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Depth-related patterns in microbial community responses to complex organic matter in the western North Atlantic Ocean

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Table S1. Amount of water filtered from each mesocosm for 16S rRNA sequencing. Note that one of the Stn. 12 bottom water amended mesocosms had 225 mL of water filtered from it, rather than the 250 mL that was filtered from the other two amended bottom water mesocosms.

	Station 12					
	Epipelagic		**Mesopelagic**		**Bathypelagic**	
	Amended	**Unamended**	**Amended**	**Unamended**	**Amended**	**Unamended**
0 d	1100 mL	2500 mL	1100 mL	2500 mL	1100 mL	2500 mL
2 d	300 mL	1900 mL	425 mL	2000 mL	1700 mL	2500 mL
7 d	300 mL	1550 mL	300 mL	1500 mL	600 mL	1800 mL
16 d	300 mL	1500 mL	300 mL	1500 mL	250 mL	1500 mL

	Station 16					
	Epipelagic		**Mesopelagic**		**Bathypelagic**	
	Amended	**Unamended**	**Amended**	**Unamended**	**Amended**	**Unamended**
0 d	1500 mL	2000 mL	1800 mL	2000 mL	2100 mL	2300 mL
2 d	300 mL	1800 mL	425 mL	2100 mL	1300 mL	2300 mL
7 d	300 mL	1500 mL	300 mL	1500 mL	600 mL	1700 mL
16 d	300 mL	1500 mL	300 mL	1500 mL	300 mL	1500 mL

Table S2. Analysis of variance (ANOVA) results for the effect of Treatment (amended vs. unamended) on bacterial community richness, evenness, and diversity. Bold denotes statistically significant ($p<0.05$) differences between amended and unamended mesocosms for a given depth and variable.

	Depth	df	F	Sig.
Richness	Epipelagic	4	1.967	0.2334
	Mesopelagic	4	1.8795	0.2423
	Bathypelagic	**4**	**27.2461**	**0.0064**
Pielous evenness	Epipelagic	4	1.2235	0.3307
	Mesopelagic	4	3.94846	0.1178
	Bathypelagic	**4**	**12.09968**	**0.0254**
Shannon diversity	Epipelagic	4	1.705	0.2617
	Mesopelagic	4	0.5336	0.5056
	Bathypelagic	**4**	**24.166**	**0.008**

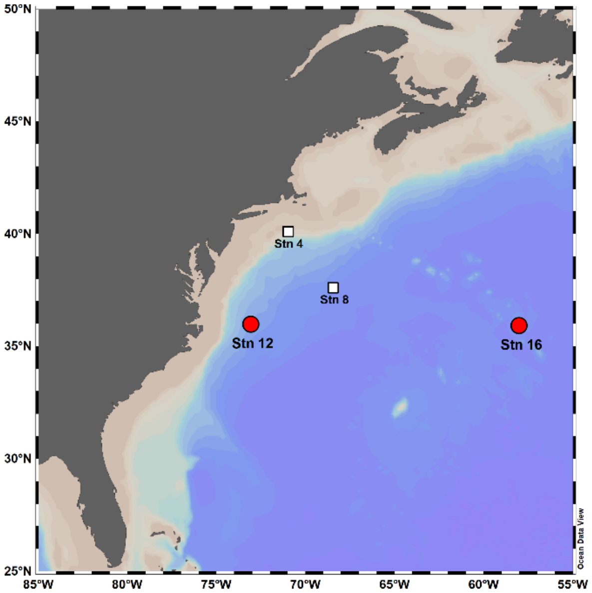

Figure S1. Stations sampled in the North Atlantic Ocean in 2015 and 2016. The white squares denote the stations sampled during April 2015 (EN556; Balmonte et al. 2019); red circles denote the stations sampled during July 2016 (EN584; current manuscript). Figure made using Ocean Data View (Schlitzer, 2015).

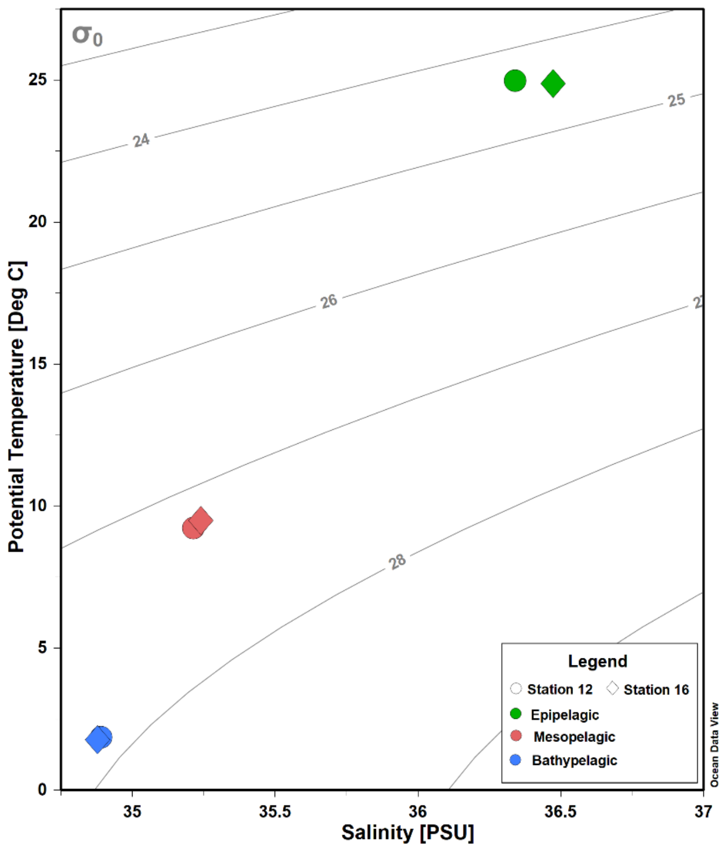

Figure S2. Temperature-salinity plot of the water masses at stations 12 and 16. The grey background lines indicate isopycnals, which were calculated from potential density with a reference pressure of 0 db.

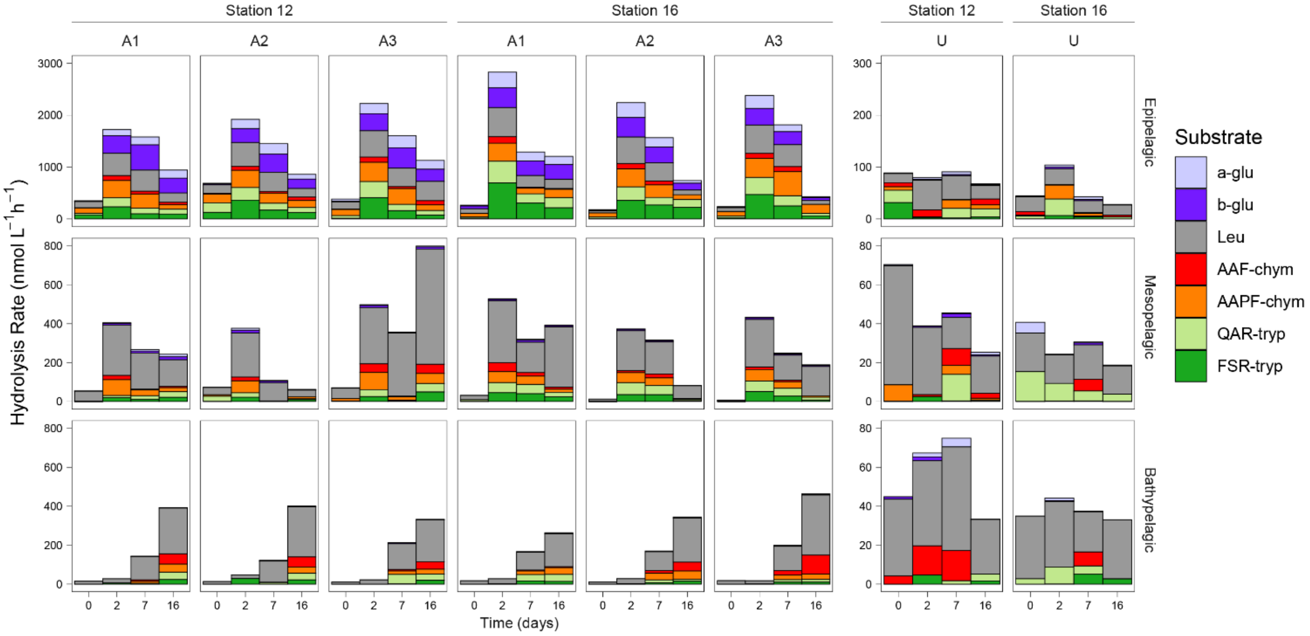

Figure S3. Average peptidase and glucosidase hydrolysis rates over a 48-hour period beginning on each sampling day (0, 2, 7, and 16 days) after HMW organic matter amendment. Note that the scales differ between amended and unamended mesocosms and between different depths. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms. a-glu = α-glucose, b-glu = β-glucose, AAF-chym = AAF-chymotrypsin, AAPF-chym=AAPF-chymotrypsin, QAR-tryp = QAR-trypsin, FSR-trypsin = FSR-trypsin, Leu = leucine-MCA.

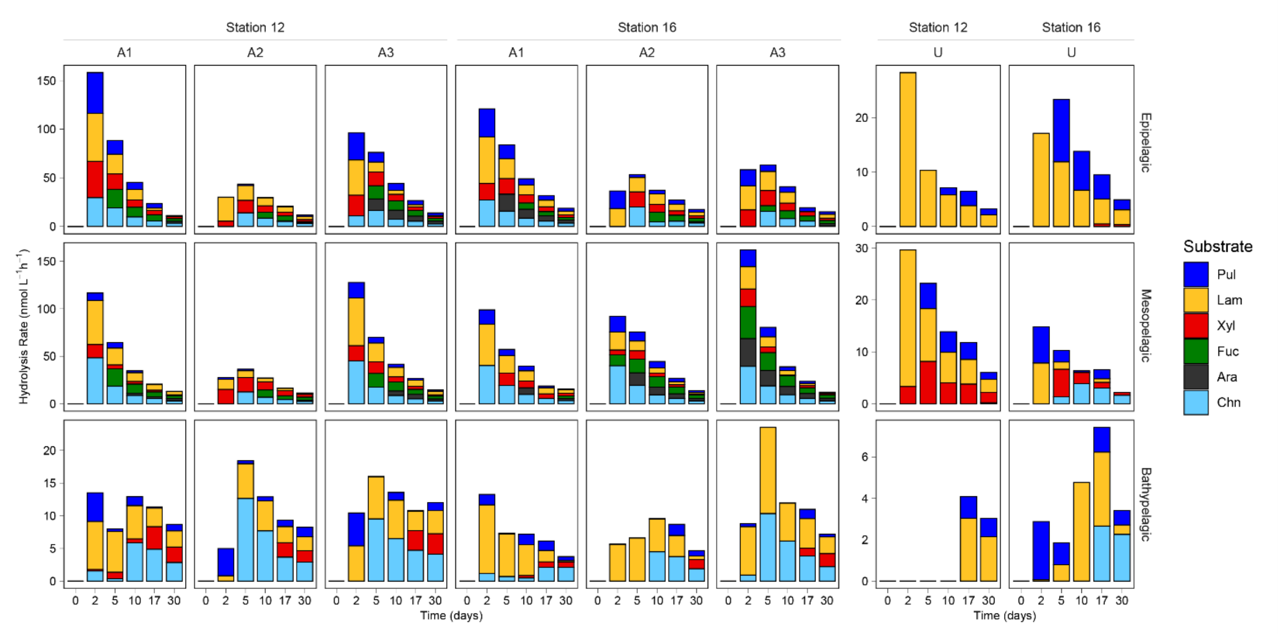

Figure S4. Average polysaccharide hydrolase rates in triplicate incubations from amended and unamended mesocosms at each station and depth. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms. Pul = pullulan, Lam = laminarin, Xyl = xylan, Fuc = fucoidan, Ara = arabinogalactan, Chn = chondroitin.

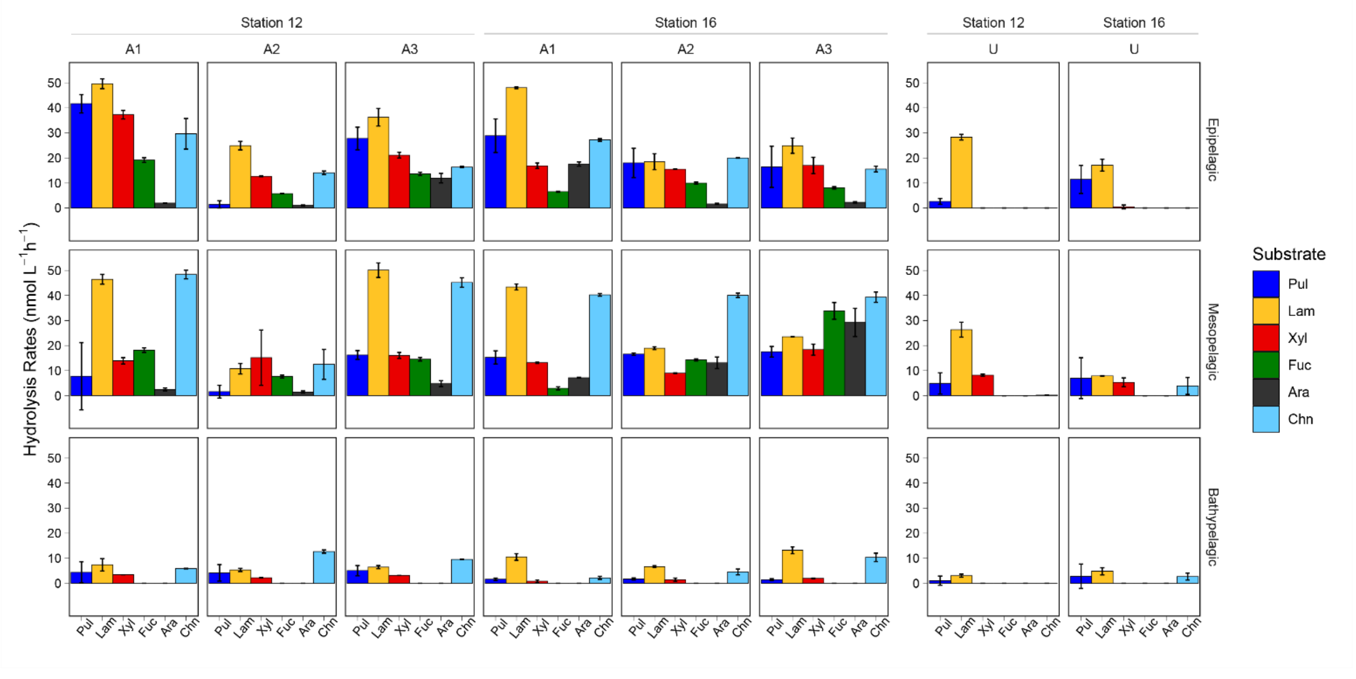

Figure S5. Maximum polysaccharide hydrolase rates over the 30 d sampling period. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms. Pul = pullulan, Lam = laminarin, Xyl = xylan, Fuc = fucoidan, Ara = arabinogalactan, Chn = chondroitin.

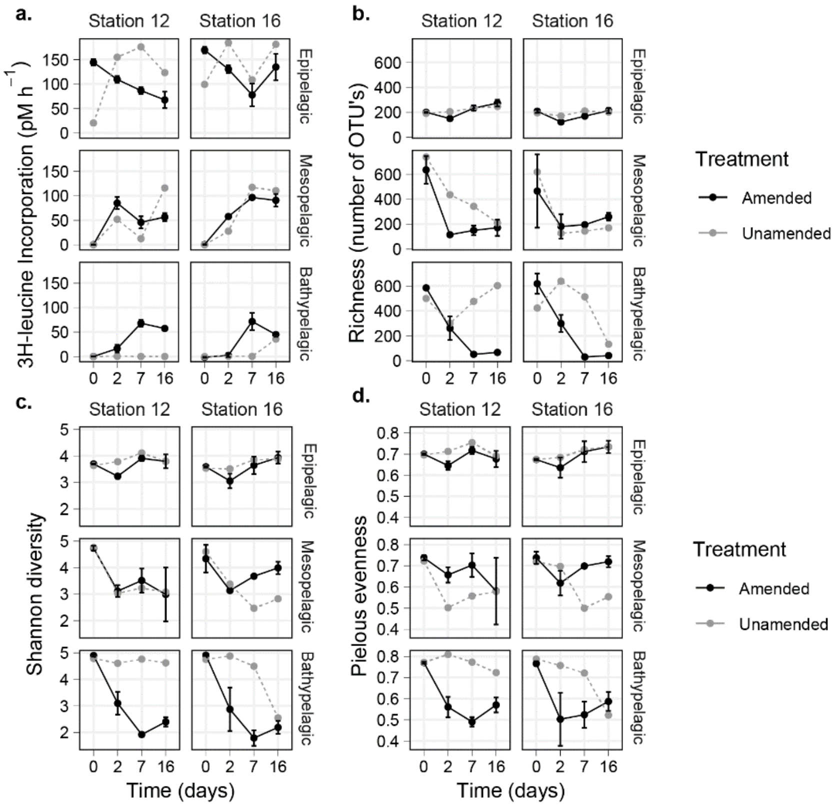

Figure S6. Average values of a) Leucine incorporation, b) Richness, in number of OTUs, c) Shannon diversity, and d) Pielous' evenness in amended and unamended mesocosms from each station and depth.

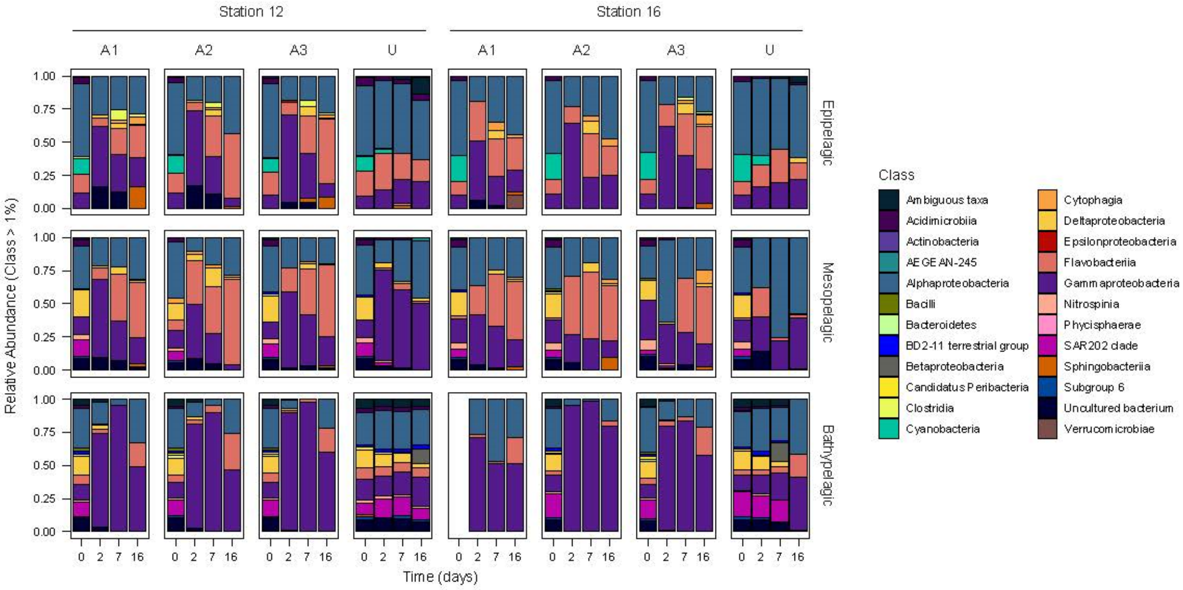

Figure S7. Class level community composition at each station and depth. Classes shown only include those with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

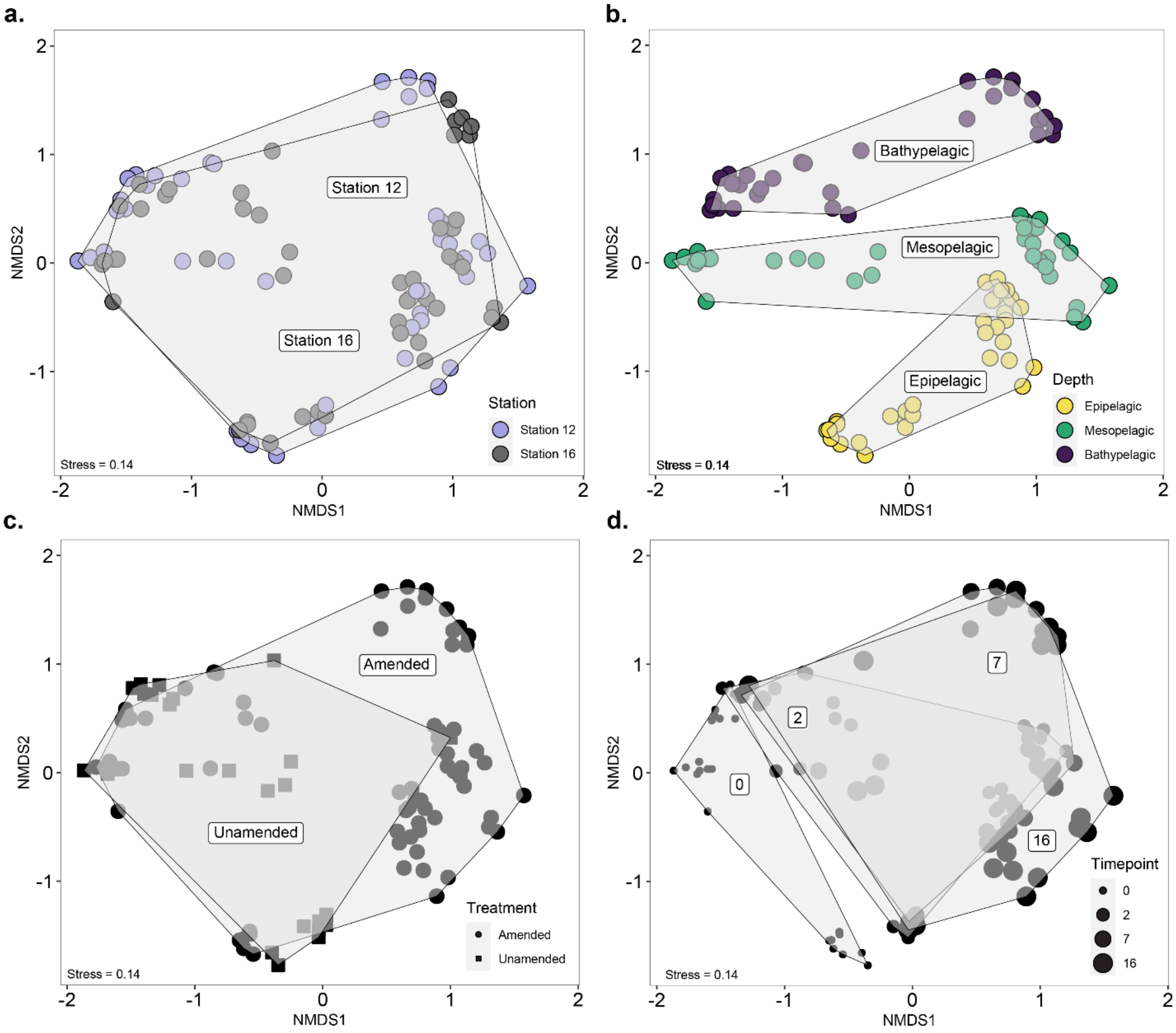

Figure S8. Non-metric multidimensional scaling (NMDS) plot of bacterial community composition based on the Bray-Curtis dissimilarity index, with communities grouped by a) station, b) depth, c) treatment, and d) timepoint. These analyses show that a) communities at Stns. 12 and 16 were very similar overall to one another in their development; b) communities were quite distinct by depth, but at later timepoints (see d) some epi- and mesopelagic communities became more similar; c) there was considerable compositional similarity between initial unamended and amended communities, which became more distinct with time (compare points to d); d) communities evolved considerably away from their initial (timepoint 0) composition.

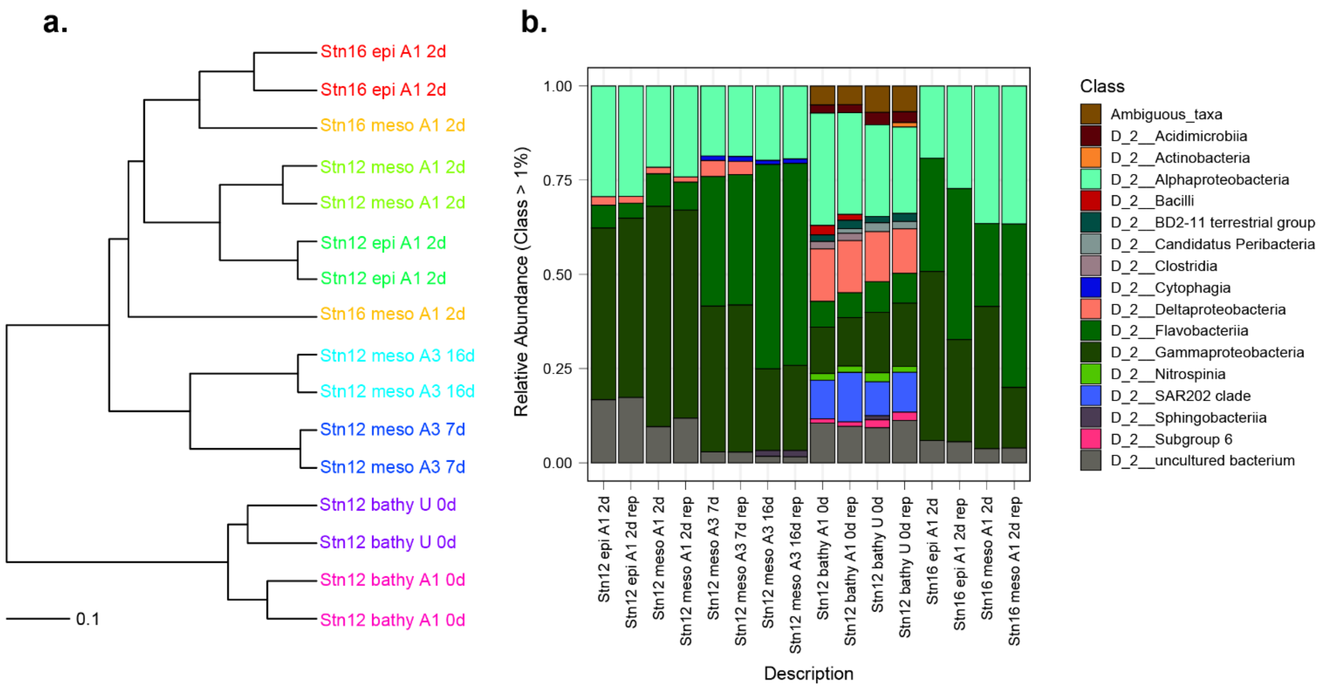

Figure S9. Reproducibility of bacterial community composition in filter duplicates (stn12_surface_amend1_t1, stn12_02minimum_amend1_t1, stn16_surface_amend1_t1, stn16_02minimum_amend1_t1) and sequencing duplicates (stn12_02minimum_amend3_t2, stn12_02minimum_amend3_t3, stn12_bottom_unamend_t0, stn12_bottom_amend1_t0). a) hierarchical clustering of duplicate filter samples, where duplicates are illustrated as different colors; b) Class level community composition of duplicate samples. Samples containing "–rep" in b. are replicate samples that were filtered out of the final community composition analysis.

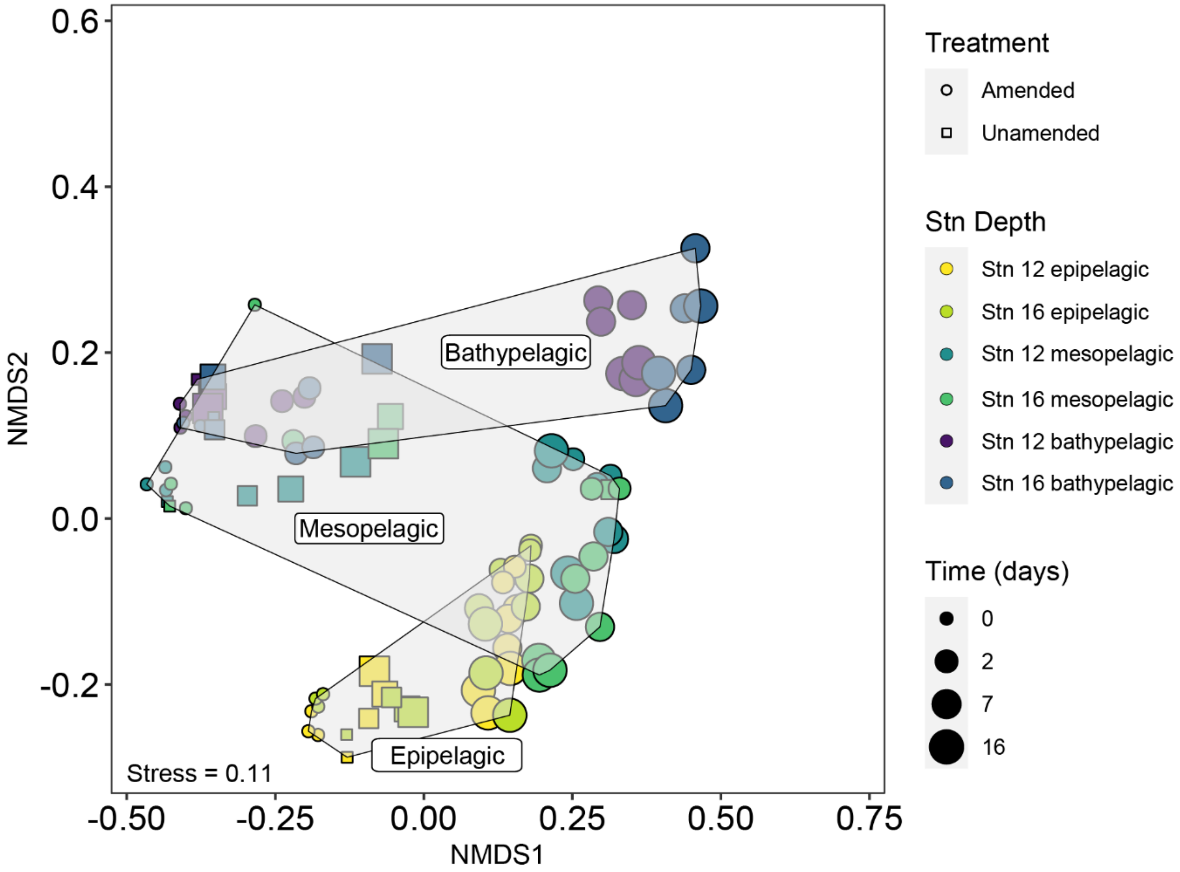

Figure S10. Non-metric multidimensional scaling (NMDS) plot of bacterial community composition based on the Unifrac dissimilarity index.

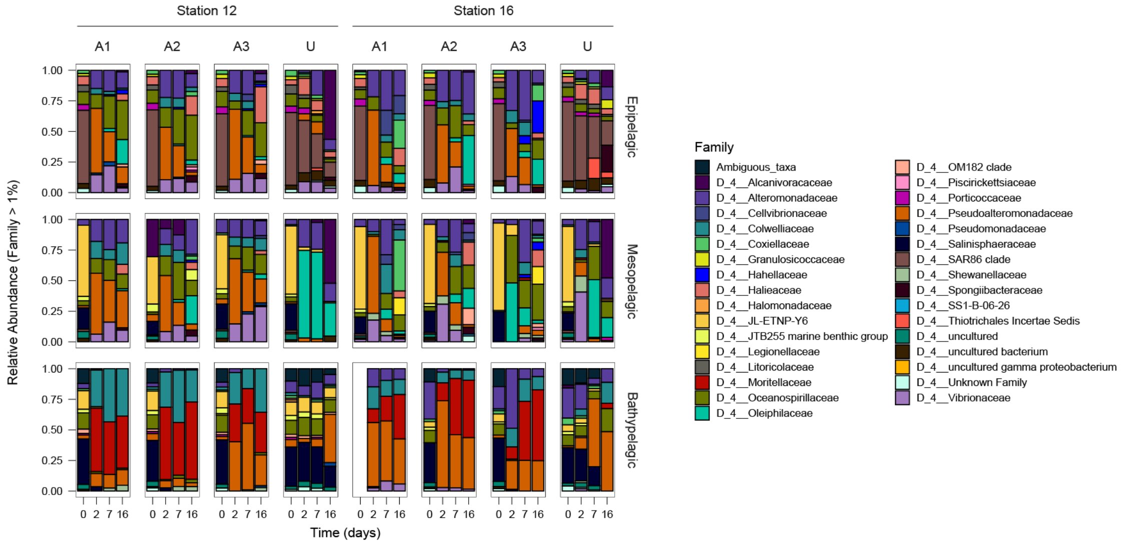

Figure S11. Relative abundance of *Gammaproteobacteria* families with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

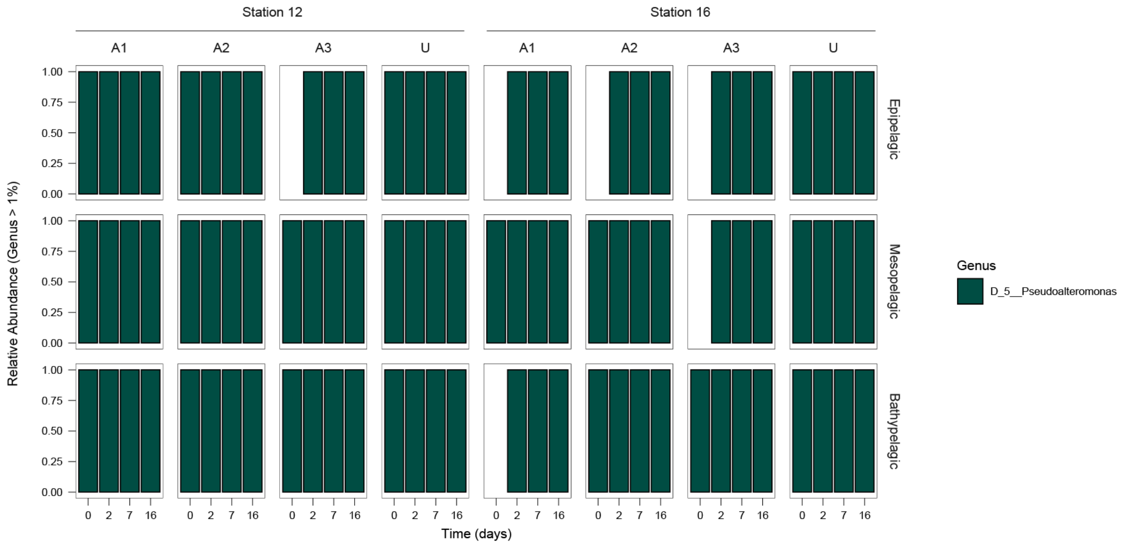

Figure S12. *Pseudoalteromonadaceae* (*Gammaproteobacteria*) genera with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

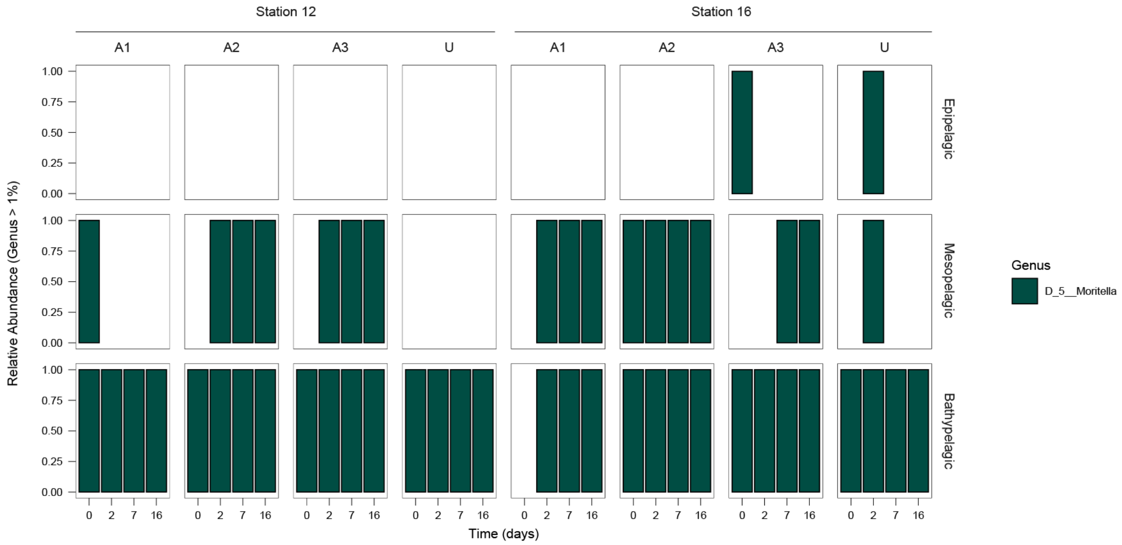

Figure S13. *Moritellaceae* (*Gammaproteobacteria*) genera with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

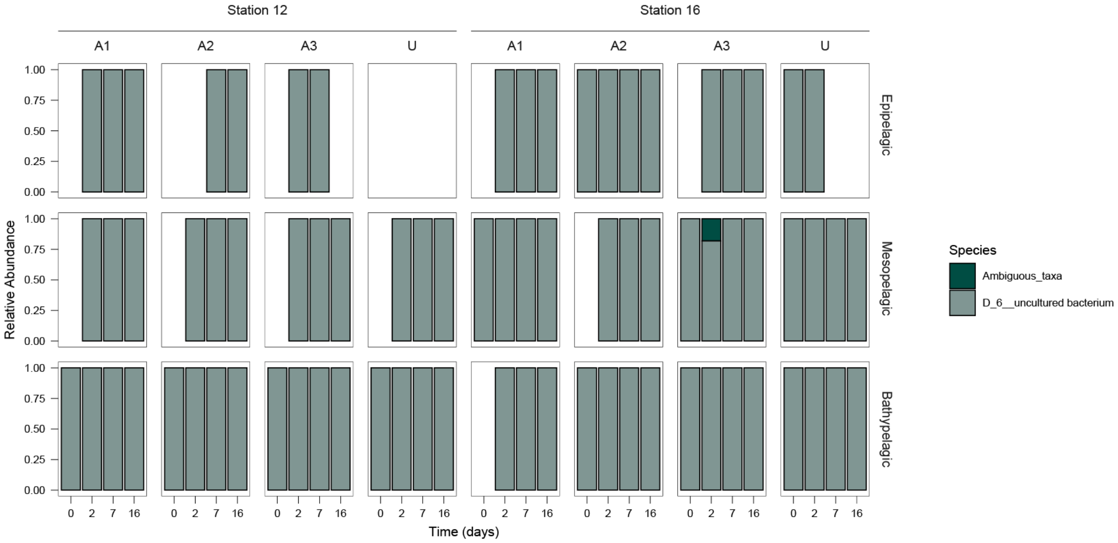

Figure S14. Relative abundance of *Colwellia* OTUs. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

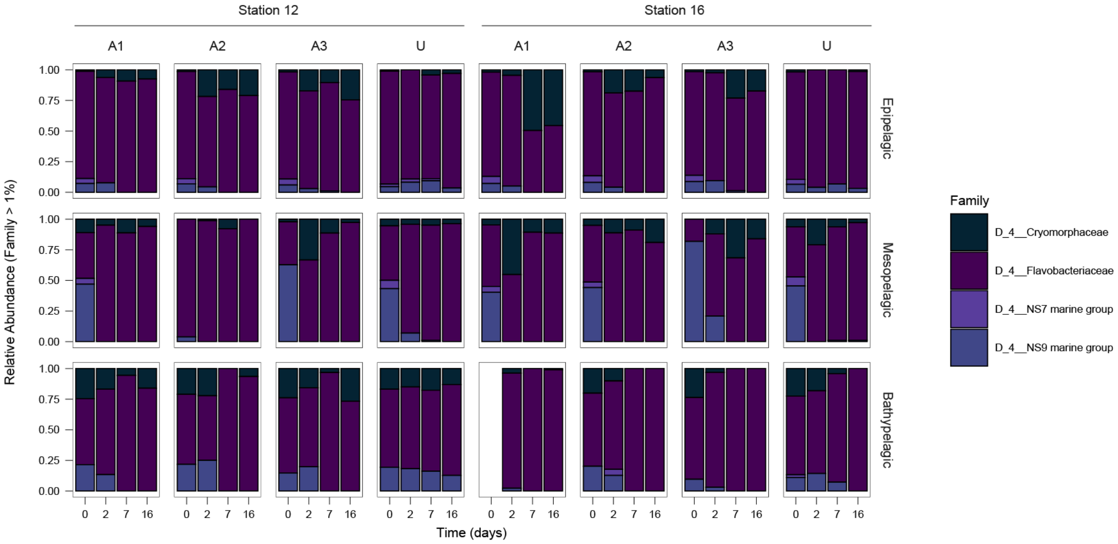

Figure S15. *Flavobacteriia* families with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

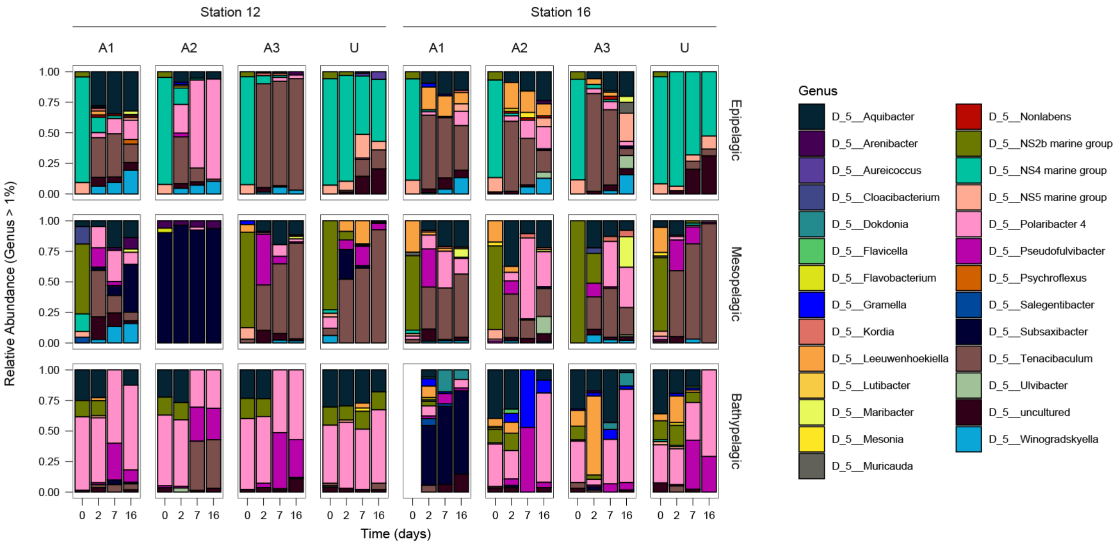

Figure S16. *Flavobacteraceae* (*Flavobacteriia*) genera with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

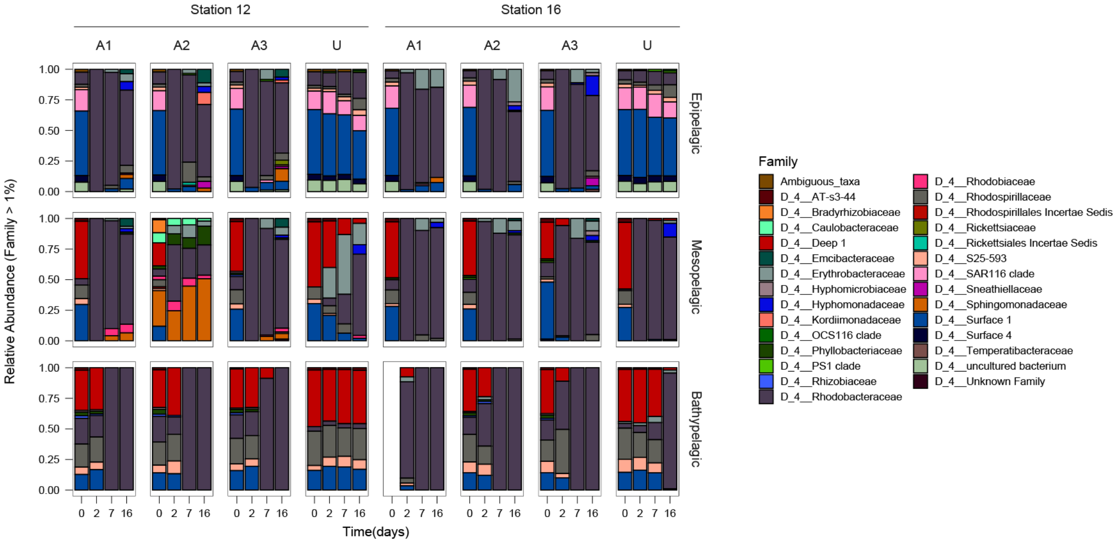

Figure S17. *Alphaproteobacteria* families with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.

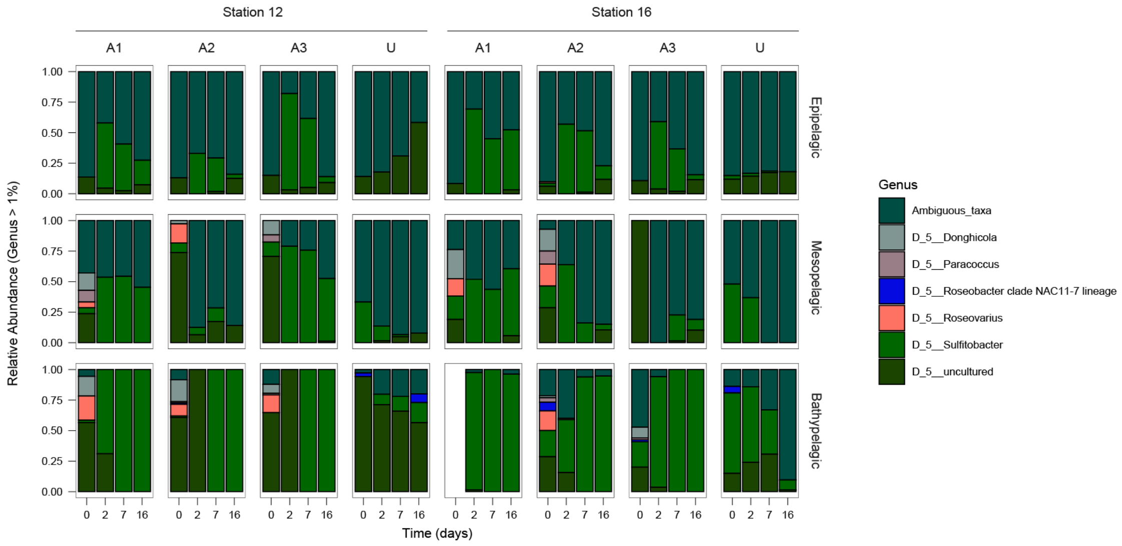

Figure S18. *Rhodobacteraceae* (*Alphaproteobacteria*) genera with an overall relative abundance greater than 1%. A1, A2, and A3 are the triplicate amended mesocosms; U are the unamended mesocosms.