

## SUPPLEMENTAL MATERIALS

Ecosystem-wide biodiversity with environmental DNA can inform management of Marine Protected Areas

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**Table S2.** Metabarcoding primers. LF indicates the forward linking sequence (5'-TCGTCGGCAGCGTCAGATGTGTATAAGCAG-3') and LR indicated the reverse linking sequence (5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-3').

Dataset	Primer sequence (5'-3')	Reference
16S	<i>Forward (515F)</i> : LF-GTGYCAGCMGCCGCGGTAA <i>Reverse (806R)</i> : LR-GGACTACNVGGGTWTCTAAT	Apprill et al. 2015 Parada et al. 2016
18S	<i>Forward (FO4)</i> : LF-GCTTGTCTCAAAGATTAAGCC <i>Reverse (R22)</i> : LR-GCCTGCTGCTGCCTTCCTTGGA	Fonseca et al. 2010
12S	<i>Forward (12S-V5)</i> : LF-ACTGGGATTAGATACCCC <i>Reverse (12S-V5)</i> : LR-TAGAACAGGCTCCTCTAG	Riaz et al. 2011

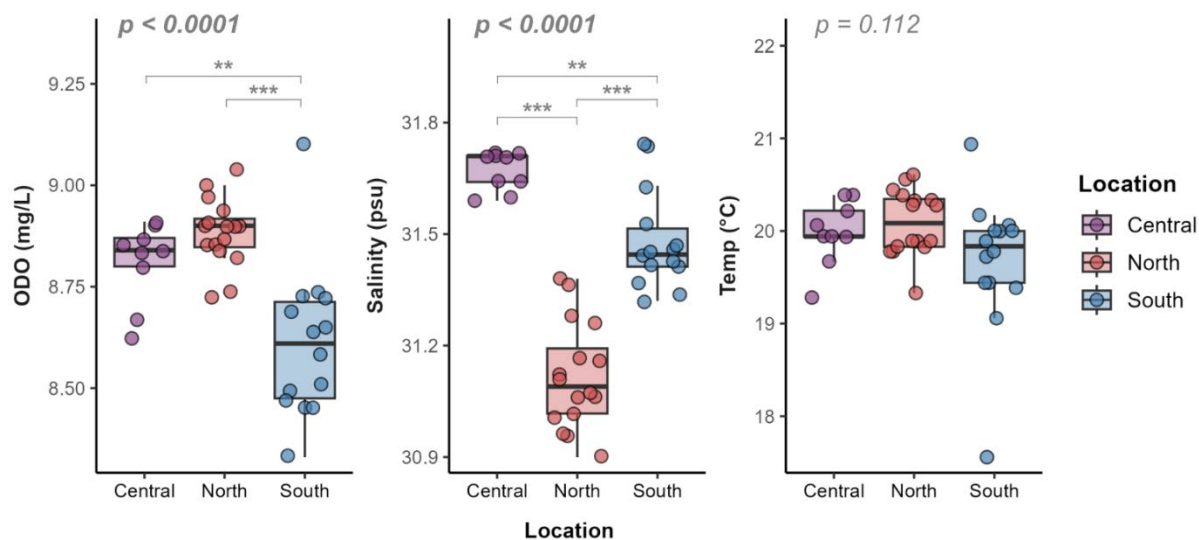
**Table S5.** Sequencing statistics

Dataset	16S	18S	12S
Total read pairs	15,887,318	16,206,469	20,018,979
QC'ed read pairs	11,446,152 (72.04%)	16,201,995 (99.97%)	16,859,079 (84.22%)
Merged reads	7,678,157 (67.08%)	13,615,971 (84.04%)	14,231,083 (84.41%)
ASVs	30,883	8,292	158
Reads mapped to ASVs	7,089,675 (92.33%)	12,309,384 (90.4%)	9,587,715 (63.37%)

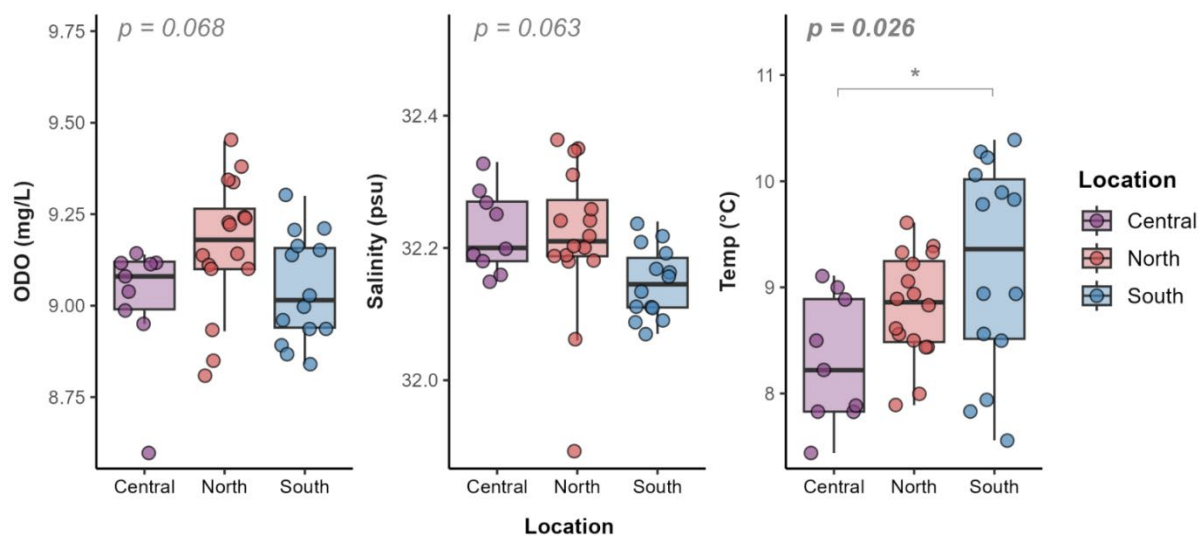
**Table S6.** Detections of species or interest in video footage, grab sample, or by onboard observers.

Site	Local date	Sand lance		Shearwater			Whale			Other marine mammals		
		Adult	YOY	Great	Cory's	Sooty	Humpback	Minke	Fin	Gray seal	Harbor seal	Harbor porpoise
S1	21-Jul-2021	0	0	0	0	0	2	0	0	0	0	0
S2	21-Jul-2021	0	0	0	0	0	0	1	0	0	0	0
S3	21-Jul-2021	0	0	1	0	0	0	0	0	0	0	0
S4	21-Jul-2021	0	0	2	0	0	0	1	0	0	0	0
S5	21-Jul-2021	0	0	0	0	0	0	1	0	0	0	0
S6	21-Jul-2021	0	0	1	0	0	0	0	0	0	0	0
S7	21-Jul-2021	0	0	1	0	0	0	0	0	0	0	0
S8	21-Jul-2021	0	0	1	0	0	0	0	0	1	0	0
S9	21-Jul-2021	0	0	1	0	0	0	0	0	0	0	0
S10	21-Jul-2021	0	0	2	0	0	0	0	0	0	0	0
S11	21-Jul-2021	0	0	1	0	0	0	0	0	0	0	0
S12	21-Jul-2021	0	0	2	0	0	0	0	0	0	0	0
S13	21-Jul-2021	3	0	1	1	0	0	0	0	0	0	0
S14	21-Jul-2021	0	0	1	1	0	0	1	0	0	0	0
C5	22-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C4	22-Jul-2021	1	1	0	0	0	0	0	0	0	0	0
C11	22-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C12	22-Jul-2021	nd	nd	0	0	0	0	0	0	0	0	0
C13	22-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C14	22-Jul-2021	0	0	2	0	0	0	0	0	0	0	0
C1	22-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C2	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C3	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
C10	23-Jul-2021	0	0	0	0	0	2	0	0	0	0	0
N16	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N1	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N2	23-Jul-2021	nd	nd	0	0	0	0	0	0	0	0	0
N15	23-Jul-2021	2	0	0	0	0	0	0	0	0	0	0
N14	23-Jul-2021	1	0	0	0	0	0	0	0	0	0	0
N3	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N4	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N13	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N12	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N5	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N6	23-Jul-2021	nd	nd	0	0	0	0	0	0	0	0	0
N11	23-Jul-2021	2	0	0	0	0	0	0	0	0	0	0
N10	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N8	23-Jul-2021	0	0	2	0	0	0	0	0	0	0	0
N9	23-Jul-2021	0	0	0	0	0	0	0	0	0	0	0
N7	23-Jul-2021	0	0	5	0	0	0	0	0	0	0	0

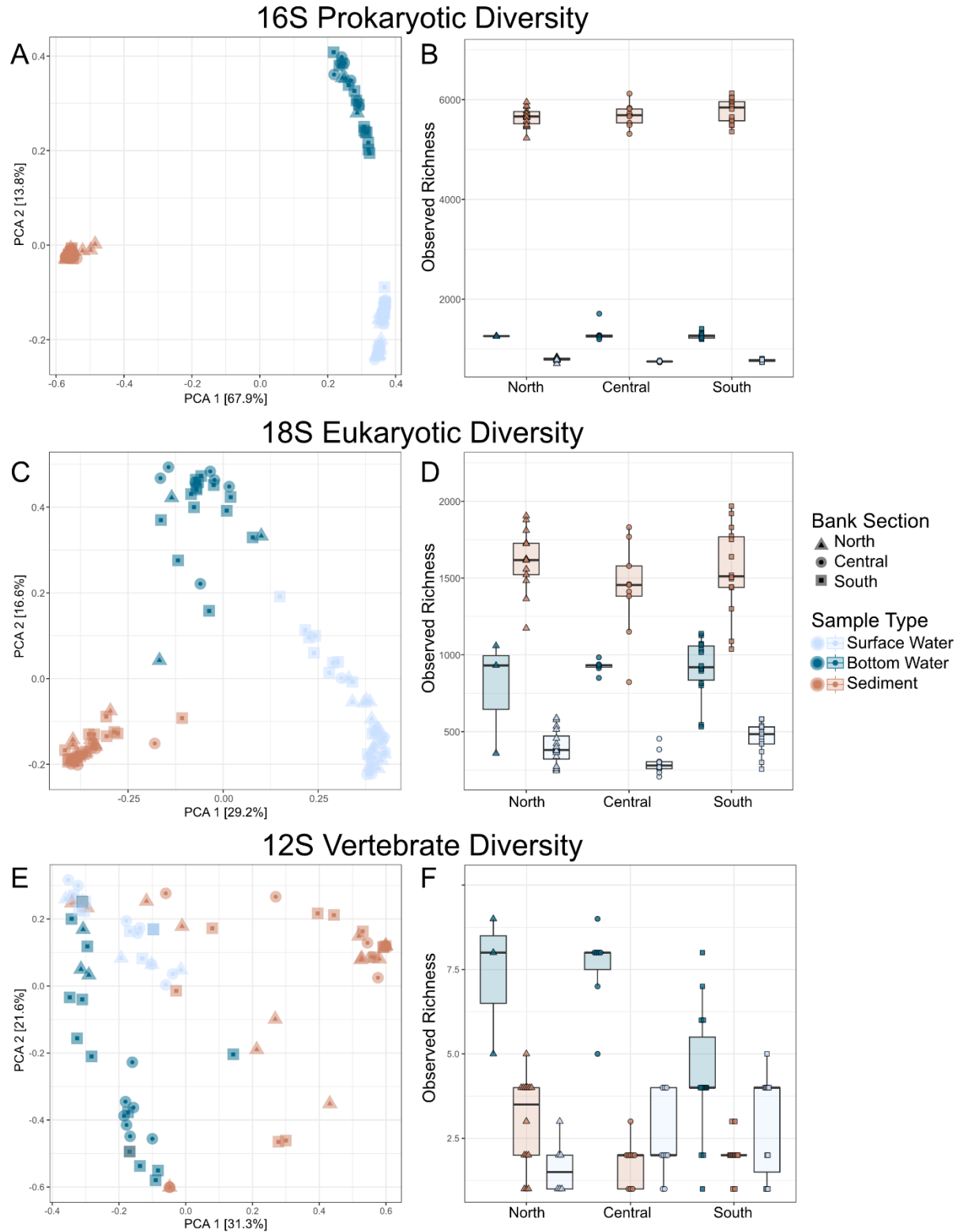
## Surface Water



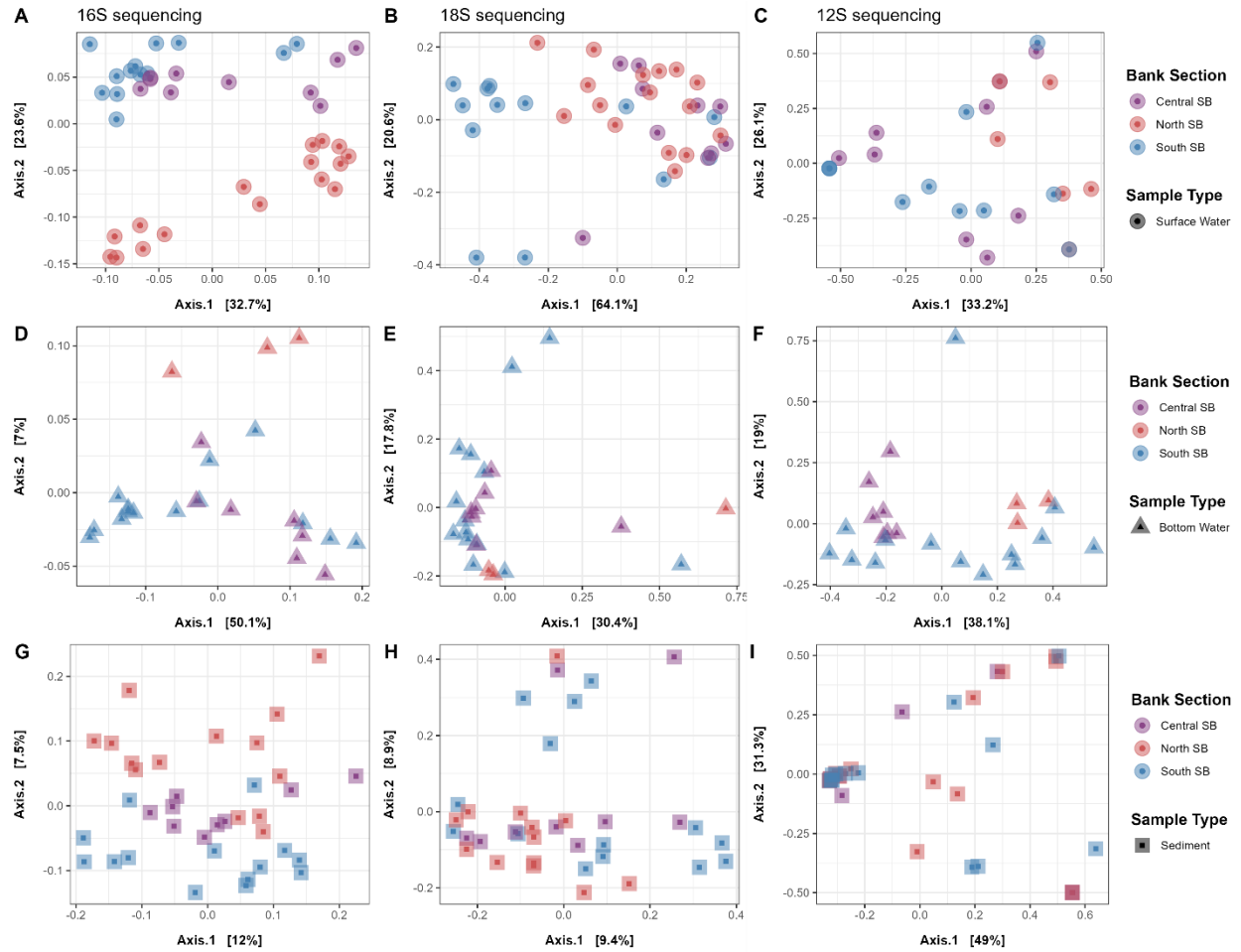
## Bottom Water



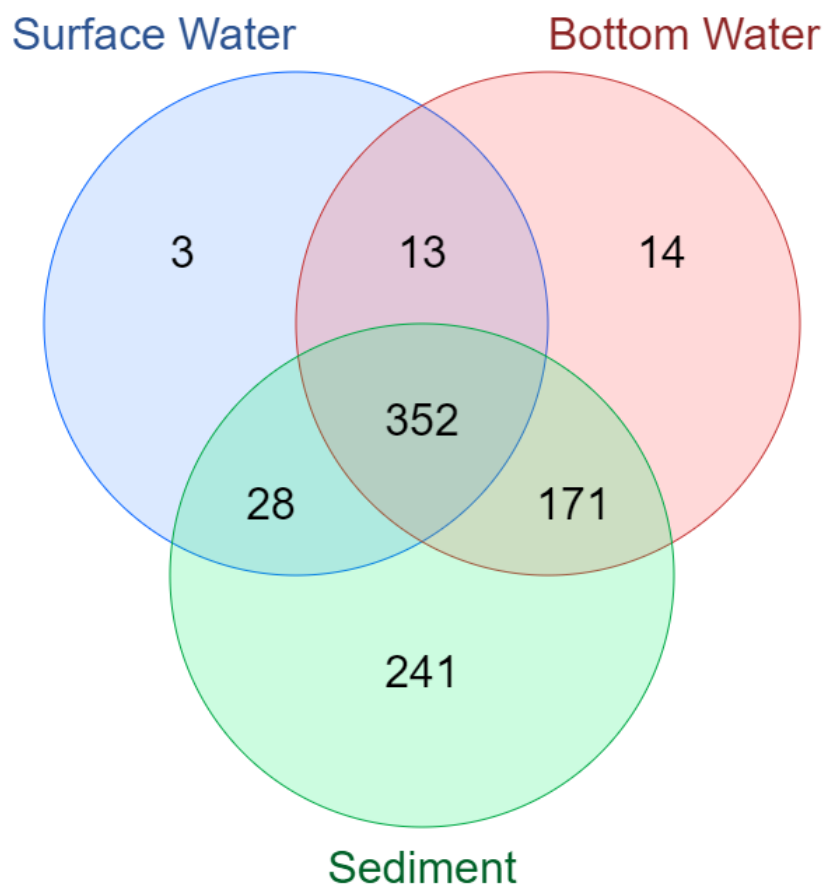
**Figure S1.** Environmental data for bottom and surface water, including ODO (mg/uL), Salinity (psu), and Temperature (°C), analyzed by Bank Section/Location. ANOVA results reported in gray text and Tukey Post-Hoc results reported with significance codes:  $p < 0.001$  (\*\*\*),  $p < 0.01$  (\*\*),  $p < 0.05$  (\*).



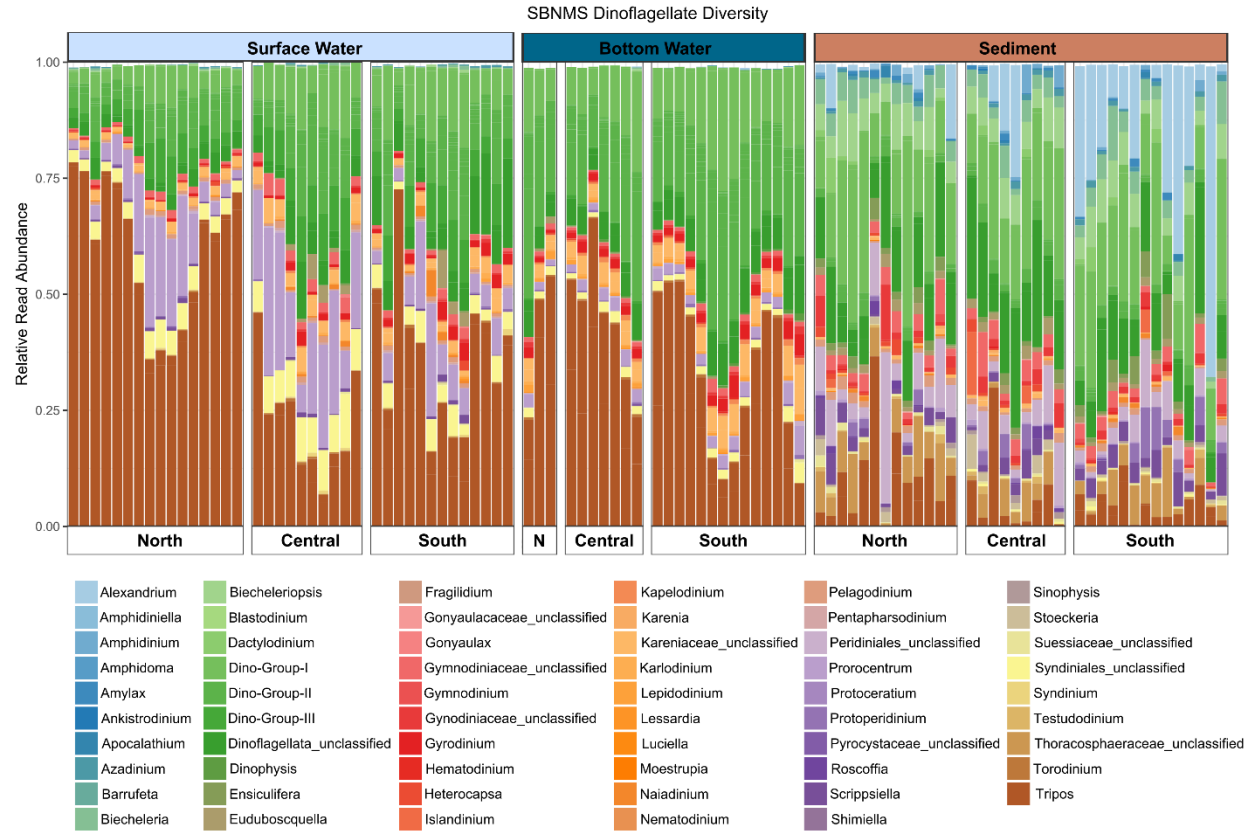
**Figure S2.** Principle Components Analysis of 16S prokaryotic (A), 18S eukaryotic (C), and 12S vertebrate (E) rarefied sequencing data. Observed richness of 16S (B), 18S (D), and 12S (F) rarefied sequencing data.



**Figure S3.** Principal Coordinates Analysis (PCoA) of Bank Section for each 16S SSU rRNA, 18S, and 12S V5 amplicon sequencing and Sample Type (Surface Water, Bottom Water, and Sediment).

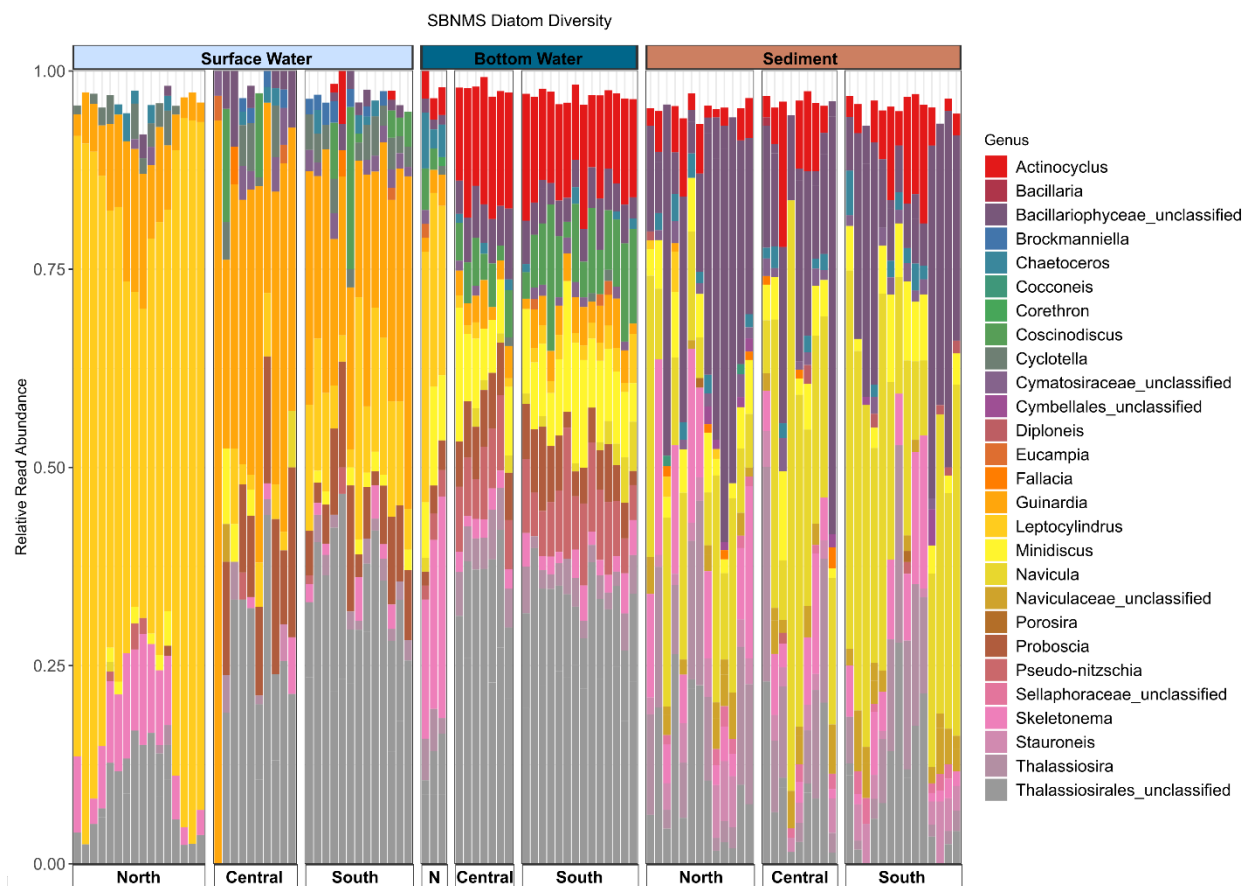


**Figure S4.** Venn diagram depicting the number of shared 18S taxa, grouped at the lowest level of taxonomic classification down to genus when possible.

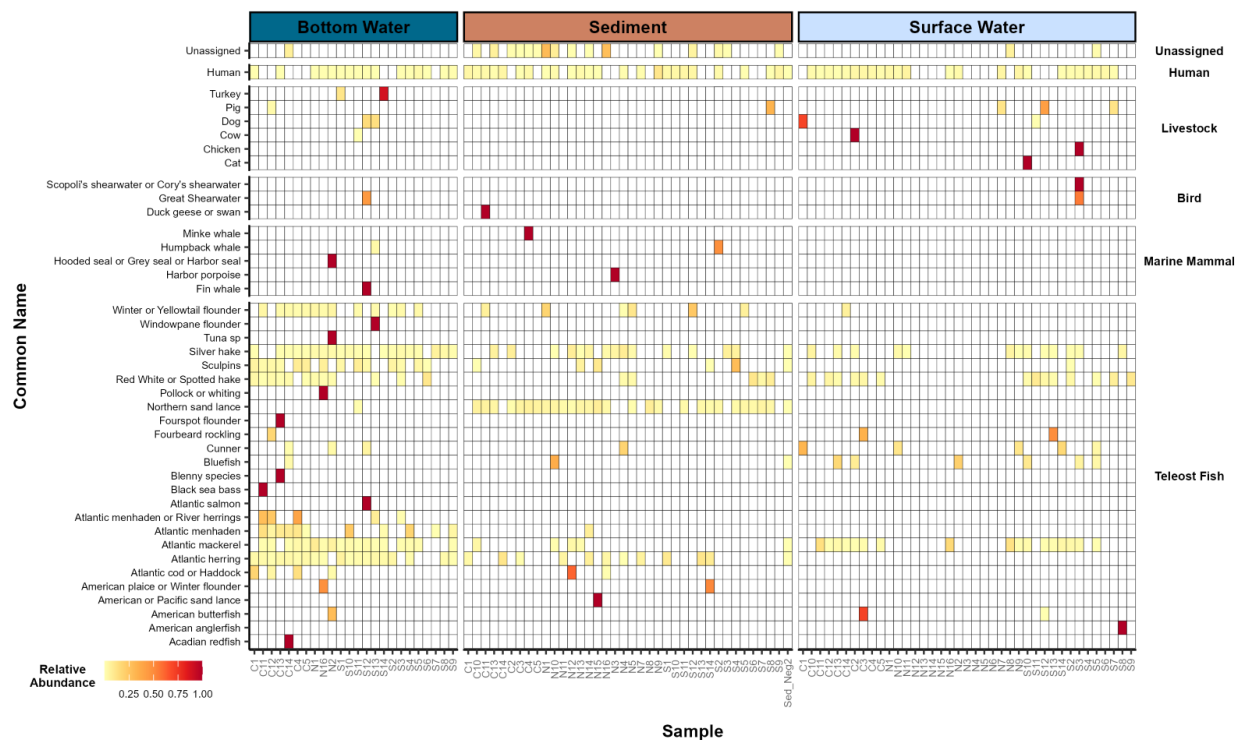


**Figure S5.** Relative abundance of dinoflagellates observed in eukaryotic (18S) data.





**Figure S6.** Relative abundance of diatom genera observed in eukaryotic (18S) data.



**Figure S7.** Relative abundance of 12S V5 amplicon sequencing unassigned and assigned to Human, Livestock, Bird, Marine Mammals, and Teleost Fish.