Table S1. List of primers and barcode sequences used in this study.

SampleID	Barcode Sequence	Linker Primer Sequence
H1	TACTCTCGTG	CCTAYGGGRBGCASCAG
H2	TAGAGACGAG	CCTAYGGGRBGCASCAG
H3	TCGTCGCTCG	CCTAYGGGRBGCASCAG
A1	ACATACGCGT	CCTAYGGGRBGCASCAG
A2	ACGCGAGTAT	CCTAYGGGRBGCASCAG
B1	ACTACTATGT	CCTAYGGGRBGCASCAG
B2	ACTGTACAGT	CCTAYGGGRBGCASCAG
B3	AGACTATACT	CCTAYGGGRBGCASCAG
B4	AGCGTCGTCT	CCTAYGGGRBGCASCAG
C1	AGTACGCTAT	CCTAYGGGRBGCASCAG
C2	ATAGAGTACT	CCTAYGGGRBGCASCAG
C3	CACGCTACGT	CCTAYGGGRBGCASCAG
D1	CAGTAGACGT	CCTAYGGGRBGCASCAG
D2	CGACGTGACT	CCTAYGGGRBGCASCAG
D3	TACACACACT	CCTAYGGGRBGCASCAG
D4	TACACGTGAT	CCTAYGGGRBGCASCAG
D5	TACAGATCGT	CCTAYGGGRBGCASCAG
E1	TACGCTGTCT	CCTAYGGGRBGCASCAG
E2	TAGTGTAGAT	CCTAYGGGRBGCASCAG
G1	TCTAGCGACT	CCTAYGGGRBGCASCAG
G2	TCTATACTAT	CCTAYGGGRBGCASCAG
G3	TGACGTATGT	CCTAYGGGRBGCASCAG
F1	ACAGTATATA	CCTAYGGGRBGCASCAG
F2	ACGCGATCGA	CCTAYGGGRBGCASCAG
I1	TCGATCACGT	CCTAYGGGRBGCASCAG
I2	TCGCACTAGT	CCTAYGGGRBGCASCAG

Table S2. Relative abundance of major phyla in each sample used for Figure 3.

Taxon	A1	A2	B1	B2	B3	B4	C1	C2	C3	D1	D2	D3	D4	D5	E1	E2	F1	F2	G1	G2	G3	H1	H2	H3	I1	I2	mean
Crenarchaeota	0.0	0.0	0.2	0.0	0.0	0.0	0.2	0.2	0.1	0.0	0.0	0.6	1.8	0.5	0.1	0.0	0.2	0.0	0.9	0.2	0.4	0.1	0.3	0.4	0.9	0.2	0.3
Euryarchaeota	36.2	0.4	0.2	7.0	7.5	16.0	0.1	0.1	16.4	0.2	0.0	28.0	1.1	37.5	3.3	3.8	0.2	1.6	0.1	0.0	0.1	0.1	0.1	0.1	0.0	0.0	6.2
Unclassified archaea	0.1	0.1	1.8	0.2	0.2	0.1	0.1	0.6	0.1	0.2	1.9	5.2	11.3	1.7	3.1	0.0	0.1	0.0	0.8	0.3	0.8	0.1	1.1	3.9	0.5	0.1	1.3
Acidobacteria	0.1	2.5	14.2	0.7	2.0	1.6	8.3	7.7	2.1	7.7	13.7	3.6	2.8	5.2	6.7	1.3	11.1	1.8	10.8	9.7	7.9	10.9	14.6	3.6	21.4	0.6	6.6
Actinobacteria	2.4	16.4	10.8	5.6	4.7	13.2	14.0	11.3	12.8	8.0	7.6	2.1	1.0	2.2	5.3	9.2	13.4	13.5	13.1	14.5	18.0	14.5	11.1	0.4	6.2	10.3	9.3
BRC1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Bacteria_incertae_sedis	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.1	0.0	0.0	0.1	0.0	0.0	1.5	0.0	1.9	0.0	0.2
Bacteroidetes	0.8	0.9	1.2	0.3	1.0	0.9	3.3	1.0	0.3	1.1	1.3	2.0	4.3	1.5	0.5	2.9	0.4	4.4	0.7	2.0	3.5	2.4	2.3	7.7	0.3	0.9	1.8
Caldiserica	0.2	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Chlamydiae	0.0	0.3	1.2	0.2	0.3	0.3	0.5	0.4	0.5	0.2	0.8	0.1	0.2	0.2	0.5	0.7	0.1	0.3	0.7	0.8	0.6	0.3	0.3	1.5	0.2	0.0	0.4
Chloroflexi	11.5	1.0	1.0	2.3	3.4	5.0	0.9	0.7	3.1	0.7	2.0	4.7	8.1	3.5	1.6	9.1	1.4	6.7	1.4	1.0	1.2	0.7	1.1	1.9	0.5	0.0	2.9
Cyanobacteria	0.0	0.2	0.1	0.3	0.0	0.1	0.0	0.5	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.5	1.1	0.4	0.1	1.7	0.0	0.0	0.2
Deinococcus-Thermus	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Fibrobacteres	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0
Firmicutes	6.0	24.3	2.1	46.8	25.0	13.6	16.0	7.9	16.6	1.2	3.3	1.2	1.6	4.2	1.5	0.3	5.5	5.2	5.5	9.2	7.2	3.2	3.3	12.9	7.3	3.6	9.0
Gemmatimonadetes	0.0	0.2	0.2	0.0	0.0	0.0	0.5	0.4	0.1	0.7	0.6	0.1	0.0	0.0	0.6	0.2	0.8	0.1	0.5	0.4	0.7	0.3	0.2	0.0	0.0	0.0	0.3
Nitrospira	0.0	0.2	0.8	0.0	0.0	0.1	0.9	0.5	0.0	0.7	0.2	0.0	0.0	0.0	0.6	0.0	0.6	0.1	1.3	0.6	0.7	0.4	0.3	0.0	0.0	0.0	0.3
Bacteria;OD1	0.2	0.0	0.4	0.1	0.0	0.0	0.1	0.1	0.1	0.4	0.4	0.1	0.1	0.5	0.3	0.3	0.1	0.1	0.4	0.4	0.4	0.3	0.3	1.6	0.1	0.0	0.3
Bacteria;OP10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0
Bacteria;OP11	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Unclassified bacteria	19.9	12.3	24.4	9.8	12.4	11.8	21.7	28.4	10.3	22.3	14.6	30.6	36.2	15.4	18.6	18.8	39.2	10.2	30.3	25.2	22.6	25.5	26.5	23.7	46.3	1.5	21.5
Planctomycetes	0.0	0.6	1.0	0.2	0.1	0.7	1.1	0.6	0.6	0.7	0.3	0.0	0.0	0.1	0.5	1.0	0.7	0.3	1.0	1.0	1.2	0.9	0.6	0.1	0.6	0.0	0.5
Proteobacteria	22.1	40.1	37.5	26.1	42.7	35.9	30.2	38.0	36.4	54.4	50.1	19.1	27.6	26.5	53.5	49.0	25.5	54.0	30.4	30.0	30.1	36.8	33.2	30.9	10.4	82.6	36.6
SR1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Spirochaetes	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Synergistetes	0.2	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
TM7	0.0	0.2	0.6	0.1	0.2	0.1	0.3	0.2	0.2	0.6	0.2	0.0	0.0	0.0	0.9	1.6	0.1	0.4	0.2	0.3	0.3	0.5	0.2	2.0	0.3	0.0	0.4
Tenericutes	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Verrucomicrobia	0.1	0.4	1.6	0.3	0.2	0.2	1.6	0.9	0.5	0.3	1.6	0.2	0.3	0.3	1.5	1.4	0.3	0.9	0.8	2.6	2.1	1.7	1.9	6.0	2.9	0.1	1.2
WS3	0.0	0.0	0.1	0.0	0.0	0.1	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.2	0.3	0.0	0.1	0.4	0.2	0.8	0.7	0.0	0.0	0.0	0.1
Unclassified;Other	0.1	0.0	0.5	0.0	0.0	0.1	0.1	0.3	0.0	0.3	1.3	2.1	3.4	0.4	0.7	0.1	0.1	0.1	0.9	0.6	1.0	0.1	0.3	1.6	0.1	0.0	0.5

Table S3. Relative abundance of *Proteobacteria* classes used for Figure 3.

Taxon	A1	A2	B1	B2	B3	B4	C1	C2	C3	D1	D2	D3	D4	D5	E1	E2	F1	F2	G1	G2	G3	H1	H2	H3	I1	I2	mean
Alphaproteobacteria	1.9	6.3	13.2	11.9	28.8	19.4	11.0	10.5	10.5	12.1	8.5	4.0	3.1	2.7	13.4	10.6	9.5	6.7	7.0	7.7	9.4	10.4	11.6	7.6	5.4	0.5	9.4
Betaproteobacteria	6.2	23.6	5.5	10.7	3.8	4.6	6.0	5.4	12.4	2.6	12.7	1.5	1.8	5.7	26.7	16.4	5.2	14.3	11.6	11.0	9.5	13.3	9.1	12.5	1.9	73.4	11.8
Deltaproteobacteria	12.8	1.4	3.6	1.9	3.1	4.2	3.4	2.6	5.7	1.5	1.7	13.0	22.1	16.4	2.5	3.5	2.0	7.1	2.3	2.9	3.2	6.1	7.6	4.9	1.4	0.1	5.3
Epsilonproteobacteria	0.0	0.0	0.0	0.1	1.1	0.0	0.0	0.0	3.4	0.0	0.9	0.0	0.0	0.2	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.2
Gammaproteobacteria	0.6	8.1	10.3	1.3	4.9	6.5	6.0	12.8	3.2	31.5	21.8	0.1	0.2	1.0	5.6	12.8	4.7	22.7	4.8	5.5	5.2	3.1	1.9	4.3	1.3	8.5	7.3
Unclassified proteobacteria	0.5	0.6	4.9	0.3	1.0	1.1	3.8	6.7	1.2	6.6	4.6	0.3	0.4	0.5	5.2	5.6	4.0	3.1	4.7	2.9	2.8	3.8	3.0	1.4	0.6	0.1	2.7

Table S4. Lineage and total abundance of fifty most prominent operational taxonomic units (OTUs).

#OTU ID	total	% total	Consensus Lineage
7163	8214	4.07	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax
42143	6814	3.38	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosaetaceae;Methanosaeta
42977	2993	1.48	Bacteria
64060	2857	1.42	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;Methylocystis
38964	2516	1.25	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella
42889	1503	0.75	Bacteria;Proteobacteria;Gammaproteobacteria
41508	1215	0.60	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus
51120	1180	0.59	Bacteria;Proteobacteria;Betaproteobacteria
804	1097	0.54	Bacteria
46070	1083	0.54	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosaetaceae;Methanosaeta
17322	1066	0.53	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae
36140	1065	0.53	Bacteria
50799	913	0.45	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter
49748	856	0.42	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosaetaceae;Methanosaeta
35899	807	0.40	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter
54656	788	0.39	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces
44690	775	0.38	Bacteria;Proteobacteria
45207	770	0.38	Archaea
11323	766	0.38	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae
35948	726	0.36	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia
10657	722	0.36	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosaetaceae;Methanosaeta
13904	715	0.35	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosaetaceae;Methanosaeta
19827	684	0.34	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;Mycobacterium
50808	666	0.33	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Desulfosporosinus
48085	642	0.32	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae
44101	638	0.32	Bacteria;Actinobacteria;Actinobacteria
13667	626	0.31	Bacteria
62246	619	0.31	Bacteria
31313	613	0.30	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae
47077	611	0.30	Archaea
884	499	0.25	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella
56805	491	0.24	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales
49398	457	0.23	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium
60579	447	0.22	Bacteria
25769	439	0.22	Bacteria;Proteobacteria;Betaproteobacteria
8729	436	0.22	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae
54563	427	0.21	Bacteria;Acidobacteria;Acidobacteria_Gp16;Gp16
20713	425	0.21	Bacteria;Proteobacteria;Gammaproteobacteria
20435	416	0.21	Bacteria;Acidobacteria;Acidobacteria_Gp6;Gp6
61491	413	0.20	Archaea
63018	407	0.20	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobium
33445	401	0.20	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella
39599	400	0.20	Bacteria;Proteobacteria
40430	390	0.19	Bacteria;Proteobacteria;Gammaproteobacteria
11351	386	0.19	Bacteria
6715	381	0.19	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae
1197	380	0.19	Bacteria
61102	367	0.18	Bacteria;Proteobacteria;Deltaproteobacteria
29799	365	0.18	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurovum
51936	338	0.17	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium