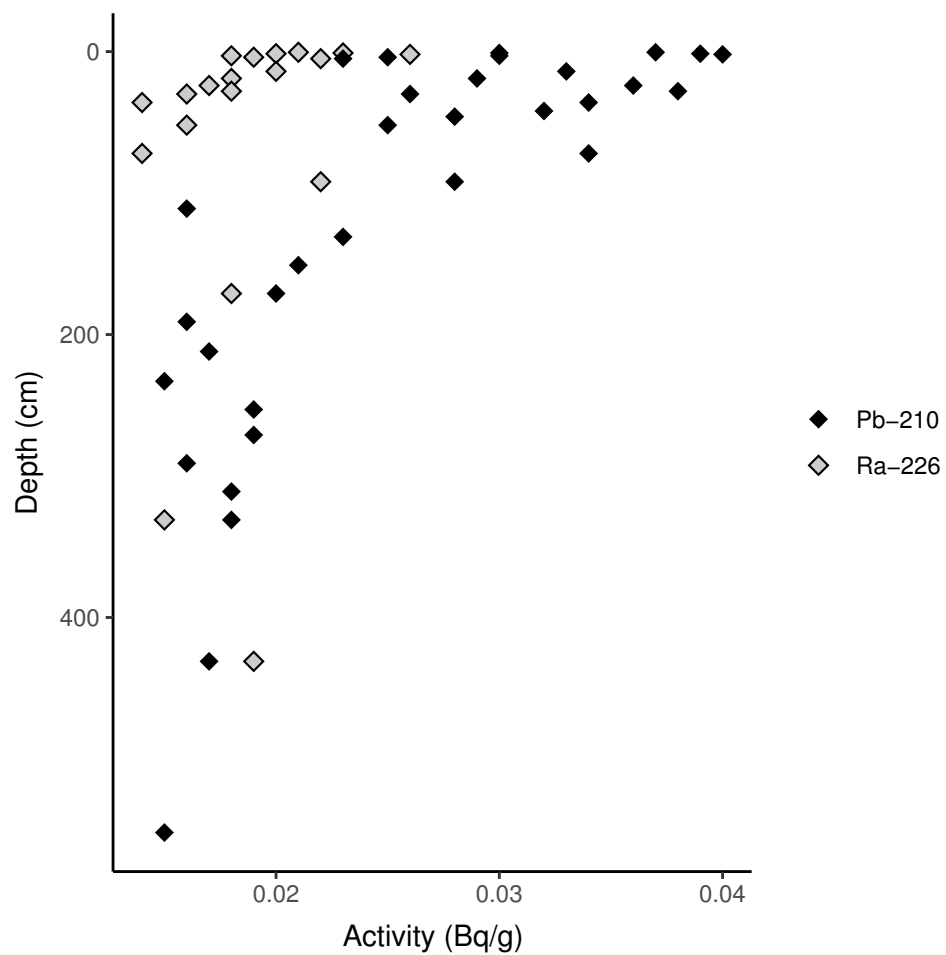


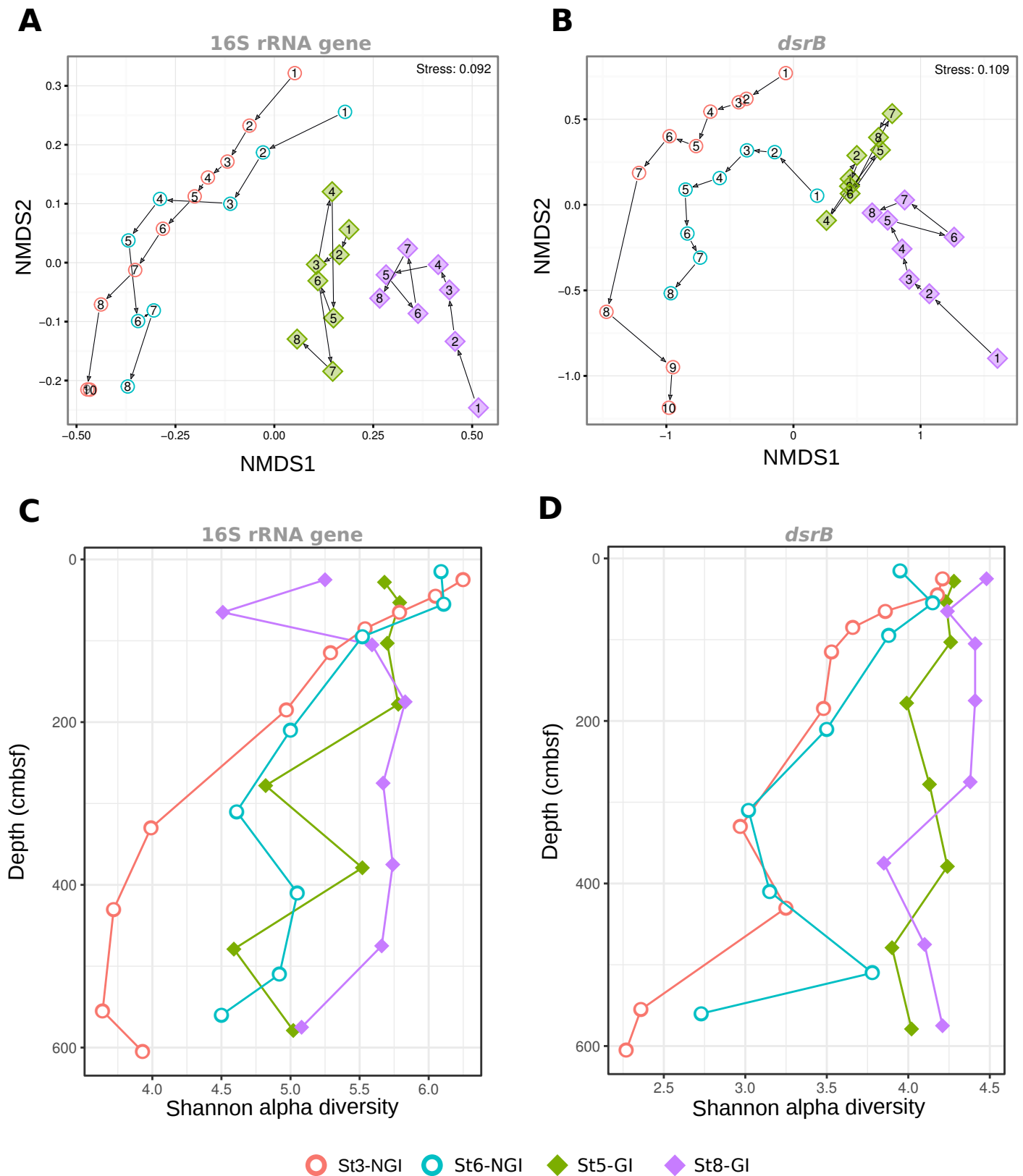
# **Glacial runoff promotes deep burial of sulfur cycling-associated microorganisms in marine sediments**

## ***Supplementary Material***

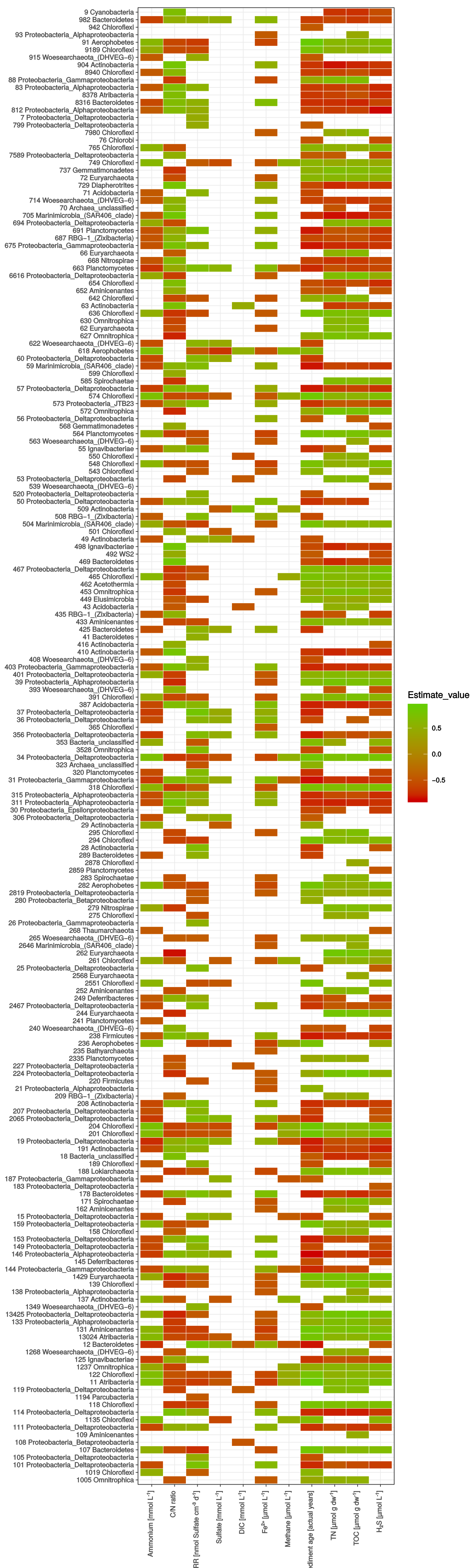
Claus Pelikan, Marion Jaussi, Kenneth Wasmund, Marit-Solveig Seidenkrantz, Christof Pearce, Zou Zou Anna Kuzyk, Craig W. Herbold, Hans Røy, Kasper Urup Kjeldsen, and Alexander Loy



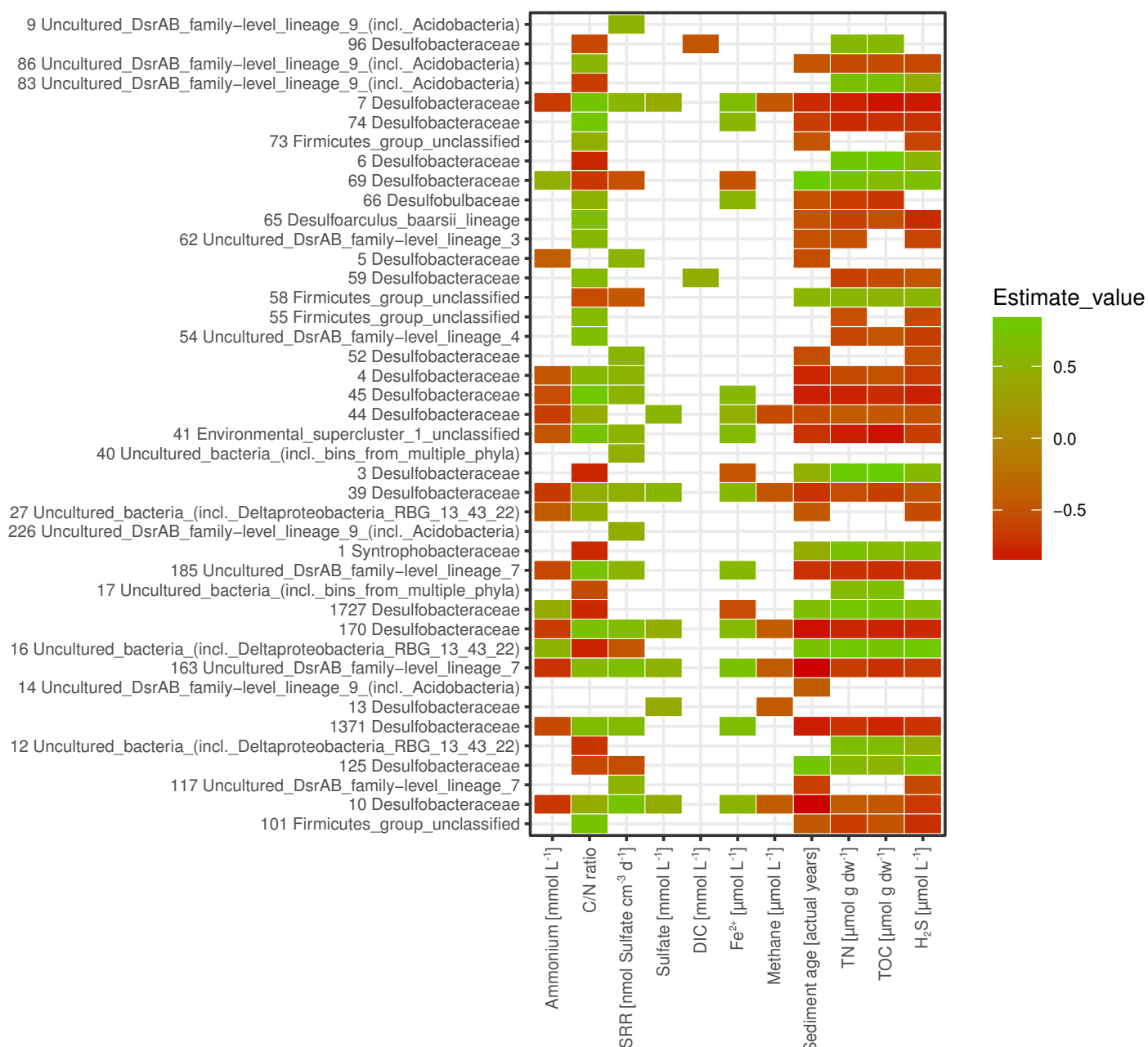
**Supplementary Figure S1. Activity of  $^{210}\text{Pb}$  (black) and  $^{226}\text{Ra}$  (grey) at station St8-GI.**



**Supplementary Figure S2. Microbial diversity across non-glacier-influenced (NGI) and glacier-influenced (GI) sediment cores and sediment depth.** A and B, Nonmetric multidimensional scaling ordinations (NMDS) of Bray-Curtis distances between 16S rRNA gene and *dsrB* communities. C and D, Shannon alpha diversity indices of 16S rRNA gene and *dsrB* communities. Colours indicate the sampling station. Numbers indicate the sediment depth according to Supplementary Table 2. St3-NGI and St6-NGI, Non-glacier-influenced stations 3 and 6. St5-GI and St8-GI, Glacier-influenced stations 5 and 8.



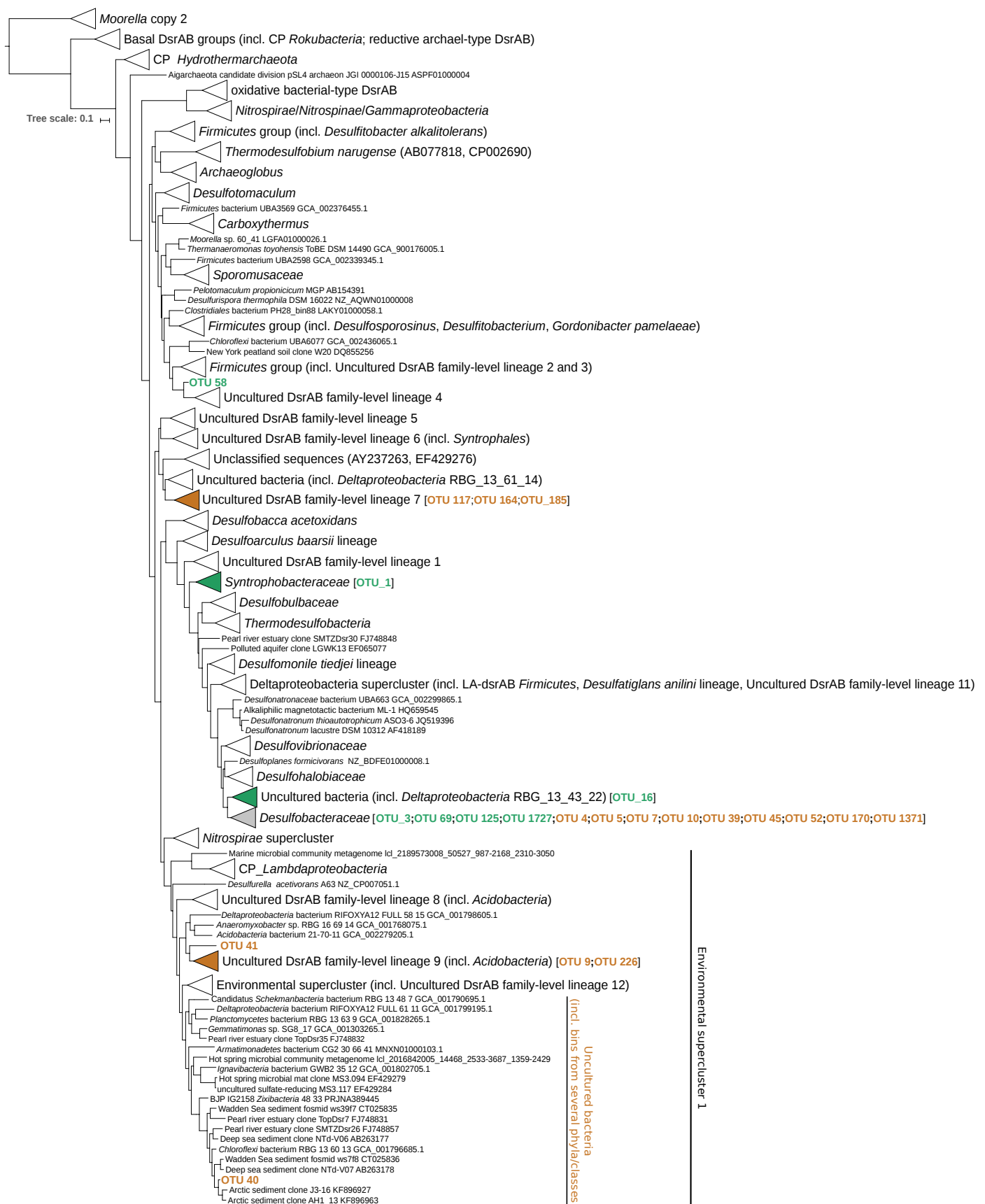
**Supplementary Figure S3. Spearman correlations between relative abundances of 16S rRNA-OTUs and physicochemical parameters.** Indicated are OTUs with significant ( $p \leq 0.05$ ) Spearman correlations to any of the tested parameters.



**Supplementary Figure S4. Spearman correlations between relative abundances of *dsrB*-OTUs and physicochemical parameters.** Indicated are OTUs with significant (p ≤ 0.05) Spearman correlations to any of the tested parameters.



**Supplementary Figure S5. Phylogenetic placement of 16S rRNA-OTUs.** Only OTUs with significant correlations to sulfate reduction rates or sediment age are shown. The reference tree was built from sequences that were closely related to 16S rRNA-OTUs. These were extracted from the SILVA database v.128 (Quast *et al.*, 2013), and used for tree construction with FastTree (Price *et al.*, 2010). 16S rRNA-OTUs were aligned to the SILVA database using the SINA aligner (Pruesse *et al.*, 2012), and placed into the reference tree using the EPA algorithm (Berger *et al.*, 2011) in RAXML (Stamatakis, 2014). The placement tree was visualized with iTOL (Letunic and Bork, 2007). OTUs that are colored in orange and green were significantly correlated to sulfate reduction rates (Figure 3) and sediment age (Figure 4), respectively. Clades that contained only OTUs with significant correlations to either sulfate reduction rates or sediment age are colored accordingly. Gray clades contain OTUs with correlations to sulfate reduction rates and OTUs with correlations to sediment age.



**Supplementary Figure S6. Phylogenetic placement of dsrB-OTUs.** Only OTUs with significant correlations to sulfate reduction rates or sediment age are shown. The reference tree was built from an extended reference alignment that contained DsrAB sequences from Müller et al., 2015 and novel DsrAB sequences from recent metagenomic surveys (Anantharaman et al., 2017; Parks et al., 2017). The reference tree was constructed with FastTree (Price et al., 2010). dsrB-OTUs were aligned to the extended reference alignment using MAFFT (Katoh et al., 2002), and added to the reference tree using the EPA algorithm (Berger et al., 2011) in RAxML (Stamatakis, 2014). The placement tree was visualized with iTOL (Letunic and Bork, 2007). OTUs that are colored in orange and green were significantly correlated to sulfate reduction rates (Figure 5) and sediment age (Figure 5), respectively. Clades that contained only OTUs with significant correlations to either sulfate reduction rates or sediment age are colored accordingly. Gray clades contain OTUs with correlations to sulfate reduction rates and OTUs with correlations to sediment age.

**Supplementary Table S1. Raw data of radiocarbon ages and output of age-depth model of stations St3-NGI, St6-NGI and St5-GI.**

Core	LabCode	Material	Depth (cm)	14C Age (yrs BP)	Error (yrs)	Calibrated age range (2 $\sigma$ )		Modelled age (cal yrs BP)	Error (yrs)
						From (cal yrs BP)	To (cal yrs BP)		
SA13-ST3-20G	AAR20067	Mollusk fragment	163.5	2362	25	2083	1896	2048	43
	AAR20068	Mollusk	346	6446	28	7038	6835	6940	49
	AAR20069	Mollusk	435	9033	39	9875	9560	9617	55
	AAR20070	Mollusk fragment	514	9896	39	11020	10700	10921	79
SA13-ST5-30G	AAR20955	Mollusk	25	652	25	386	250	265	42
	AAR20956	Mollusk	539	815	25	505	403	457	26
SA13-ST6-40G	AAR21687	Marine macroalgae	50	1372	24	986	840	919	32
	AAR21690	Marine macroalgae	173.5	2668	28	2452	2294	2362	43
	AAR21691	Marine macroalgae	196	3356	30	3326	3120	3218	54
	AAR21692	Marine macroalgae	260	4458	40	4787	4516	4647	75



**Supplementary Table S2. Sample numbering and sediment depth of the four sediment cores.**

<b>Coring station</b>	<b>Sample numbering</b>	<b>Sediment depth (cmbsf)</b>
Station 3	1	25
Station 3	2	45
Station 3	3	65
Station 3	4	85
Station 3	5	115
Station 3	6	185
Station 3	7	330
Station 3	8	430
Station 3	9	555
Station 3	10	605
Station 5	1	28
Station 5	2	53
Station 5	3	103
Station 5	4	178
Station 5	5	278
Station 5	6	379
Station 5	7	479
Station 5	8	579
Station 6	1	15
Station 6	2	55
Station 6	3	95
Station 6	4	210
Station 6	5	310
Station 6	6	410
Station 6	7	510
Station 6	8	560
Station 8	1	25
Station 8	2	65
Station 8	3	105
Station 8	4	175
Station 8	5	275
Station 8	6	375
Station 8	7	475
Station 8	8	575

**Supplementary Table S3. dsrB-targeted primer sets that were used in this study**

Name	Target	Sequence (5'-3')	Reference
DSR1762F1	dsrB	CAYACCCAGGGNTGG	Steger et al., 2011
DSR1762F4	dsrB	CACACDCAGGGNTGG	Steger et al., 2011
DSR1762F2	dsrB	CAYACBCAAGGNTGG	Steger et al., 2011
DSR1762F3	dsrB	CATACDCAGGGHTGG	Steger et al., 2011
DSR1762F5	dsrB	CATACHCAGGGNTAY	Steger et al., 2011
DSR1762F6	dsrB	CACACSCAGGGKTAY	Pelikan et al., 2016
DSR1762F7	dsrB	CACACBCAGGGMTAC	Pelikan et al., 2016
DSR1762F8	dsrB	CACACHCAGGGCTAT	Pelikan et al., 2016
DSR1762F9	dsrB	CACACCCAGGGWTTT	Pelikan et al., 2016
DSR1762F10	dsrB	CAYACACAAGGATGG	Pelikan et al., 2016
DSR2107R1	dsrB	CAGTTDCCRCARTACAT	Pelikan et al., 2016
DSR2107R2	dsrB	CAGTTACRCAGAACAT	Pelikan et al., 2016
DSR2107R3	dsrB	CAGTTGSCGCAGAACAT	Pelikan et al., 2016
DSR2107R4	dsrB	CAGTTYCCGCAGAACAT	Pelikan et al., 2016
DSR2107R5	dsrB	CAGTTKCCACAGAACAT	Pelikan et al., 2016
DSR2107R6	dsrB	CAATTWCCACAGAACAT	Pelikan et al., 2016
DSR2107R7	dsrB	CAGTTGCCGCAAAACAT	Pelikan et al., 2016
DSR2107R8	dsrB	CAGGCACCGCAGAACAT	Pelikan et al., 2016
DSR2107R9	dsrB	CAGTTAGCGCACATCAT	Pelikan et al., 2016
DSR2107R10	dsrB	CAATTGGCACAGTACAT	Pelikan et al., 2016
DSR2107R11	dsrB	CAATTTCCGCAGTACAT	Pelikan et al., 2016
DSR2107R12	dsrB	CAATTGCCGCAGAACAT	Pelikan et al., 2016
DSR2107R13	dsrB	CAGTTGGCACATAACAT	Pelikan et al., 2016

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