



OTU	Phylum	Class	Order	Family	Genus
1	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae	unclassified
2	Synergistetes	Synergistia	Synergistales	Synergistaceae	Thermovirga
3	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Desulfobulbus
4	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	unclassified	unclassified
5	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	Denitrovibrio
6	Hyd24-12	unclassified	unclassified	unclassified	unclassified
7	Spirochaetae	Spirochaetes	Spirochaetales	PL-11B10	unclassified
8	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Proteiniphilum
9	Bacteroidetes	vadinHA17	unclassified	unclassified	unclassified
10	Tenericutes	Mollicutes	NB1-n	unclassified	unclassified
11	Synergistetes	Synergistia	Synergistales	Synergistaceae	Aminivibrio
12	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Smithella
13	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
14	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter
15	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae	unclassified
16	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Thauera
17	Candidate division OP8	unclassified	unclassified	unclassified	unclassified
18	Spirochaetae	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta
19	Chlorobi	Ignavibacteria	Ignavibacteriales	unclassified	unclassified
20	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	unclassified
21	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	WCHB1-69	unclassified
22	Deferribacteres	Deferribacteres	Deferribacterales	SAR406 clade (Marine group A)	unclassified
23	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Defluviimonas
24	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	WCHB1-69	unclassified
25	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Meniscus

Figure S4: Bacterial community composition of the enrichment culture based on percent relative abundance.

The figure includes the 25 bacterial OTUs observed with the highest relative abundance which constituted 80% of the total bacterial sequences.