Table S1. Sequencing depth (as number of V6 tag sequences), observed number of OTUs (operational taxonomic units), richness estimators (ACE and Chao1), and Simpson's Reciprocal Index of diversity for all archaeal and bacterial OTUs in this study

	Archaea	Bacteria
V6 tag sequences	167,031	43,027
Unique sequence types	2,635 (1,163)	2,082
OTUs (3% distance)	817 (444)	1,135
ACE (3% distance)	980–1,024 (543–642)	2,203–2,362
Chao1 (3% distance)	943–1078 (524–641)	1,692–2,048
Simpson's Reciprocal Index (3% distance)	2.3 (2.3)	12.5
OTUs (10% distance)	116 (81)	653
ACE (10% distance)	142–191 (85–111)	1,215–1,294
Chao1 (10% distance)	130–246 (83–124)	922–1189
Simpson's Reciprocal Index (10% distance)	2.04 (2.04)	11.1

Values in parentheses are derived from randomly resampling the 167,031 archaeal tags down to 43,027 tags to compare archaeal diversity with bacterial diversity at equal sequencing efforts. The 167,031 archaeal tags includes 139,086 tags from the 454 Life Sciences FLX pyrosequencer and 27,945 tags from the 454 Life Sciences GS20 pyrosequencer.