

Supplementary Information (Figures S1-3)

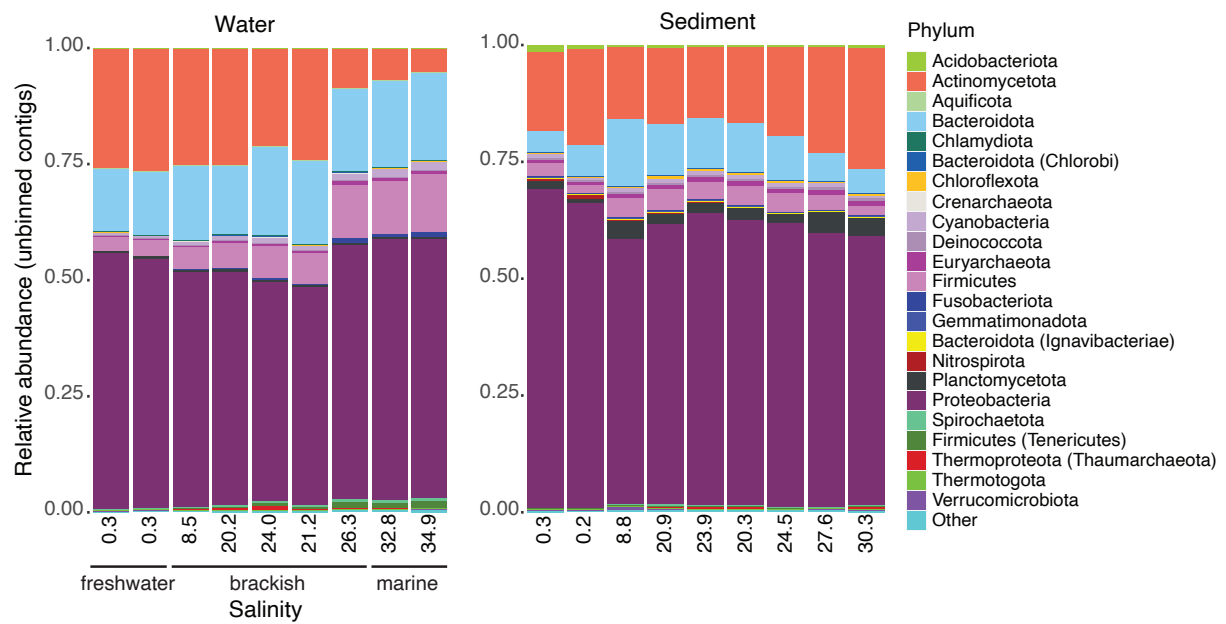


Figure S1. Bar plots showing taxa relative abundances across the salinity gradient in the water column and sediments based on unbinned contigs. Plots show phyla relative abundance in water (left) and sediment (right). Sediment values are averages of spatial replicates (x3).

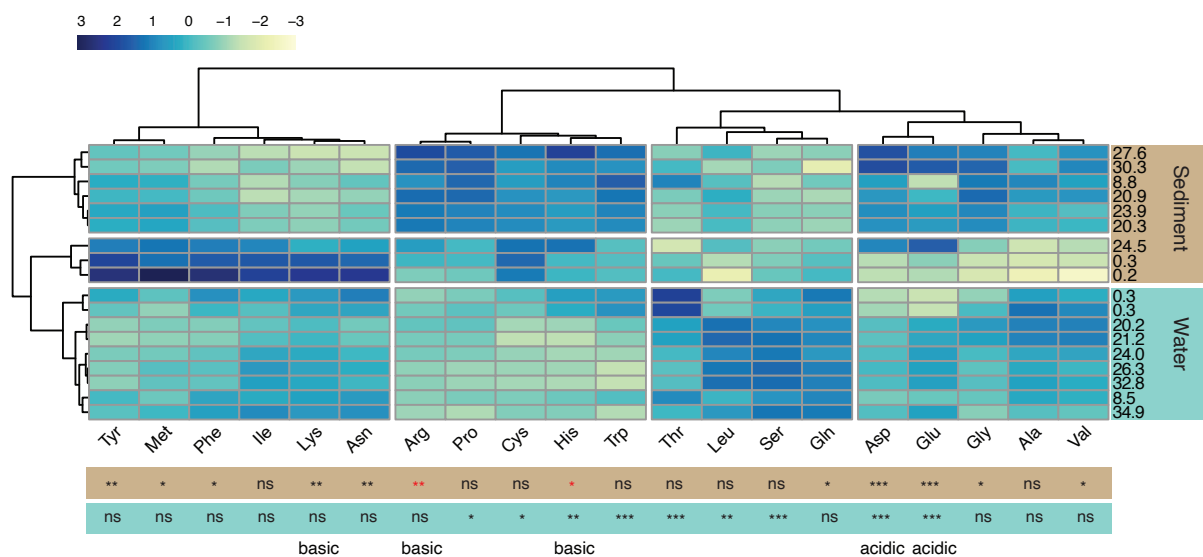


Figure S2. Heatmap showing hierarchical clustering of amino acid composition in water and sediment samples across the salinity gradient. Values are scaled by column as z-scores. Clustering uses Ward's method. Asterisks indicate significant Pearson's correlations (* $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$) between amino acids and salinity (ns = not significant). Averaged amino acid proportions per site were weighted by MAG coverage (and scaled by total MAG coverage across all samples). Red font indicates a trend for a charged amino acid is opposite to that predicted (i.e. the association with salinity is negative for acidic and positive for basic amino acids). Only aspartate (Asp) and glutamate (Glu) yielded strong correlations with salinity in both water and sediment.

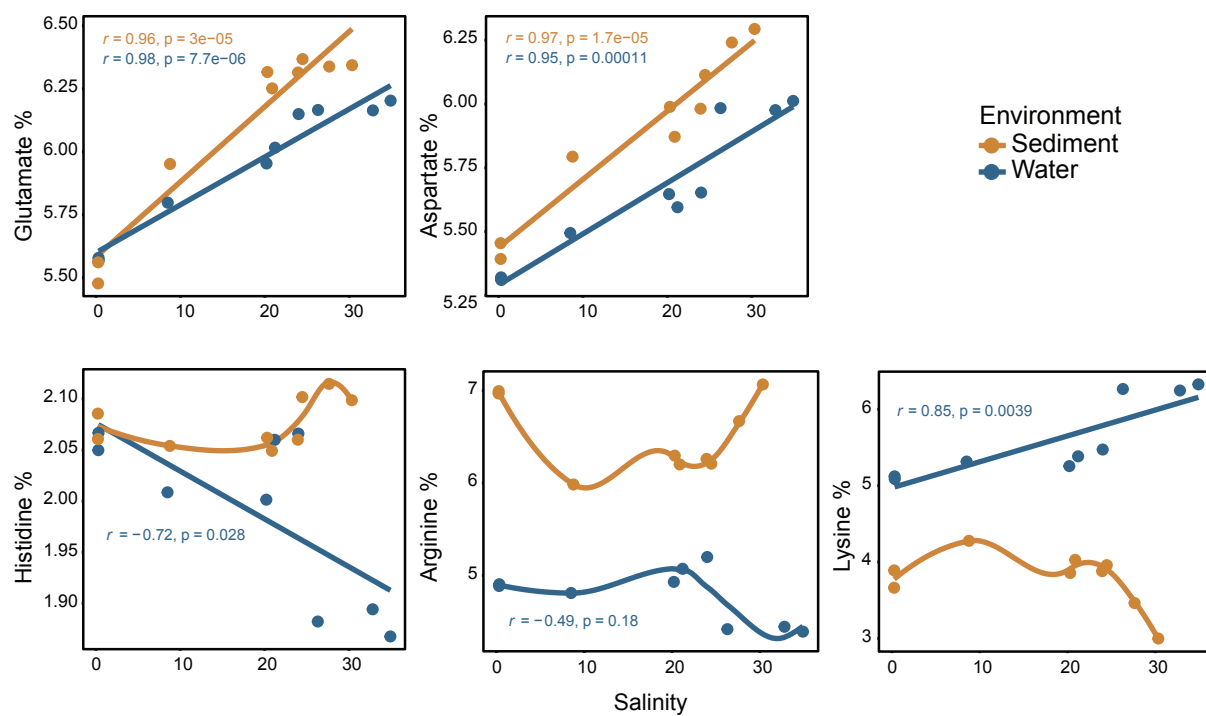


Figure S3. Scatter plot showing the acidic and basic amino acid proportions across salinity in water column and sediment samples using unbinned data. Regression lines, Pearson's correlation coefficients (r), and the associated p-values are shown in the plots.