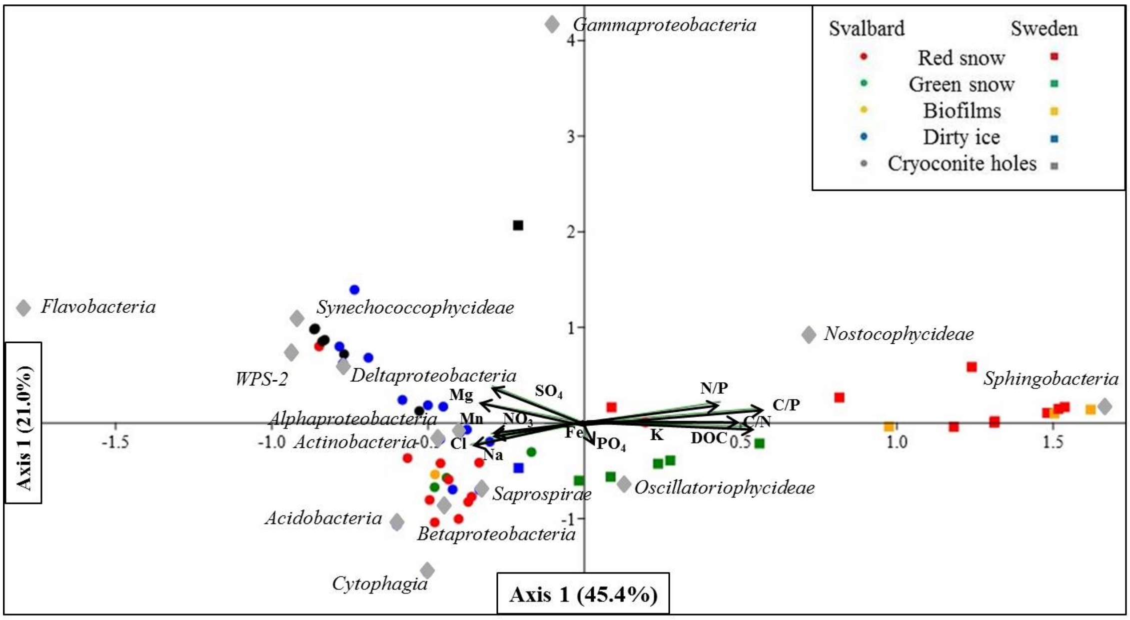

Figure S4: C/N and C/P ratios for the analysed Svalbard and Arctic Sweden samples. Lines show optimal Redfield ratios (solid line: C/N, dashed line: C/P). Most samples were above the optimal Redfield ratio for C/N but only the samples from the red snow habitats from Arctic Sweden were above the optimal C/P ratio. Samples cluster according to habitats within their respective location.

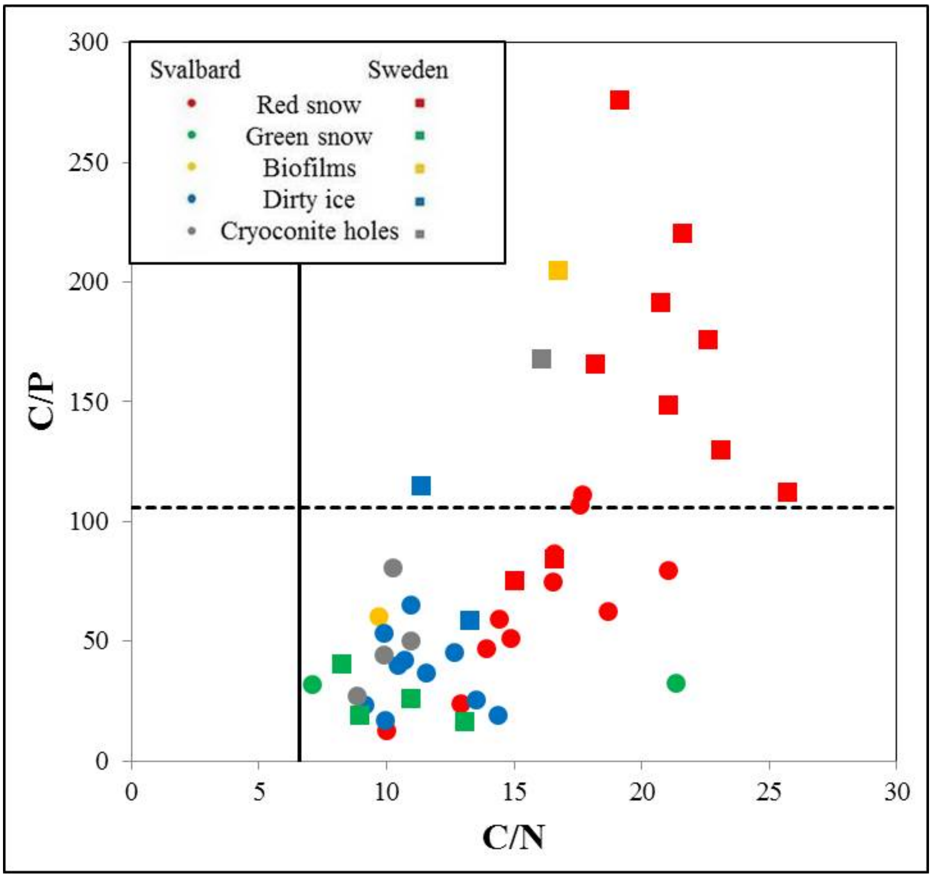

Figure S5: Carbon and nitrogen isotopes. $\delta^{15}N$ values were predominately negative but show no significant trend ($p>0.05$) for habitats or locations. $\delta^{13}C$ values varied over a narrow range and significant trends ($p=0.004$) were only established for habitats in Svalbard (left plot), where on average most red snow samples showed more negative values than the dirty ice and cryoconite hole samples. No significant trends were observed for samples from Arctic Sweden (right plot).

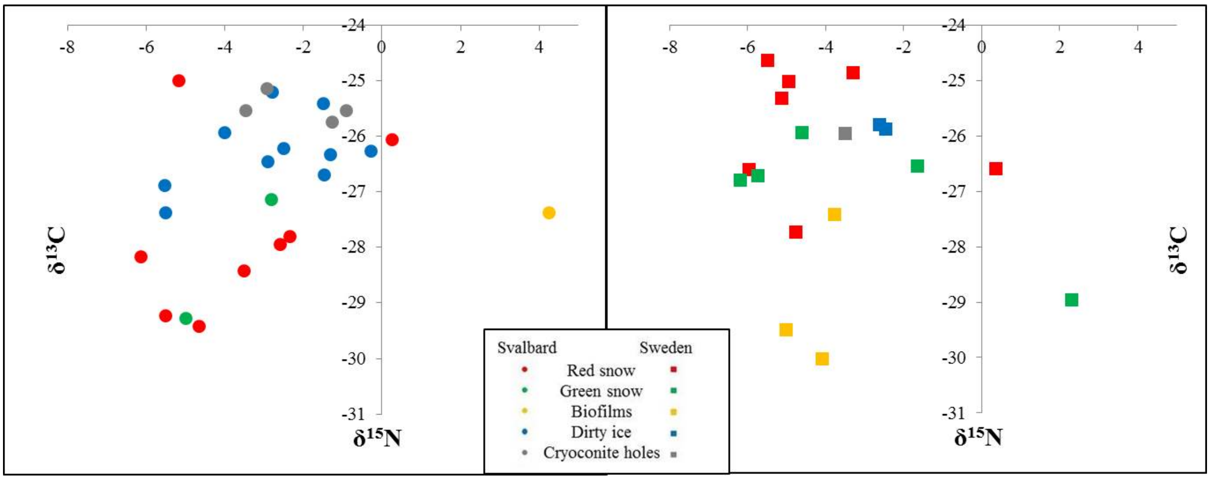

Figure S6: Relative abundance of functional group corresponding to lipids and proteins showing that samples cluster according to algal habitats. Lipids and proteins show highest values in red snow (specifically in the Arctic Sweden samples), whereas in the Svalbard samples lipids were significantly higher but not proteins.