

**Table S1**

Relative abundance and close relatives of some OTUs ( $\geq 0.2\%$  of total reads at least in one of the communities).

"0.00%" implies no reads detected. Uncultured/environmental sample sequences were included in descriptions if 16S rRNA gene sequence identity was below 90% nt to any known species.

Phylum	OTUs	Relative abundance		Descriptions (Accession No.)	Identity (%)
		Wall Site	Steram Site		
<i>Acidobacteria</i>	denovo34541	0.00%	0.32%	Uncultured Acidobacteria bacterium clone YNP_SBC_BP4_B26 (HM448257)	96.4%
					<i>Stenotrophobacter roseus</i> strain Ac_15_C4 (NR_146022), <i>Stenotrophobacter namibiensis</i> strain Ac_17_F2 (NR_146021)
<i>Aquificae</i>	denovo14971	65.4%	50.3%	<i>Sulfurihydrogenibium azorense</i> Az-Fu1 (NR_102858), <i>Sulfurihydrogenibium kristjanssonii</i> I6628 (NR_042660)	100%
	denovo48891	5.65%	11.30%	<i>Thermocrinis ruber</i> strain DSM 23557 (CP007028)	96.0%
	denovo14492	1.17%	0.37%	<i>Sulfurihydrogenibium azorense</i> Az-Fu1 (NR_102858)	96.8%
	denovo15700	0.59%	0.18%	<i>Hydrogenobacter subterraneus</i> HGP1 (NR_024729), <i>Thermothrix azorenensis</i> strain TM (NR_104832)	99.6%
	denovo18902	0.31%	0.36%	<i>Thermocrinis ruber</i> DSM 23557 (CP007028), <i>Thermocrinis ruber</i> OC 1/4 (NR_121741)	94.1%
	denovo53671	0.23%	0.05%	<i>Sulfurihydrogenibium azorense</i> Az-Fu1 (NR_102858)	98.4%
	denovo50041	0.22%	0.07%	<i>Sulfurihydrogenibium azorense</i> Az-Fu1 (NR_102858)	98.4%
	denovo26756	0.21%	0.03%	<i>Sulfurihydrogenibium azorense</i> Az-Fu1 (NR_102858)	97.2%
	denovo29919	0.08%	0.20%	<i>Thermocrinis jamiesonii</i> GBS1 (NR_145905), <i>Hydrogenobacter subterraneus</i> strain HGP1 (NR_024729)	96.4%
<i>Armatimonadetes</i>	denovo15330	0.00%	2.48%	Uncultured Armatimonadetes bacterium, clone: ST-B09_1 (AB735180)	100%
				<i>Pelotomaculum thermopropionicum</i> strain SI (NR_074685)	87.3%
	denovo36368	0.00%	0.48%	Uncultured bacterium clone NKB_56_N2 (JF826973) <i>Carboxydotherrnus islandicus</i> strain SET IS-9 (NR_108577), <i>Thermoterrabacterium ferrireducens</i> (U76364)	100% 86.8%
<i>Chlorobi</i>	denovo54962	0.01%	0.98%	Uncultured Chlorobi bacterium DNA, fosmid clone: JFF027_B02 (AP011715) <i>Rhodothermus clarus</i> (AB252420), <i>Rhodothermus marinus</i> (AY986798)	99.6% 88.4%
					<i>Dictyoglomus turgidum</i> DSM 6724 (CP001251)
<i>Dictyoglomi</i>	denovo10055	0.28%	0.11%		
<i>Firmicutes</i>	denovo9761	0.49%	0.01%	<i>Caldicellulosiruptor lactoaceticus</i> 6A (NR_074772), <i>Caldicellulosiruptor kristjanssonii</i> I77R1B (NR_074768), <i>Caldicellulosiruptor acetigenus</i> X6B (NR_115321)	100%
					<i>Caldimicrobium rimae</i> DS (NR_044283)
<i>Thermodesulfobacteria</i>	denovo20616	1.08%	0.21%		
	denovo155	0.42%	0.04%	<i>Caldimicrobium thiodismutans</i> (LC055107)	100%
<i>Thermotogae</i>	denovo34660	1.01%	0.00%	<i>Fervidobacterium nodosum</i> Rt17-B1 (NR_074093)	100%
<i>Thermotogae</i> (EM3)	denovo46213	0.00%	1.15%	Uncultured Bacteroidetes bacterium clone HGM-U-2 (AB539622)	98.0%
				<i>Actinomadura rayongensis</i> strain RY35-68 (NR_134688)	82.7%
				Uncultured bacterium clone NKB_56_T2 (JF826975) <i>Actinomadura atramentaria</i> strain DSM 43919 (NR_114850)	77.1% 82.3%
<i>Thermus</i>	denovo18496	2.17%	3.69%	<i>Thermus arciformis</i> TH92 (NR_116251)	100%
uncultured division	denovo56209	0.02%	0.67%	Uncultured bacterium clone NKB_56_V 16S ribosomal RNA gene	99.6%
				<i>Thermoanaerobacter cellulolyticus</i> IFO 14436 (L09183)	81.7%