Supplementary Material

Supplementary Methods

DNA extraction. To extract and purify DNA from seawater filters in the laboratory, small pieces of frozen filters (~ 35 mg filter mass) were put into 2-ml centrifuge tubes (one tube per depth) containing 200 µl of 10 mM Tris-1 mM EDTA buffer (TE) with 0.5 % (w/v) sodium dodecyl sulfate and proteinase K (50 µg ml^{-1}). Tubes were incubated at room temperature for 30 min; tubes with buffer and no filter material served as blanks. DNA was extracted by adding 200 µl of a pH 8-equibrated phenol: chloroform: iso-amyl alcohol mixture (25:24:1 [v/v/v]) and incubated for 5 min at room temperature. Tubes were then centrifuged for 5 min at highest speed, and aqueous phases were transferred into new centrifuge tubes. The phenol phases were mixed with 200 µl TE, incubated for 5 min at room temperature, and centrifuged for 5 min. The aqueous extracts were combined with the previous aqueous phases. DNA was precipitated in 10 % (v/v) 5 M NaCl and 2.5 volume of 100% ethanol overnight at room temperature. Tubes were then centrifuged for 15 min at highest speed, and pellets were washed with 70 % ethanol, air dried, and resuspended in 200 µl sterile RNA-free water (Qiagen). DNA from sediment was extracted and purified from 250 mg sediment using the MoBio UltraClean Soil DNA Kit (MoBio Laboratories, Inc, Solana Beach, CA.), following the manufacturer's instructions.

Supplementary Results

Bacteroidetes. Members of the phylum *Bacteroidetes* constituted the dominant clone library fraction in the surface water sample (58%), nearly disappeared in the bottom water sample (a single clone), and reappeared with ca. 12% and 16% clone library representation in the sediments. Strong phylogenetic partitioning between water column and sediment was also observed in the phylum *Bacteroidetes* (Fig. S1). Following the taxonomic outline of Bergeys Manual, 2nd edition that divides this phylum into the orders *Flavobacteriales* and *Bacteroidales* (S1), the surface water clones fell exclusively into the *Flavobacteriales*, where they form sister lineages to marine, heterotrophic and aerobic genera and species such as the vacuolated psychrophile *Polaribacter* (S2), or the genera *Algibacter* (S3), *Actibacter* (S4) and *Ulvibacter* (S5) that often use marine algae and biopolymers as carbon source. A number of these clones were very similar to those previously recovered from the surface water and bottom water in Kongsfjord (S6), designated as Svalbard bottom or shallow water clones (Fig. S1)

The *Flavobacteriales* disappeared almost completely in the bottom water sample and in the surface and subsurface sediment. In the sediment samples they were replaced by different lineages within the *Bacteroidales:* an uncultured cluster of marine sediment clones, including the Svalbard clone 1083 that was recovered previously from Svalbard marine sediments (S7); lineages affiliated with the fermentative marine psychrophile *Prolixibacter bellariivorans* (S8), or the fermenting obligate anaerobe *Paludibacter propionicigenes* within the *Porphyraceae* (S9). This taxonomic shift is congruent with

metabolism: the aerobic *Flavobacteriales* in the water column and on the sediment surface yielded to anaerobic *Bacteroidales* within the sediment.

In addition to the *Verrucomicrobiaceae*, members of the *Flavobacteria* and the *Planktomycetes* are strong candidates as mediators of polysaccharide hydrolysis in the water column. The single cell amplified genomes AAA168_G15 and AAA164_L19 represent xylan and laminarin-binding cells within the *Flavobacteria* (Fig. S1). While they do not match specific Svalbard clones closely, a role for *Flavobacteria* in carbohydrate degradation in the water column would be consistent with the heterotrophic culture characteristics of flavobacterial genera and species, and the abundance of hydrolase genes in published genomes across the phylum *Bacteroidetes* (S10).

Proteobacteria. A wide range of *Proteobacteria*, predominantly from the Alpha-, Gamma- and Deltaproteobacterial subdivisions, were found in the water column and sediment (Fig. S2). The *Gammaproteobacteria* accounted for approximately 20% of both water column clone libraries, and occur in similar proportions (but in changing genus- and family-level composition) in the sediment layers. The gammaproteobacterial clones belonged to the mostly uncultured lineages OCMS-1 group (S11), the GMS3 group (S12), and the ARCTIC96BD-19 group (S13) and originated mostly from surficial sediment, with the exception of a water column cluster and a deep sediment cluster related to the marine microaerophilic heterotroph *Haliea rubra* (S14). Members of these groups have been detected previously in clone libraries from the Svalbard water column (EU919783, S7) and sediments (EU050803, S15; AJ240991, S7). The Smeerenburg phylotypes overlapped with bacterial strains isolated from Svalbard sediments and water samples within the genus *Pseudomonas* (S16).

In addition to the *Verrucomicrobia* and *Bacteroidetes*, a third phylogenetically defined group of bacteria active in carbohydrate degradation is indicated within the *Gammaproteobacteria*, where a single cell amplified genome (AAA168_O11) is closely related to the genus *Pseudomonas* and a deep-water Svalbard clone (Fig. S2). No such association was found for the *Haliela rubra*-associated gammaproteobacterial phylotypes from the Svalbard water column (Fig. S2).

The *Alphaproteobacteria* accounted for only approximately 5% of the water column clone libraries, a much reduced proportion compared to their frequent detection in methodologically identical clone libraries obtained from the Smeerenburg fjord water column in the summer of 2007 (S11). The alphaproteobacterial clones were mostly obtained from the deep water column and branched with the marine *Roseobacter* clade of heterotrophic, often organosulfur-degrading bacteria that are abundant in coastal waters (S17, S18).

Members of the *Deltaproteobacteria* were almost exclusively recovered from the sediment samples; most clones were affiliated with the *Desulfosarcinales* and the psychrophilic sulfate-reducing genera *Desulfofrigus* and *Desulfofaba*, isolated previously from Svalbard sediments (S19) (Fig. S2). Other clones were affiliated to previously recovered Svalbard clones within uncultured deltaproteobacterial lineages (Sva0812b; S7). In contrast to the water column samples, the sediment samples contained a larger number of phylum-level lineages: the *Chloroflexi*, *Firmicutes*, *Actinobacteria*, *Planktomycetes*, and the *Nitrospina* lineage were represented by a few clones each (Fig. S3).

***Planctomycetes*.** A fourth hot spot of carbohydrate-degrading cells within the phylum *Planctomycetes* is suggested by a laminarin-associated single amplified genome (phylotype AAA164_M21) near *Rhodopirellula baltica*. The genome of this marine planctomycete contains an unusually large number of sulfatases, whose function is probably connected with accessing the carbon skeleton of sulfated complex organic compounds (S20); recent work demonstrates that *R. baltica* grows particularly well on chrondroitin sulfate (S21). While clones within the *Planctomycetes* phylum are commonly found in Svalbard marine sediments, water column clones were not recovered (S11, S15, this study); the *Planctomycetes* are therefore not among the conspicuous carbohydrate-utilizing bacteria in the water column but may play a greater role in the sediment.

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Supplementary Tables

Table S1. Summary of clone names organized by sample isolation source, including GenBank accession numbers, phylogenetic affiliation, and number of repeats for each representative sequence in the clone libraries. Red shading corresponds to higher relative abundance.

SOURCE	CLONE	ACCESSION NUMBER	PHYLOGENY	REPEATS
WATER COLUMN: 2 m	WS08_002	KJ566246	Flavobacteriales	1
	WS08_007	KJ566221	Verrucomicrobia	9
	WS08_009	KJ566243	Flavobacteriales	8
	WS08_012	KJ566245	Flavobacteriales	4
	WS08_014	KJ566258	Actinobacteria	2
	WS08_015	KJ566261	Actinobacteria	1
	WS08_016	KJ566249	Flavobacteriales	4
	WS08_017	KJ566250	Flavobacteriales	4
	WS08_021	KJ566267	Cyanobacteria	1
	WS08_023	KJ566247	Flavobacteriales	3
	WS08_039	KJ566224	Verrucomicrobia	1
	WS08_048	KJ566248	Flavobacteriales	1
	WS08_058	KJ566226	Verrucomicrobia	4
WATER COLUMN: 205 m	WD08_001	KJ566222	Verrucomicrobia	1
	WD08_002	KJ566282	γ-proteobacteria	11
	WD08_004	KJ566223	Verrucomicrobia	35
	WD08_005	KJ566225	Verrucomicrobia	7
	WD08_006	KJ566303	α-proteobacteria	1
	WD08_009	KJ566297	δ-proteobacteria	1
	WD08_015	KJ566242	Flavobacteriales	1
	WD08_020	KJ566302	α-proteobacteria	1
	WD08_045	KJ566287	γ-proteobacteria	1
	WD08_055	KJ566281	γ-proteobacteria	1
	WD08_060	KJ566299	ε-proteobacteria	1
	WD08_065	KJ566301	α-proteobacteria	1

SOURCE	CLONE	ACCESSION NUMBER	PHYLOGENY	REPEATS
SEDIMENT: 0-2 cmbsf	SS08_003	KJ566234	Verrucomicrobia	1
	SS08_005	KJ566266	Chlorophyta	1
	SS08_006	KJ566294	δ-proteobacteria	1
	SS08_012	KJ566251	Bacteroidales	1
	SS08_013	KJ566285	γ-proteobacteria	1
	SS08_014	KJ566268	γ-proteobacteria	2
	SS08_016	KJ566286	γ-proteobacteria	1
	SS08_018	KJ566284	γ-proteobacteria	2
	SS08_021	KJ566228	Verrucomicrobia	1
	SS08_022	KJ566220	Verrucomicrobia	2
	SS08_024	KJ566298	δ-proteobacteria	1
	SS08_029	KJ566230	Verrucomicrobia	1
	SS08_031	KJ566289	δ-proteobacteria	1
	SS08_036	KJ566270	γ-proteobacteria	1
	SS08_039	KJ566291	δ-proteobacteria	3
	SS08_040	KJ566272	γ-proteobacteria	1
	SS08_042	KJ566300	α-proteobacteria	1
	SS08_045	KJ566236	Planctomycetales	2
	SS08_046	KJ566259	Actinobacteria	2
	SS08_047	KJ566232	Verrucomicrobia	3
	SS08_048	KJ566244	Flavobacteriales	1
	SS08_049	KJ566229	Verrucomicrobia	4
	SS08_050	KJ566231	Verrucomicrobia	1
	SS08_052	KJ566275	γ-proteobacteria	1
	SS08_056	KJ566254	Bacteroidales	1
	SS08_058	KJ566280	γ-proteobacteria	1
	SS08_061	KJ566274	γ-proteobacteria	1
	SS08_062	KJ566255	Bacteroidales	1
	SS08_064	KJ566262	Chloroflexi	1
	SS08_065	KJ566296	δ-proteobacteria	1
	SS08_067	KJ566265	Firmicutes	1
	SS08_068	KJ566278	γ-proteobacteria	1

SOURCE	CLONE	ACCESSION NUMBER	PHYLOGENY	REPEATS
SEDIMENT: 3-9 cmbsf	SD08_004	KJ566264	Firmicutes	1
	SD08_005	KJ566295	δ-proteobacteria	1
	SD08_006	KJ566238	Planctomycetales	1
	SD08_008	KJ566263	Nitrospina	2
	SD08_009	KJ566260	Actinobacteria	1
	SD08_010	KJ566237	Planctomycetales	3
	SD08_011	KJ566257	Bacteroidales	1
	SD08_013	KJ566293	δ-proteobacteria	1
	SD08_014	KJ566271	γ-proteobacteria	3
	SD08_015	KJ566290	δ-proteobacteria	6
	SD08_020	KJ566269	γ-proteobacteria	1
	SD08_022	KJ566277	γ-proteobacteria	1
	SD08_023	KJ566227	Verrucomicrobia	1
	SD08_027	KJ566283	γ-proteobacteria	4
	SD08_032	KJ566239	Planctomycetales	1
	SD08_033	KJ566288	β-proteobacteria	1
	SD08_034	KJ566252	Bacteroidales	2
	SD08_036	KJ566292	δ-proteobacteria	1
	SD08_046	KJ566233	Verrucomicrobia	1
	SD08_047	KJ566253	Bacteroidales	2
	SD08_051	KJ566273	γ-proteobacteria	1
	SD08_054	KJ566256	Bacteroidales	1
	SD08_056	KJ566235	Lentisphaerae	1
	SD08_057	KJ566241	OP3	1
	SD08_063	KJ566240	OP3	1
	SD08_064	KJ566279	γ-proteobacteria	1
	SD08_065	KJ566304	α-proteobacteria	1
	SD08_066	KJ566276	γ-proteobacteria	2

Supplementary Figures

FIG. S1. Neighbor-Joining phylogeny of Smeerenburg Fjord *Bacteroidetes*, based on a ~1200-bp alignment of bacterial 16S rRNA sequences. The Svalbard phylotypes are labeled with habitat indicator (water_surface = WS; water_deep = WD; sediment_surface = SS; sediment_deep = SD), followed by clone designation, and highlighted in boldface.

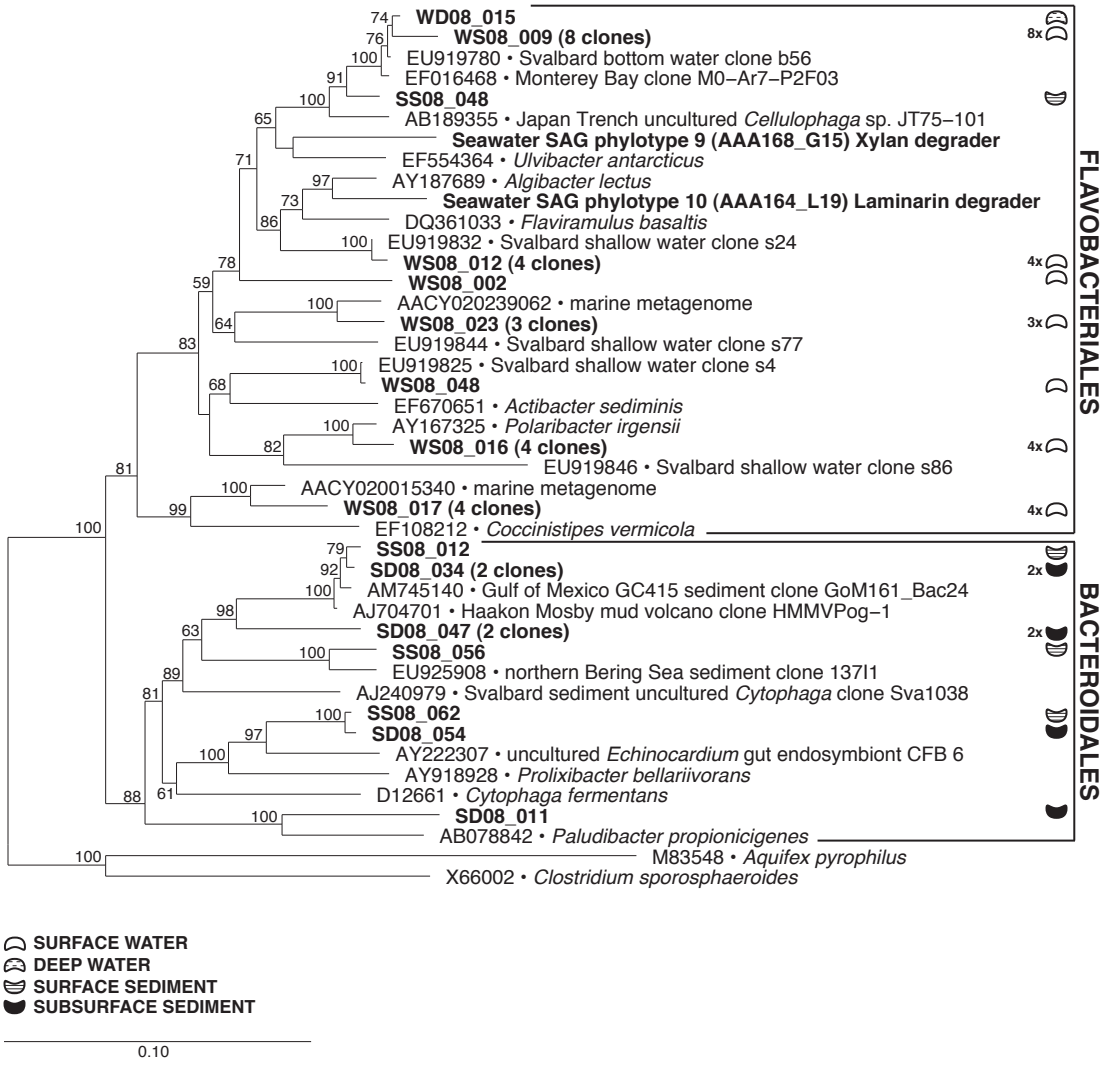

FIG. S2. Neighbor-Joining phylogeny of Smeerenburg Fjord alpha-, beta-, gamma-, delta-, and epsilonproteobacterial phylotypes, based on a ~1200-bp alignment of bacterial 16S rRNA sequences. The Svalbard phylotypes are labeled with habitat indicator (water_surface = WS; water_deep = WD; sediment_surface = SS; sediment_deep = SD), followed by clone number, and highlighted in boldface.

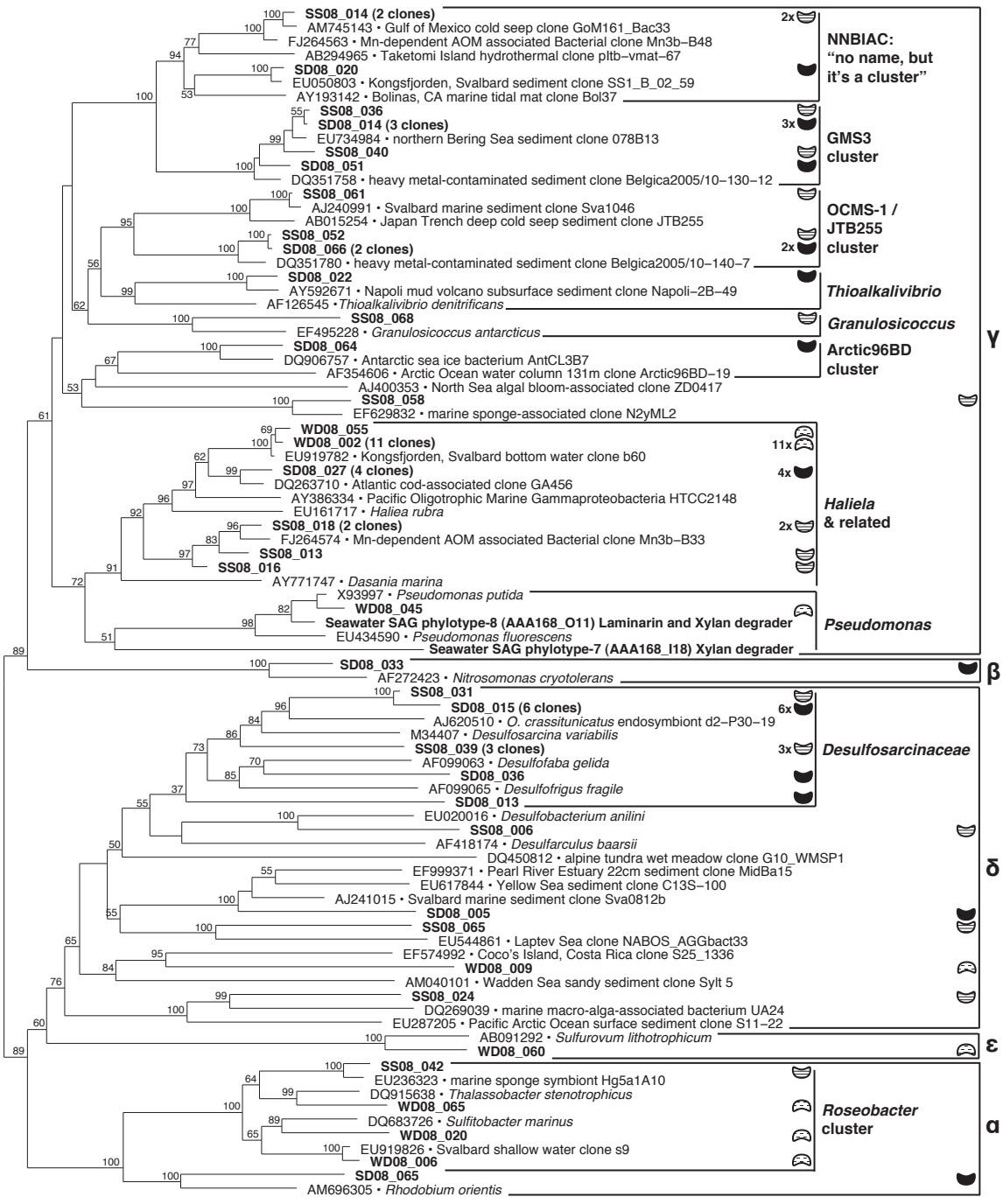
SS08_014 (2 clones)
AM745143 • Gulf of Mexico cold seep clone GoM161_Bac33
FJ264563 • Mn-dependent AOM associated Bacterial clone Mn3b–B48
AB294965 • Taketomi Island hydrothermal clone pItb–vmat–67
SD08_020
EU050803 • Kongsfjorden, Svalbard sediment clone SS1_B_02_59
AY193142 • Bolinas, CA marine tidal mat clone Bol37
2x
NNBIAC: "no name, but it's a cluster"
SS08_036
SD08_014 (3 clones)
EU734984 • northern Bering Sea sediment clone 078B13
SS08_040
SD08_051
DQ351758 • heavy metal-contaminated sediment clone Belgica2005/10–130–12
3x
GMS3 cluster
SS08_061
AJ240991 • Svalbard marine sediment clone Sva1046
AB015254 • Japan Trench deep cold seep sediment clone JTB255
SS08_052
SD08_066 (2 clones)
DQ351780 • heavy metal-contaminated sediment clone Belgica2005/10–140–7
2x
OCMS-1 / JTB255 cluster
SD08_022
AY592671 • Napoli mud volcano subsurface sediment clone Napoli–2B–49
AF126545 • Thioalkalivibrio denitrificans
Thioalkalivibrio
SS08_068
EF495228 • Granulosicoccus antarcticus
Granulosicoccus
SD08_064
DQ906757 • Antarctic sea ice bacterium AntCL3B7
AF354606 • Arctic Ocean water column 131m clone Arctic96BD–19
Arctic96BD cluster
γ
AJ400353 • North Sea algal bloom-associated clone ZD0417
SS08_058
EF629832 • marine sponge-associated clone N2yML2
WD08_055
WD08_002 (11 clones)
EU919782 • Kongsfjorden, Svalbard bottom water clone b60
11x
SD08_027 (4 clones)
DQ263710 • Atlantic cod-associated clone GA456
AY386334 • Pacific Oligotrophic Marine Gammaproteobacteria HTCC2148
EU161717 • Haliea rubra
4x
SS08_018 (2 clones)
FJ264574 • Mn-dependent AOM associated Bacterial clone Mn3b–B33
SS08_013
SS08_016
AY771747 • Dasania marina
2x
Haliela & related
X93997 • Pseudomonas putida
WD08_045
Seawater SAG phylotype-8 (AAA168_O11) Laminarin and Xylan degrader
EU434590 • Pseudomonas fluorescens
Seawater SAG phylotype-7 (AAA168_I18) Xylan degrader
Pseudomonas
SD08_033
AF272423 • Nitrosomonas cryotolerans
β
SS08_031
SD08_015 (6 clones)
AJ620510 • O. crassitunicatus endosymbiont d2–P30–19
M34407 • Desulfosarcina variabilis
SS08_039 (3 clones)
AF099063 • Desulfofaba gelida
SD08_036
AF099065 • Desulfofrigus fragile
SD08_013
6x
3x
Desulfosarcinaceae
EU020016 • Desulfobacterium anilini
SS08_006
AF418174 • Desulfarculus baarsii
DQ450812 • alpine tundra wet meadow clone G10_WMSP1
EF999371 • Pearl River Estuary 22cm sediment clone MidBa15
EU617844 • Yellow Sea sediment clone C13S–100
AJ241015 • Svalbard marine sediment clone Sva0812b
SD08_005
SS08_065
EU544861 • Laptev Sea clone NABOS_AGGbact33
EF574992 • Coco's Island, Costa Rica clone S25_1336
WD08_009
AM040101 • Wadden Sea sandy sediment clone Sylt 5
SS08_024
DQ269039 • marine macro-alga-associated bacterium UA24
EU287205 • Pacific Arctic Ocean surface sediment clone S11–22
δ
AB091292 • Sulfurovum lithotrophicum
WD08_060
ε
SS08_042
EU236323 • marine sponge symbiont Hg5a1A10
DQ915638 • Thalassobacter stenotrophicus
WD08_065
DQ683726 • Sulfitobacter marinus
WD08_020
EU919826 • Svalbard shallow water clone s9
WD08_006
Roseobacter cluster
α
SD08_065
AM696305 • Rhodobium orientis
DEEP WATER
SURFACE SEDIMENT
SUBSURFACE SEDIMENT
0.10

FIG. S3. Neighbor-Joining phylogeny of other Smeerenburg Fjord phylotypes within the *Actinobacteria*, *Firmicutes*, *Chloroflexi*, *Chlorophyta*, *Cyanobacteria* and the *Nitrospina* lineage, based on a ~1200-bp alignment of bacterial 16S rRNA sequences. The Svalbard phylotypes are labeled with habitat indicator (water_surface = WS; water_deep = WD; sediment_surface = SS; sediment_deep = SD), followed by clone number, and highlighted in boldface.

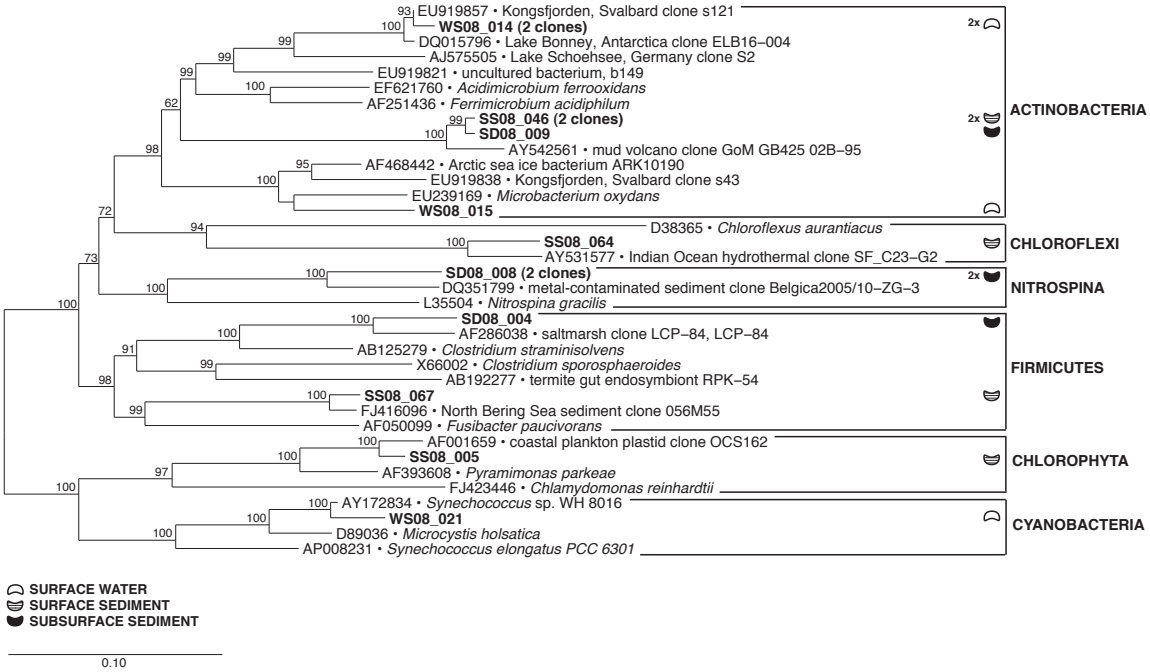

FIG. S4. Hydrolysis rates of polysaccharides in surface (horizontal striped bars) and bottom water (vertical striped bars) samples (A) and in homogenized sediments from 0-2 cm (grey bars) and 3-9 cm (black bars) depth (B) from Smeerenburgfjord in 2007. Substrate labels are as in Fig. 1. Asterisk: no data. Data replotted from (S11).