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Supplement of

Carbohydrates, enzyme activities, and microbial communities across depth gradients in the western North Atlantic Ocean

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Table S1. Station locations

Location	Stn. 17	Stn. 18	Stn. 19	Stn. 20
	34.514 N -75.670 E	37.503 N -72.022 E	42.836 N -53.394 E	34.637 N -53.923 E

Table S2. Environmental parameters of sampling sites.

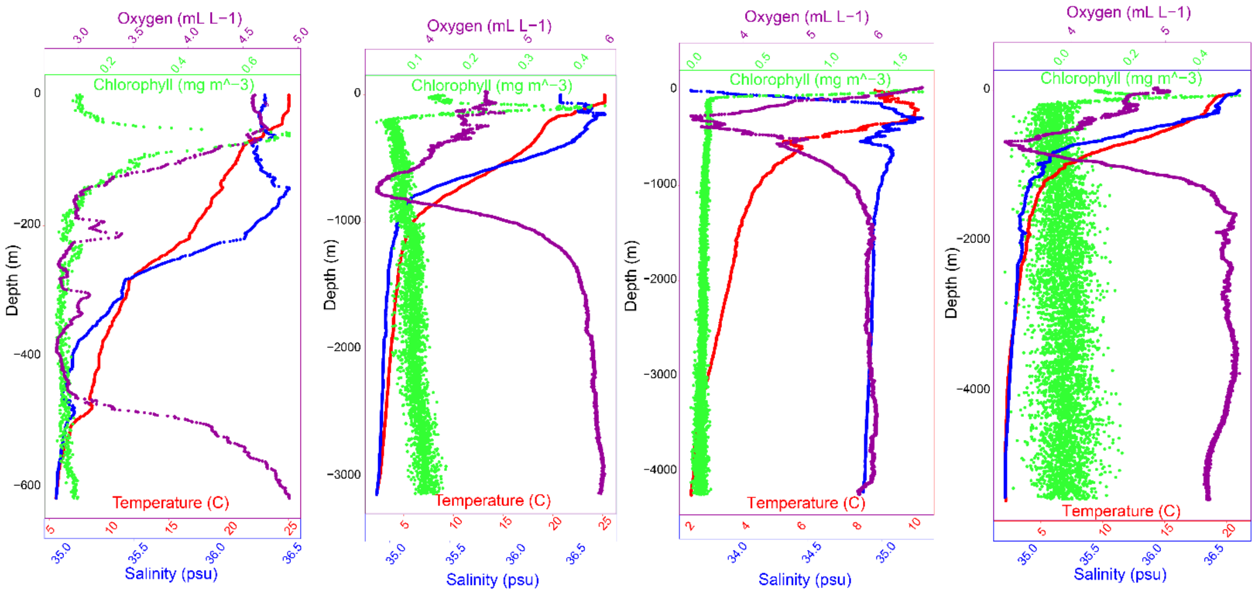
Stn	Depth (m)	T (°C)	S (psu)	Oxygen (ml L^{-1})	Chlorophyll-*a* (mg m^{-3})	POC (mg L^{-1})	Cell Counts (cells L^{-1})	Leucine Incorporation (pmol L^{-1} hr^{-1})
17	2	25.0	36.39	4.61	0.118	0.0353	6.84E08	3.9
17	64	22.9	36.45	4.54	0.690	0.0511	4.28E08	3
17	625	5.6	35.04	4.92	0.111	0.0187	8.97E07	0
18	2	25.2	36.42	4.48	0.147	0.0203	4.00E08	6
18	104	23.4	36.67	4.53	0.401	0.0204	3.55E08	5
18	300	18.8	36.61	4.30	0.070	0.00096	1.43E08	0.5
18	800	9.2	35.21	3.18	0.079	0.00326	3.83E07	0.2
18	1500	4.4	34.99	5.63	0.088	0.00573	2.60E07	0.1
18	3190	2.3	34.89	5.89	0.116	0.00859	2.42E07	0.1
19	2	8.8	33.72	6.63	1.49	0.160	9.71E08	88.1
19	33	9.3	33.94	6.45	1.32	0.136	1.62E09	60.2
19	300	9.9	35.21	3.36	0.110	0.0106	1.44E08	1.2
19	850	5.1	35.03	5.32	0.102	0.00599	2.38E07	0.2
19	1500	3.9	34.94	5.89	0.093	0.00582	1.62E07	0.3
19	3000	2.8	34.92	5.90	0.044	0	2.18E07	0.1
19	4325	2.2	34.88	5.73	0.082	0.00852	2.08E07	0.2
20	2	21.0	36.73	4.92	0.110	0.0253	3.66E08	191
20	64	20.1	36.68	5.03	0.212	0.0253	4.29E08	99.7
20	300	18.3	36.56	4.69	0.019	0.00306	2.45E08	23.5
20	800	10.1	35.33	3.46	0.00	0.00900	5.35E07	0.5
20	1500	4.6	35.01	5.54	0.00	0.00147	2.23E07	5.5
20	3000	3.0	34.93	5.66	0.058	0.00057	1.12E07	0.4
20	5580	2.2	34.85	5.46	0.0087	0.00242	9.67E06	1.2

Table S3. Volumes of water filtered (L) for POM analyses.

Depth	Stn. 17	Stn. 18	Stn. 19	Stn. 20
Surface	6.0	9.5	5.0	13.5
DCM	5.5	8.5	5.5	12.5
300 m	-	13.5	15.0	14.5
Meso	9.0	11.0	14.5	12.5
1500 m	-	14.0	14.0	15.0
3000 m	-	-	13.7	13.5
Bottom	-	13.5	12.5	13.0

Table S4. Summed signal for polysaccharide epitopes by station and depth, including the specific antibodies used to determine relative abundance. Although samples from all depths (Suppl. Table 2) were included in the analyses only depths at which a positive signal was detected are listed here (surface, DCM, bottom). Note that signal intensity can be compared for single epitopes detected at multiple stations, but signal intensity cannot be compared across epitopes, which have different relative affinities for their targets (see Methods).

	Epitope	Fucoidan (I)	Fucoidan (II)	Rhamnogalacturonan I backbone	Cellulose (1,4-β-D-glucan	1,3-β-D-glucan	1,4-β-D-(galacto)(gluco)mannan	Xylosul residues	Alginate – mannuronate-guluronate
	Antibody	BAM1	BAM2	INRA-RU1	CBM3a	BS-400-2	LM21	LM23	BAM7
Station	**Depth**	**Signal**							
17	Surface	0	14.5	0	0	30.25	0	0	19.75
	DCM	0	0	0	0	25.75	0	0	9.75
	Bottom	0	0	0	0	0	7.5	0	0
18	Surface	0	0	0	0	20	0	0	16.25
	DCM	0	0	0	0	6	0	0	10
	Bottom	0	0	0	0	0	0	0	0
19	Surface	24.5	0	12.25	8.5	28.5	6	4	29.75
	DCM	23.75	0	6.5	0	30	6	4.5	35.5
	Bottom	0	0	0	0	0	0	0	0
20	Surface	62.75	12.5	0	0	28.25	4.75	0	33.75
	DCM	0	0	0	0	33	0	0	9.5
	Bottom	0	0	0	0	0	0	0	0



Station 17 Station 18 Station 19 Station 20

Figure S1. Temperature, salinity, dissolved oxygen, and chlorophyll-*a* profiles, measured from the conductivity, temperature, and depth (CTD) profile for each station.

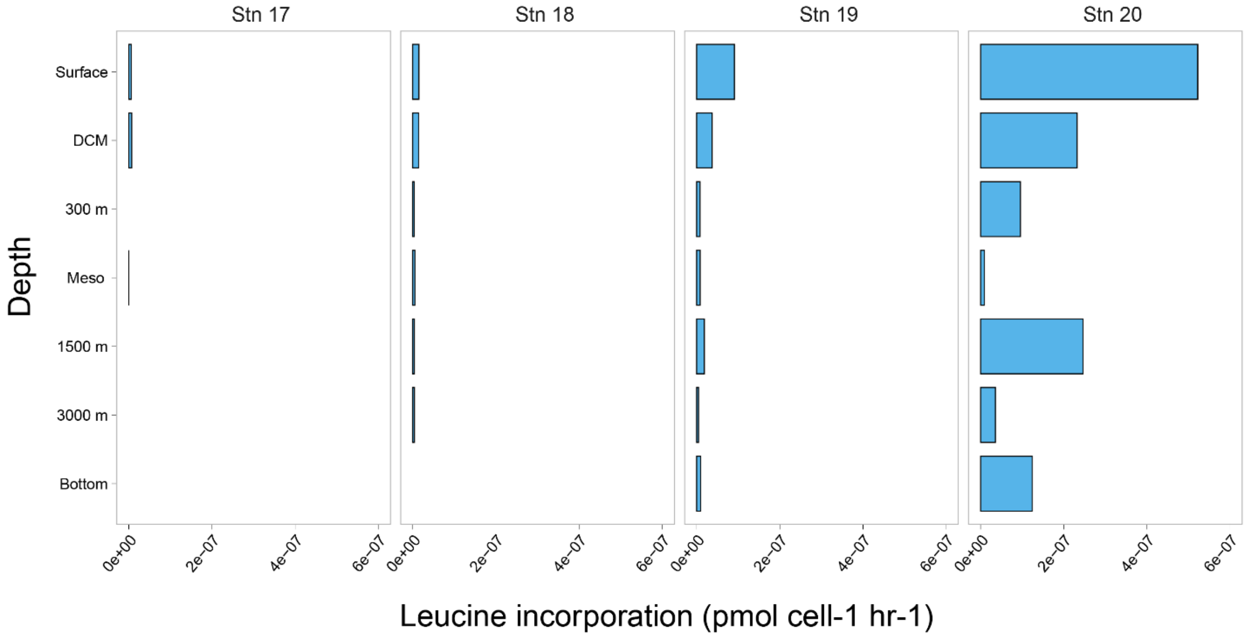


Figure S2. Bacterial protein production per cell, as measured by incorporation of tritiated leucine (^{3}H-Leu).

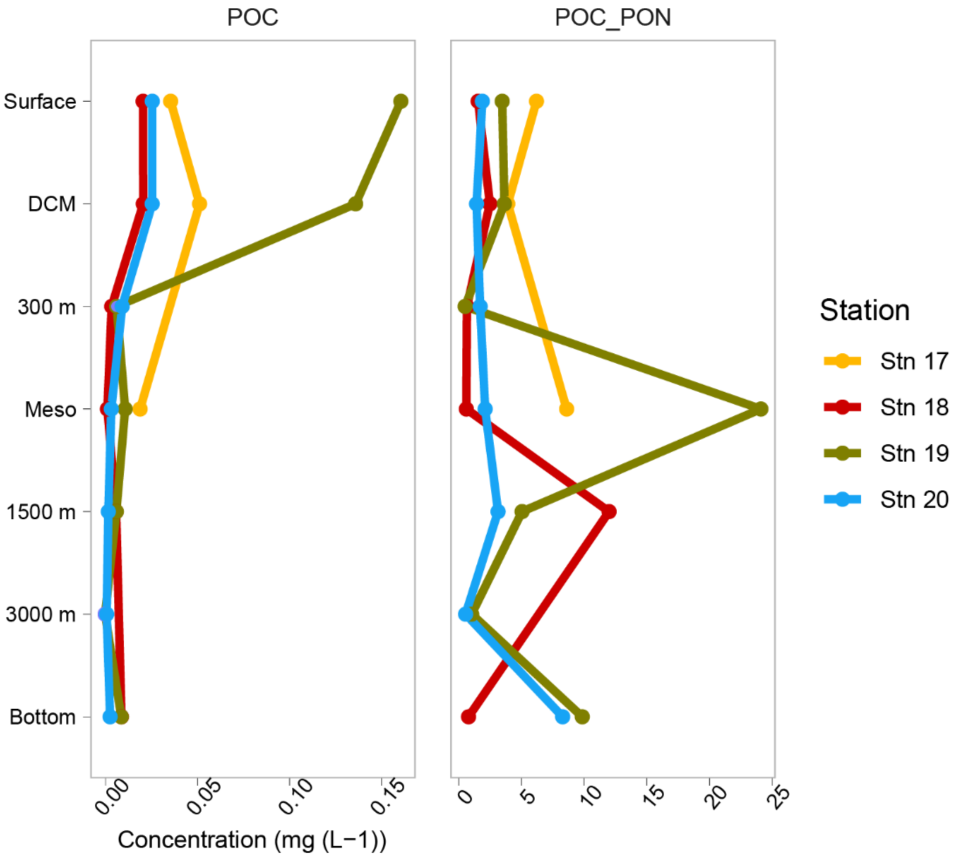


Figure S3. Particulate organic carbon and the POC:PON ratio for each station and depth. Stations are distinguished by color.

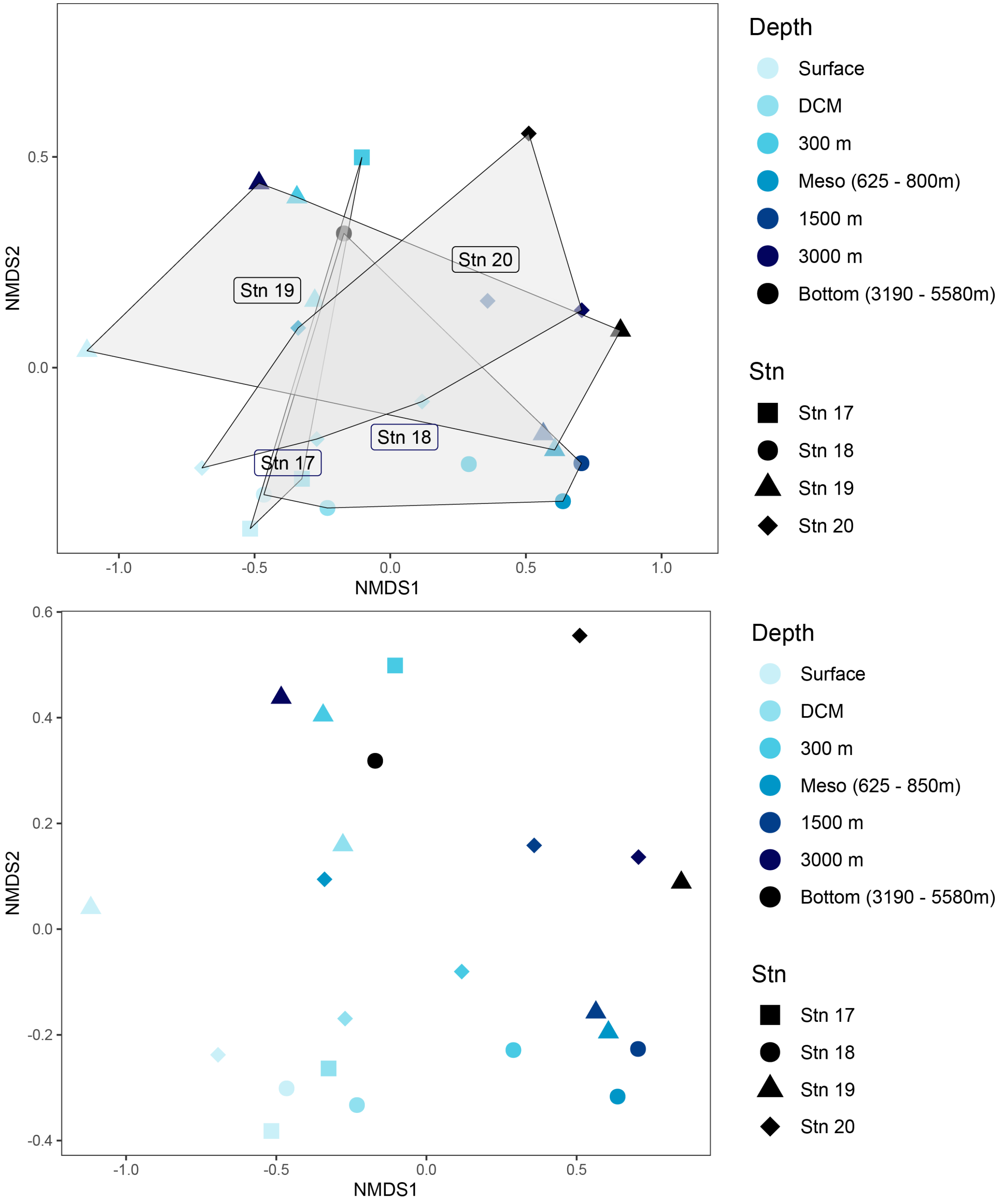


Fig. S4. Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis dissimilarity shows bacterial communities clustered by station (A) as well as the same data without gray hulls (B).

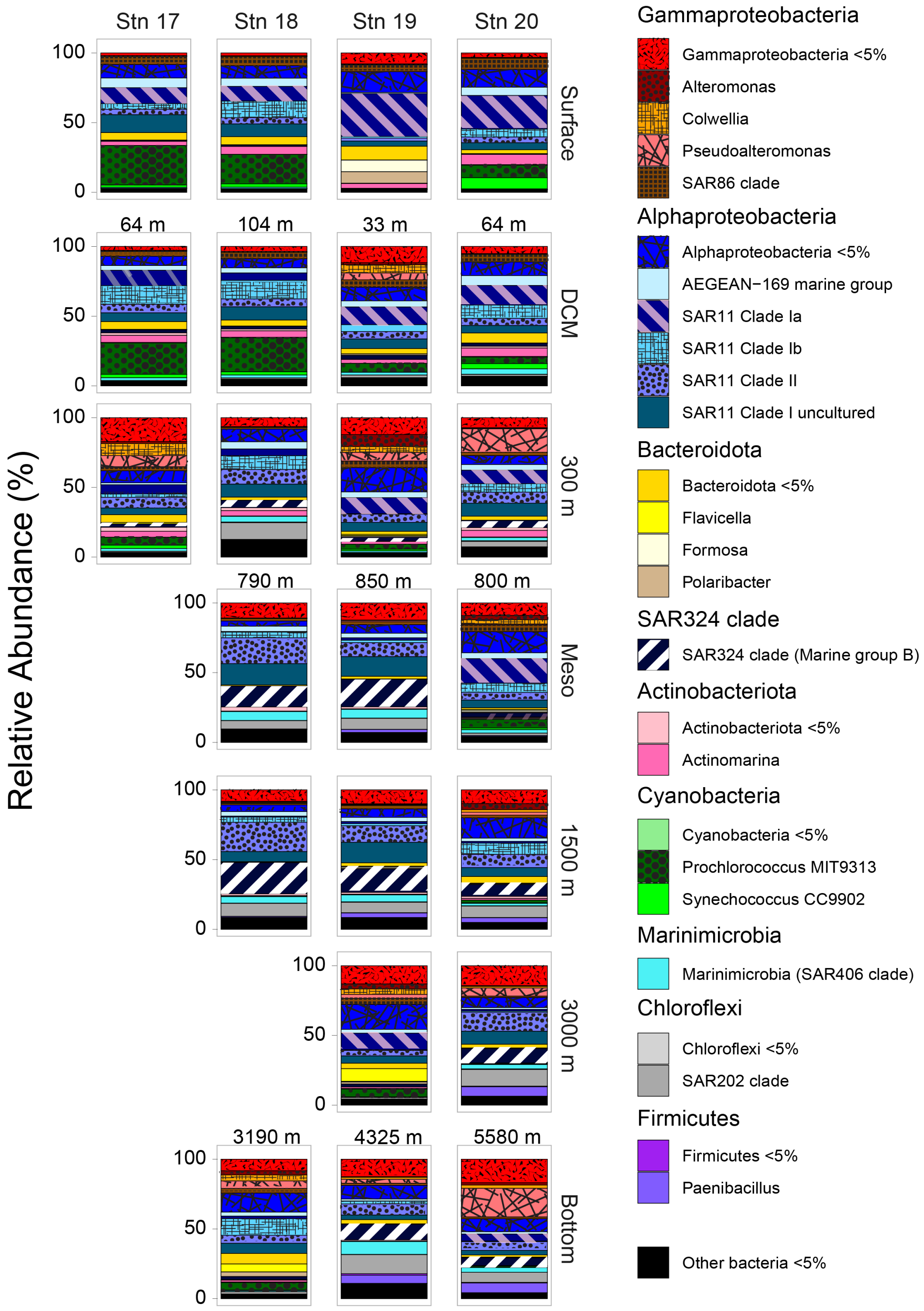


Figure S5. Bacterial community composition, expressed as relative abundance. Operational taxonomic units are grouped by similar colors; select taxa are differentiated by pattern for better visualization.

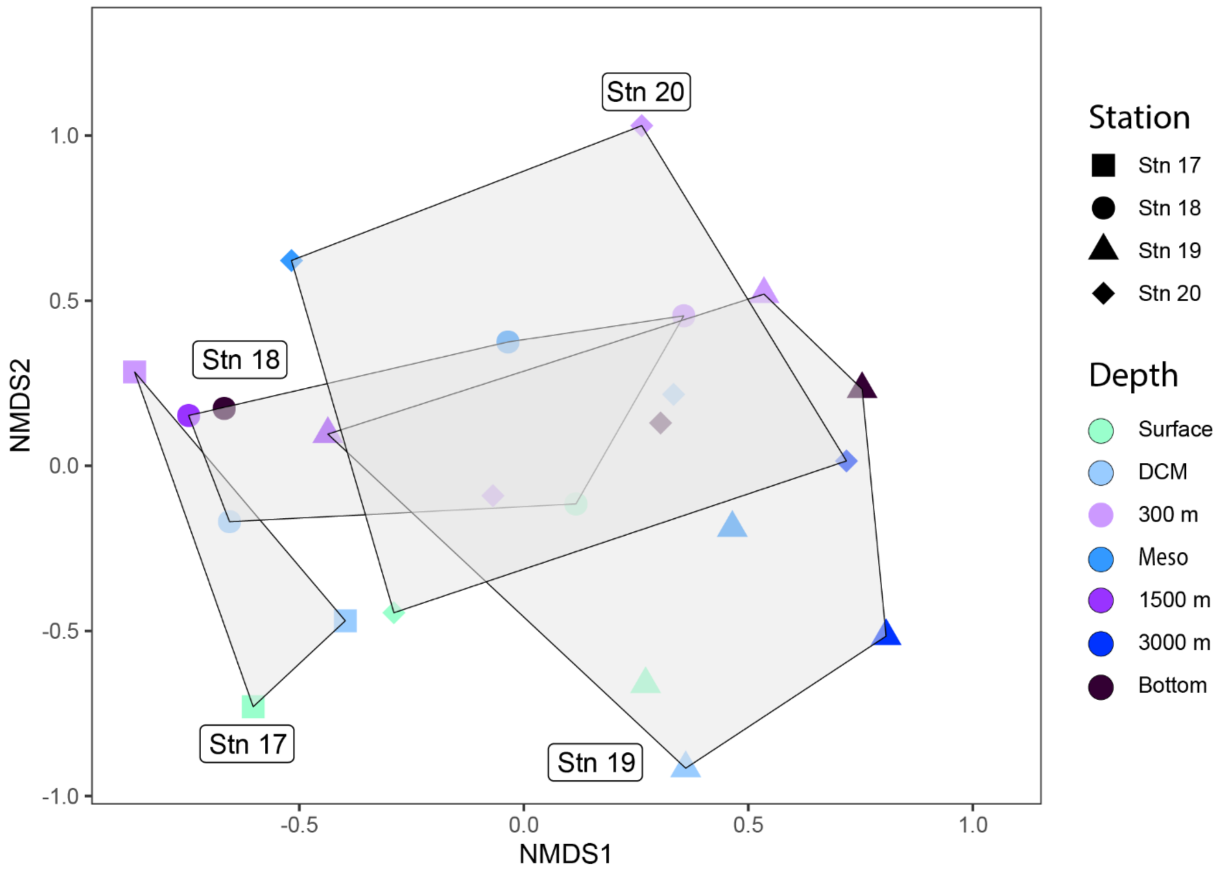


Figure S6. Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis dissimilarity shows glucosidase and peptidase activities clustered by station.

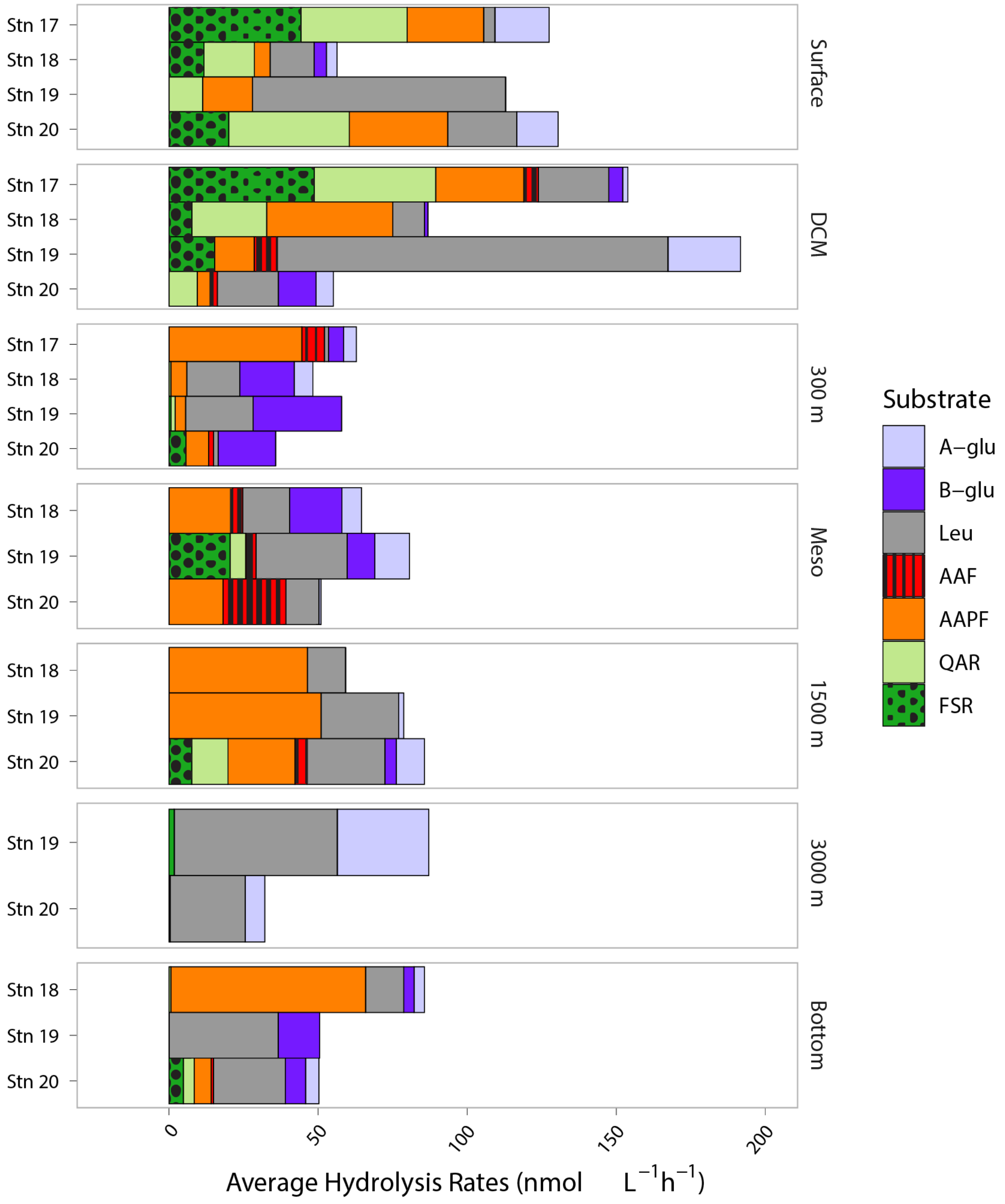


Figure S7. Summed glucosidase and peptidase activities for each station and depth. Bars represent the average hydrolysis rate calculated over 12 hours. A-glu: alpha-glucosidase; B-glu: beta-glucosidase; Leu: leucine aminopeptidase; AAF: alanine-alanine-phenylalanine; AAPF: alanine-alanine-proline-phenylalanine; QAR: glutamine-alanine-arginine; FSR: phenylalanine-serine-arginine.

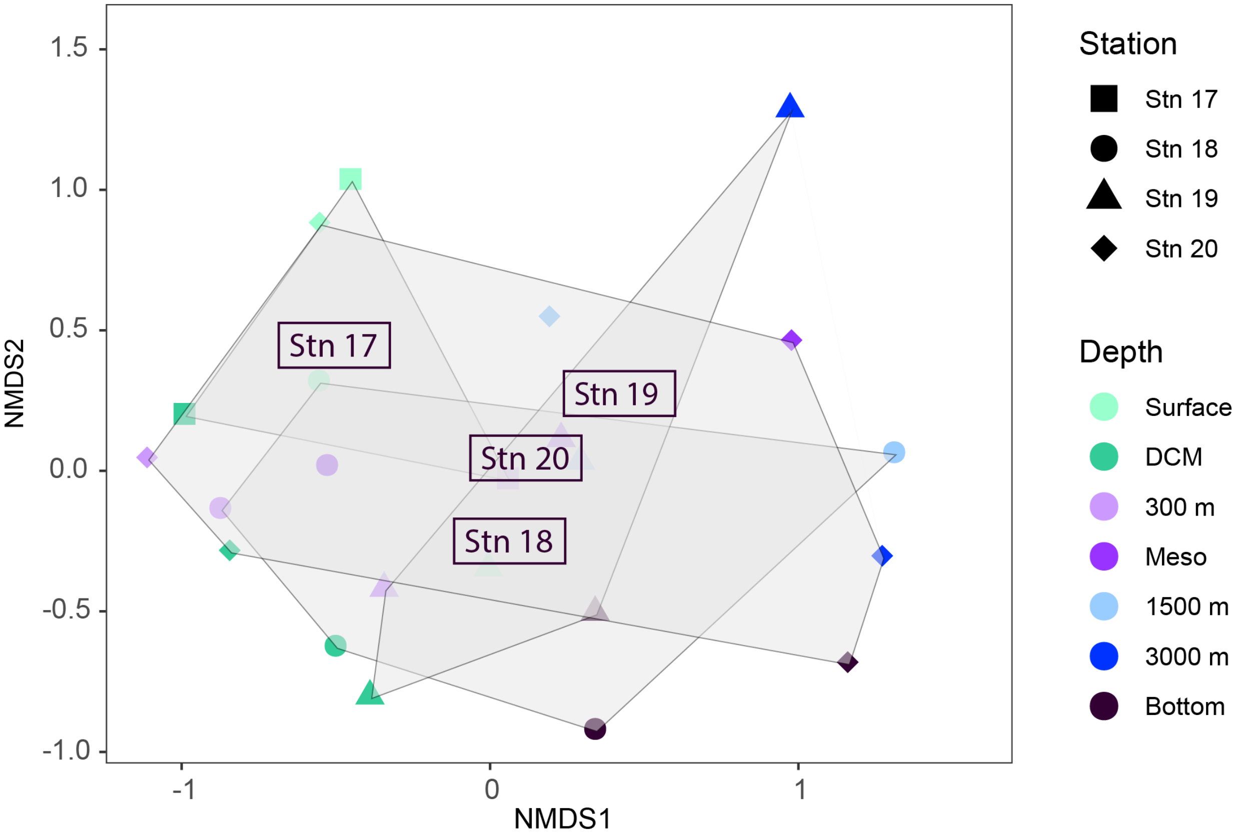


Figure S8. Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis dissimilarity shows polysaccharide hydrolase activities clustered by station.

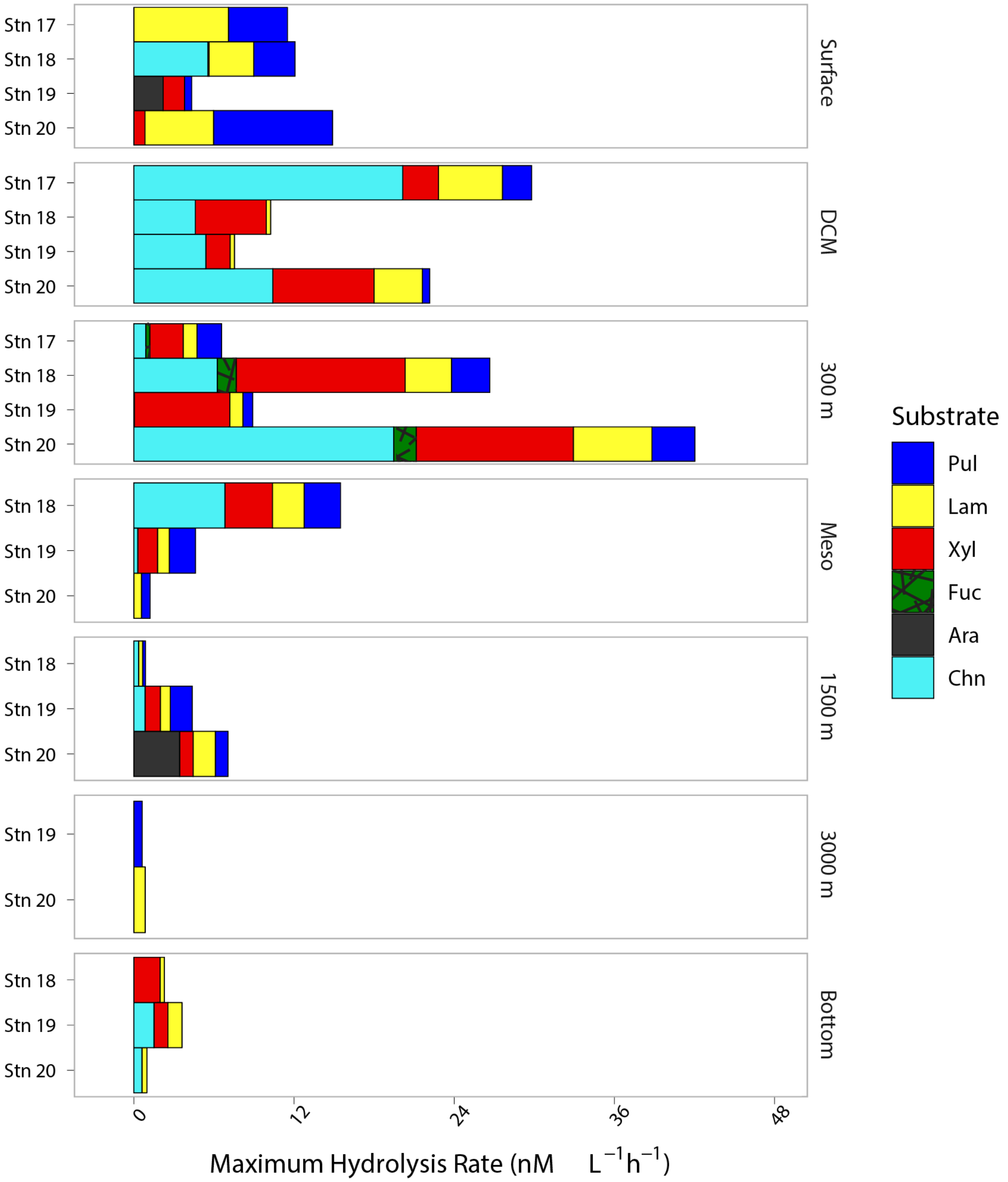


Figure S9. Summed polysaccharide hydrolase activities for each station and depth. Bars represent the maximum hydrolysis rate calculated. Pul = pullulan; Lam = laminarin; Xyl = xylan; Fuc = fucoidan from *Fucus vesiculosis*; Ara = arabinogalactan; Chn = chondroitin sulfate.

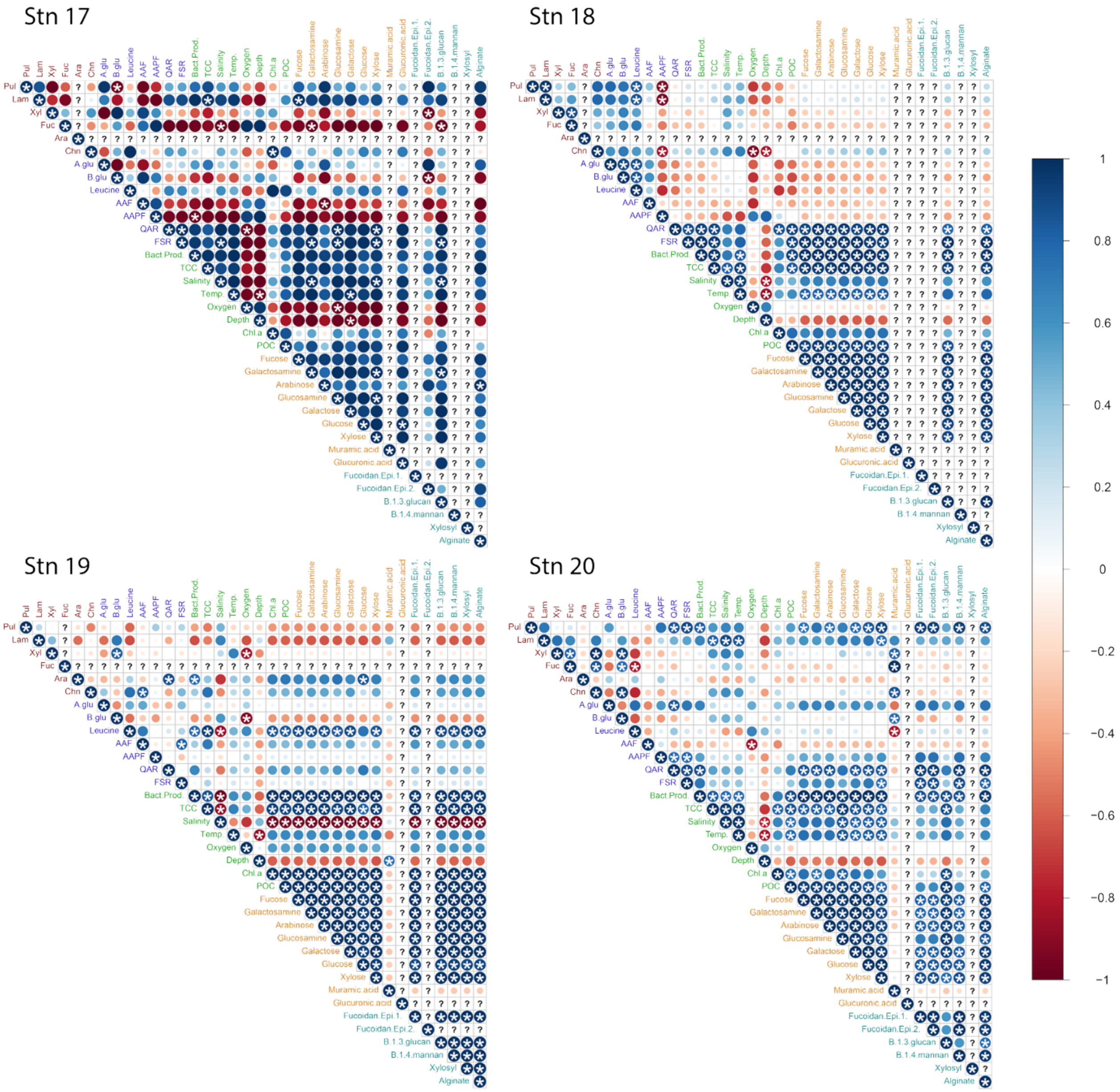


Figure S10. Correlation plot displaying Pearson's correlations between environmental parameters, enzymatic activities, and carbohydrate constituents at all stations. Blue denotes positive correlations while red denotes negative correlations. The shade and size of the circle demonstrates the intensity of correlation between environmental parameters and enzymatic activities. * denotes statistical significance ($p < 0.05$).