Supplementary Materials

Table S1. Pearson product-moment correlation coefficients of the LH metagenome taxonomic and functional reads under different cutoff *E values* $\leq 10^{-5}$, 10^{-10}, 10^{-15}, and 10^{-20}

Taxonomy		**1.00E-10**	**1.00E-15**	**1.00E-20**
1.00E-05	$\mathbf{R}^2$	1	0.987563	0.73459
	P-value	< 2.2e-16	< 2.2e-16	1.93E-05
Function				
1.00E-05	$\mathbf{R}^2$	0.999999	0.995174	0.908828
	P-value	< 2.2e-16	< 2.2e-16	2.27E-11

TABLE S2. The percentages of genera related to the genes encoding enzymes facilitating nitrogen cycles in LH metagenome

Genus/Enzyme/EC	**%**	**Phylum/Class of Proteobacteria**
Copper-containing nitrite reductase (EC 1.7.2.1)		
Burkholderia	2.4	*Betaproteobacteria*
Bdellovibrio	15	*Deltaproteobacteria*
Propionibacterium	1.2	*Actinobacteria*
Gramella	3.6	*Bacteroidetes*
Kangiella	23	*Gammaproteobacteria*
Neisseria	7.1	*Betaproteobacteria*
Maribacter	13	*Bacteroidetes*
Flavobacterium	32	*Bacteroidetes*
Leeuwenhoekiella	1.2	*Bacteroidetes*
Flavobacteria	1.2	*Bacteroidetes*
Nitrous-oxide reductase (EC 1.7.99.6/1.7.2.4)		
Magnetospirillum	11	*Alphaproteobacteria*
Campylobacter	68	*Deltaproteobacteria*
Nitratiruptor	3.6	*Deltaproteobacteria*
Sulfurovum	11	*Deltaproteobacteria*
Magnetospirillum	3.6	*Alphaproteobacteria*
Gramella	3.6	*Bacteroidetes*
Nitrogenase (EC 1.18.6.1)		
Nostoc	50	*Cyanobacteria*
Cyanothece	50	*Cyanobacteria*
Nitrite reductase [NAD(P)H] (EC 1.7.1.4)		
Thermobaculum	1.4	*Bacteroidetes*
Pseudomonas	1.4	*Gammaproteobacteria*
Cytophaga	10	*Cyanobacteria*
Escherichia	2.9	*Gammaproteobacteria*
Spirosoma	7.2	*Bacteroidetes*
Klebsiella	2.9	*Bacteroidetes*
Polaromonas	1.4	*Betaproteobacteria*
Geobacillus	1.4	*Firmicutes*
Polaribacter	11.6	*Bacteroidetes*

Saccharophagus	1.4	*Gammaproteobacteria*
Acinetobacter	2.8	*Gammaproteobacteria*
Chitinophaga	7.2	*Bacteroidetes*
Dyadobacter	2.9	*Bacteroidetes*
Psychrobacter	10	*Gammaproteobacteria*
Mycobacterium	1.4	*Bacteroidetes*
Rhodoferax	1.4	*Betaproteobacteria*
Dokdonia	8.7	*Bacteroidetes*
Leptothrix	2.9	*Betaproteobacteria*
Psychromonas	4.3	*Gammaproteobacteria*
Methylococcus	2.8	*Gammaproteobacteria*
Thiobacillus	1.4	*Betaproteobacteria*
Sorangium	5.8	*Deltaproteobacteria*
Croceibacter	5.8	*Bacteroidetes*
Ferredoxin--nitrite reductase (EC 1.7.7.1)		
Synechocystis	24	*Cyanobacteria*
Cyanothece	16	*Cyanobacteria*
Trichodesmium	8	*Cyanobacteria*
Nostoc	44	*Cyanobacteria*
Thermosynechococcus	4	*Cyanobacteria*
Microcystis	4	*Cyanobacteria*
Assimilatory nitrate reductase (EC 1.7.99.4)		
RhodoPseudomonas	0.7	*Alphaproteobacteria*
Flavobacterium	0.7	*Bacteroidetes*
Psychrobacter	30	*Gammaproteobacteria*
Thermobaculum	0.7	*Unclassidied Bacteria*
Streptosporansium	0.7	*Actinobacteria*
Bacillus	5.7	*Firmicutes*
Trichodesmium	1.4	*Cyanobacteria*
Mycobacterium	0.7	*Bacteroidetes*
Methylococcus	1.4	*Gammaproteobacteria*
Burkholderia	2.8	*Betaproteobacteria*
Pectobacterium	0.7	*Gammaproteobacteria*
Cyanothece	4.3	*Cyanobacteria*
Shewanella	0.7	*Gammaproteobacteria*
Pseudomonas	0.7	*Gammaproteobacteria*
Bradyrhizobium	2.2	*Gammaproteobacteria*

Azoarcus	0.7	*Betaproteobacteria*
Alcanivorax	1.4	*Gammaproteobacteria*
Anabaena	6.5	*Cyanobacteria*
Chitinophaga	0.7	*Bacteroidetes*
Cytophaga	2.9	*Bacteroidetes*
Rhodococcus	0.7	*Actinobacteria*
Marinomonas	0.7	*Gammaproteobacteria*
Roseobacter	1.4	*Alphaproteobacteria*
Nostoc	12	*Cyanobacteria*
Methylibium	2.2	*Betaproteobacteria*
Pseudoalteromonas	0.7	*Gammaproteobacteria*
Microcystis	2.2	*Cyanobacteria*
Polaromonas	0.7	*Betaproteobacteria*
Novosphingobium	0.7	*Alphaproteobacteria*
Crocosphaera	0.7	*Cyanobacteria*
Thiobacillus	2.2	*Betaproteobacteria*
Pseudomonas	0.7	*Gammaproteobacteria*
Azorhizobium	2.2	*Alphaproteobacteria*
Acidovorax	1.4	*Betaproteobacteria*
Maribacter	0.7	*Bacteroidetes*
Acinetobacter	2.2	*Gammaproteobacteria*
Mesorhizobium	0.7	*Alphaproteobacteria*
Rhizobium	1.4	*Alphaproteobacteria*

TABLE S3. The percentages of genera related to the genes encoding enzymes facilitating Sulfate reduction in LH metagenome

Genus/Enzyme/EC	**%**	**Phylum/Class of Proteobacteria**
Adenylylsulfate kinase (EC 2.7.1.25)		
Roseiflexus	16.3	*Chloroflexi*
Aquifex	16.3	*Aquificae*
Chloroflexus	5.8	*Chloroflexi*
Schizosaccharomyces	5.2	*Opisthokonta*
Caulobacter	4.6	*Alphaproteobacteria*
Halothermothrix	4.7	*Firmicutes*
Xanthomonas	3.5	*Gammaproteobacteria*
Paracoccus	2.9	*Alphaproteobacteria*
Zymomonas	2.9	*Alphaproteobacteria*
Trichodesmium	2.3	*Cyanobacteria*
Cyanothece	2.3	*Cyanobacteria*
Bacteroides	1.7	*Bacteroidetes*
Erythrobacter	1.7	*Alphaproteobacteria*
Magnetococcus	1.7	*Alphaproteobacteria*
Microcystis	1.7	*Cyanobacteria*
Solibacter	1.7	*Acidobacteria*
Francisella	1.8	*Gammaproteobacteria*
Pseudomonas	1.8	*Gammaproteobacteria*
Vibrio	1.2	*Gammaproteobacteria*
Burkholderia	1.2	*Betaproteobacteria*
Chlorobium	1.2	*Bacteroidetes*
Deinococcus	1.2	*Deinococcus*
Frankia	1.2	*Actinobacteria*
Hydrogenobaculum	1.2	*Aquificae*
Oceanobacillus	1.2	*Firmicutes*
Rhodopseudomonas	1.2	*Alphaproteobacteria*
Synechocystis	1.2	*Cyanobacteria*
Ashbya	0.6	*Opisthokonta*
Aurantimonas	0.6	*Alphaproteobacteria*
Campylobacter	0.6	*Deltaproteobacteria*
Crocosphaera	0.6	*Cyanobacteria*
Delftia	0.6	*Betaproteobacteria*

Geobacter	0.6	*Deltaproteobacteria*
Methylococcus	0.6	*Gammaproteobacteria*
Mycobacterium	0.6	*Actinobacteria*
Neurospora	0.6	*Opisthokonta*
Oceanicaulis	0.6	*Alphaproteobacteria*
Parvibaculum	0.6	*Alphaproteobacteria*
Pelobacter	0.6	*Deltaproteobacteria*
Prochlorococcus	0.6	*Cyanobacteria*
Roseobacter	0.6	*Alphaproteobacteria*
Shewanella	0.6	*Gammaproteobacteria*
Sphingomonas	0.6	*Alphaproteobacteria*
Thermobispora	0.6	*Actinobacteria*
Thermosynechococcus	0.6	*Cyanobacteria*
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)/ Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10)		
Marinobacter	29.2	*Gammaproteobacteria*
Acinetobacter	17	*Gammaproteobacteria*
Azotobacter	9.8	*Gammaproteobacteria*
Reinekea	9.8	*Gammaproteobacteria*
Cyanothece	4.8	*Cyanobacteria*
Pseudomonas	4.8	*Gammaproteobacteria*
Crocosphaera	4.9	*Cyanobacteria*
Hahella	4.9	*Gammaproteobacteria*
Alkalilimnicola	2.4	*Gammaproteobacteria*
Anabaena	2.4	*Cyanobacteria*
Bordetella	2.4	*Betaproteobacteria*
Cellvibrio	2.4	*Gammaproteobacteria*
Croceibacter	2.4	*Bacteroidetes*
Nostoc	2.4	*Cyanobacteria*
Sulfate adenylyltransferase, dissimilatory-type (EC 2.7.7.4)		
Aquifex	12.6	*Aquificae*
Roseiflexus	12.7	*Chloroflexi*
Anabaena	5.9	*Cyanobacteria*
Chloroflexus	4.5	*Chloroflexi*
Cytophaga	3.6	*Cyanobacteria*

Synechococcus	4.2	*Cyanobacteria*
Caulobacter	3.7	*Alphaproteobacteria*
Nitrosococcus	1.8	*Gammaproteobacteria*
Xanthomonas	3.3	*Gammaproteobacteria*
Nostoc	2.7	*Cyanobacteria*
Maribacter	3.7	*Bacteroidetes*
Paracoccus	2.3	*Alphaproteobacteria*
Microcystis	1.8	*Cyanobacteria*
Thermosynechococcus	1.8	*Cyanobacteria*
Pseudomonas	1.4	*Gammaproteobacteria*
Trichodesmium	1.4	*Cyanobacteria*
Erythrobacter	1.4	*Alphaproteobacteria*
Francisella	1.4	*Gammaproteobacteria*
Leeuwenhoekiella	2.3	*Bacteroidetes*
Magnetococcus	1.4	*Alphaproteobacteria*
Pseudoalteromonas	1.9	*Gammaproteobacteria*
Robiginitalea	2.3	*Bacteroidetes*
Streptosporangium	1.4	*Actinobacteria*
Aeropyrum	0.9	*Crenarchaeota*
Bacillus	0.9	*Firmicutes*
Deinococcus	0.9	*Deinococcus*
Hydrogenobaculum	0.9	*Aquificae*
Pyrococcus	0.9	*Euryarchaeota*
Frankia	0.9	*Actinobacteria*
RhodoPseudomonas	0.9	*Alphaproteobacteria*
Saccharophagus	0.9	*Gammaproteobacteria*
Cyanothece	0.5	*Cyanobacteria*
Ferroplasma	0.5	*Euryarchaeota*
Neurospora	0.5	*Opisthokonta*
Petrotoga	0.5	*Thermotogae*
Roseobacter	0.5	*Alphaproteobacteria*
Staphylococcus	0.5	*Firmicutes*
Staphylothermus	0.5	*Crenarchaeota*
Thermobispora	0.5	*Actinobacteria*
Flavobacterium	0.5	*Bacteroidetes*
Geobacter	0.5	*Deltaproteobacteria*
Hahella	0.5	*Gammaproteobacteria*
Kytococcus	0.5	*Actinobacteria*

Opitutus	1	*Verrucomicrobia*
Psychromonas	1	*Gammaproteobacteria*
Aurantimonas	0.5	*Alphaproteobacteria*
Chromobacterium	0.5	*Betaproteobacteria*
Leptospira	0.5	*Spirochaetes*
Methylococcus	0.5	*Gammaproteobacteria*
Mycobacterium	0.5	*Actinobacteria*
Nocardioides	0.5	*Actinobacteria*
Oceanicaulis	0.5	*Alphaproteobacteria*
Parvibaculum	0.5	*Alphaproteobacteria*
Pelobacter	0.5	*Deltaproteobacteria*
Salmonella	0.5	*Gammaproteobacteria*
Shewanella	0.5	*Gammaproteobacteria*
Sphingomonas	0.5	*Alphaproteobacteria*
Nitrosomonas	1.8	*Betaproteobacteria*
Sulfite reductase (EC 1.8.99.1)/ Ferredoxin--sulfite reductase (EC 1.8.7.1)/ Sulfite reductase [NADPH] hemoprotein (EC 1.8.1.2)/ Sulfite reductase, dissimilatory-type (EC 1.8.99.3)		
Thiobacillus	31.3	*Betaproteobacteria*
Nostoc	10.8	*Cyanobacteria*
Cyanothece	9.9	*Cyanobacteria*
Synechocystis	8.9	*Cyanobacteria*
Alkalilimnicola	6.3	*Gammaproteobacteria*
Anabaena	5.4	*Cyanobacteria*
Thioalkalivibrio	4.5	*Gammaproteobacteria*
Microcystis	3.6	*Cyanobacteria*
Xanthomonas	2.7	*Gammaproteobacteria*
Magnetospirillum	2.7	*Alphaproteobacteria*
Xylella	1.8	*Gammaproteobacteria*
Vesicomyosocius	1.8	*Gammaproteobacteria*
Trichodesmium	1.8	*Cyanobacteria*
Shewanella	0.9	*Gammaproteobacteria*
Polaribacter	0.9	*Bacteroidetes*
Nitrosospira	0.9	*Betaproteobacteria*
Myxococcus	0.9	*Deltaproteobacteria*

Halorhodospira	0.9	*Gammaproteobacteria*
Flavobacterium	0.9	*Bacteroidetes*
Crocosphaera	0.9	*Cyanobacteria*
Chromobacterium	0.9	*Betaproteobacteria*
Acinetobacter	0.9	*Gammaproteobacteria*
Sulfur oxidation protein SoxB		
Thiomicrospira	20.2	*Gammaproteobacteria*
Chlorobium	15.9	*Bacteroidetes*
Dechloromonas	12.6	*Betaproteobacteria*
Herminiimonas	7.9	*Betaproteobacteria*
Thiobacillus	6.3	*Betaproteobacteria*
Congregibacter	5.6	*Gammaproteobacteria*
Janthinobacterium	5.3	*Betaproteobacteria*
Chlorobaculum	4.3	*Bacteroidetes*
Polaromonas	3.6	*Betaproteobacteria*
Bradyrhizobium	3.3	*Alphaproteobacteria*
Ralstonia	3.0	*Betaproteobacteria*
Vesicomyosocius	2.6	*Gammaproteobacteria*
Pelodictyon	2.0	*Bacteroidetes*
Thioalkalivibrio	1.3	*Gammaproteobacteria*
Nitrobacter	1.3	*Alphaproteobacteria*
Acidiphilium	1.3	*Alphaproteobacteria*
Polynucleobacter	1.0	*Betaproteobacteria*
Methylobacterium	0.7	*Alphaproteobacteria*
Arcobacter	0.7	*Deltaproteobacteria*
Oligotropha	0.3	*Alphaproteobacteria*
Anaeromyxobacter	0.3	*Deltaproteobacteria*

TABLE S4. Representatives of genes/proteins related to oxidative stress in LH metagnome

Function	**Protein names**	**Unique hits**	**Total hits**	**Phyla**
Oxidative stress	Catalase	67	29592	*Bacteroidetes* (74.0%), *Cyanobacteria* (11.0%), *Proteobacteria* (11.6%), *Acidobacteria* (1.1%), *Chlorobi* (0.3%), *Actinobacteria* (1.3%), *Firmicutes* (0.5%), *Deinococcus-Thermus* (0.2%)
	Superoxide dismutase	46	57074	*Cyanobacteria* (66.9%), *Bacteroidetes* (29.4%), *Chloroflexi* (0.4%), *Proteobacteria* (2.9%), *Bacteria* (0.3%), *Firmicutes* (0.3%), *Thermotoga* (0.1%)
	Peroxidase	41	18062	*Bacteroidetes* (65.8%), *Cyanobaceria* (18.0%), *Proteobacteria* (11.9%), *Acidobacteria* (1.7%), *Chlorobi* (0.5%), *Firmicutes* (0.5%), *Actinobacteria* (1.6%)
	Iron-binding ferritin-like antioxidant protein	17	19709	*Cyanobacteria* (28.4%), *Bacteroidetes* (66.2%), *Proteobacteria* (5.4%)
	Organic hydroperoxide resistant protein	11	609	*Verrucomicrobia* (71.8%), *Firmicutes* (28.2%)

TABLE S5. Representatives of genes/proteins related to osmotic stress in LH metagenome

Function	**Protein names**	**Unique hits**	**Total hits**	**Phyla**
Synthesis of osmoregulated periplasmic glucan	Cyclic beta-1,2-glucan synthase	34	4475	*Acidobacteria* (12.1%), *Proteobacteria* (57.8%), *Chloroflexi* (15.6%), *Planctomycetes* (5.4%), *Firmicutes* (7.3), *Euryarchaeota* (1.8)
	Glucans biosynthesis protein C	3	2563	*Bacteroidetes* (95.3%), *Proteobacteria* (4.7%)
Choline and Betaine Uptake and Betaine Biosynthesis	Sarcosine oxidase	30	10504	*Acidobacteria* (7.4%), *Actinobacteria* (30.0%), *Proteobacteria* (62.6%)
	L-proline glycine betaine ABC transport system permease protein	14	4233	*Acidobacteria* (64.6%), *Proteobacteria* (30.0%), *Actinobacteria* (3.2%), *Firmicutes* (2.2%)
	Choline dehydrogenase	12	8386	*Cyanobacteria* (88.4%), *Proteobacteria* (6.9%), *Actinobacteria* (4.7%)
	Betaine aldehyde dehydrogenase	2	7	*Fungi* (85.7%), *Proteobacteria* (14.3%)

TABLE S6. Representatives of genes/proteins related to cold adaptation in LH metagenome

Functions	**Protein or subsystem names**	**Unique hits**	**Total hits**	**Phyla**
DNA replication	gyrA (DNA Gyrase A)	96	58535	*Cyanobacteria* (55.6%), *Bacteroidetes* (40.8%), *Proteobacteria* (2.3%), *Actinobacteria* (0.6%), *Firmicutes* (0.7%)
	recA (Recombination factor A)	36	28954	*Cyanobacteria* (48.4%), *Bacteroidetes* (46.5%), *Proteobacteria* (2.6%), *Chlorobi* (0.3%), *Deinococcus-Thermus* (0.3%), *Actinobacteria* (1.8%), *Chloroflexi* (0.1%)
	dnaA (Replication initiator Protein)	30	28928	*Cyanobacteria* (33.7%), *Bacteroidetes* (63.4%), *Actinobacteria* (1.0%), *Proteobacteria* (1.5%), *Deinococcus-Thermus* (0.4%)
Unsaturated fatty acids	Fatty acid desaturases	36	54030	*Cyanobacteria* (99.7%), *Proteobacteria* (0.3%)
	dnaJ	53	57229	*Cyanobacteria* (75.3%), *Bacteroidetes* (21.3%), *Proteobacteria* (2.9%), *Firmicutes* (0.4%), *Actinobacteria* (0.1%)
Protein folding	Prolyl-isomerase	64	7063	*Bacteroidetes* (60.5%), *Proteobacteria* (33.3%), *Acidobacteria* (4.4%), *Cyanobacteria* (1.5%), *Synergistetes* (0.3%)
Nucleosides and Nucleotides	aceE	79	55118	*Cyanobacteria* (57.0%), *Bacteroidetes* (38.5%), *Acidobacteria* (0.6%), *Proteobacteria* (3.0%),

				Chloroflexi (0.4%), *Actinobacteria* (0.3%), *Deinococcus-Thermus* (0.1%), *Chlamydiae* (0.1%)
Pyruvate metabolism	aceF	72	52841	*Cyanobacteria* (49.6%), *Bacteroidetes* (43.3%) *Proteobacteria* (6.1%), *Acidobacteria* (0.6%), *Actinobacteria* (0.2%), *Deinococcus-Thermus* (0.1%), *Firmicutes* (0.1%)
Transcription	nusA	26	28035	*Cyanobacteria* (49.4%), *Bacteroidetes* (45.3%), *Bacteria* (0.5%), *Firmicutes* (1.2%), *Actinobacteria* (3.6%)
RNA helicase	Cold-shock DEAD-box protein A	61	25563	*Bacteroidetes* (49.8%) *Cyanobacteria* (48.4%) *Proteobacteria* (1.6%) *Methanococcales* (0.1%) *Firmicutes* (0.1%) *Verrucomicrobia* (1.0%)
	cspA	9	14	*Bacteroidetes* (71.4%) *Proteobacteria* (21.4%) *Firmicutes* (7.2%)

TABLE S7. Dereplication hits of active bacterial 16S ribosomal cDNA based on 98% similarity

No. of reads	**Dereplicated representative**	**Best hit**	**Accession No.**	**Identity**
103	SB-1	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	94%
84	SB-2	*Stenotrophomonas* sp. NOE8	JX842835.1	100%
73	SB-3	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	93%
73	SB-4	*Rhodothalassium* sp. PHT1	HE806302.1	91%
65	SB-5	*Pseudomonas aeruginosa* strain PM389	JF899310.2	99%
63	SB-6	*Roseateles* sp. R-45571	FR775142.1	98%
60	SB-7	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	95%
55	SB-8	*Pedobacter heparinus*	AB680215.1	98%
54	SB-9	*Pseudomonas aeruginosa* strain PM389	JF899310.2	99%
43	SB-10	*Enterobacter* sp. DHL-02	AB714445.1	99%
38	SB-11	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
31	SB-12	*Desulfobulbus* sp.	AF132865.1	99%
30	SB-13	*Stenotrophomonas* sp. NOE8	JX842835.1	99%
22	SB-14	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	93%
17	SB-15	*Delftia lacustris*	HE861943.1	100%
9	SB-16	*Acidovorax* sp. CNE 29	FR749857.1	99%
7	SB-17	*Enterobacter* sp. DHL-02	AB714445.1	99%
7	SB-18	*Desulfobulbus* sp.	AF132865.1	98%
6	SB-19	*Pseudomonas aeruginosa* strain PM389	JF899310.2	98%
6	SB-20	*Enterobacter* sp. DHL-02	AB714445.1	99%
6	SB-21	*Stenotrophomonas* sp. NOE8	JX842835.1	99%
6	SB-22	*Pseudomonas* sp. RB5-M5	JN019027.1	97%
5	SB-23	*Staphylococcus aureus* 08BA02176	CP003808.1	99%
5	SB-24	*Marinobacter* sp. V3H-008	JN106689.1	98%
5	SB-25	*Verrucomicrobia* bacterium	HQ675558.1	95%

		SCGC AAA240-C14		
5	SB-26	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	94%
5	SB-27	*Pseudomonas aeruginosa* strain PM389	JF899310.2	99%
5	SB-28	*Desulfobulbus* sp.	AF132865.1	99%
4	SB-29	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
4	SB-30	*Microlunatus panaciterrae*	NR_041517.1	93%
4	SB-31	*Stenotrophomonas* sp. NOE8	JX842835.1	99%
4	SB-32	*Pedobacter heparinus*	AB680215.1	98%
4	SB-33	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	93%
4	SB-34	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	93%
4	SB-35	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	94%
3	SB-36	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	96%
3	SB-37	*Stenotrophomonas maltophilia* strain BXCC-58	JF431276.1	98%
3	SB-38	*Pseudomonas* sp. PC IW 25	FM164626.1	98%
3	SB-39	*Pseudomonas aeruginosa* strain PM389	JF899310.2	99%
3	SB-40	*Stenotrophomonas* sp. NOE3	JX842830.1	99%
3	SB-41	*Pseudomonas aeruginosa* strain 9Cit	JN969597.1	92%
3	SB-42	*Pedobacter heparinus*	AB680215.1	97%
3	SB-43	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
3	SB-44	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	91%
3	SB-45	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	97%
3	SB-46	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	95%
3	SB-47	*Delftia lacustris*	HE861943.1	99%

3	SB-48	*Pseudomonas aeruginosa* strain PM389	JF899310.2	96%
3	SB-49	*Mitsuaria* sp. H29L1B	EU714912.1	96%
3	SB-50	*Tessaracoccus* sp. SL014B-79A	GU111568.2	93%
3	SB-51	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	97%
2	SB-52	*Pseudomonas aeruginosa* strain N83	JQ900543.1	92%
2	SB-53	*Pseudomonas aeruginosa*	AB037548.1	96%
2	SB-54	*Pseudomonas aeruginosa* strain RsB-29	DQ666628.1	94%
2	SB-55	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
2	SB-56	*Stenotrophomonas maltophilia* strain GGI-22	GU815943.1	96%
2	SB-57	*Enterobacter* sp. DHL-02	AB714445.1	98%
2	SB-58	*Roseateles* sp. AKB-2008-KU7	AM989118.1	95%
2	SB-59	*Rhodothalassium salexigens*	FR682008.1	90%
2	SB-60	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	92%
2	SB-61	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
2	SB-62	*Afifella marina* strain P530	GU370095.1	88%
2	SB-63	*Roseateles* sp. R-45571	FR775142.1	95%
2	SB-64	*Klebsiella oxytoca* E718	CP003683.1	99%
2	SB-65	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	96%
2	SB-66	*Stenotrophomonas maltophilia* clone FH030	GU420674.1	97%
2	SB-67	*Pseudomonas aeruginosa*	AY499109.1	99%
2	SB-68	*Sphingomonadaceae* bacterium KF016	AB269802.2	91%
2	SB-69	*Pedobacter heparinus*	AB680215.1	94%
2	SB-70	*Stenotrophomonas* sp. NOE8	JX842835.1	98%
2	SB-71	*Desulfobulbus* sp.	AF132865.1	91%
2	SB-72	*Stenotrophomonas* sp. NOE8	JX842835.1	97%

2	SB-73	*Alcaligenes faecalis* strain N8	EU567029.1	98%
2	SB-74	*Pseudomonas* sp. AMAAS232	JN391539.1	98%
2	SB-75	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	99%
2	SB-76	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	96%
2	SB-77	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	91%
2	SB-78	*Acidovorax* sp. CNE 29	FR749857.1	97%
2	SB-79	*Desulfobulbus* sp.	AF132865.1	97%
2	SB-80	*Stenotrophomonas* sp. NOE8		94%
2	SB-81	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	93%
1	SB-82	*Pedobacter heparinus*	AB680215.1	98%
1	SB-83	*Alcaligenes faecalis* strain N8	EU567029.1	98%
1	SB-84	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	94%
1	SB-85	*Sphingomonadaceae* bacterium KF016	AB269802.2	90%
1	SB-86	*Mitsuaria* sp. H29L1B	EU714912.1	89%
1	SB-87	*Pseudomonas aeruginosa*	AB037548.1	94%
1	SB-88	*Alcaligenes faecalis* strain N8	EU567029.1	97%
1	SB-89	*Pseudomonas aeruginosa* strain S85R	JF513140.1	94%
1	SB-90	*Roseateles* sp. R-45571	FR775142.1	94%
1	SB-91	*Enterobacter* sp. 2391	JX174268.1	92%
1	SB-92	*Afifella marina* strain P530(0)	GU370095.1	88%
1	SB-93	*Stenotrophomonas* sp. NOE8	JX842835.1	94%
1	SB-94	*Pseudomonas aeruginosa* strain NGKCTS	FJ556919.1	95%
1	SB-95	*Pseudomonas aeruginosa* strain ASFP-38	HQ018741.1	98%
1	SB-96	*Roseateles* sp. MC12	AB013425.1	92%
1	SB-97	*Desulfobulbus* sp.	AF132865.1	97%
1	SB-98	*Pseudomonas aeruginosa* strain TERIPS9002	AY499109.1	97%
1	SB-99	*Porphyrobacter cryptus*	FR774566.1	87%
1	SB-100	*Porphyrobacter cryptus*	FR774566.1	89%

1	SB-101	*Roseateles* sp. R-45571	FR775142.1	97%
1	SB-102	*Pedobacter heparinus*	AB680215.1	97%
1	SB-103	*Pseudomonas aeruginosa* strain XRF-6	GU212673.1	99%
1	SB-104	*Desulfobulbus* sp.	AF132865.1	99%
1	SB-105	*Sphingomonadaceae* bacterium KF016	AB269802.2	89%
1	SB-106	*Pseudomonas aeruginosa* strain PM389	JF899310.2	97%
1	SB-107	*Sphingomonadaceae* bacterium KF016	AB269802.2	91%
1	SB-108	*Sphingomonadaceae* bacterium KF016	AB269802.2	88%
1	SB-109	*Enterobacter* oryzae strain R5-362	JQ659749.1	95%
1	SB-110	*Stenotrophomonas* sp. NOE8	JX842835.1	99%
1	SB-111	*Pseudomonas aeruginosa* strain PM389	JF899310.2	98%
1	SB-112	*Sphingomonas* sp. V3M21	FN794222.1	93%
1	SB-113	*Pedobacter heparinus*	AB680215.1	96%
1	SB-114	*Acidovorax* sp. CNE 29	FR749857.1	91%
1	SB-115	*Microlunatus* sp. M5_21	AB468984.1	90%
1	SB-116	*Desulfobulbus* sp.	AF132865.1	97%
1	SB-117	*Tessaracoccus* sp. SL014B-79A	GU111568.2	89%
1	SB-118	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	92%
1	SB-119	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	92%
1	SB-120	*Pedobacter heparinus*	AB680215.1	98%
1	SB-121	*Desulfobulbus* sp.	AF132865.1	91%
1	SB-122	*Porphyrobacter cryptus*	FR774566.1	91%
1	SB-123	*Pseudomonas aeruginosa* strain PM389	JF899310.2	99%
1	SB-124	*Roseateles* sp. R-45571	FR775142.1	95%
1	SB-125	*Staphylococcus aureus* subsp. aureus ST228	HE579073.1	96%
1	SB-126	*Roseateles* sp. R-45571	FR775142.1	94%

1	SB-127	*Enterobacter* sp. SP1	JQ001784.1	99%
1	SB-128	*Pseudomonas* sp. PC IW 25	FM164626.1	97%
1	SB-129	*Pseudomonas aeruginosa*	AB062598.1	96%
1	SB-130	*Musa acuminata*	EU017026.1	99%
1	SB-131	*Pseudomonas aeruginosa* strain TERIPS9002	AY499109.1	97%
1	SB-132	*Verrucomicrobia* bacterium SCGC AAA240-C14	HQ675558.1	96%
1	SB-133	*Pedobacter heparinus*	AB680215.1	91%
1	SB-134	*Pseudomonas* stutzeri	EU520400.1	90%
1	SB-135	*Microlunatus panaciterrae* strain Gsoil 954	NR_041517.1	93%
1	SB-136	*Tessaracoccus* sp. SL014B-79A	GU111568.2	92%
1	SB-137	*Pedobacter heparinus*	AB680215.1	93%
1	SB-138	*Pseudomonas aeruginosa* strain M10	JQ927361.1	100%
1	SB-139	*Sneathiella* sp. BFLP-8	FN687912.1	87%
1	SB-140	*Pseudomonas* sp. RB5-M5	JN019027.1	97%
1	SB-141	*Pedobacter* sp. 9-15	HM151618.1	96%
1	SB-142	*Pseudomonas aeruginosa*	AB680503.1	95%
1	SB-143	*Mitsuaria* sp. RV4	JQ433927.1	91%
1	SB-144	*Pantoea agglomerans* strain GS2	GQ374474.1	93%
1	SB-145	*Delftia* acidovorans strain IAC/BECa-020	JX155410.1	98%
1	SB-146	*Pseudomonas* sp. INBio2893C	HM771055.1	91%
1	SB-147	*Rhodothalassium salexigens*	FR682008.1	90%
1	SB-148	*Pedobacter heparinus*	AB680215.1	96%
1	SB-149	*Enterobacter* cloacae strain M-5	HM030748.1	99%
1	SB-150	*Desulfobulbus* sp.	AF132865.1	94%

TABLE S8. The dereplication hits of active archaeal 16S ribosomal cDNA based on 98% similarity

No. of reads	Dereplicated representative	Best hit	Accession No.	Identity
206	SA-1	*Candidatus* Nitrososphaera gargensis clone RHGA41c	EU281334.1	84%
172	SA-2	anaerobic methanogenic archaeon ET1-9	AJ244285.1	94%
168	SA-3	*Vulcanisaeta* sp. CBA1501	HM594677.1	99%
116	SA-4	*Candidatus* Nitrososphaera gargensis	CP002408.1	86%
82	SA-5	*Thermoproteus uzoniensis* 768-20	CP002590.1	98%
49	SA-6	*Vulcanisaeta distributa*	AB063641.1	87%
36	SA-7	*Aeropyrum pernix*	AB263905.1	86%
33	SA-8	*Thermogladius cellulolyticus* 1633	CP003531.1	85%
24	SA-9	*Sulfolobus* sp. JP3	AY907890.1	95%
13	SA-10	anaerobic methanogenic archaeon ET1-8	AJ244284.1	95%
9	SA-11	anaerobic methanogenic archaeon ET1-9	AJ244285.1	93%
8	SA-12	*Candidatus* Nitrosocaldus yellowstonii strain HL72	EU239960.1	99%
6	SA-13	*Desulfurococcus amylolyticus*	AB661712.1	86%
4	SA-14	Methanobacterium sp. AL-21	CP002551.1	99%

3	SA-15	*Candidatus* Nitrososphaera gargensis Ga9.2	CP002408.1	85%
3	SA-16	*Thermogymnomonas acidicola* strain JCM 13583	NR_041513.1	87%
3	SA-17	*Vulcanisaeta* sp. CBA1501	HM594677.1	85%
1	SA-18	*Candidatus* Nitrososphaera gargensis clone RHGA41c	EU281334.1	83%
1	SA-19	*Vulcanisaeta* sp. CBA1501	HM594677.1	97%
1	SA-20	*Vulcanisaeta* sp. CBA1501	HM594677.1	90%
1	SA-21	*Methanocella arvoryzae* MRE50	AM114193.2	92%
1	SA-22	*Vulcanisaeta* sp. CBA1501	HM594677.1	92%
1	SA-23	*Pyrobaculum* sp. D11	AJ630373.1	99%
1	SA-24	*Candidatus* Nitrososphaera gargensis Ga9.2	CP002408.1	85%
1	SA-25	*Vulcanisaeta distributa*	AB063641.1	86%

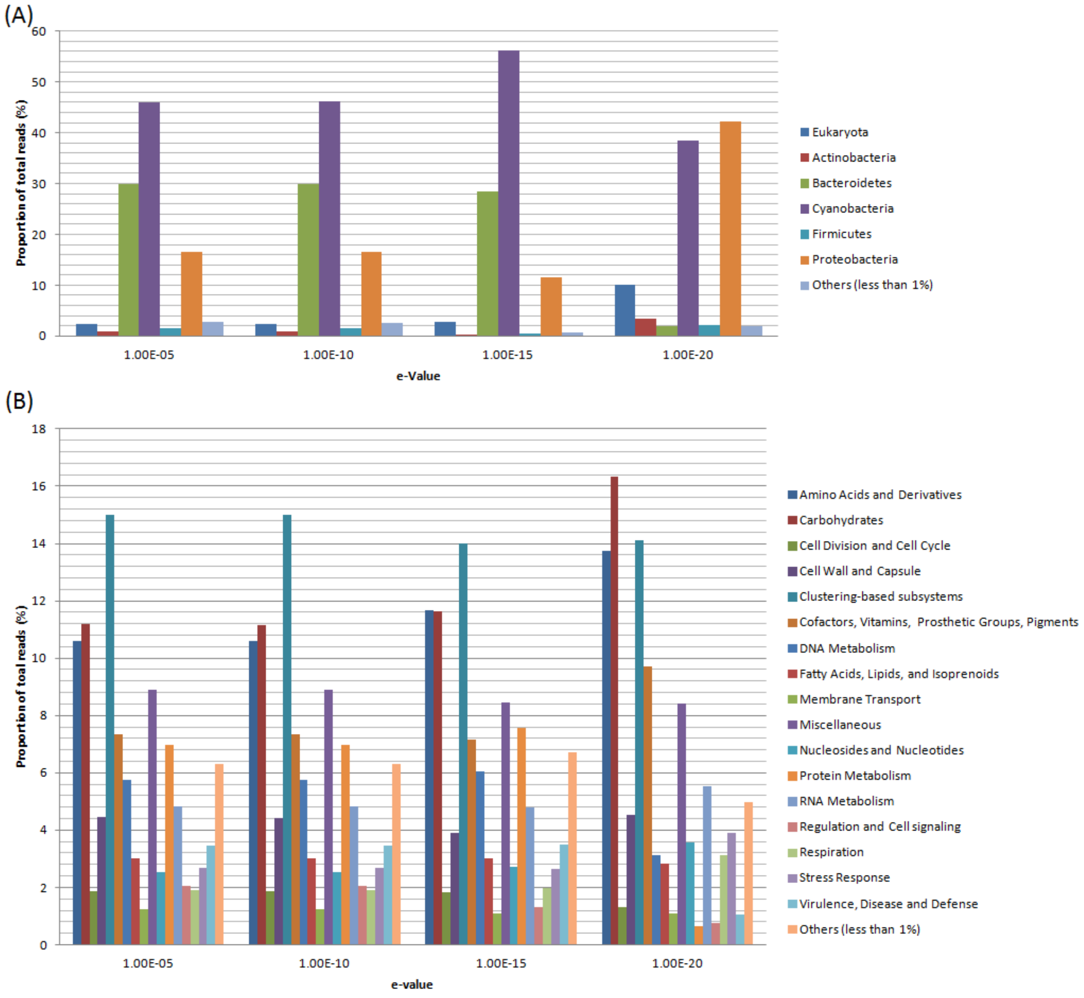

FIG S1 The proportions of (A) taxonomic and (B) functional classifications of the total metagenomic reads under E values $\leq 10^{-5}$, 10^{-10}, 10^{-15}, and 10^{-20} at phylum (except Eukaryota) and subsystem levels.

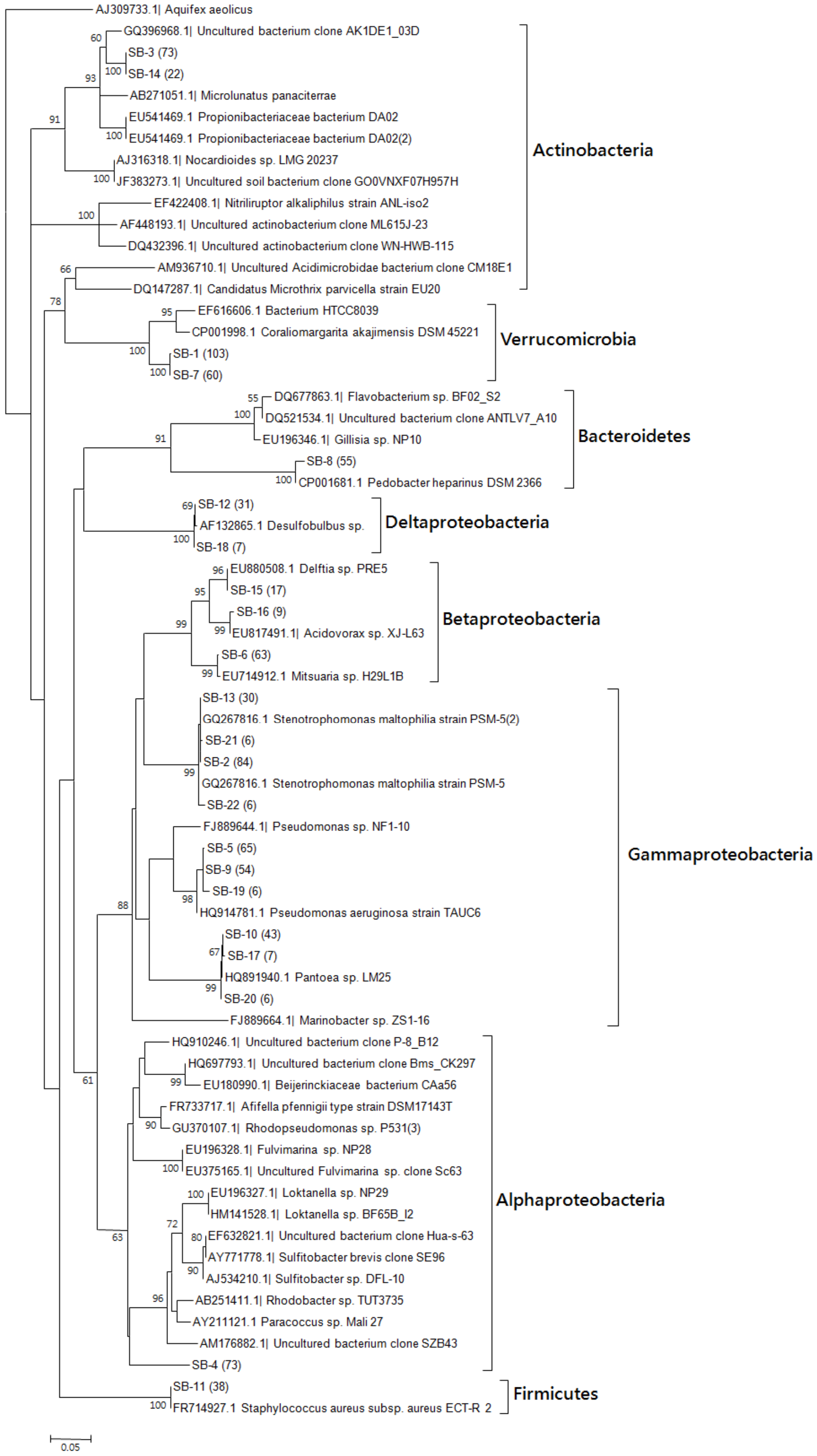
AJ309733.1| Aquifex aeolicus
60
GQ396968.1| Uncultured bacterium clone AK1DE1_03D
SB-3 (73)
93
100
SB-14 (22)
AB271051.1| Microlunatus panaciterrae
91
EU541469.1 Propionibacteriaceae bacterium DA02
100
EU541469.1 Propionibacteriaceae bacterium DA02(2)
AJ316318.1| Nocardioides sp. LMG 20237
100
JF383273.1| Uncultured soil bacterium clone GO0VNXF07H957H
EF422408.1| Nitriliruptor alkaliphilus strain ANL-iso2
100
AF448193.1| Uncultured actinobacterium clone ML615J-23
DQ432396.1| Uncultured actinobacterium clone WN-HWB-115
66
AM936710.1| Uncultured Acidimicrobidae bacterium clone CM18E1
DQ147287.1| Candidatus Microthrix parvicella strain EU20
Actinobacteria
78
95
EF616606.1 Bacterium HTCC8039
CP001998.1 Coraliomargarita akajimensis DSM 45221
100
SB-1 (103)
100
SB-7 (60)
Verrucomicrobia
55
DQ677863.1| Flavobacterium sp. BF02_S2
100
DQ521534.1| Uncultured bacterium clone ANTLV7_A10
91
EU196346.1| Gillisia sp. NP10
SB-8 (55)
100
CP001681.1 Pedobacter heparinus DSM 2366
Bacteroidetes
69
SB-12 (31)
AF132865.1 Desulfobulbus sp.
100
SB-18 (7)
Deltaproteobacteria
96
EU880508.1 Delftia sp. PRE5
95
SB-15 (17)
SB-16 (9)
99
99
EU817491.1| Acidovorax sp. XJ-L63
SB-6 (63)
99
EU714912.1 Mitsuaria sp. H29L1B
Betaproteobacteria
SB-13 (30)
GQ267816.1 Stenotrophomonas maltophilia strain PSM-5(2)
SB-21 (6)
SB-2 (84)
99
GQ267816.1 Stenotrophomonas maltophilia strain PSM-5
SB-22 (6)
FJ889644.1| Pseudomonas sp. NF1-10
SB-5 (65)
SB-9 (54)
SB-19 (6)
88
98
HQ914781.1 Pseudomonas aeruginosa strain TAUC6
SB-10 (43)
67
SB-17 (7)
HQ891940.1 Pantoea sp. LM25
99
SB-20 (6)
FJ889664.1| Marinobacter sp. ZS1-16
Gammaproteobacteria
HQ910246.1| Uncultured bacterium clone P-8_B12
HQ697793.1| Uncultured bacterium clone Bms_CK297
61
99
EU180990.1| Beijerinckiaceae bacterium CAa56
FR733717.1| Afifella pfennigii type strain DSM17143T
90
GU370107.1| Rhodopseudomonas sp. P531(3)
EU196328.1| Fulvimarina sp. NP28
100
EU375165.1| Uncultured Fulvimarina sp. clone Sc63
100
EU196327.1| Loktanella sp. NP29
HM141528.1| Loktanella sp. BF65B_I2
72
63
80
EF632821.1| Uncultured bacterium clone Hua-s-63
AY771778.1| Sulfitobacter brevis clone SE96
90
AJ534210.1| Sulfitobacter sp. DFL-10
96
AB251411.1| Rhodobacter sp. TUT3735
AY211121.1 Paracoccus sp. Mali 27
AM176882.1| Uncultured bacterium clone SZB43
SB-4 (73)
Alphaproteobacteria
SB-11 (38)
100
FR714927.1 Staphylococcus aureus subsp. aureus ECT-R 2
Firmicutes
0.05

FIG S2.

Neighbor-joining phylogenetic tree of the bacterial representative sequences from the LH 16S ribosomal cDNA pyrosequencing dataset with the number of representing reads indicated in parentheses. Bootstrap values ≧ 60% of 1000 replicates are indicated at the nodes.

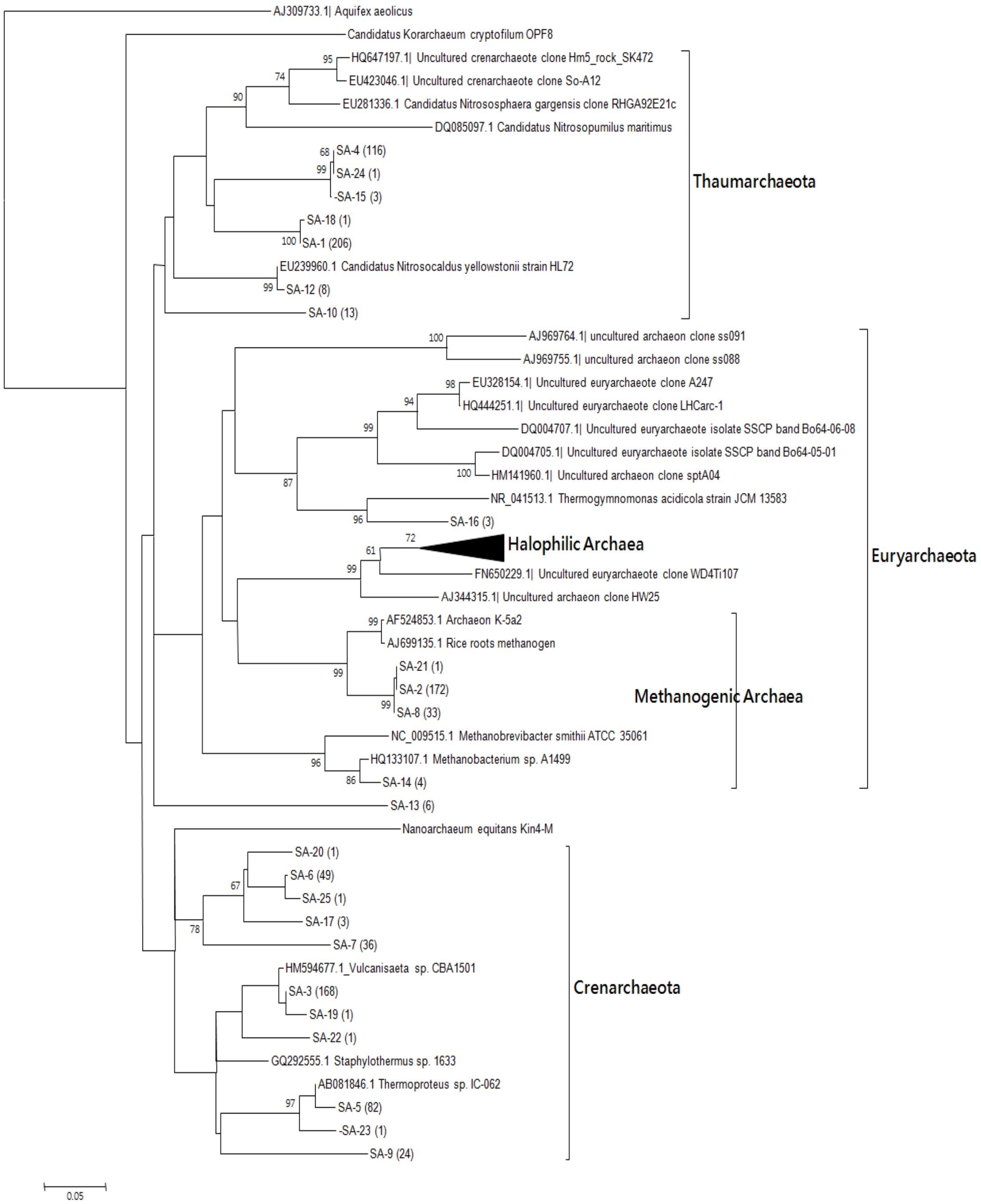

FIG S3.

Neighbor-joining phylogenetic tree of the archaeal representative sequences from the LH 16S ribosomal cDNA pyrosequencing dataset with the number of representing reads indicated in parentheses. Bootstrap values ≧ 60% of 1000 replicates are indicated at the nodes.

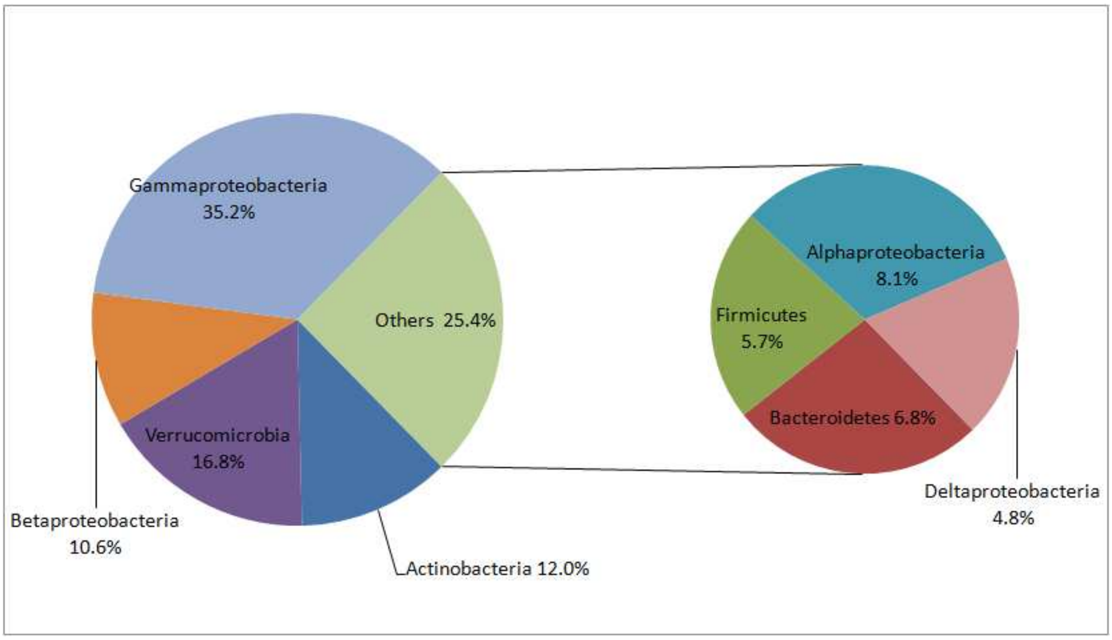

FIG S4.

The active bacterial composition of LH spring sediments based on 16S ribosomal cDNA pyrosequencing analyses.

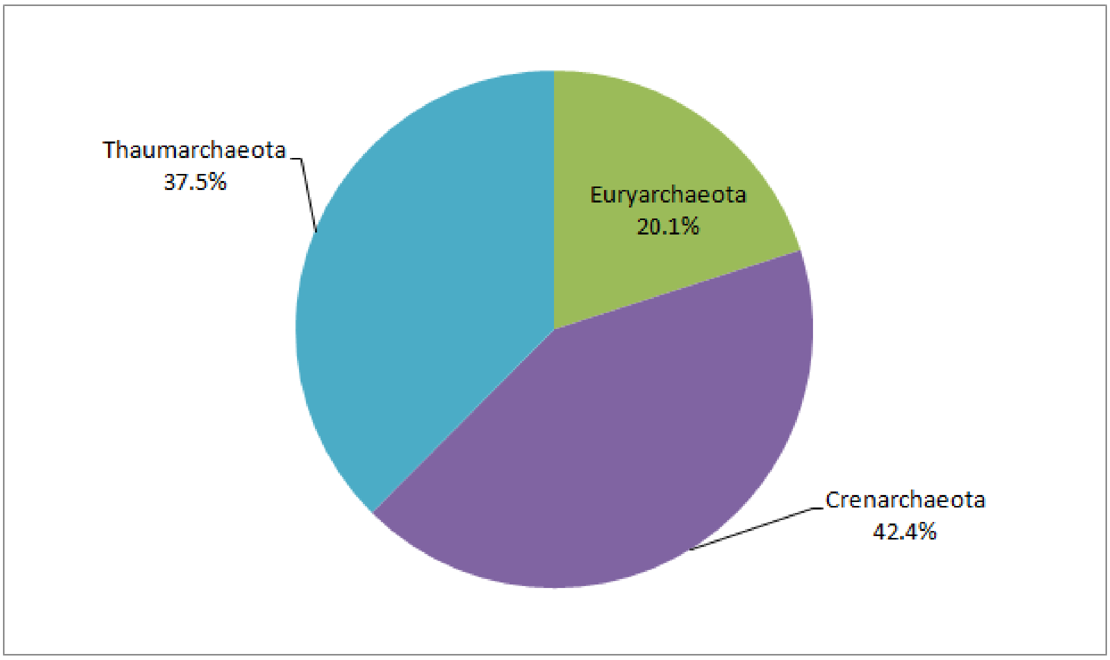

FIG S5.

The active archaeal composition of LH spring sediments based on 16S ribosomal cDNA pyrosequencing analyses.

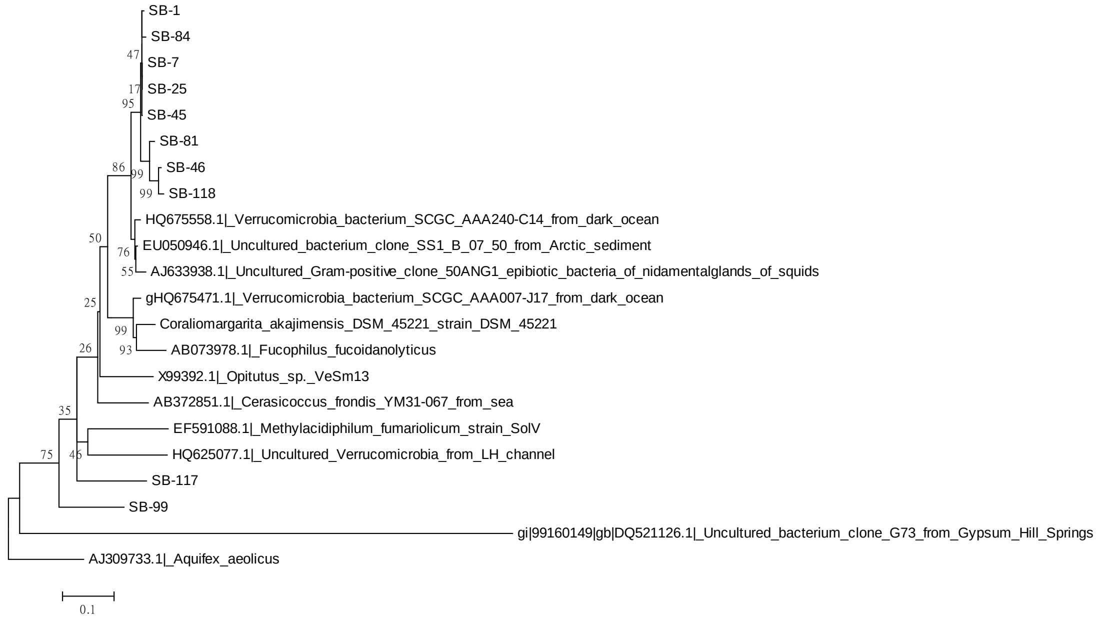

FIG S6.

Neighbor-joining phylogenetic tree of the verrucomicrobial representative sequences (phylotypes with the initial of SB) from the LH 16S ribosomal cDNA pyrosequencing dataset based on 437 bp. EF591088 is a sequence of methanotrophic *Verrucomicrobia* and its clustering sequence (HQ625077.1) originates from a clone of our previous study on LH channel sediment.

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