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*Supplement of*

## **Differences in microbial community composition between injection and production water samples of water flooding petroleum reservoirs**

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## Supplementary Text

### *Pyrosequencing of partial 16S rRNA genes and sequences analysis*

Broadly conserved primers 27F (5'-AGA GTT TGA TCC TGG CTC AG-3') and 533R (5'-TTA CCG CGG CTG CTG GCA C-3') containing the A and B sequencing adaptors, were used to amplify bacterial 16S rRNA gene sequences, while primers 344F (5'-ACG GGG YGC AGC AGG CGC GA-3') and 915R (5'-GTG CTC CCC CGC CAA TTC CT-3') were used to amplify archaeal 16S rRNA gene sequences. The PCRs were carried out in triplicate using 20  $\mu$ L reactions with 10.5  $\mu$ L sterile ddH<sub>2</sub>O, 4  $\mu$ L 5 $\times$  *TransStart®FastPfu* Buffer (TransGen Biotech, China), 2  $\mu$ L 2.5 mM dNTPs, 0.5  $\mu$ L *TransStart® FastPfu* DNA Polymerase, 0.5  $\mu$ L forward primer (10  $\mu$ M), 0.5  $\mu$ L reverse primer (10  $\mu$ M), and 2  $\mu$ L sample DNA. For bacteria, samples were denatured for 2 min at 95°C followed by 25 cycles at 94°C for 30 s, 50°C for 30 s, 72°C for 30 s and a final elongation step at 72°C for 5 min. For archaea, samples were denatured for 2 min at 95°C followed by 30 cycles at 94°C for 30 s, 50°C for 30 s, 72°C for 30 s and a final elongation step at 72°C for 5 min.

Sequences generated from pyrosequencing were analyzed using default settings in the open source software package MOTHUR (Schloss et al., 2009). All sequences were sorted into different samples according to barcodes. Sequences were subjected to systematic checks to remove replicates, duplicates, barcodes, primer sequences and low-quality reads. Briefly, high quality sequences (> 200bp in length, quality score > 25, exact match to barcode and primer, and containing no ambiguous characters) were remaining. These sequences were simplified using the 'unique.seqs' command to generate a unique set of sequences, and then were aligned using the 'align.seqs' command and compared with Bacterial SILVA database. The aligned sequences were clustered into OTUs with 97% similarity.

### *Miseq-sequencing of partial 16S rRNA genes and sequences analysis*

Pairs of reads from the original DNA fragments are merged by using FLASH (Magoc and Salzberg, 2011)-a very fast and accurate software tool which is designed to merge pairs of reads when the original DNA fragments are shorter than twice the length of reads. Sequencing reads was assigned to each sample according to the unique barcode of each sample. Raw sequences were firstly demultiplexed and then quality-filtered using the default parameters in QIIME software package (Quantitative Insights Into Microbial Ecology) and UPARSE pipeline (Caporaso et al., 2011).

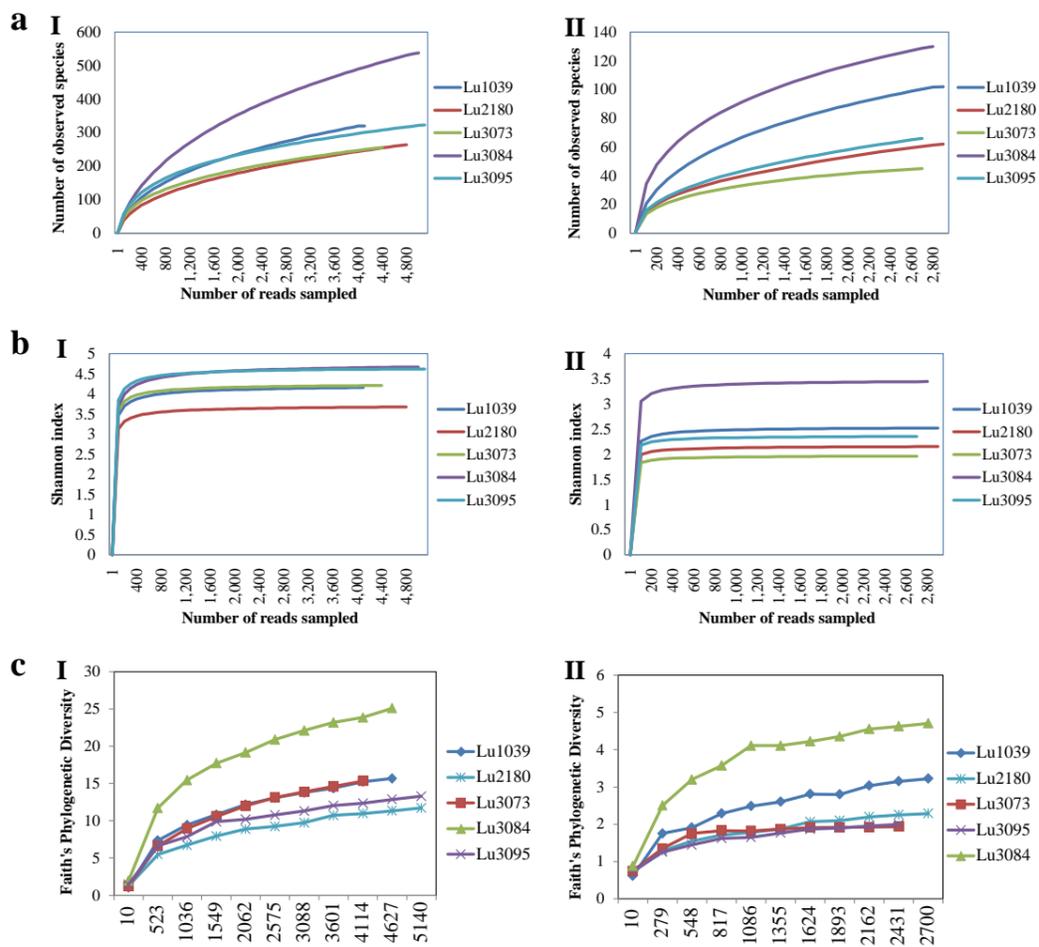
First, the reads were filtered by QIIME quality filters. Default settings for Illumina processing in QIIME was used ( $r = 3$   $p = 0.75$  total read length;  $q = 3$ ;  $n = 0$ ). ( $p$ ) min\_per\_read\_length: minimum number of consecutive high-quality base calls to retain read (as percentage of total read length); ( $r$ ) max\_bad\_run\_length: maximum number of consecutive low-quality base calls allowed before truncating a read; ( $n$ ) sequence\_max\_n: maximum number of ambiguous (N) characters allowed in a sequence; ( $q$ ) phred\_quality\_score: last quality score considered low quality

Then, we use UPARSE pipeline to picking operational taxonomic units (OTUs) through making OTU table. Sequences were assigned to OTUs at 97% similarity. The resulting representative sequence set were aligned and given a taxonomic classification using RDP (Wang et al., 2007). In order to compute Alpha Diversity, we rarify the OTU table and calculate three metrics: Chao1 metric estimates the species richness, the Observed Species metric is simply the count of unique OTUs found in the sample, and shannon index. QIIME calculates both weighted and unweighted unifracs, which were used to do Principal Coordinate Analysis (PCoA).

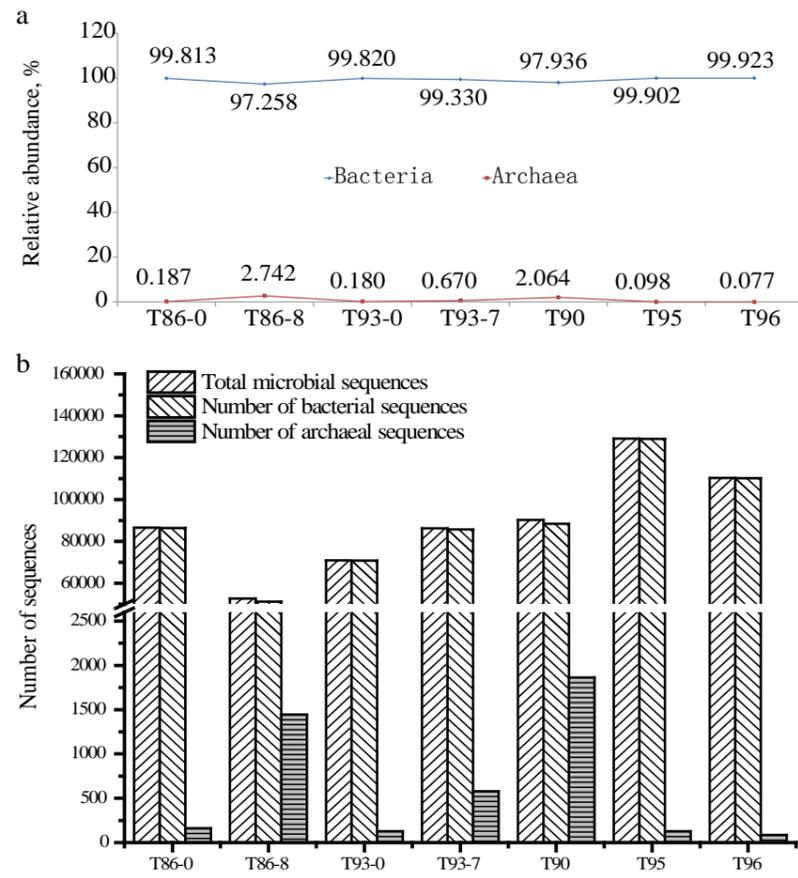
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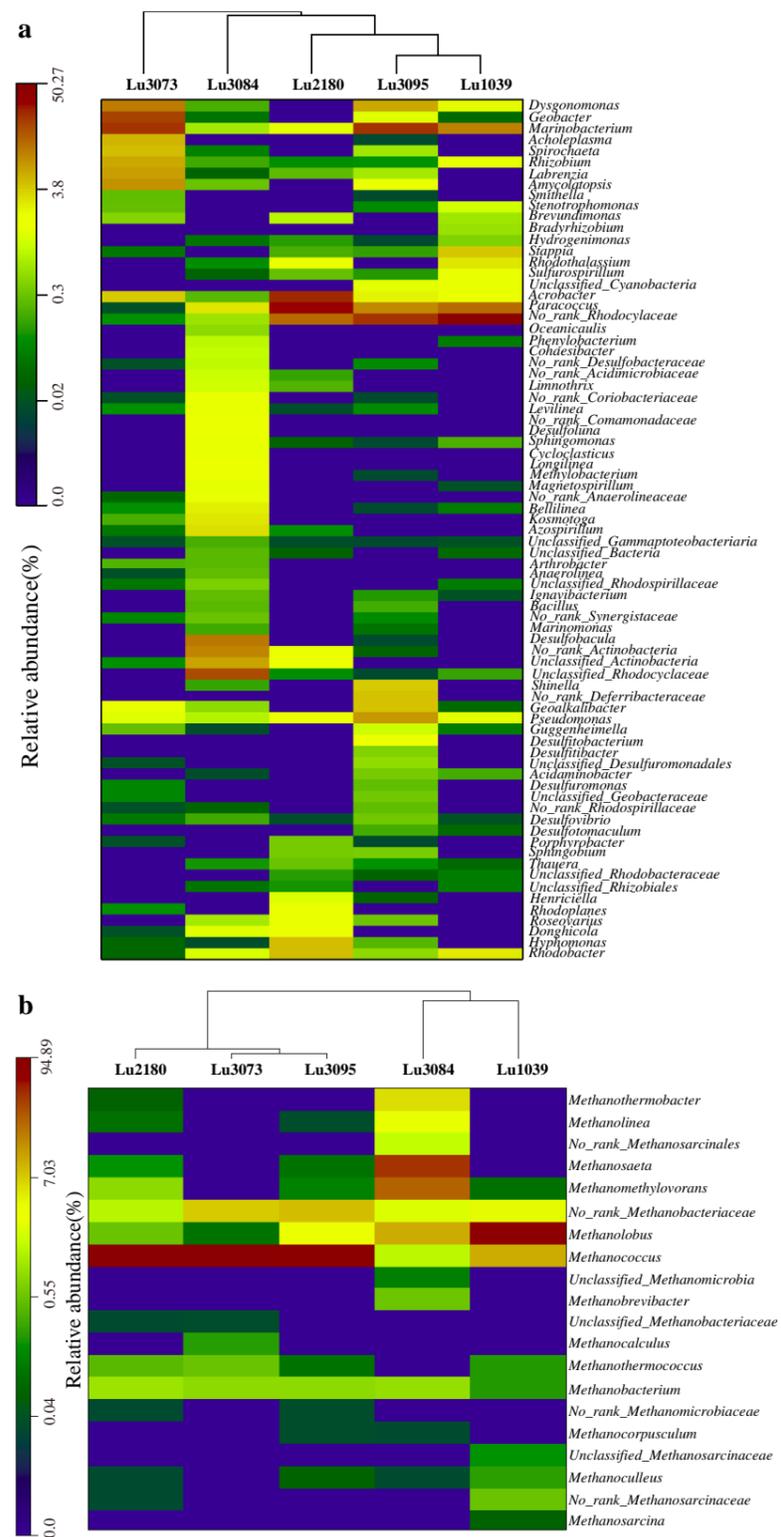
Supplementary Figure: Figure S1 to Figure S3



**Figure S1** Rarefaction curves (a), Shannon curves (b) and phylogenetic diversity (PD) (c) of the bacterial (I) and archaeal (II) 16S rRNA gene libraries of injection and production wells in Lu-field block reservoir.



**Figure S2** Statistical analyses of communities sequencing in L-field block reservoir. a, represents the relative percent of bacteria and archaea in a whole community; b, represents the number of bacterial and archaeal sequences obtained by miseq-sequencing.



**Figure S3** Heatmap showing the relative abundance and distribution of representative bacterial (a) and archaeal (b) taxa in injection and production water samples obtained from Lu-field block reservoir.

**Supplementary Table: Table S1 to S4****Table S1** Sequencing depth and alpha diversity of the microbial communities in Lu field block reservoir

Library	Reads	OTUs	Chao I	Shannon	Simpson
Bacterial					
Lu3084	4957	538	892.04	4.67	0.03
Lu1039	4016	320	556.33	4.16	0.04
Lu2180	4776	264	482.90	3.68	0.07
Lu3073	4395	256	377.42	4.21	0.03
Lu3095	5060	323	486.58	4.62	0.02
Archaeal					
Lu3084	2793	139	180.65	3.44	0.06
Lu1039	2824	102	151.4	2.52	0.15
Lu2180	2857	62	101	2.15	0.18
Lu3073	2692	45	51.11	1.97	0.23
Lu3095	2688	66	108	2.36	0.14

**Table S2** Sequencing depth and alpha diversity of the microbial communities in Liu field block reservoir

Library	Reads	OTUs	Chao1	Shannon
T86-0	86526	1555	4403.944	6.890032
T86-8	52719	1680	4439.167	6.896292
T93-0	70930	1284	4224.441	6.103269
T93-7	86256	1580	4248.355	6.683729
T90	90303	1571	3731.311	6.421689
T95	129106	1420	4256.786	5.956687
T96	110341	1284	4224.441	6.103269

**Table S3** The relative abundance of bacterial genera detected in Lu field block reservoir

Taxa (Phylum-Class-Order-Family-Genus)	Lu3084	Lu1039	Lu2180	Lu3073	Lu3095
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;g_Propionibacterium	0.04	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0	0	0	0.02	0.04
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Paludibacter	0	0	0	0.05	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Proteiniphilum	0.2	2.39	0	10.44	6.09
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Gillisia	0	0	0	0	0.02
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Leptolinea	0.28	0	0	0	0
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Levilinea	0.12	0	0	0	0
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Longilinea	0.14	0	0	0	0
p_Deferribacteres;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Geovibrio	0	0	0	0	0.06
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Acetobacterium	0	0.02	0	0	0.1
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Christensenella	0.06	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfitibacter	0	0	0	0	0.42
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfitobacterium	0	0	0	0	1.62
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfosporosinus	0	0	0	0	0.1
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfurispora	0.32	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Fastidiosipila	0.16	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;g_Fusibacter	0	0.07	0	0.41	1.09
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Erysipelothrix	0	0	0	0	0.04
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas	0	0.57	0.59	0.32	0
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium	0.87	0.02	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Salinarimonas	0	0	0	0	0.02
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum	0.04	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Filomicrobium	0.06	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Pleomorphomonas	0.02	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Rhizobium	0.34	0.07	0.08	5.94	4.09
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Hyphomonas	0.02	0	6.16	0.05	0.28
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Maricaulis	0.16	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Oceanicaulis	0.46	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Labrenzia	0	0	0	4.07	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Pannonibacter	0.04	0	0.25	0	0.67
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	0	0.02	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter	0	0.02	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodovulum	0.04	0	0.02	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rubellimicrobium	0	0	0	0	0.02
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Stappia	0	4.16	0.19	0	0.16
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Thioclava	0	0.02	3.94	0.05	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Azospirillum	2.93	0	0.08	0.07	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Caenispirillum	0.08	0	0.06	0	0.06
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Magnetospirillum	0.04	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Marispirillum	0	0	0.04	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Novispirillum	0.1	3.14	1.97	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Oceanibaculum	0.02	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Rhodospirillum	0.28	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Roseospirillum	0.1	0	0	0.02	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Roseovarius	0.59	0	1.95	0	0.32
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Thalassospira	0.08	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Tistrella	0.14	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Altererythrobacter	0	0	0.36	0.02	0.02
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	0.24	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium	0	0	0.36	0	0.38
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	1.96	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Burkholderia	0	0	0	0	0.04
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Pusillimonas	0.1	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Aquabacterium	0.06	0	0	0	0.02
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Brachymonas	0.14	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas	0	0	0	0.02	0.08
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Delftia	0	0	0	0	0.06
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Diaphorobacter	0.04	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Azoarcus	0.02	0	0	0.02	0
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Thauera	0.12	0	0.06	0	0.12
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfarculales;f_Desulfarculaceae;g_Desulfarculus	2.2	0	0	0.02	0.1
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobacteriales;f_Desulfobulbaceae;g_Desulfobulbus	0.2	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobacteriales;f_Desulfobulbaceae;g_Desulfofustis	0.12	0	0	0	0

p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfomicrobiaceae;g_Desulfomicrobium	0	0.02	0	0.05	0.14
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0.08	0.05	0.02	0.07	0.04
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Desulfuromonadaceae;g_Desulfuromonas	0	0.02	0	11.92	1.48
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Desulfuromonadaceae;g_Donghicola	1.09	0	1.7	0.02	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Desulfuromonadaceae;g_Pelobacter	0.36	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Geobacteraceae;g_Alkalibacter	0.04	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Geobacteraceae;g_Geoalkalibacter	0	0.05	0	2.09	4.37
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Geobacteraceae;g_Geobacter	0.06	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfococcus	0.1	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfotignum	0.28	0	0	0	0.02
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophaceae;g_Desulfomonile	0.04	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophaceae;g_Smithella	0	0	0	0.27	0.02
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophobacteraceae;g_Desulfoglaeba	0.08	0	0	0	0
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Arcobacter	0.24	2.04	25.1	4.1	2.63
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Sulfurospirillum	0.04	2.17	0.4	0	0.16
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_Sulfurimonas	0.04	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_[Chromatiaceae];g_Alishewanella	0.06	0.15	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Shewanellaceae;g_Shewanella	0	0	0	0.02	0
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	0.02	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Marinobacterium	0.61	8.42	1.51	22.3	22.37
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Marinobacterium	0.06	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Nitrincola	0	0	0.02	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Oceanobacter	0.04	0	0.06	0.05	0
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Thalassolituus	0.18	0	0	0	0.06
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	0.99	1.44	1.93	1.3	7.37
p_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Piscirickettsiaceae;g_Methylophaga	0	0.1	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	0	1.12	0	0.25	0.1
p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Spirochaeta	0.08	0	0	4.66	0.61
p_Synergistetes;c_Synergistia;o_Synergistales;f_Aminiphilaceae;g_Aminiphilus	0.12	0	0	0.05	0
p_Synergistetes;c_Synergistia;o_Synergistales;f_Thermovirgaceae;g_Thermovirga	0.18	0	0	0.02	0.06
p_Tenericutes;c_Mollicutes;o_Acholeplasmatales;f_Acholeplasmataceae;g_Acholeplasma	0	0	0	5.32	0.02
p_Thermi;c_Deinococci;o_Thermales;f_Thermaceae;g_Thermus	0.02	0	0.02	0	0
p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_Kosmotoga	2.82	0	0	0.05	0
Total percent	20.56	26.08	46.87	74.06	55.47

**Table S4** The relative abundance of bacterial genera detected in L-field block reservoir

Taxa (Phylum-Class-Order-Family-Genus)	T86-0	T86-8	T93-0	T93-7	T90	T95	T96
p_Acidobacteria;c_Solibacterales;o_Solibacterales;f_Solibacteraceae;g_Candidatus Solibacter	0.0000	0.0000	0.0026	0.0000	0.0000	0.0180	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Actinotalea	0.0231	0.0079	0.0591	0.0258	0.0105	0.0000	0.0026
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Cellulomonas	0.0026	0.0000	0.0051	0.0103	0.0000	0.0026	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium	0.0000	0.0079	0.0026	0.0052	0.0026	0.0103	0.0128
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dietziaceae;g_Dietzia	0.0051	0.0079	0.0309	0.0103	0.0524	0.6501	0.8426
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Phycococcus	0.0026	0.0000	0.0000	0.0000	0.0000	0.0180	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Jonesiaceae;g_Jonesia	0.0026	0.0000	0.0000	0.0078	0.0000	0.0000	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter	0.0103	0.0053	0.0900	0.0103	0.0079	0.0000	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Salinibacterium	0.0051	0.0000	0.0360	0.0000	0.0000	0.0026	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter	0.0000	0.0053	0.0000	0.0103	0.0000	0.0000	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium	0.0000	0.0000	0.0000	0.0000	0.0026	0.0899	0.0180
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;g_Rhodococcus	0.0000	0.0000	0.0000	0.0000	0.0026	0.2518	3.7070
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioideae;g_Aeromicrobium	0.2237	0.0449	1.0724	0.0698	0.0760	0.0026	0.0026
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioideae;g_Nocardioides	0.0026	0.0026	0.0360	0.0000	0.0000	0.0000	0.0000
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae;g_Propionibacterium	0.0000	0.0026	0.0051	0.0000	0.0105	0.0077	0.0257
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Tsukamurellaceae;g_Tsukamurella	0.0000	0.0000	0.0000	0.0000	0.0052	0.0026	0.0051
p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Patulibacteraceae;g_Patulibacter	0.0000	0.0000	0.0026	0.0000	0.0000	0.1002	0.0077
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Butyricimonas	0.0129	0.0000	0.0026	0.0000	0.0000	0.0000	0.0000
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0.9747	0.0897	2.0213	0.1938	0.0550	13.151	0.1901
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Dysgonomonas	0.0026	0.0079	0.0077	0.0129	0.0079	0.0180	0.0000
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Parabacteroides	1.9237	0.6150	1.0055	0.6099	0.1153	0.0360	0.2107
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Aequorivita	0.0360	0.0026	0.0257	0.0026	0.0026	0.0719	0.0077
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Flavobacterium	0.0154	0.1188	0.0540	0.0388	0.0052	0.1490	0.0103
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Wautersiella	0.0154	0.0000	0.0026	0.0052	0.0105	0.0000	0.0000
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Amoebophilaceae;g_Candidatus Amoebophilus	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0539
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium	0.0026	0.0000	0.0103	0.0000	0.0000	0.0000	0.0000
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_C1_B004	0.0077	0.0475	0.0129	0.0284	0.1048	0.0771	0.0103
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_SHD-231	0.0180	0.0977	0.0334	0.0491	0.1546	0.1824	0.0437
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_T78	0.1029	1.3329	0.0951	0.1706	2.3721	0.6989	0.2209
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_WCHB1-05	0.0026	0.0264	0.0000	0.0078	0.0131	0.0257	0.0000
p_Deferribacteres;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Denitrovibrio	0.0129	0.0106	0.0103	0.0052	0.0157	0.0000	0.0026
p_Deferribacteres;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Flexistipes	0.1723	0.1135	0.2083	0.1060	0.2123	0.0668	0.0719
p_Deferribacteres;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Geovibrio	0.0026	0.0000	0.0026	0.0052	0.0052	0.0000	0.0000
p_Fibrobacteres;c_Fibrobacteriia;o_Fibrobacteriales;f_Fibrobacteraceae;g_Fibrobacter	0.0000	0.0000	0.0026	0.0026	0.0000	0.0231	0.0000
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	1.1085	0.7205	0.7509	0.6848	0.7260	0.1079	0.1284
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Virgibacillus	0.6841	0.3721	0.3317	0.4264	0.4063	0.0000	0.0000
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Brevibacillus	0.0000	0.0000	0.0000	0.0000	0.0000	0.0206	0.0051
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Cohnella	0.0051	0.0000	0.0051	0.0026	0.0000	0.0000	0.0000
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Paenibacillus	0.0000	0.0000	0.0103	0.0026	0.0026	0.1002	0.0719
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Facklamia	0.0926	0.0370	0.1440	0.2223	0.0315	0.0000	0.0000
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Trichococcus	0.0077	0.0264	0.0180	0.0594	0.0026	1.4903	0.1696
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Acetobacterium	0.0180	0.0185	0.0180	0.0078	0.0105	0.0822	0.0514
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Anaerostipes	0.0051	0.0026	0.0000	0.0310	0.0026	0.0308	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Dehalobacter	0.0103	0.0633	0.0026	0.0181	0.0157	0.0000	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfobacterium	0.0026	0.0290	0.0051	0.0026	0.0026	0.0000	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfosporosinus	0.0051	0.0000	0.0026	0.0000	0.0000	0.0103	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfotomaculum	0.0000	0.0000	0.0000	0.0000	0.0000	0.0231	0.0026
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfurispora	0.0026	0.0026	0.0000	0.0000	0.0000	0.0051	0.0026
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Niigata-25	0.0231	0.0317	0.0283	0.0594	0.0131	0.0257	0.0026
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Pelotomaculum	0.0000	0.0000	0.0000	0.0000	0.0000	0.0077	0.0051
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_SJA-118	0.0000	0.0000	0.0000	0.0000	0.0000	0.0103	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Sporotomaculum	0.0000	0.0000	0.0000	0.0000	0.0000	0.0154	0.0026
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Peptostreptococcus	0.0026	0.0000	0.0026	0.0078	0.0000	0.0000	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerofilum	0.0051	0.0026	0.0051	0.0052	0.0026	0.3186	0.0334
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus	0.0000	0.0000	0.0026	0.0000	0.0079	0.0000	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira	0.0463	0.0581	0.0283	0.0413	0.0262	0.0000	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus	0.0746	0.3167	0.0900	0.3360	0.0813	0.0360	0.0128
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas	0.0129	0.1980	0.0180	0.0207	0.0603	0.0026	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Acidaminococcus	0.0000	0.0053	0.0026	0.0284	0.0026	0.0077	0.0000
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_vadinHB04	0.0257	0.1795	0.0334	0.5582	0.0367	0.1773	0.0334
p_Firmicutes;c_Clostridia;o_Desulfobacterales;f_Desulfobacteraceae;g_Desulfobacter	0.0077	0.0713	0.0180	0.0078	0.0131	0.0000	0.0000
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Erysipelothrix	0.0026	0.0053	0.0000	0.0052	0.0000	0.0000	0.0000

p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_PSB-M-3	0.0051	0.0211	0.0026	0.0078	0.0105	0.0000	0.0000
p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_Thermodesulfovibrionaceae;g_Thermodesulfovibrio	0.0386	0.0026	0.0411	0.0078	0.0026	0.0026	0.0000
p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata	0.0000	0.0000	0.0000	0.0000	0.0000	0.0206	0.0026
p_Planctomycetes;c_Planctomycetia;o_Planctomycetales;f_Planctomycetaceae;g_Planctomyces	0.0000	0.0000	0.0051	0.0078	0.0026	0.0077	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas	0.0051	0.0000	0.0000	0.0052	0.0000	0.2004	0.2954
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Mycoplana	0.0000	0.0000	0.0000	0.0000	0.0000	0.4625	0.0411
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium	0.0026	0.0000	0.0051	0.0000	0.0052	0.0308	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Kiloniellales;f_Kiloniellaceae;g_Thalassospira	0.1312	0.0158	0.0051	0.0078	0.0105	0.0180	0.0334
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum	0.8281	0.4302	0.8769	0.6590	0.6055	0.2878	0.2261
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Devosia	0.0180	0.0053	0.0951	0.0181	0.0157	0.1053	0.0411
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	0.0000	0.0026	0.0077	0.0000	0.0000	0.0051	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Parvibaculum	0.1003	0.0079	0.0823	0.0078	0.0472	1.3104	0.4650
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Rhodoplanes	0.0000	0.0000	0.0077	0.0000	0.0000	0.0026	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_Methylobacterium	0.0000	0.0000	0.0000	0.0000	0.0000	0.0103	0.0206
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Aminobacter	0.0026	0.0026	0.0077	0.0026	0.0000	0.0051	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Agrobacterium	0.0103	0.0079	0.0977	0.0207	0.0052	0.1182	0.1002
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Hyphomonas	0.0051	0.0053	0.0103	0.0155	0.0708	0.5267	0.3699
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Maricaulis	0.0000	0.0000	0.0000	0.0000	0.0000	0.0874	0.0437
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae;g_Oceanicaulis	0.0000	0.0000	0.0000	0.0000	0.0000	0.1182	0.0591
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Antarctobacter	0.0540	0.1056	0.0797	0.0388	0.1992	0.0976	0.0796
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	1.4711	0.4276	0.9772	1.7651	0.4141	0.0077	0.0308
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter	0.0000	0.0026	0.0000	0.0000	0.0000	0.0283	0.0231
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodovulum	0.0000	0.0026	0.0129	0.0000	0.0000	0.1259	0.0360
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseomonas	0.0026	0.0000	0.0000	0.0000	0.0000	0.0385	0.0154
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Azospirillum	0.0000	0.0026	0.0026	0.0000	0.0000	0.0591	0.0822
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Magnetospirillum	0.0000	0.0000	0.0000	0.0000	0.0000	0.0437	0.0308
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Novispirillum	0.1157	0.0845	0.1414	0.1344	0.1756	0.1747	0.1259
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Phaeospirillum	0.0000	0.0000	0.0000	0.0000	0.0000	0.0719	0.0103
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Erythrobacter	0.0000	0.0000	0.0000	0.0000	0.0000	0.0206	0.0026
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_Lutibacterium	0.0000	0.0000	0.0077	0.0026	0.0000	0.0000	0.0000
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	0.0000	0.0053	0.0154	0.0362	0.0079	0.0668	0.0257
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium	0.0026	0.0026	0.0951	0.0026	0.0052	0.0000	0.0026
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	0.0000	0.0026	0.0154	0.0026	0.0052	0.1542	0.0899
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis	0.0103	0.0000	0.0051	0.0026	0.0000	0.1722	0.0103
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter	0.0823	0.0343	0.0643	0.0569	0.0524	0.0154	0.0257
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Denitrobacter	0.0026	0.0000	0.0000	0.0078	0.0000	0.0000	0.0000
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Pigmentiphaga	0.0000	0.0000	0.0051	0.0000	0.0000	0.0103	0.0180
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Aquabacterium	0.0231	0.1029	0.0154	0.0129	0.0026	0.0103	0.1310
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Hydrogenophaga	0.0000	0.0000	0.0000	0.0000	0.0000	0.0797	0.0206
p_Proteobacteria;c_Betaproteobacteria;o_Hydrogenophilales;f_Hydrogenophilaceae;g_Thiobacillus	0.0386	0.0554	0.0283	0.0439	0.0603	0.1644	0.0154
p_Proteobacteria;c_Betaproteobacteria;o_Procabbacteriales;f_Procabbacteriaceae;g_Procabbacter	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0411
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Azovibrio	0.0103	0.0132	0.0103	0.0078	0.0288	0.0334	0.0565
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Dechloromonas	0.0463	0.0633	0.0309	0.1318	0.0157	0.0051	0.0000
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Hydrogenophilus	0.0026	0.0000	0.0000	0.0103	0.0000	0.0026	0.0026
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Thauera	1.9392	1.4780	0.9155	1.2715	0.5006	0.0360	0.0617
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Z-35	0.0026	0.0000	0.0026	0.0000	0.0000	0.0026	0.0026
p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoracaceae;g_Bacteriovorax	0.0051	0.0053	0.0283	0.0052	0.0079	0.0745	0.1978
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0.0283	0.1557	0.0463	0.1783	0.0524	0.0103	0.0077
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfomicrobiaceae;g_Desulfomicrobium	0.0643	0.1293	0.0694	0.2300	0.0681	0.0283	0.0257
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfomicrobiaceae;g_Desulfovibrio	0.3883	0.1029	0.1697	0.1240	0.1651	0.3340	0.2338
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Desulfuromonadaceae;g_Desulfuromonas	0.0000	0.0000	0.0000	0.0026	0.0000	0.0077	0.0360
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfobacter	0.0411	0.0475	0.0591	0.7262	0.0393	0.0026	0.0026
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfobacterium	0.0000	0.0053	0.0000	0.0000	0.0210	0.0077	0.0000
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfococcus	0.0000	0.0106	0.0000	0.0026	0.0131	0.0026	0.0000
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Desulfobacteraceae;g_Desulfotignum	0.1415	0.1927	0.1517	0.1835	0.4508	0.0463	0.0617
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophaceae;g_Syntrophus	0.0180	0.0185	0.0077	0.0155	0.0236	0.0051	0.0000
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophobacteraceae;g_Syntrophobacter	0.0000	0.0000	0.0000	0.0000	0.0000	0.0103	0.0051
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Arcobacter	0.6352	1.7974	0.7201	0.7288	10.5394	22.1594	14.2630
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Sulfurospirillum	0.3266	0.3510	0.4063	0.3334	1.2136	0.0437	0.1387

p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacteriales;f_Helicobacteraceae;g_Sulfurimonas	0.1363	0.4988	0.1440	0.6332	0.1179	0.2518	3.0108
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_[Chromatiaceae];g_Alishewanella	0.0489	0.2798	0.0514	0.1111	0.0472	0.0642	0.3622
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_HB2-32-21	0.0411	0.0264	0.3240	0.0413	0.0734	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Marinobacter	0.7535	0.3484	0.4320	0.4574	2.9094	1.8706	4.9016
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_ZD0117	0.0231	0.0106	0.1569	0.0181	0.0157	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Idiomarinaceae;g_Pseudidiomarina	0.3240	0.5912	0.5658	0.2998	0.0996	0.3674	0.7245
							10.859
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Shewanellaceae;g_Shewanella	0.0386	0.0818	0.0360	0.0388	0.0262	0.8608	1
p_Proteobacteria;c_Gammaproteobacteria;o_Chromatiales;f_Halothiobacillaceae;g_Halothiobacillus	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0617
p_Proteobacteria;c_Gammaproteobacteria;o_Chromatiales;f_Halothiobacillaceae;g_Thiofaba	0.0103	0.0000	0.0103	0.0000	0.0026	0.0026	0.0051
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia	0.0129	0.0053	0.0411	0.0646	0.0341	0.0051	0.0026
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Morganella	0.0129	0.0000	0.0077	0.0026	0.0026	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Trabulsiella	0.0077	0.0106	0.0103	0.0388	0.0026	0.3829	1.1201
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Alcanivoracaceae;g_Alcanivorax	0.3755	0.0686	0.5066	0.0827	0.0917	0.2390	0.0360
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	0.5041	0.1557	0.3472	0.2894	0.2385	0.3983	0.8015
					19.537		
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Marinobacterium	2.3481	3.7716	2.5613	7.9183	6	1.4826	3.1342
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Nitrincola	0.0540	0.0290	0.0180	0.0284	0.0288	0.0103	0.0385
p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Oceanospirillaceae;g_Oleibacter	1.6280	6.3952	1.0338	2.0597	1.7614	0.2313	0.3519
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	0.0926	0.4144	0.2932	0.0517	0.0498	0.1490	0.3648
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	0.0000	0.0000	0.0000	0.0000	0.0000	0.0051	0.0077
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Psychrobacter	0.0000	0.0000	0.0000	0.0026	0.0000	0.0000	0.0077
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Azorhizophilus	0.0026	0.0185	0.0103	0.0129	0.0157	0.0026	0.0154
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	1.7514	1.1983	1.3604	1.5454	3.0510	1.1537	5.2715
p_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Piscirickettsiaceae;g_Methylophaga	0.0026	0.0000	0.0077	0.0078	0.0052	0.0591	0.1927
p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	0.0051	0.0026	0.0283	0.0155	0.0079	0.0000	0.0128
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_Hydrocarboniphaga	0.0026	0.0000	0.0051	0.0026	0.0052	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Arenimonas	0.0000	0.0000	0.0000	0.0000	0.0000	0.1259	0.0077
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas	0.0077	0.0000	0.0000	0.0000	0.0026	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Lysobacter	0.0000	0.0026	0.0026	0.0129	0.0000	0.0000	0.0000
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	0.0000	0.0000	0.0000	0.0000	0.0000	0.3726	0.0283
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Rhodanobacter	0.0077	0.0000	0.0000	0.0052	0.0026	0.0128	0.0308
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas	0.0077	0.0396	0.0206	0.0594	0.0210	0.0051	0.0103
p_Spirochaetes;c_[Leptospirae];o_[Leptospirales];f_Sediment-4;g_SJA-88	0.0000	0.0132	0.0000	0.0026	0.0000	0.0000	0.0000
p_Spirochaetes;c_Spirochaetes;o_Sphaerochaetales;f_Sphaerochaetaceae;g_Sphaerochaeta	4.6884	4.5450	3.5591	0.3463	4.1177	0.0385	0.4290
p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Treponema	0.0411	0.1452	0.0977	0.0594	0.3853	0.1876	0.0231
p_Spirochaetes;c_WWE1;o_[Cloacamonales];f_[Cloacamonaceae];g_W22	0.2032	8.9712	0.1569	0.3902	0.6553	0.0154	0.0051
p_Synergistetes;c_Synergistia;o_Synergistales;f_Aminiphilaceae;g_Aminiphilus	0.0026	0.0000	0.0051	0.0052	0.0000	0.0103	0.0257
p_Synergistetes;c_Synergistia;o_Synergistales;f_Anaerobaculaceae;g_Anaerobaculum	0.0514	0.0026	0.0463	0.0026	0.0026	0.0000	0.0000
p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_Aminobacterium	0.1003	0.0079	0.0386	0.0543	0.0157	0.0000	0.0334
p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_Dethiosulfovibrio	0.0129	0.0475	0.0026	0.0284	0.0026	0.0488	0.0154
p_Synergistetes;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_HA73	1.4222	0.8103	0.6198	0.7546	0.4744	0.1079	0.1850
p_Synergistetes;c_Synergistia;o_Synergistales;f_Synergistaceae;g_vadinCA02	0.2186	3.7426	0.2520	3.9824	0.4089	0.0463	0.2029
p_Synergistetes;c_Synergistia;o_Synergistales;f_Thermovirgaceae;g_Thermovirga	0.0051	0.0026	0.0000	0.0052	0.0026	0.0000	0.0000
p_Tenericutes;c_Mollicutes;o_Acholeplasmatales;f_Acholeplasmataceae;g_Acholeplasma	0.3215	2.4995	0.3446	0.2998	1.4704	0.0180	0.0128
p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_RFN20	0.0103	0.0739	0.0103	0.0103	0.0262	0.0000	0.0000
p_Thermi;c_Deinococci;o_Thermales;f_Thermaceae;g_Thermus	0.0026	0.0053	0.0026	0.0000	0.0052	0.0026	0.0026
p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_Kosmotoga	0.0463	0.3273	0.0360	0.0413	0.5006	0.1567	0.0771
p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_Petrotoga	0.0077	0.0026	0.0000	0.0026	0.0000	0.0000	0.0000
p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g_Opitutus	0.1234	0.0079	0.2057	0.0233	0.0157	0.0231	0.5241
	27.778	45.542	25.034	30.541	55.761	54.309	56.473
Total percent	2	1	7	4	2	0	8