



OTU	Class	Order	Family	Genus
1	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanofollis
2	Methanomicrobia	Methanosarcinales	Methanosarcinaceae	Methanosarcina
3	Methanomicrobia	Methanomicrobiales	Methanospirillaceae	Methanospirillum
4	Thermoplasmata	WCHA1-57	unclassified	unclassified
5	Methanomicrobia	Methanosarcinales	Methanosaetaceae	Methanosaeta
6	Halobacteria	Halobacteriales	Deep Sea Hydrothermal Vent Gp 6	unclassified
7	Thermoplasmata	Thermoplasmatales	Thermoplasmatales Incertae Sedis	Candidatus Methanomethylophilus
8	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium

**Figure S2:** Dual hierarchal clustering of the archaeal communities.

The eight OTUs identified based on 97% similarity, represent >99% of the total archaeal sequences observed in the enrichment culture and G1, G2, G3 digesters. The gradient scale ranges from 0 to 100% relative abundance. Sample names x1, x2 and x3 represent the enrichment culture. The sample names for digesters are denoted as follows: for example “nB1” – the prefix “n” represents “non-bioaugmented, the middle letter “B” represents Set-B and the suffix “1” represent the replicate number. The enrichment culture is dominated by *Methanosaeta* (OTU 5), *Methanospirillum* (OTU 4) and *WCHA1-57* (OTU 3). Set-A, B & C digesters, belonging to group G1 are dominated by *Methanosarcina* (OTU 2). G2 digesters, Set-D, E, F and G, are dominated by *Methanobacterium* (OTU 8). Set H and I are dominated by sequences related to *Methanobacterium* (OTU 8) and *DHVEG6* (OTU 6).