

Supplemental Information

Hydrothermal trace metal release and microbial metabolism in the Northeast Lau Basin of the south Pacific Ocean

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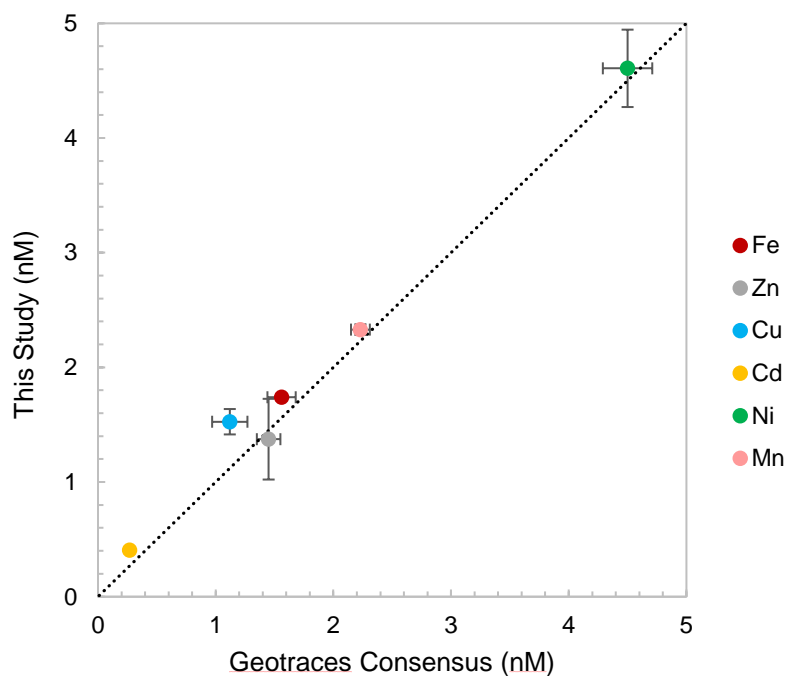
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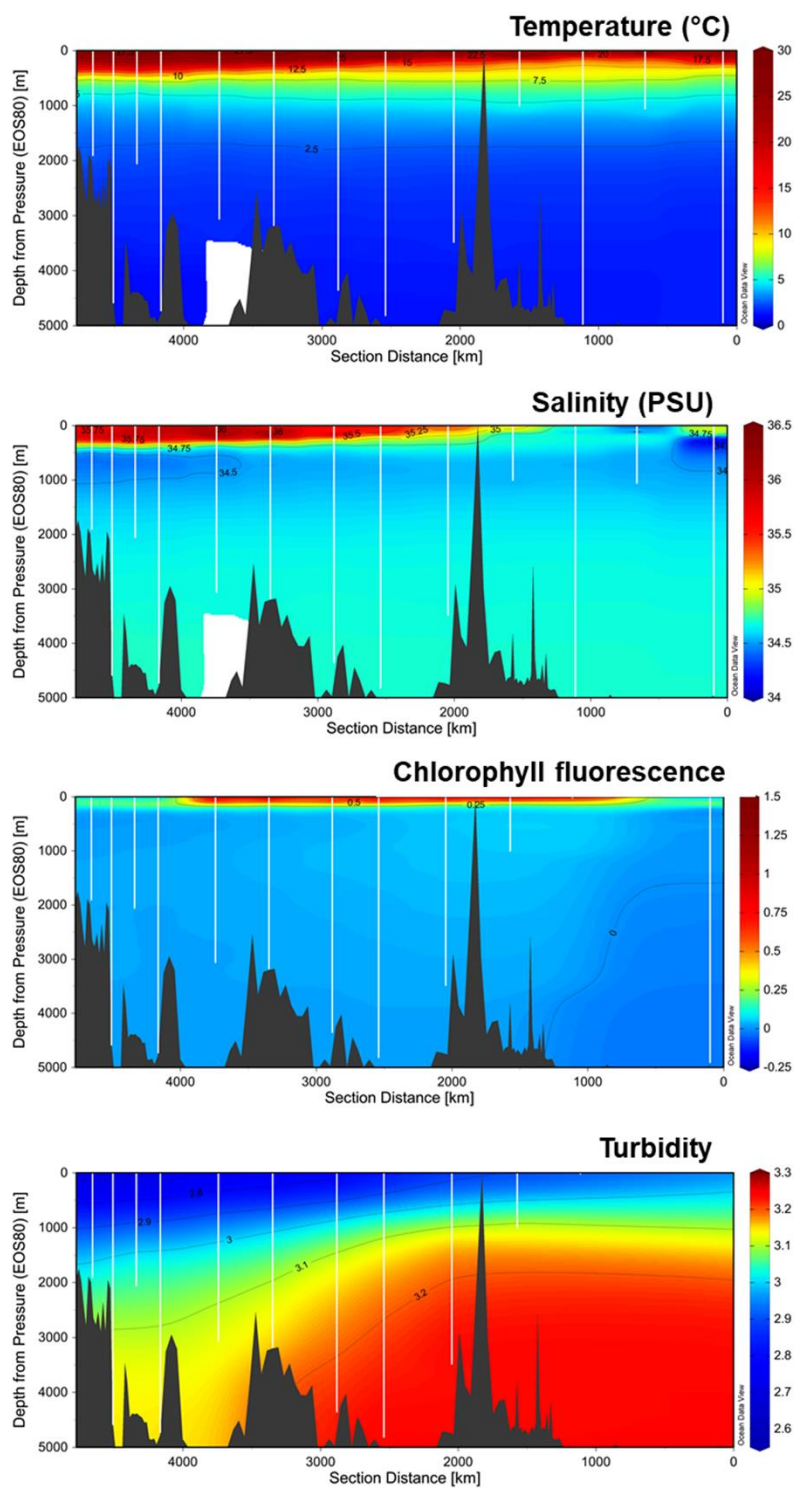
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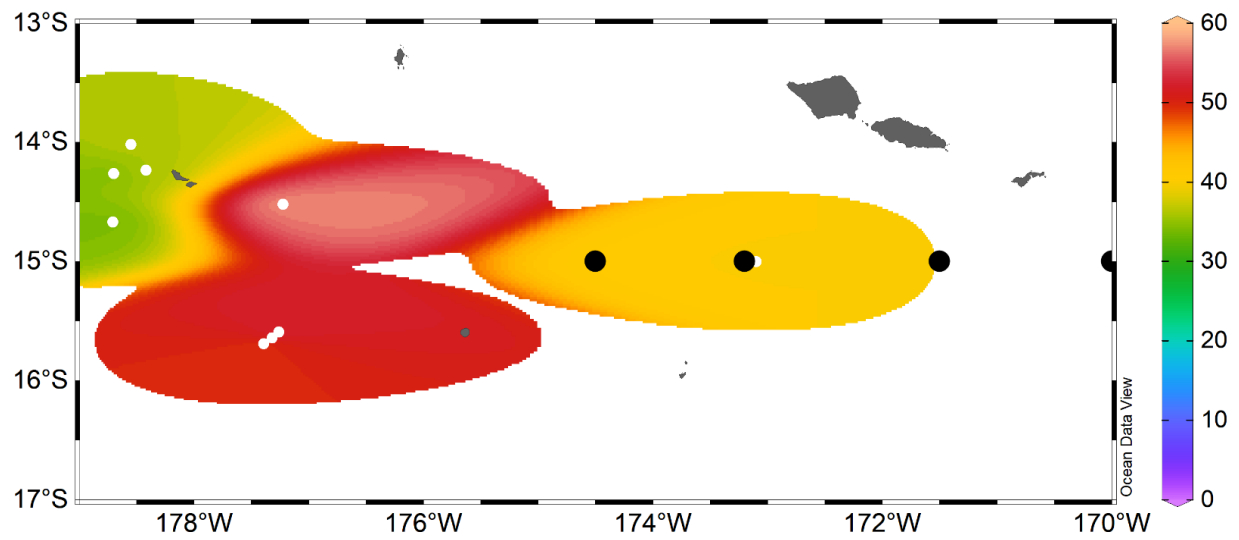
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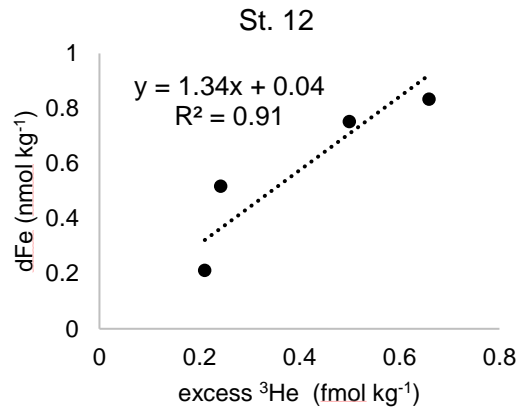
Supplemental Fig. 1. Comparison of Geotraces coastal surface seawater (GSC) standard concentrations between this study (n=3) and the Geotraces community consensus, as shown in Table 1. The dotted line shows a 1:1 relationship. Vertical and horizontal error bars represent the standard deviation.



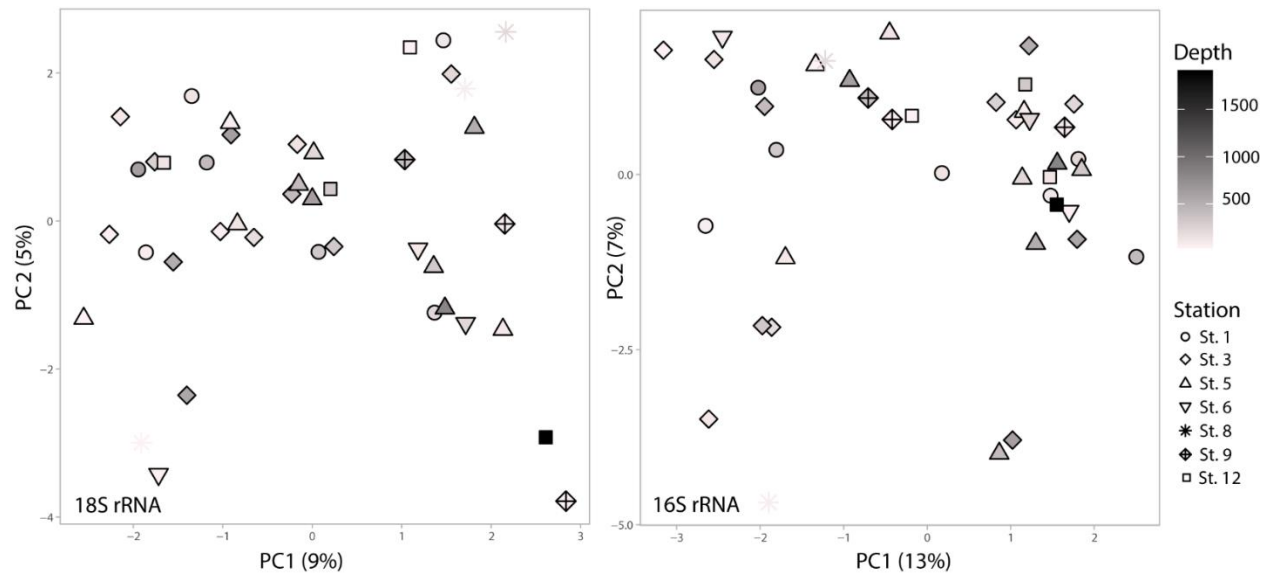
Supplemental Fig. 2. Temperature, salinity, fluorescence, and turbidity sections from the trace metal rosette CTD, plotted using weighted-gridding interpolation in Ocean Data View.



Supplemental Fig. 4. $\delta^3\text{He}$ in the southwest Pacific at 1,900m collected from the Global Oceanic Database of Tritium and Helium (Jenkins et al. 2019), plotted in Ocean Data View. $\delta^3\text{He}$ data points are shown in white, Metzyme stations are shown in black.

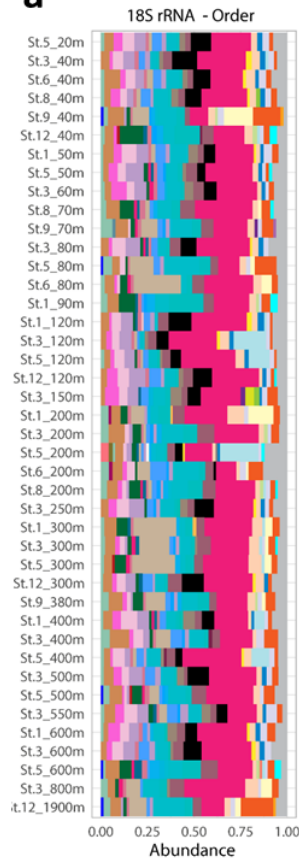


Supplemental Fig. 5 Estimated relationship between dissolved iron and excess helium in the NE Lau Basin using $\delta^3\text{He}$ reported in Lupton et al. (2004) at the same coordinates as Metzyme St. 12, and iron concentrations from St. 12. For comparison, the $\text{dFe}:\text{}^3\text{He}$ ratio obtained using Fe concentrations from St. 13 is shown in Fig 5C. A Type II linear regression is plotted (Glover et al., 2012). Total He and Ne concentrations were not available and were estimated for this region (Jenkins et al., 2019a). Upper water column ^3He concentrations were extrapolated using historical data from Lupton et al. (2004). St. 12 has two Fe maxima, neither of which align with the 1,726 m ^3He maximum, and therefore only the top of the profile is used in the regression.

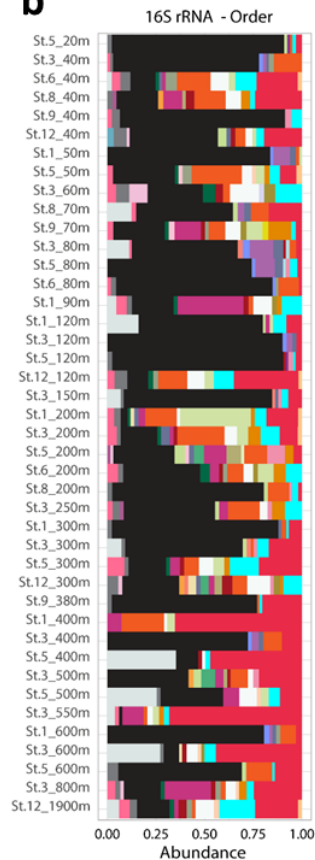


Supplemental Fig. 6. Principal coordinate analysis (PCoA) of 16S rRNA (left) and 18S rRNA (right) OTUs using Bray-Curtis dissimilarity within the R package *vegan*. OTUs were center-log-ratio transformed. The color scale represents surface to deep, with the deepest and hydrothermal sample in black. Each station is represented by a unique shape. Axes show the percent variation explained by each eigenvalue. These 16S rRNA and 18S rRNA data sets were published in Cohen et al. 2021.

a



b



Supplemental Fig. 7. Order-level community composition based on 16S rRNA OTU (left) and 18S rRNA OTU (right) relative abundance, depicted as stacked bar plots. Low abundance taxa contributing to less than 1% of the community were removed. Higher class or supergroup identification is indicated in parentheses. If no order-level assignment was available, the lowest classification was provided. These 16S rRNA and 18S rRNA data sets were published in Cohen et al. 2021.

Table S1. Metzyme sampling stations, depths, flow volumes, and protein concentrations.

Table S2. Metaproteomic spectral counts associated with proteins detected in deep waters (≥ 200 m). Only peptide spectral counts matching open reading frames (ORFs) with a classified taxonomic annotation and lineage probability index greater than 0.7 are shown. Exclusive spectral counts were normalized following the NSAF (normalized spectral abundance factor) approach. Relative abundance of proteins in the plume (St. 12, 1,900m) was compared to background deep sites (n=20) using a permutation test followed by Benjamini-Hochberg multiple test correction. Blue rows indicate differentially abundant proteins in hydrothermally-influenced seawater (FDR < 0.1).