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*Supplement of*

## **Microbial assemblages on a cold-water coral mound at the SE Rockall Bank (NE Atlantic): interactions with hydrography and topography**

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1 **Supplementary information**

2 **S.I. Table 1.** Taxons that are indicators for five groups (biotopes) of samples taken at Haas  
 3 Mound. Only those with the highest statistics values are listed. The number of strong  
 4 indicators is the number of indicators with  $A > 0,85$  over the total number of significant  
 5 ( $p < 0,0001$ ) indicators found for that group. w\_CTD = water sampled at 400 m and 5+10  
 6 mab; Near-bottom water (w\_bc). A = given the indicator is present, the probability that the  
 7 sample belongs to the sample group. B = taking one sample from the group, the probability  
 8 that it contains the indicator.

Sample group (#strong indicators)	Indicator	A	B	stat	p.value	Reads avg % in sample group
w_CTD (4/38)	uncl. SAR11 clade Deep 1	0,8833	1,0000	0,940	0,0001	2,61
	Rhodospirillaceae	0,8796	1,0000	0,938	0,0001	2,20
	AEGEAN-169 marine group					
	uncl. Verrucomicrobia	0,8751	1,0000	0,935	0,0001	0,45
	Arctic97B-4 marine group					
	uncl. Thermoplasmatales	0,8721	1,0000	0,934	0,0001	1,00
	Marine Group III					
	uncl. Oceanospirillales	0,8361	1,0000	0,914	0,0001	2,85
	ZD0405					
w_bc (8/13)	uncl. Dehalococcoidia	0,9437	1,0000	0,971	0,0001	0,36
	vadinBA26					
	uncultured	0,9460	0,8571	0,900	0,0001	0,05
	Oceanospirillaceae					
	uncl. Dehalococcoidia GIF3	1,0000	0,7143	0,845	0,0001	0,27
	uncl. BHI80-139	0,8931	0,7857	0,838	0,0001	0,07
	uncl. Dehalococcoidia	1,0000	0,6429	0,802	0,0001	0,09

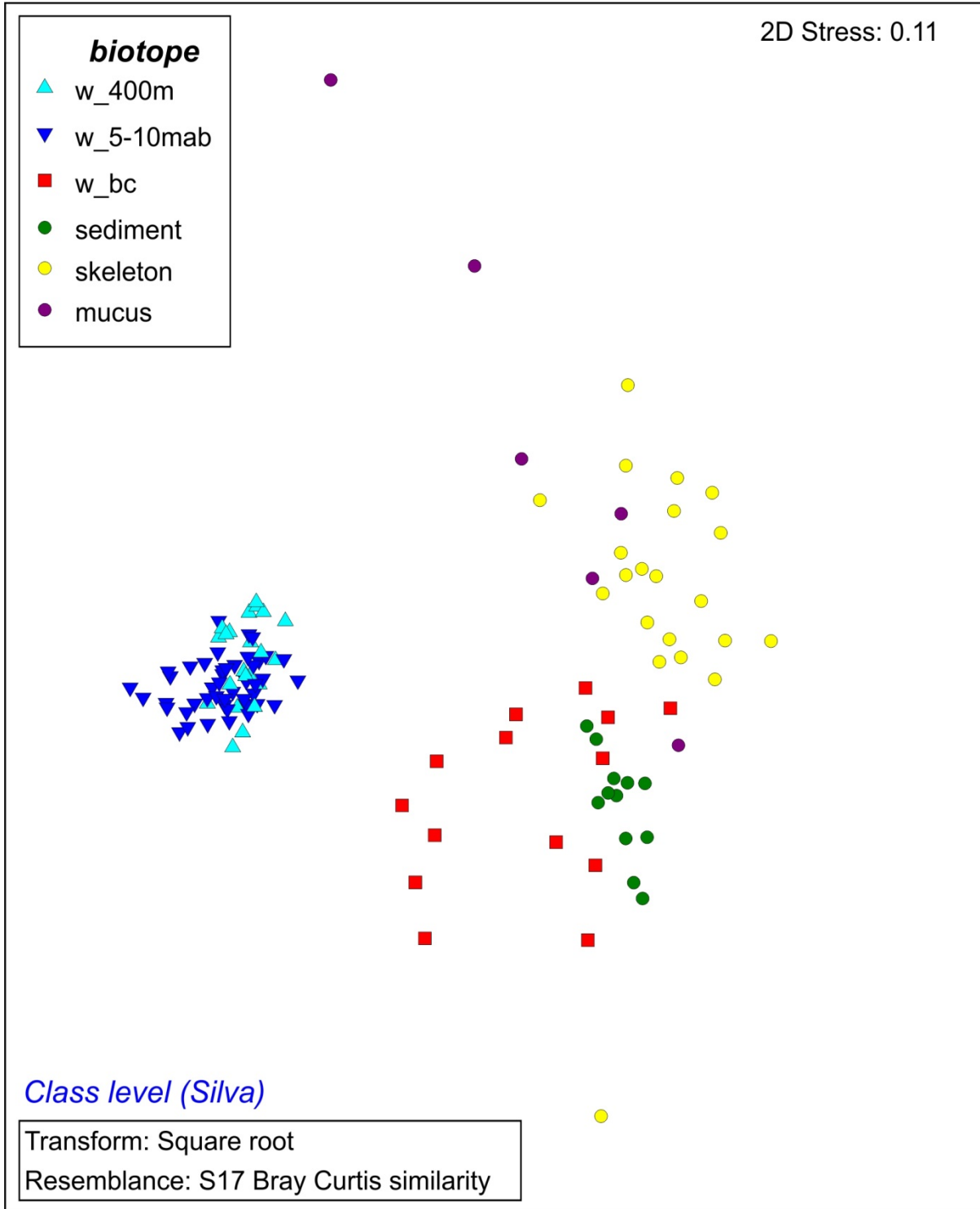
	Sh765B-AG-111					
	Sphingobacteriales KD1-131	0,8881	0,7143	0,796	0,0001	0,09
	Thaumarchaeota Group C3	1,0000	0,5714	0,756	0,0001	0,03
	Brocadiaceae W4	0,9982	0,5000	0,706	0,0001	0,83
sediment (0/3)	Phycisphaerae C86	0,6982	1,0000	0,836	0,0001	0,25
	uncl. Chloroflexi JG30-KF-CM66	0,5118	1,0000	0,715	0,0001	0,56
	uncl. Rhodospirillales AT-s3-44	0,3669	1,0000	0,606	0,0001	0,32
skeleton (0/12)	uncul. Caldilineaceae	0,7979	1,0000	0,893	0,0001	0,71
	Granulosicoccus	0,7513	1,0000	0,867	0,0001	1,87
	Profundibacterium	0,7602	0,9524	0,851	0,0001	0,22
mucus (12/12)	uncl. Oceanospirillales G02-CR02-full	0,9982	1,0000	0,999	0,0001	0,36
	Acinetobacter	0,9872	1,0000	0,994	0,0001	9,11
	uncult. Helicobacteraceae	0,9699	1,0000	0,985	0,0001	0,48
	uncl. Oceanospirillales BPS-CK174	0,9651	1,0000	0,982	0,0001	0,29
	Alteromonadaceae BD1-7 clade	0,9636	1,0000	0,982	0,0001	22,00
	Corynebacterium	0,9259	1,0000	0,962	0,0001	0,11
	Staphylococcus	0,9169	1,0000	0,958	0,0001	0,06
	Sphingomonas	0,9000	1,0000	0,949	0,0001	0,15

	Enhydrobacter	0,9963	0,8333	0,911	0,0001	0,17
	Methylobacterium	0,9705	0,8333	0,899	0,0001	0,24
	Tumebacillus	0,9106	0,8333	0,871	0,0001	0,13
	Micrococcus	0,9773	0,5000	0,699	0,0001	0,06

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11 **S.I. Figure 1.** MDS plot of microbial community on class level of 125 samples shows  
12 clustering according to sample category: overlaying water (400m and 5+10 mab), near-bottom  
13 water (w\_bc), sediment, skeleton and mucus.

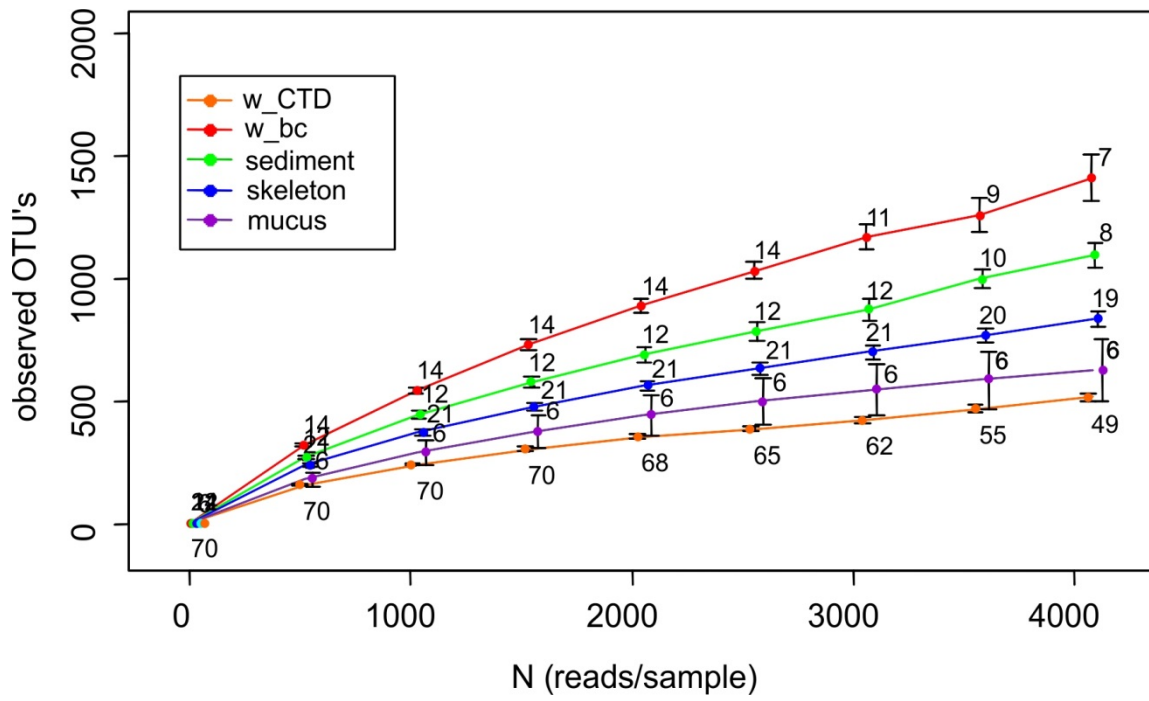


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16 **S.I. Figure 2.** Rarefaction curves of OTU's plotted against reads per sample.

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