

Vertical profiles of microbial trace element utilization in marine environments

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Supplementary figures

Figure S1. Geographic locations of marine metagenomic samples. The Red Sea and the Sargasso Sea areas contain two metagenomic datasets from different projects.

Figure S2. Distribution of cuproproteomes in marine metagenomic samples. The boundary lines for cuproprotein-rich and -poor samples are indicated.

Figure S3. Distribution of molybdoproteomes in marine metagenomic samples. The boundary lines for molybdoprotein-rich and -poor samples are indicated.

Figure S4. Distribution of tungstoproteomes in marine metagenomic samples. The boundary lines for tungstoprotein-rich and -poor samples are indicated.

Figure S5. Distribution of Ni-dependent proteomes in marine metagenomic samples. The boundary lines for Ni-dependent-protein-rich and -poor samples are indicated.

Figure S6. Distribution of Co-dependent proteomes in marine metagenomic samples. The boundary lines for Co-dependent-protein-rich and -poor samples are indicated.

Figure S7. Putative taxonomic affiliation of RNR II sequences detected in the metagenomic dataset.

Figure S8. Distribution of selenoproteomes in marine metagenomic samples. The boundary lines for selenoprotein-rich and -poor samples are indicated.

Figure S1

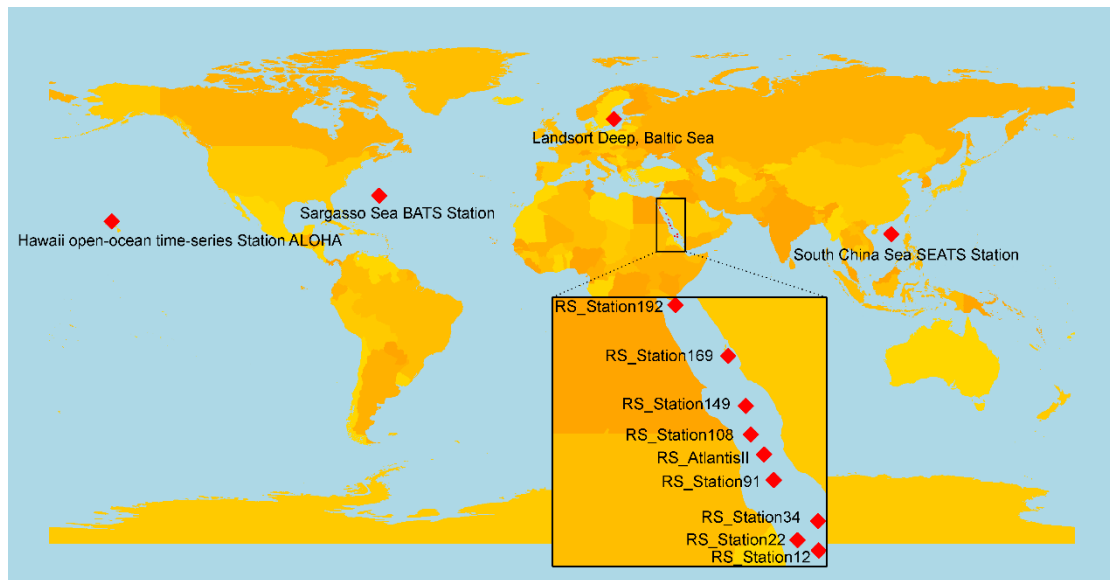


Figure S2

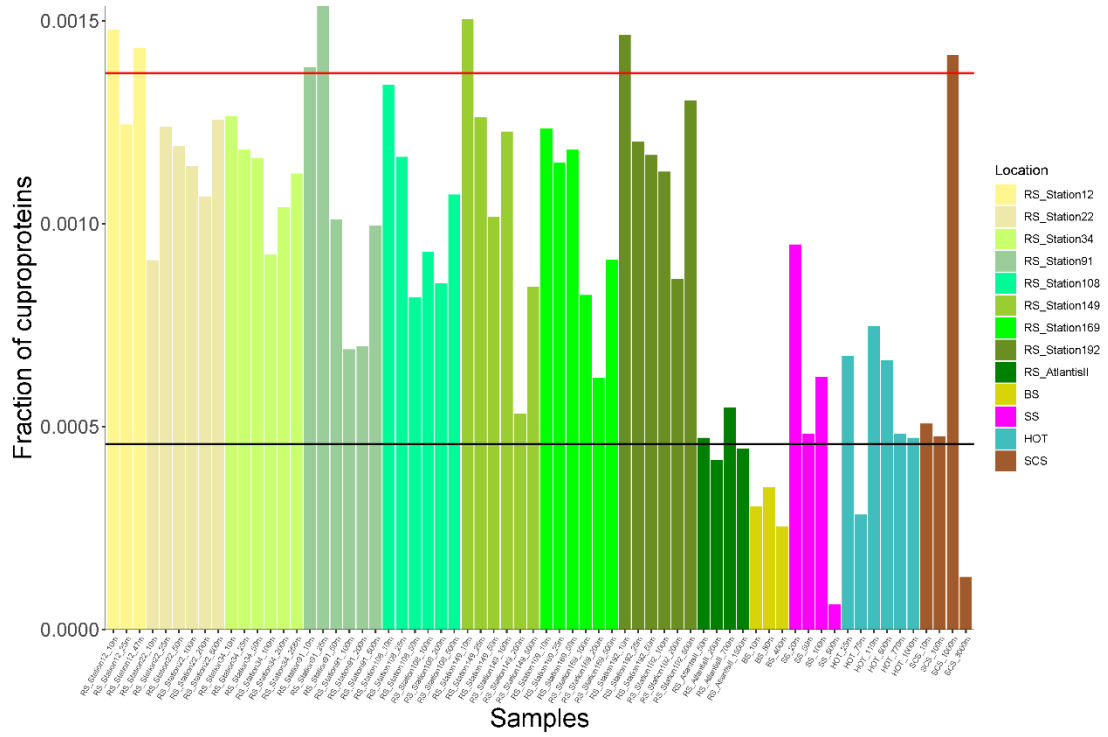


Figure S3

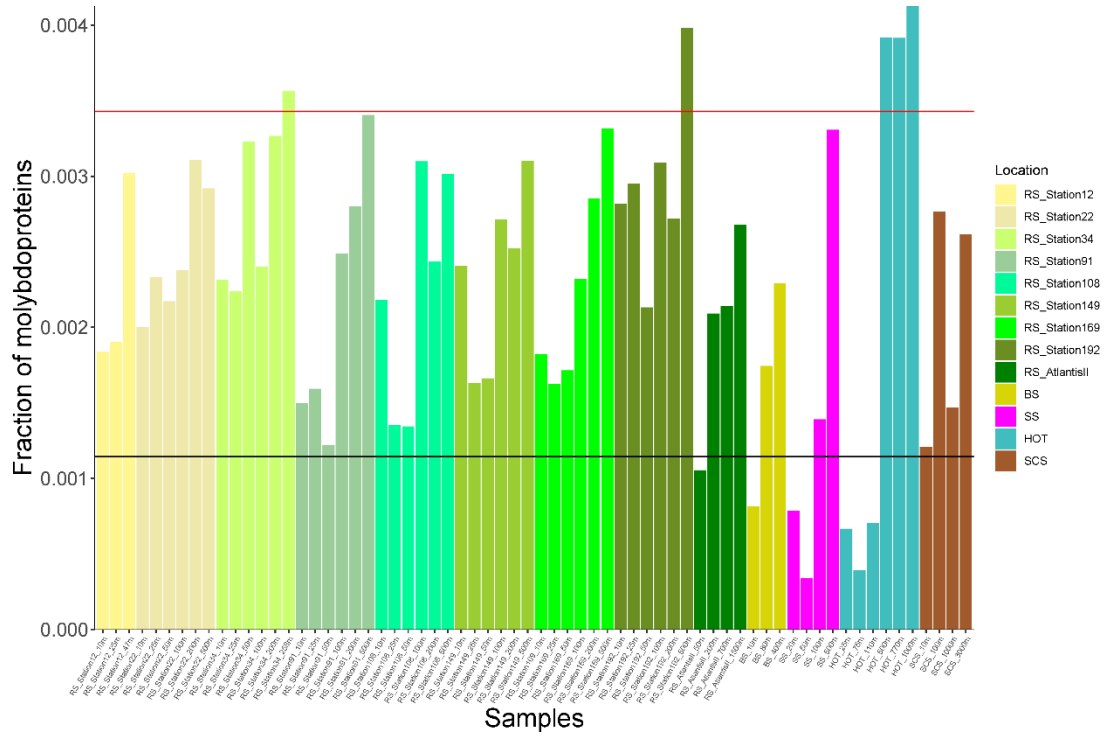


Figure S4

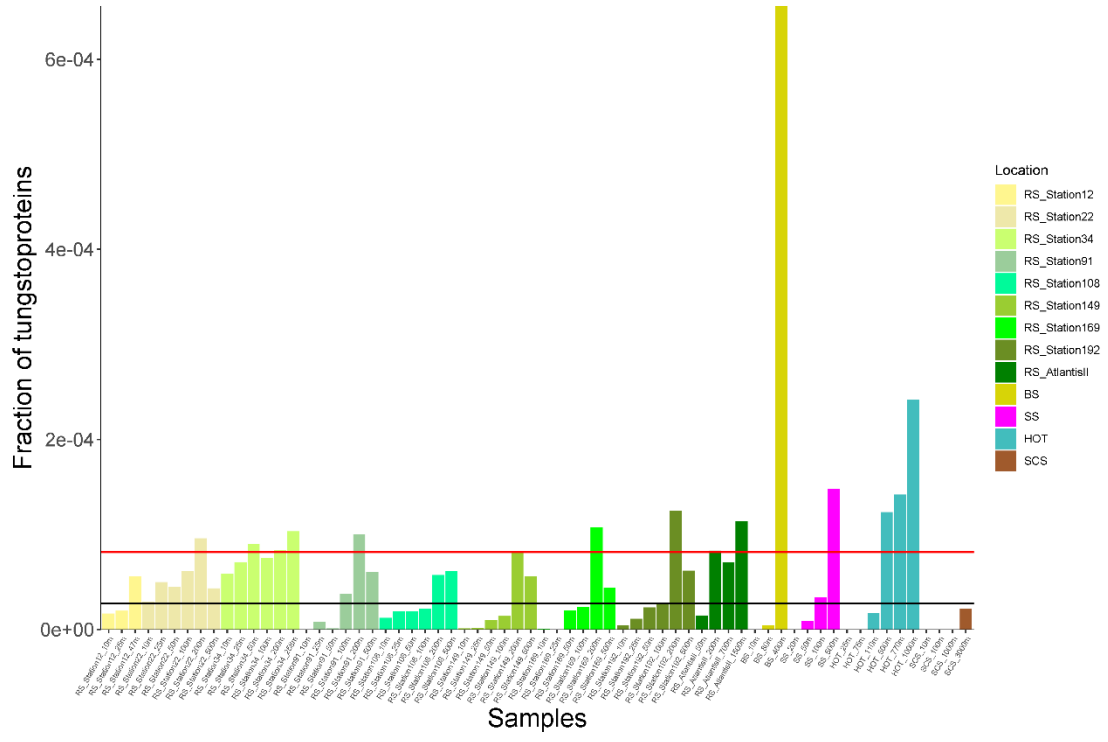


Figure S5

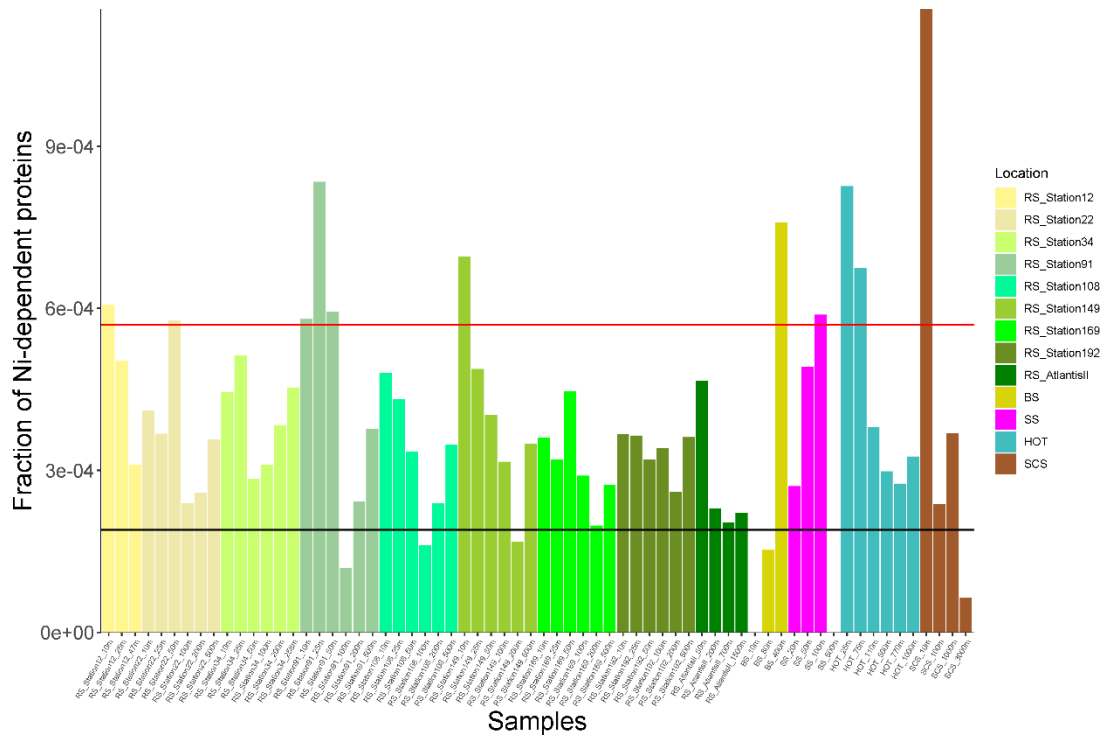


Figure S6

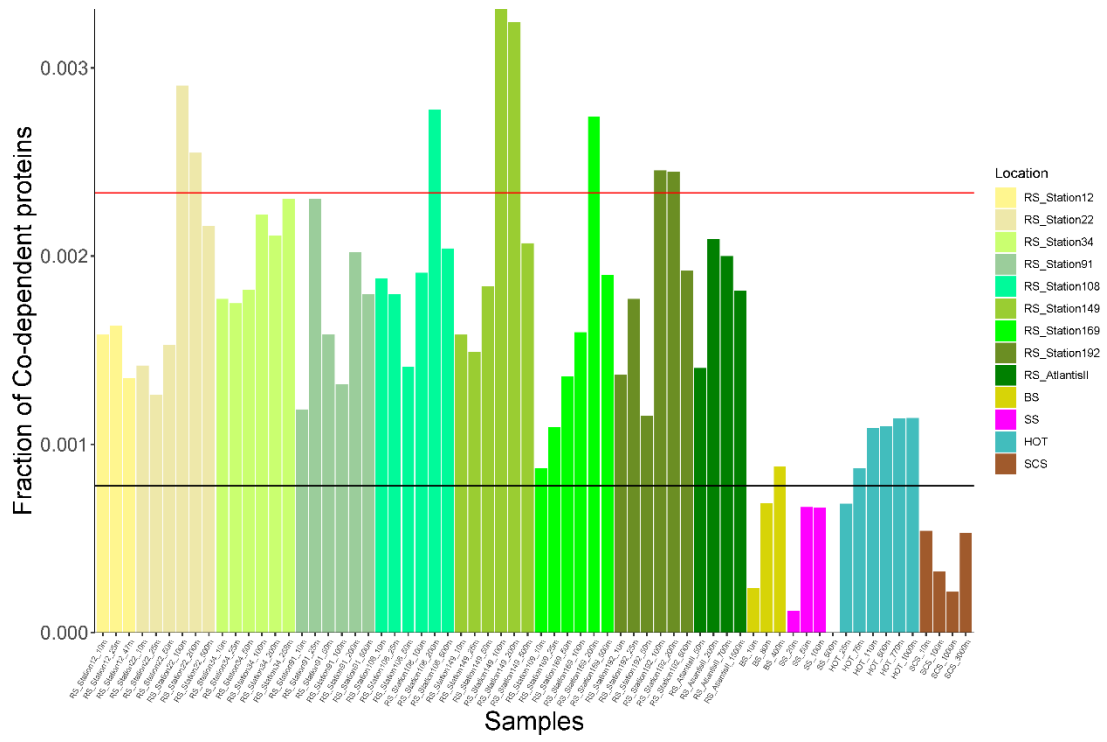


Figure S7

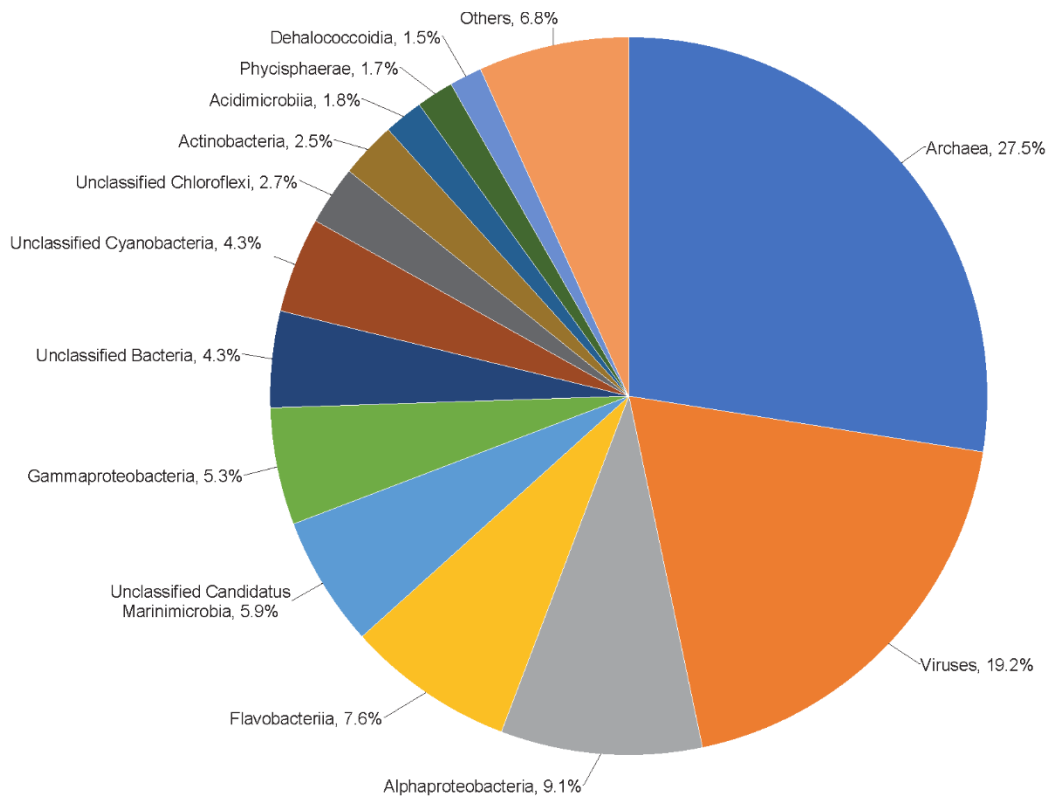


Figure S8

