

Table S3. Numbers of bacterial 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)		Sample 2 (43 yr)		Sample 3 (128 yr)		Sample 4 (1,245 yr)	
			Tags	OTUs	Tags	OTUs	Tags	OTUs	Tags	OTUs
Acidobacteria	Acidobacteria	Acidobacteriales	0	0	0	0	10	7	3	2
Acidobacteria	Unassigned	Unassigned	0	0	0	0	1	1	0	0
Actinobacteria	Actinobacteria	Misc.	0	0	2	2	12	5	23	9
Actinobacteria	Unassigned	Unassigned	0	0	0	0	3	1	14	2
Bacteroidetes	Bacteroidia	Bacteroidales	0	0	0	0	3	1	1	1
Bacteroidetes	Flavobacteria	Flavobacteriales	27	7	103	18	301	37	40	10
Bacteroidetes	Sphingobacteria	Sphingobacteriales	42	4	29	8	39	21	11	9
Bacteroidetes	Unassigned	Unassigned	36	2	11	4	48	12	3	1
BRC1	Unassigned	Unassigned	0	0	0	0	89	5	163	9
Chloroflexi	Anaerolineae	Unassigned	2	1	0	0	0	0	0	0
Chloroflexi	Caldilineae	Caldilineales	1	1	3	1	11	1	1	1
Chloroflexi	Dehalococcoidetes	Unassigned	0	0	0	0	1,083	17	518	8
Deferribacteres	Deferribacteres	Deferribacterales	5	1	0	0	7	2	1	1
Deferribacteres	Unassigned	Unassigned	0	0	0	0	1	1	0	0
Deinococcus- Thermus	Deinococci	Misc.	31	4	0	0	0	0	0	0
Firmicutes	Bacilli	Misc.	0	0	1	1	2	1	0	0
Firmicutes	Clostridia	Misc.	1,073	42	426	31	228	21	57	9
Nitrospira	Nitrospira	Nitrospirales	0	0	3	1	601	8	83	3
OD1	Unassigned	Unassigned	0	0	8	2	62	10	10	5
Proteobacteria	Alphaproteobacteria	Misc.	15	3	24	10	14	9	9	7
Proteobacteria	Alphaproteobacteria	Rhodobiales	121	3	15	6	64	6	45	13
Proteobacteria	Alphaproteobacteria	Rhodobacteriales	273	19	1294	40	545	39	2146	50
Proteobacteria	Alphaproteobacteria	Unassigned	102	9	108	7	149	25	140	16
Proteobacteria	Betaproteobacteria	Burkholderiales	15	3	11	5	72	6	13	7
Proteobacteria	Betaproteobacteria	Misc.	0	0	3	1	6	3	0	0
Proteobacteria	Deltaproteobacteria	Desulfobacteriales	5	2	52	9	379	30	96	13
Proteobacteria	Deltaproteobacteria	Desulfobacteriales	15	5	3	3	2	2	1	1
Proteobacteria	Deltaproteobacteria	Misc.	0	0	14	6	18	11	14	9
Proteobacteria	Epsilonproteobacteria	Campylobacteriales	158	9	29	9	36	11	21	4
Proteobacteria	Epsilonproteobacteria	Nautiliales	0	0	0	0	1	1	0	0
Proteobacteria	Gammaproteobacteria	Methylococcales	0	0	54	3	233	7	221	6
Proteobacteria	Gammaproteobacteria	Thiotrichales	3,483	42	3,122	56	371	21	1,429	30
Proteobacteria	Gammaproteobacteria	Misc.	114	10	153	21	459	42	192	32
Proteobacteria	Unassigned	Unassigned	2	2	52	11	325	14	182	15
Tenericutes	Mollicutes	Acholeplasmatales	0	0	1	1	35	4	5	2
Thermomicrobia	Unassigned	Unassigned	2	1	3	1	23	1	2	2
Misc. assigned*			42	6	7	7	63	23	21	11
Unassigned			3	1	36	6	271	22	102	19
Bacteria total			5,567	177	5,567	270	5,567	428	5,567	307

Taxonomies were assigned with the GAST algorithm (1). Numbers of tag sequences have been normalized down to a total of 5,567 sequences per sample by random resampling after OTU clustering. Prenormalized total numbers of tag sequences were 21,582 (sample 1); 5,567 (sample 2); 7,162 (sample 3); and 8,716 (sample 4). All of the *Thiomicrospira* sequences in Fig. 6 of the main text are included under *Thiotrichales* here. Most of the "misc" *Clostridia* sequences have high sequence similarity to previously published *Desulfotomaculum*-like clones (2).

*Misc. assigned includes: *Chlamydiae*, *Chlorobi*, *Cyanobacteria*, *Fibrobacteres*, *Fusobacteria*, *Gemmatimonadetes*, *Lentisphaerae*, *Planctomycetes*, *Spirochaetes*, *Thermotogae*, TM7, and *Verrucomicrobia*