

**Table S1.** Phylogenetic affiliation and relative abundance of bacterial and archaeal 16S rRNA gene sequences retrieved from the clone libraries.

Phylogenetic group	Relative abundance, %		The most similar sequence	
	day 20	day 120	Closest relative species	Similarity, %
Archaea				
<i>Methanosaeta</i> ( <i>Methanotherix</i> )	4.3	0.0	<i>Methanosaeta thermophila</i> PT	95.8
<i>Methanosarcina</i>	86.0	25.0	<i>Methanosarcina thermophila</i> TM-1	100.0
<i>Methanomassiliicoccus</i>	3.2	21.9	<i>Methanomassiliicoccus luminyensis</i> B10	95.7
<i>Methanothermobacter</i>	3.2	53.1	<i>Methanothermobacter</i> <i>thermautotrophicus</i> Delta H	100.0
<i>Thermoprotei</i>	2.2	0.0	<i>Thermofilum uzonense</i> 1807-2	83.2
Bacteria				
<i>Thermacetogenium</i>	5.1	7.1	<i>Thermacetogenium phaeum</i> DSM 12270	97.1
<i>Syntrophaceticus</i>	30.4	42.9	<i>Syntrophaceticus schinkii</i> Sp3	96.4
<i>Syntrophomonas</i>	2.5	26.2	<i>Syntrophomonas wolfei</i> DSM 4212	
<i>Firmicutes</i>	2.5	26.2	<i>Hydrogenispora ethanolica</i> LX-B	87.6
<i>Anaerobaculum</i>	38.0	14.3	<i>Anaerobaculum hydrogeniformans</i> OS1	100.0
<i>Atribacteria</i>	1.3	2.4	<i>Caldanaerobacter subterraneus</i> DSM 13054	81.2
<i>Tepidiphilus</i>	2.5	0.0	<i>Tepidiphilus margaritifer</i> N2-214	99.4
<i>Anaerolineae</i>	15.3	7.1	<i>Thermanaerotherix daxensis</i> GNS-1	96.0
<i>Mesotoga</i>	1.3	0.0	<i>Mesotoga infera</i> VNs100	99.9
<i>Thermotoga</i>	1.3	0.0	<i>Pseudothermotoga profunda</i> AZM34c06	97.4