Table S2. Numbers of archaeal tag sequences and OTUs clustered with a 3% distance threshold for the most frequently detected phyla, classes, and orders

Phylum	Class	Order	Sample 1 (34 yr) Tags	OTUs	Sample 2 (43 yr) Tags	OTUs	Sample 3 (128 yr) Tags	OTUs	Sample 4 (1,245 yr) Tags	OTUs
Crenarchaeota	MBGA	Unassigned	3	2	0	0	0	0	0	0
Crenarchaeota	MGI	Unassigned	5	3	0	0	0	0	0	0
Crenarchaeota	Thermoprotei	Unassigned	45	11	0	0	3	1	2	1
Crenarchaeota	Unassigned	Unassigned	259	27	0	0	10	5	7	4
Euryarchaeota	Methanomicrobia	Methanosarcinales	14,689	281	16,258	264	16,199	256	12	4
Euryarchaeota	Methanomicrobia	Methanosaetaceae	0	0	0	0	0	0	265	5
Euryarchaeota	Misc.		4	1	0	0	0	0	2	1
Euryarchaeota	Unassigned	Unassigned	53	15	0	0	2	1	15,935	116
Korarchaeota	Unassigned	Unassigned	2	1	0	0	0	0	0	0
Unassigned	Unassigned	Unassigned	1020	1	2	1	46	1	37	4
Archaea total			16,260	342	16,260	265	16,260	265	16,260	135

Taxonomies were assigned with the GAST algorithm (1). Numbers of tag sequences have been normalized down to a total of 16,260 sequences per sample by random resampling after OTU clustering. Prenormalized total numbers of tag sequences were 16,260 (sample 1); 32,345 (sample 2); 25,471 (sample 3); and 21,983 (sample 4). Most of the OTUs labeled 'LCMS' in Fig. 3 of the main text were assigned to order *Methanosarcinales*; most ANME-1 OTUs were assigned to *Euryarchaeota* unassigned; and most MGI OTUs were assigned to "*Crenarchaeota* unassigned" or "unassigned."