

Supplementary Information

Supplementary Dataset legends:

Supplementary Dataset 1. Information on each sample's coordinates, physicochemical parameters, ocean, habitat type, and diversity of sequences detected, among other features. Used sample metadata for all figures. Used diversity data for Figure 4.

Supplementary Dataset 2. Information on the VOG profiles used to detect the phage marker sequences and the virus detection tool outputs.

Supplementary Dataset 3. RPKM tables of reads mapped from each sample for the phage and prokaryotic sequences. Used for Figure 2.

Supplementary Dataset 4. Information on the number of each sequence present in a file and the ecological statistics reported and the manuscript (ANOSIMs, Mantel tests, correlations) used to benchmark the sequences.

Supplementary Dataset 5. Sequence information for TerL and RNAP B on which samples they were found, their classifications, and their envfit test results. Used for Figure 3.

Supplementary Figure legends

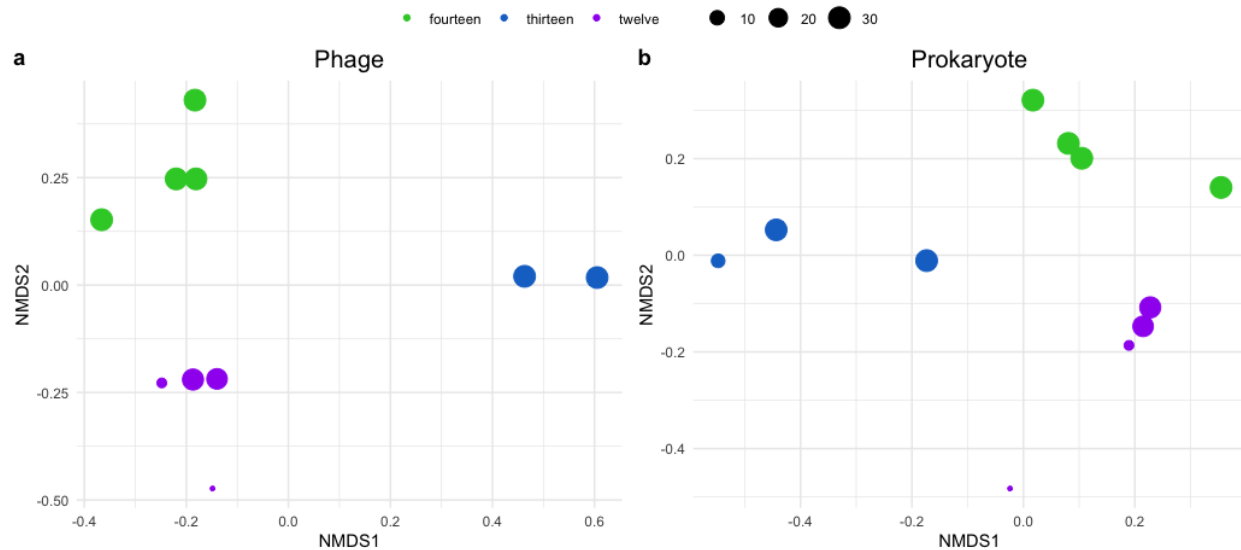
Supplementary Fig. 1. NMDS plot of samples based on bray-curtis distances of phage (a) and prokaryote (b) relative abundance with data points colored by river and size of point scaled to salinity (ppt).

Supplementary Fig. 2. Violin plots of the physicochemical parameters measured for the WA samples (top row) and EP samples (bottom row) between mangroves and reefs. Stars correspond to significance (*=0.05, **=0.01, ***=0.001, ns or NS = not significant)

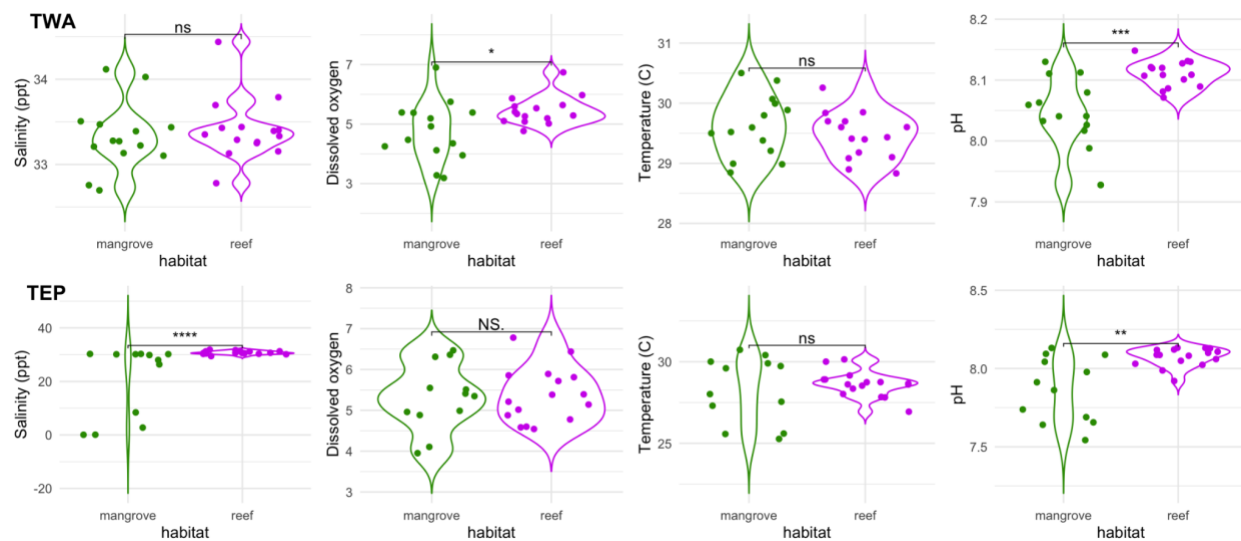
Supplementary Fig. 3. Shannon's Diversity of phages (a,b) and prokaryotes (c,d) in reefs (a,c) and mangrove (b,d) samples examined separately. Stars correspond to significance (*=0.05, **=0.01, ***=0.001, ns or NS = not significant).

Supplementary Fig. 4. NMDS plots of WA samples based on phage sequences (top row) or prokaryotic sequences (bottom row) color by habitat type that included WAM_TWN.

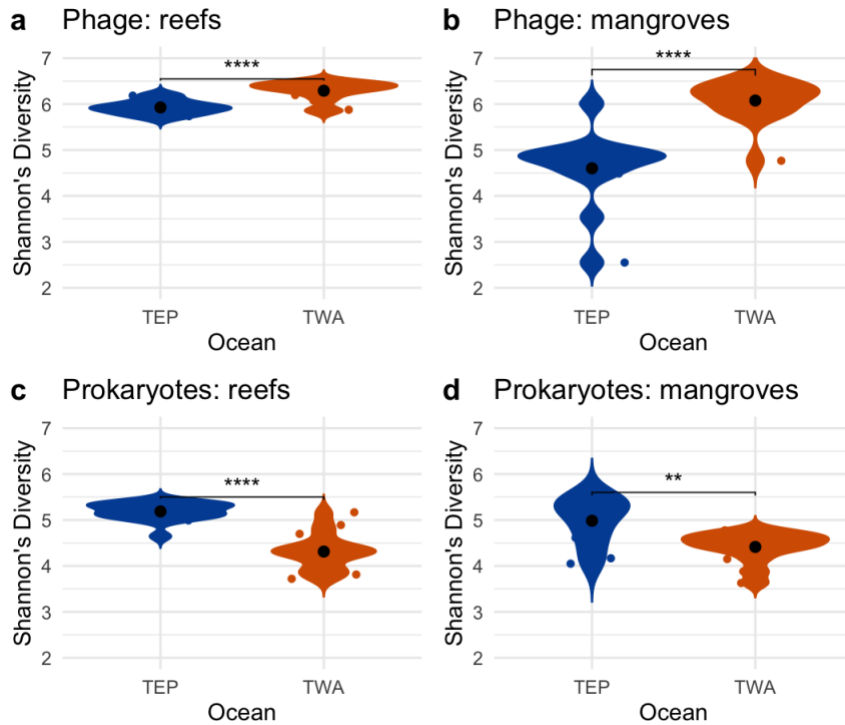
Supplementary Fig. 5. NMDS plots of EP samples based on phage sequences (top row) or prokaryotic sequences (bottom row) color by habitat type that included EPM_13A1.



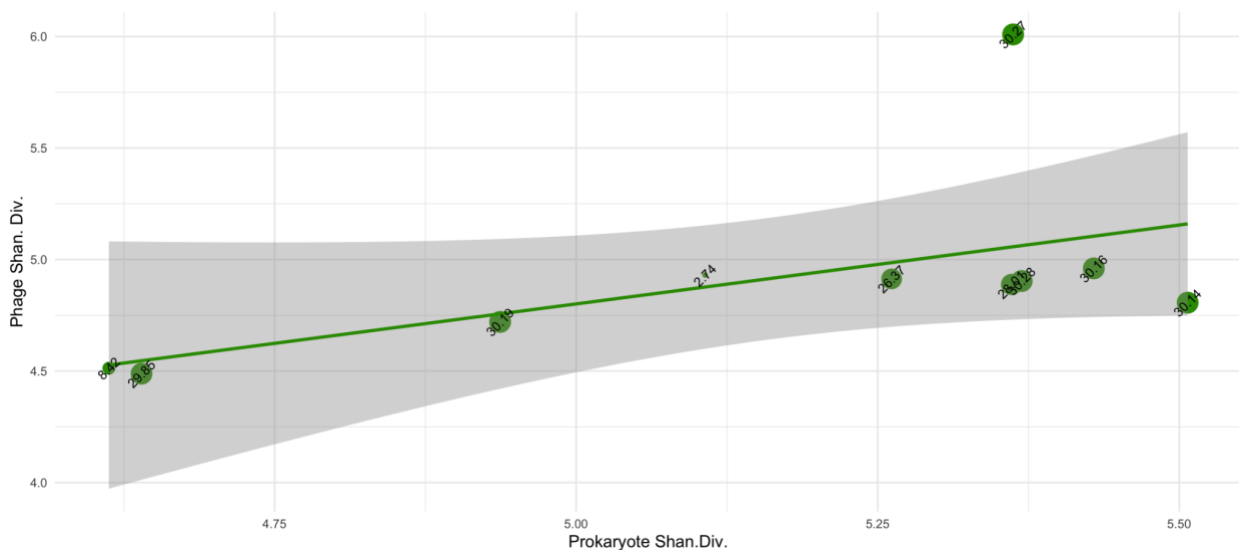
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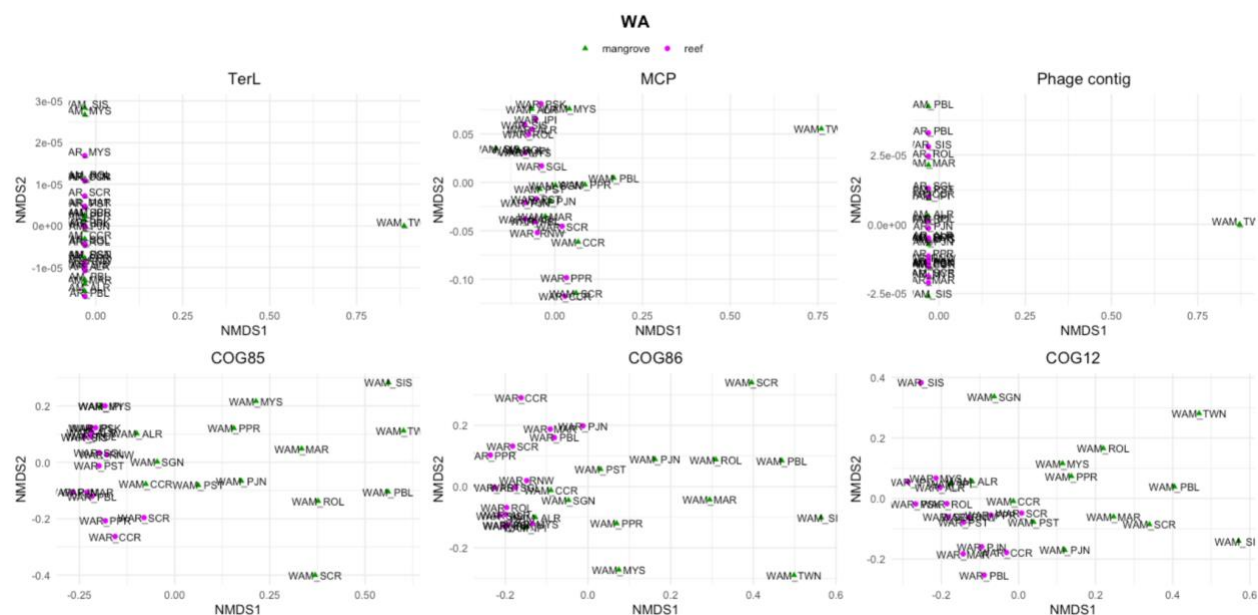
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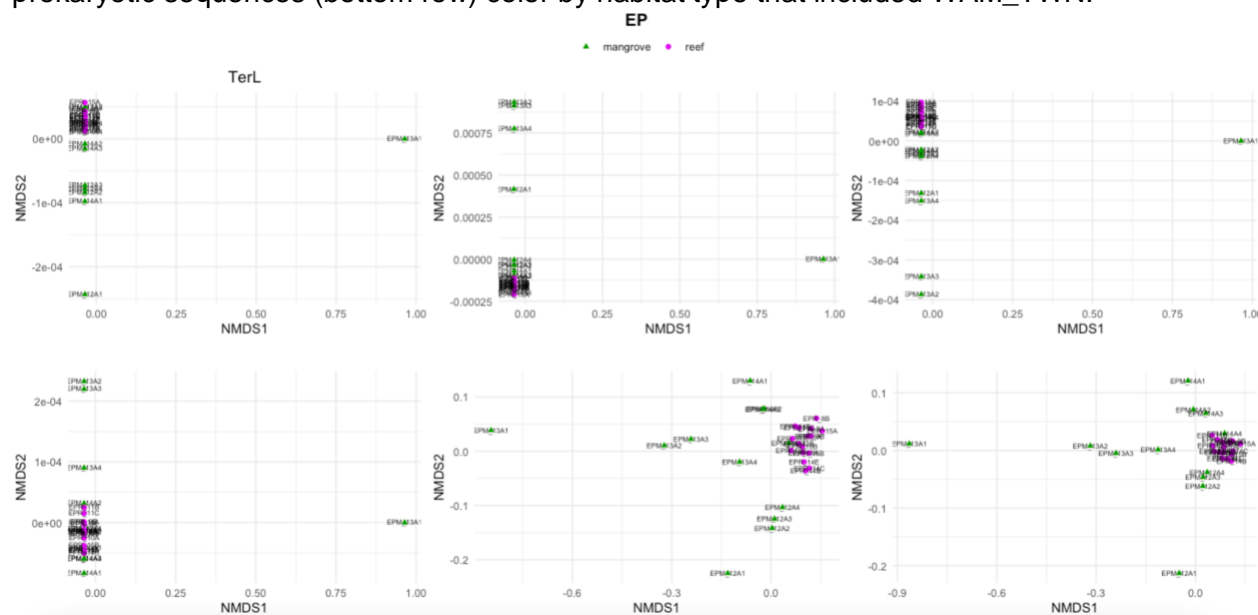
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Supplementary Figure 4. Phage Shannon's Diversity (Shan. Div.) versus prokaryotic Shannon's Diversity of TEP mangrove samples with the two freshest samples (EPM_13A1 and EPM_12A1) removed. No significant correlation. Text labels refer to salinity (ppt). Point sizes correspond to salinity.



Supplementary Figure 5. NMDS plots of WA samples based on phage sequences (top row) or prokaryotic sequences (bottom row) color by habitat type that included WAM_TW.



Supplementary Figure 6. NMDS plots of EP samples based on phage sequences (top row) or prokaryotic sequences (bottom row) color by habitat type that included EPM_13A1.