Table S1. Results from pairwise PERMANOVA analyses of Bray Curtis dissimilarity beta diversity metrics of 16S microbial community data grouped by mineral used during the incubations. Comparisons highlighted in yellow indicated no statistically significant differences between the two treatment groups, indicated by a p-value greater than 0.05.

Treatment 1	**Treatment 2**	**P-value**
Ferrihydrite	Hematite	0.196
Ferrihydrite	Initial	0.001
Ferrihydrite	No Mineral	0.001
Hematite	Initial	0.001
Hematite	No Mineral	0.028
Initial	No Mineral	0.001

Table S2. Results from pairwise PERMANOVA analyses of Bray Curtis dissimilarity beta diversity metrics of 16S microbial community data grouped by inhibitor used during the incubations.

Treatment 1	**Treatment 2**	**P-value**
Molybdate	BES	0.001
BES	Initial	0.001
BES	No Inhibitor	0.017
Molybdate	Initial	0.001
Molybdate	No Inhibitor	0.001
Initial	No Inhibitor	0.001

Figure S1. Aqueous concentrations (mM) of sulfate, sulfide, butyrate, acetate, and methane over the duration of the experiment (71 days) for the 6 conditions. Error bars represent one standard deviation of experimental triplicates

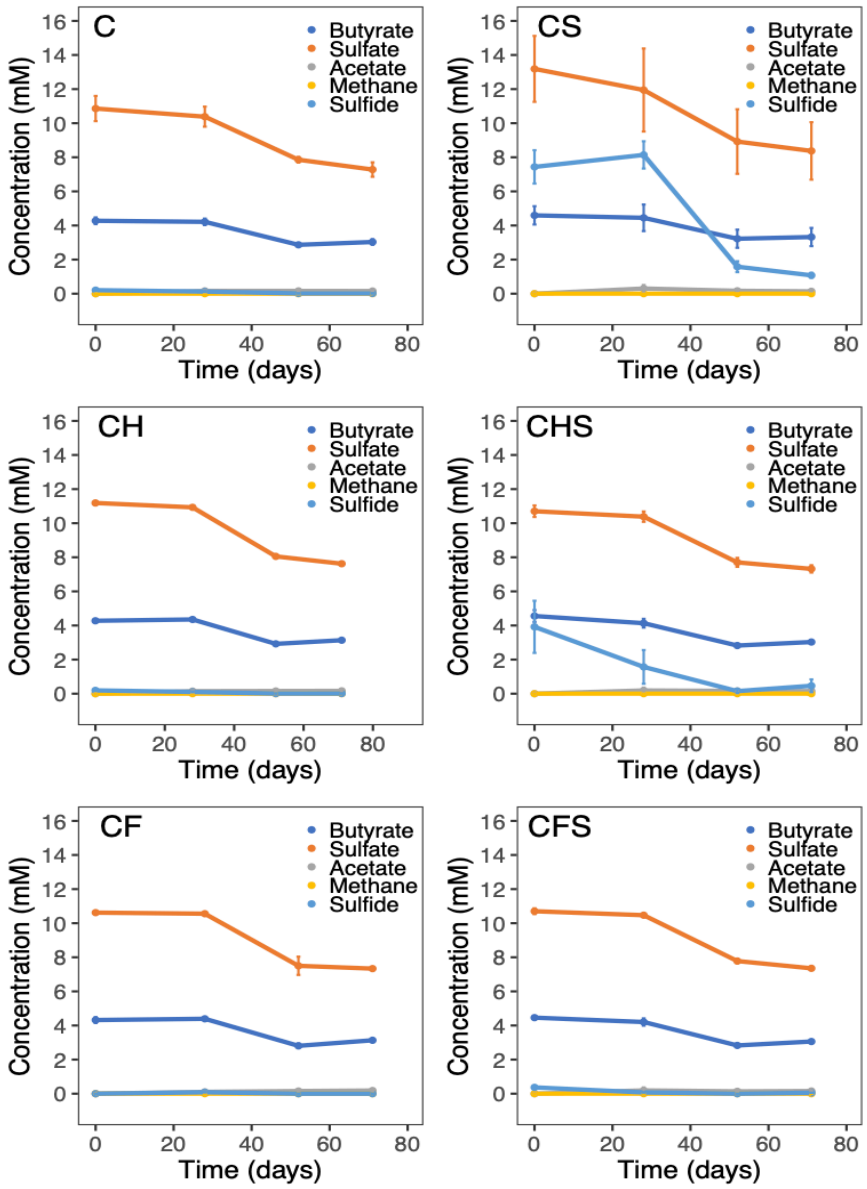

Figure S2. Fourier-transformed Fe K-edge extended x-ray absorption fine structure (EXAFS) data in samples collected after biotic incubations with either hematite (SH) or ferrihydrite (SF) compared with samples from abiotic control incubations using added sulfide with either hematite (CHS) or ferrihydrite (CFS). Fe K-edge EXAFS spectra from pure hematite and ferrihydrite are shown to identify potential similarities in the coordination environment with the experimental samples.

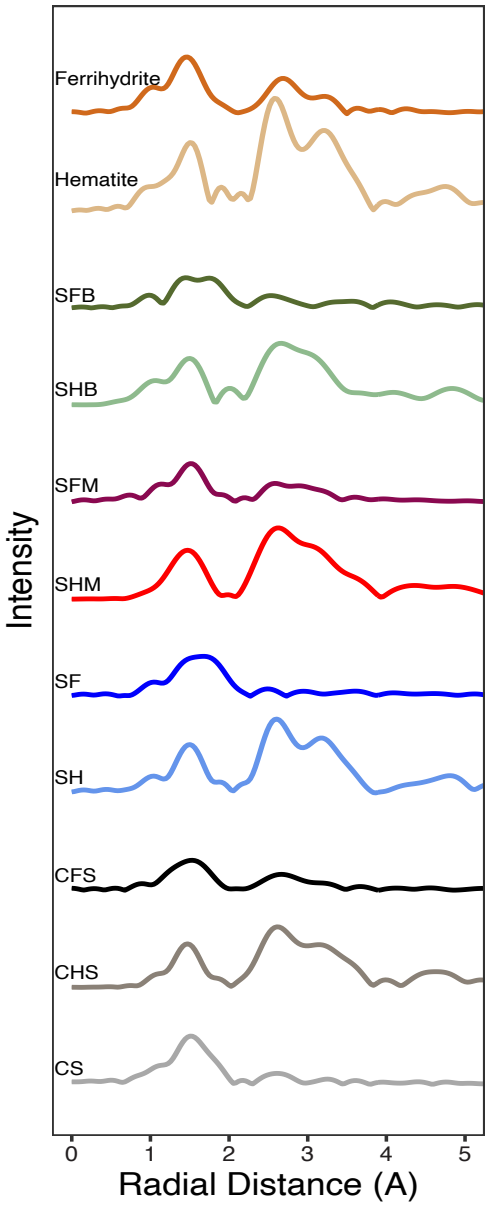

Figure S3. Alpha diversity statistical metrics for 16S community composition of initial inoculum and experimental samples grouped by mineral used during incubations. Error bars represent one standard deviation of experimental triplicates.

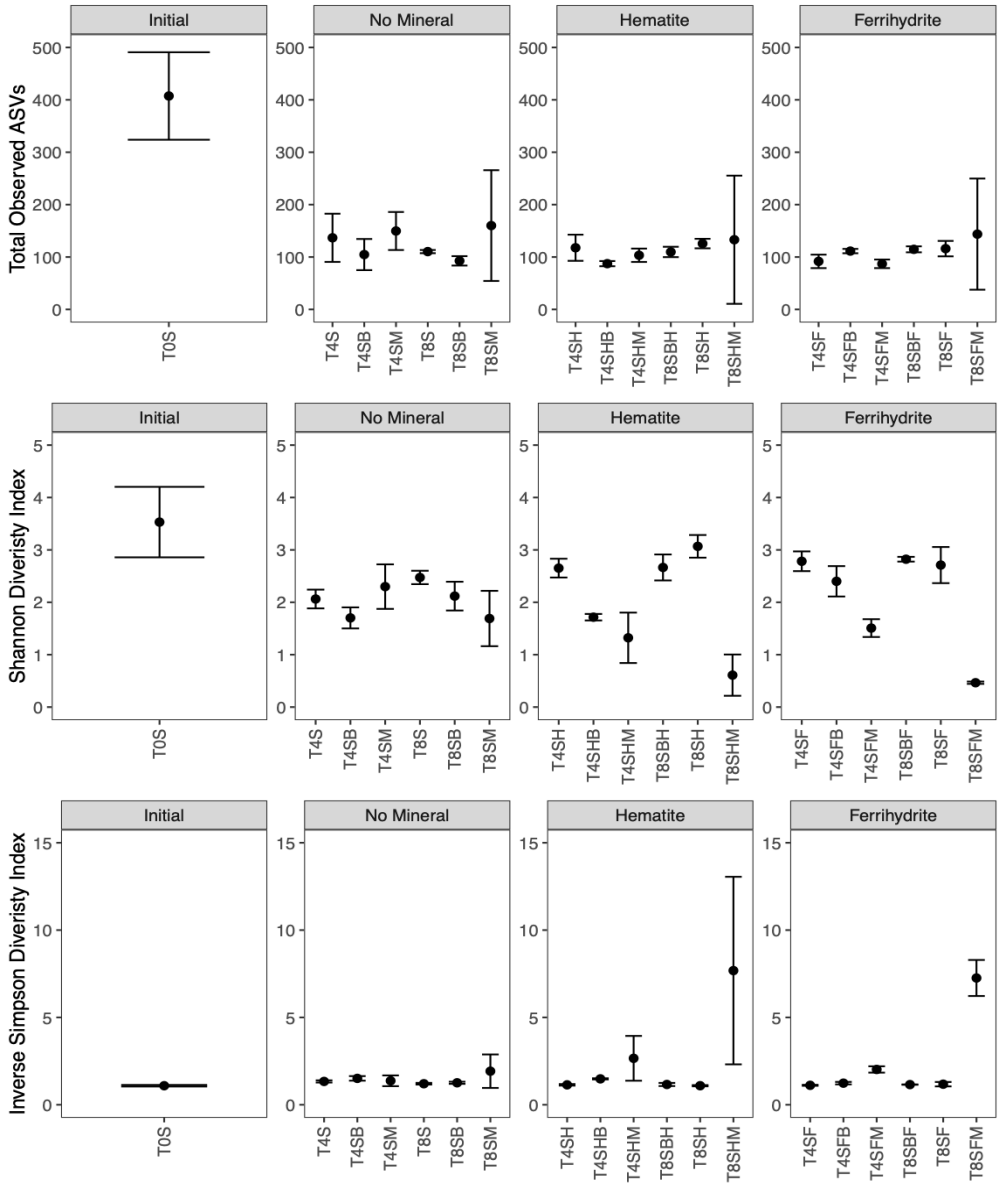

Figure S4. NMDS plot showing beta diversity of 16S microbial community data from samples taken at Days 0, 36, and 87 calculated using Bray Curtis dissimilarity metrics. Ellipses were overlaid for each mineral treatment group representing a 95% confidence interval for the standard deviation of the ellipses centroids.

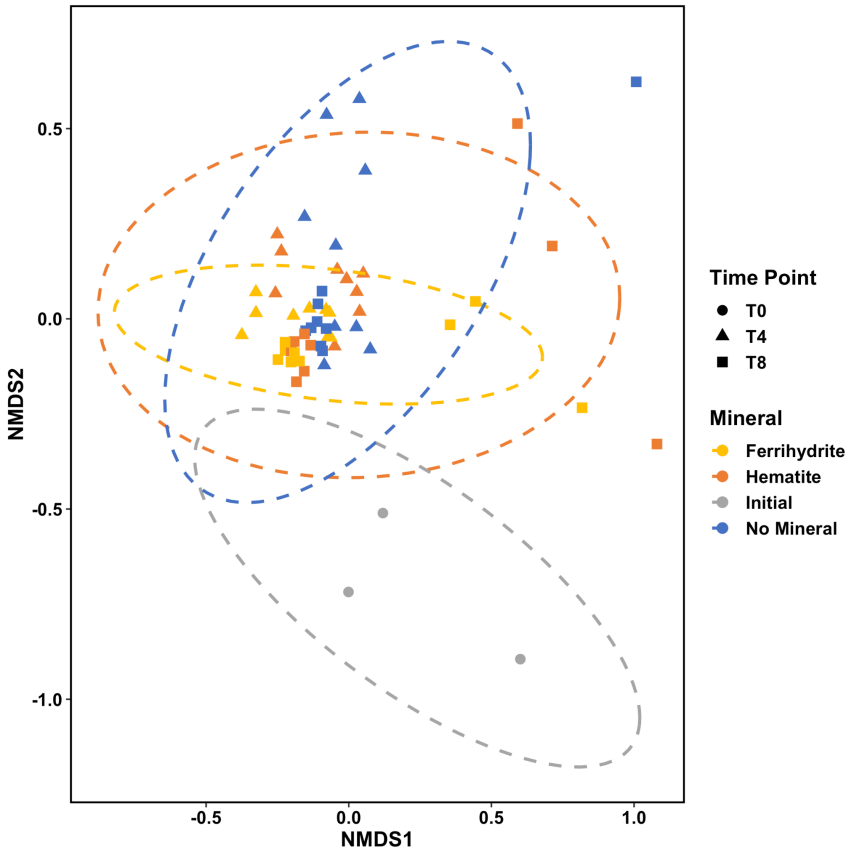

Figure S5. Microbial community composition data based on 16S rRNA phylogenetics using archaeal specific 519F/915R primers . Samples labeled with T4 or T8 were collected at Days 0, 36, or 87, respectively. Bar plots were grouped according to the mineral used during the incubation. DNA was extracted and sequenced for each experimental triplicate when possible.

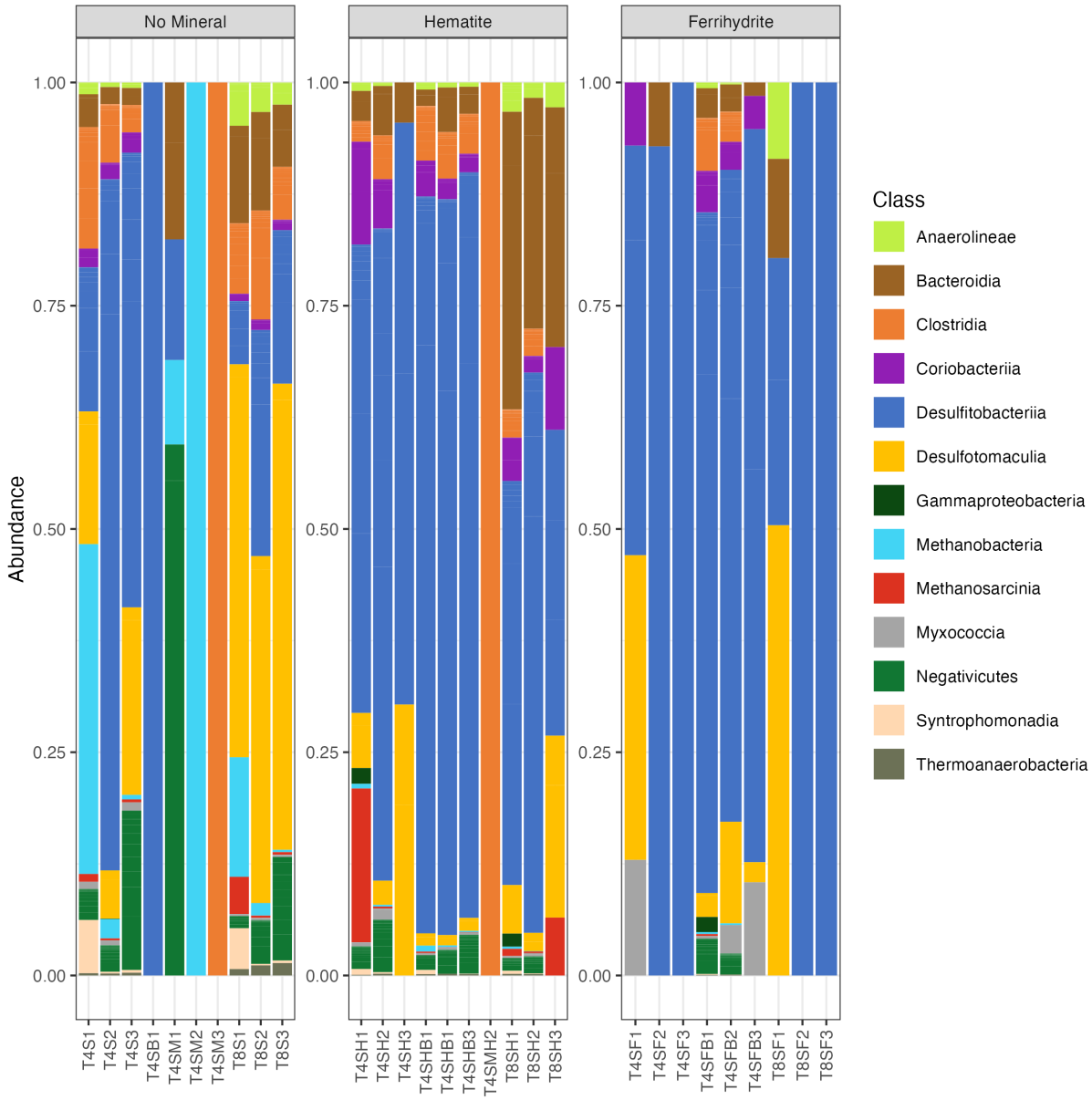

Figure S6. Microbial community composition data based on 16S rRNA phylogenetics. Bar plots were grouped according to the inhibitor used during the incubation. Samples labeled with T0, T4, or T8 were collected at Days 0, 36, or 87, respectively. DNA was extracted and sequenced

Figure S7. Acid extractable Fe(II) concentrations (uM) over the duration of our experiment. Cultures were sampled twice at each time point to obtain two technical replicates and error bars represent one standard deviation of experimental triplicates.