

1 **Supplemental Table 1.** Environmental parameters of sampling sites.

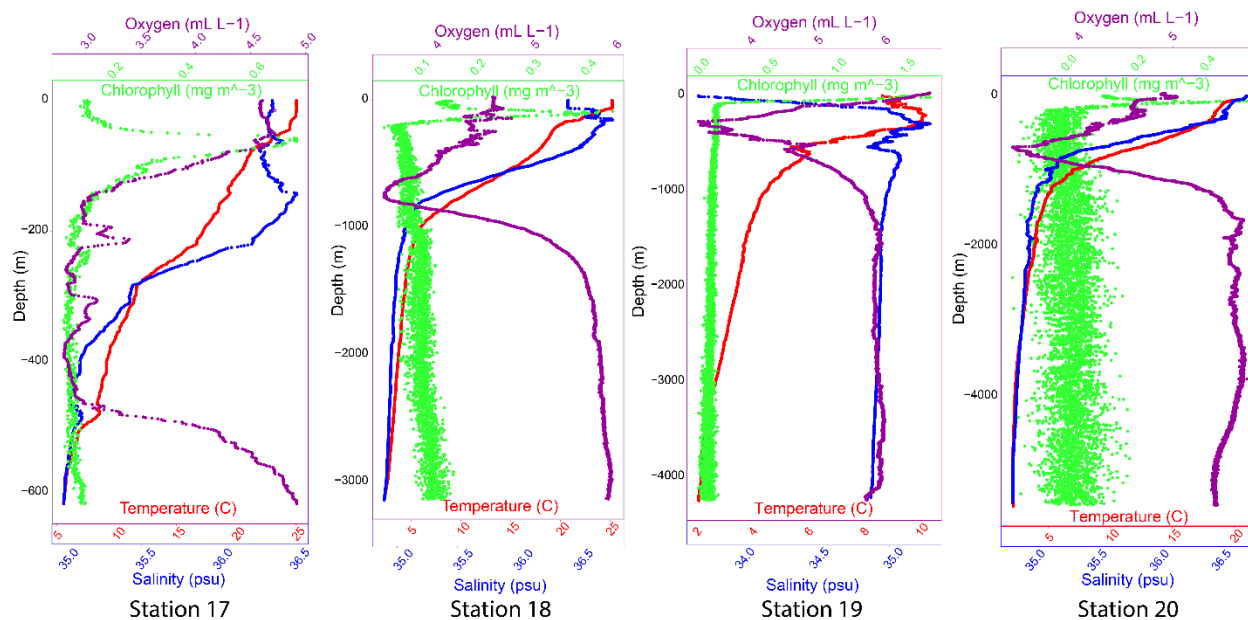
Stn	Depth (m)	T (°C)	S (psu)	Oxygen (ml/L)	Chlorophyll- <i>a</i> (mg/m ³)	POC (mg/L)	Cell Counts (cells/L)
17	2	25.0	36.39	4.61	0.118	0.0353	6.84E08
17	64	22.9	36.45	4.54	0.690	0.0511	4.28E08
17	625	5.6	35.04	4.92	0.111	0.0187	8.97E07
18	2	25.2	36.42	4.48	0.147	0.0203	4.00E08
18	104	23.4	36.67	4.53	0.401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

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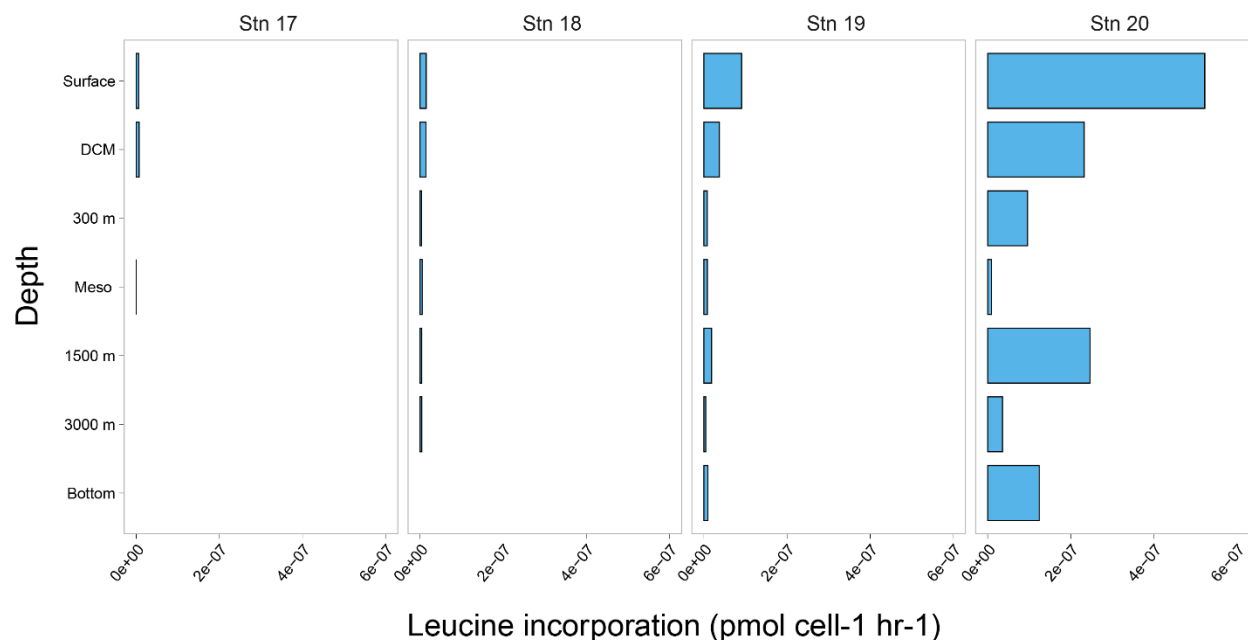
3 **Supplemental Table 2.** Volume of water filtered (L) for POM analyses.

Depths	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

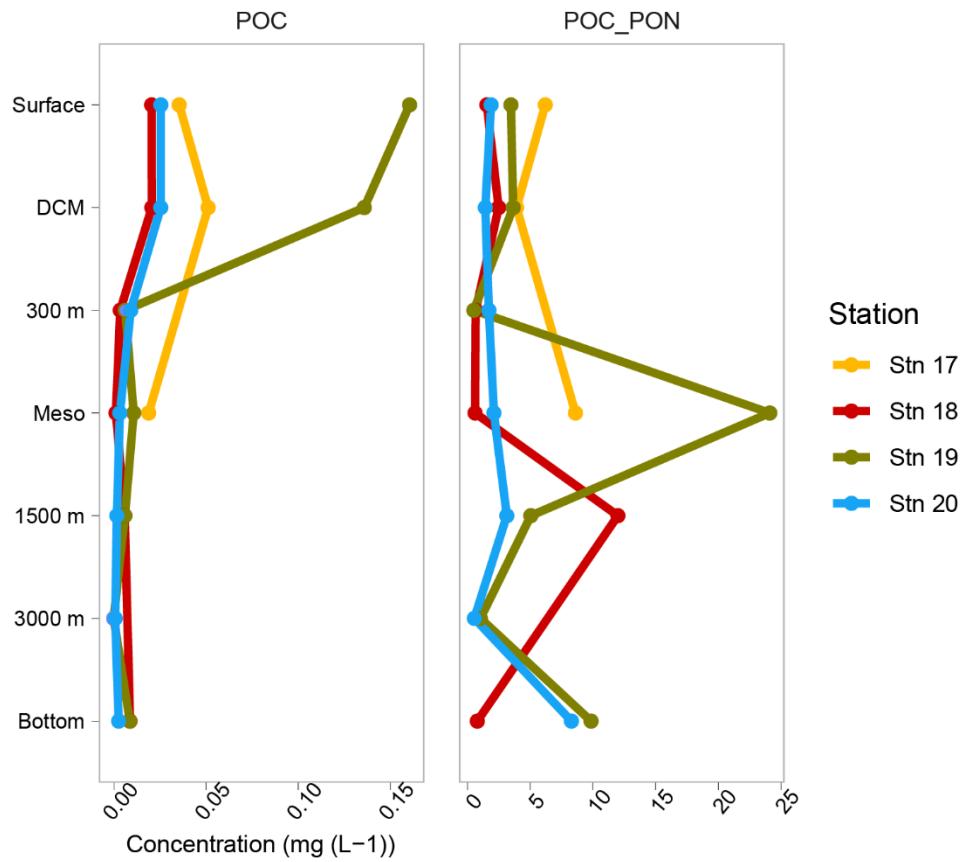
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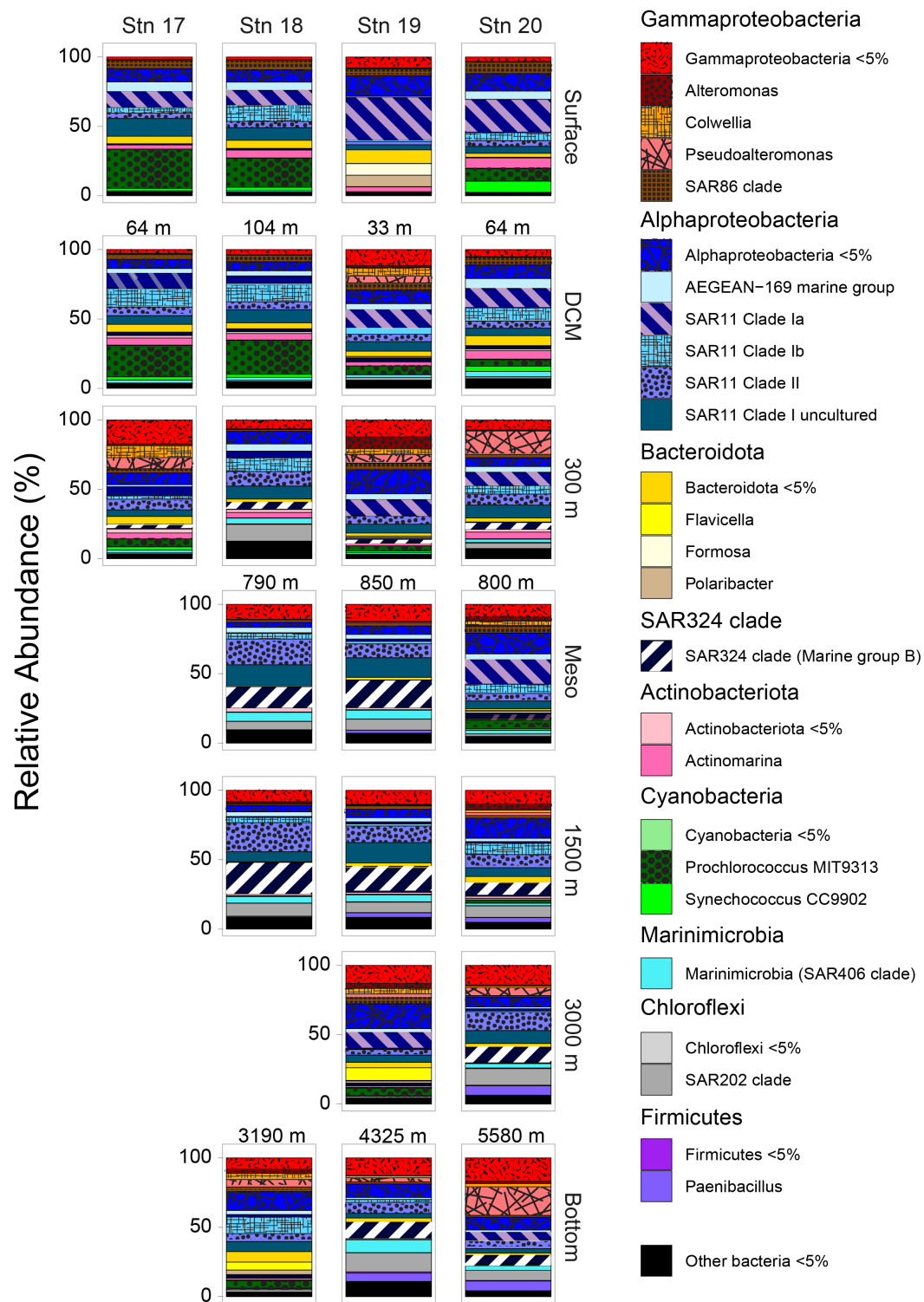
Supplemental Figure 1. Temperature, salinity, dissolved oxygen, and chlorophyll-*a* profiles, measured from the conductivity, temperature, and depth (CTD) profile for each station.



Supplemental Figure 2. Bacterial protein production per cell, as measured by incorporation of tritiated leucine (^3H -Leu).

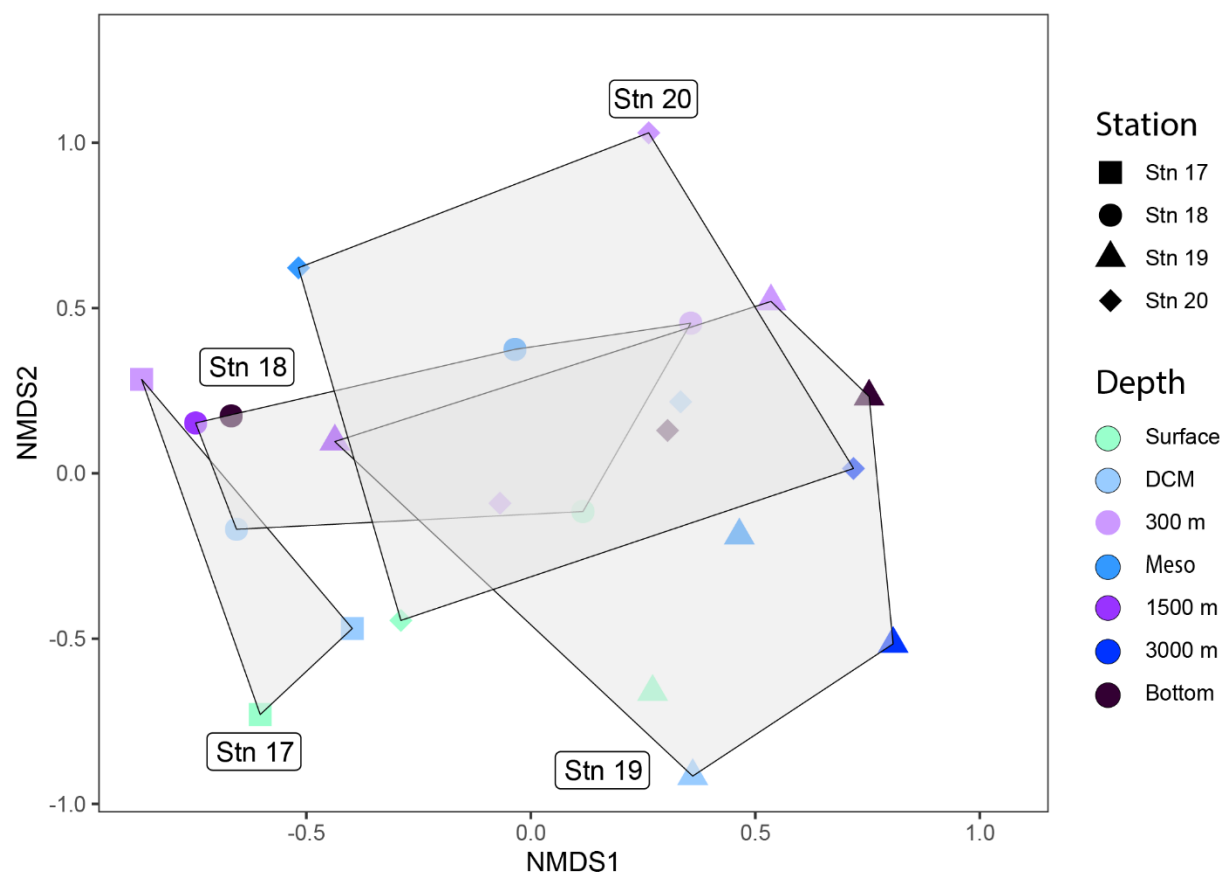


Supplemental Figure 3. Particulate organic carbon and the POC:PON ratio for each station and depth. Stations are separated by color.



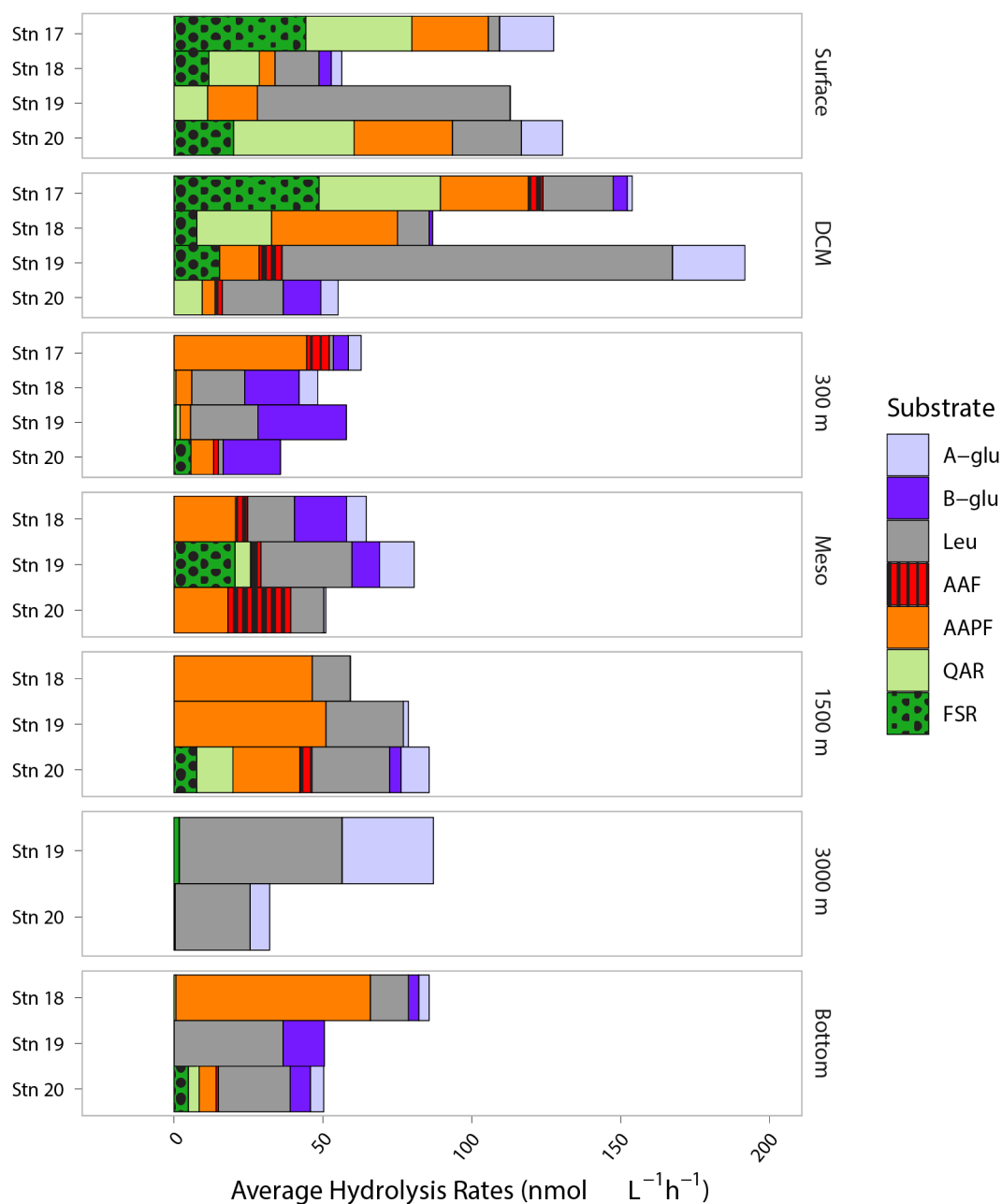
Supplemental Figure 4. Bacterial community composition, expressed as relative abundance. Operational taxonomic units are grouped by similar colors; select taxa are differentiated by pattern for better visualization.

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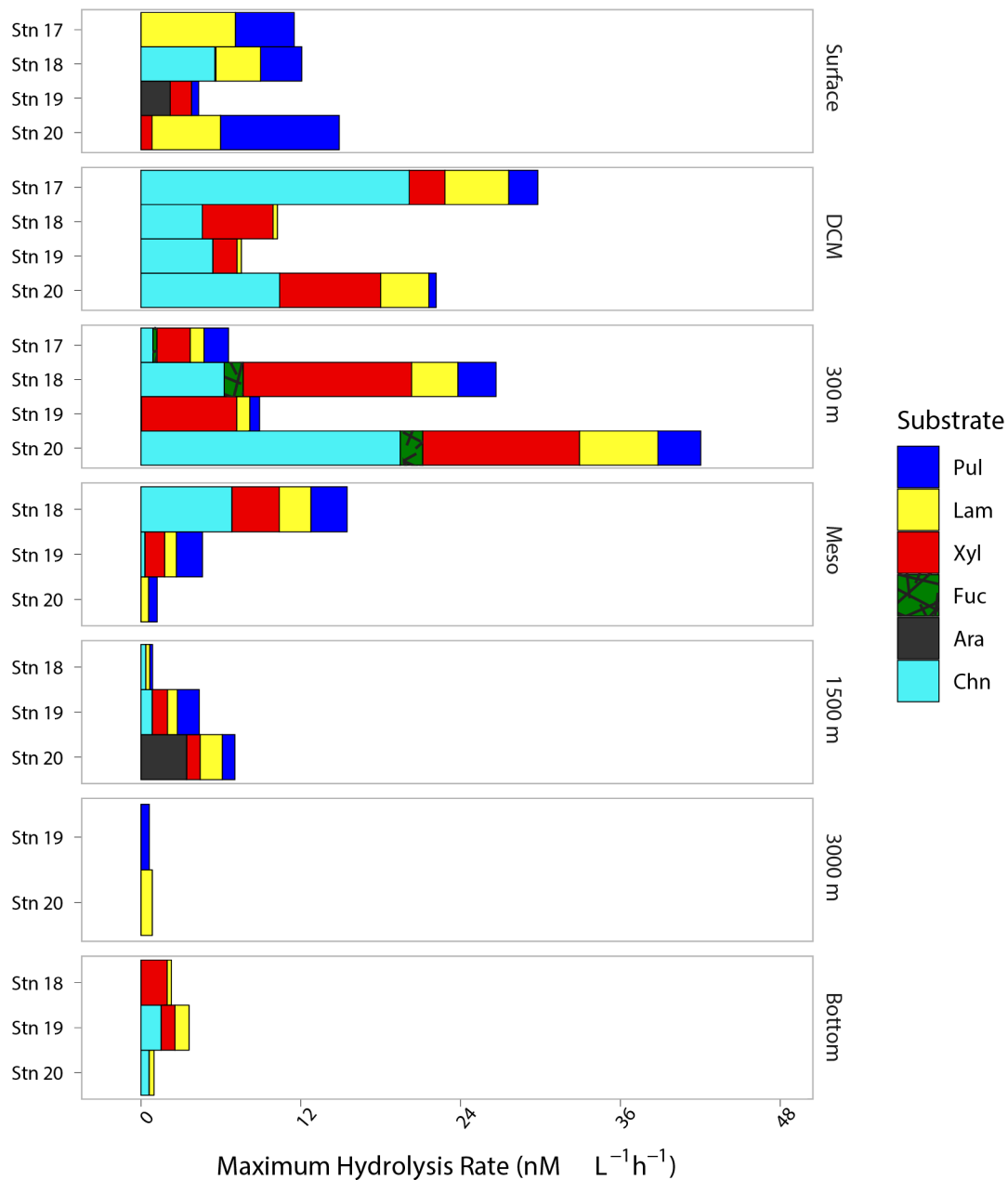


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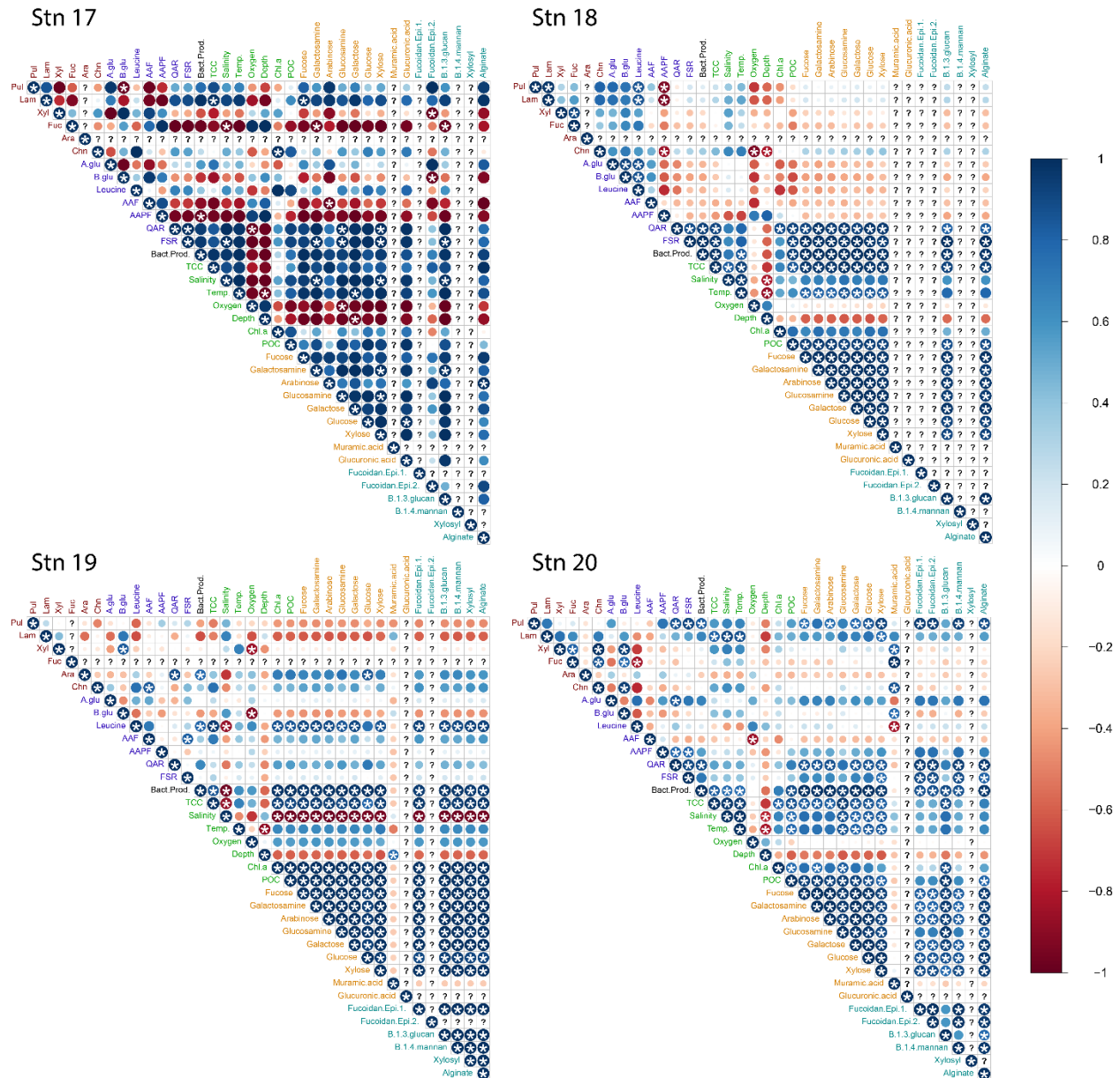
Supplemental Figure 5. Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis dissimilarity shows glucosidase and peptidase activities clustered by station.



Supplemental Figure 6. 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.



Supplemental Figure 7. 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 vesiculosus*; Ara = arabinogalactan; Chn = chondroitin sulfate.



Supplemental Figure 8. Correlation plot displaying Pearson's correlations between environmental parameters, monosaccharide constituents, and enzymatic activities 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 ($p < 0.05$).