## TABLE CAPTIONS

***Table S1*** Overview of the BSF metagenomic assemblies used in this study, including quality measurements, number of contigs, and number of predicted proteins per assembly.

***Table S2*** Summary table with completion and contamination of the BSF MAGs used in this study (as determined through checkM).

***Table S3*** Functional read abundance for genes of interest in each assembly, normalized as transcripts per million (*TPM*).

***Table S4*** Genomic organization of aerobic CODH (*cox*) genes in the BSF MAGs and their associated enzyme form.

***Table S5*** Table of average nucleotide identity (ANI) results for the haloarchaeal MAGs compared against reference genomes of cultured haloarchaea carboxydovores.

***Table S6*** BLAST results for nitrogenase genes in the BSF metagenomes. Best BLAST hit reported here was determined by highest bit score and lowest e-value.

***Table S7*** BLAST results for *dsrAB* genes in the BSF metagenomes. Best BLAST hit reported here was determined by highest bit score and lowest e-value.

## FIGURE CAPTIONS

***Figure S1*** Recovered 13CH4 from the headspace of 13CO2 incubations for 4 sites at the BSF: 12B, 33, 41, and 56. Incubations were done aerobically and anaerobically with and without the addition of hydrogen gas, in triplicate. The x-axis represents layers in the sediment column at each site. Anaerobic incubations for layer 4 at site 56 failed.

***Figure S2*** Heatmap of normalized gene abundance (as scaled *TPM* values) for genes and complexes of interest at the BSF. Names on the left represent KEGG pathways associated with these genes, but overlaps with other functions are possible.