**Supplemental Files**

**Table S1:** Other MAGs greater than 18% complete and under 10% contamination as determined by CheckM. PhyloPhythiaS+ taxonomic consensus is reported if one third or more of the contigs in the MAG were assigned the same taxonomic grouping.

**Table S2:** Assembly quality statistics for each quality MAG.

**Table S3:** BLAST results for previously sequenced *nifH* genes.

**Table S4:** BLAST results for previously sequenced *mcrA* genes.

**Table S5:** Accession numbers for reference proteins used in Figure S2.

**Dataset S1:** KEGG.Module.Overview.For.Supplemental.xlsx - Complete and incomplete KEGG modules for the Methanosarcinales, Sulfurovum, Chloroflexi MAGs.

**Figure S1:** Coverage of taxonomic assignments of contigs in the assembly. Taxonomy is reported at the level of order. Exceptions are *Sulfurovum* and contigs with unassigned order, where lowest assignment is reported.

**Figure S2**: Phylogenetic trees of Lost City Methanosarcinales (LCMS) MAG genes in methanogenic pathways. **a.** formylmethanofuran-tetrahydromethanopterin formyltransferase (*ftr*), **b.** N5N10-methenyl-tetrahydromethanopterin cyclohydrolase (*mch*), **c.** F420-dependent N5N10-methylene-tetrahydromethanopterin dehydrogenase (*mtd*), **d.** and F420-dependent N5N10-methylene- tetrahydromethanopterin reductase (*mer*). Accession numbers for reference proteins can be found in Table S5.