

Figure S1. Mineral composition of the B3 sediment layers. The major mineral component of B3-1 (sediment depth 30 cm) and B3-2 (sediment depth 40 cm) was estimated by X-ray diffraction measurement.

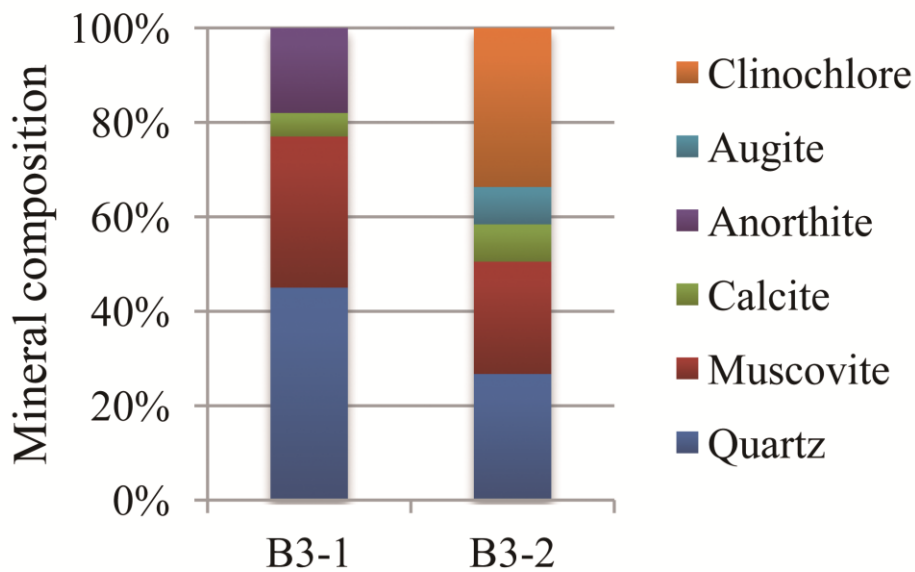


Figure S2. 16S rRNA operational taxonomic units (OTUs) in B3. Taxonomic classification of the representative reads in the OTUs (>97% similarity) was performed through comparing with sequences of SILVA database.

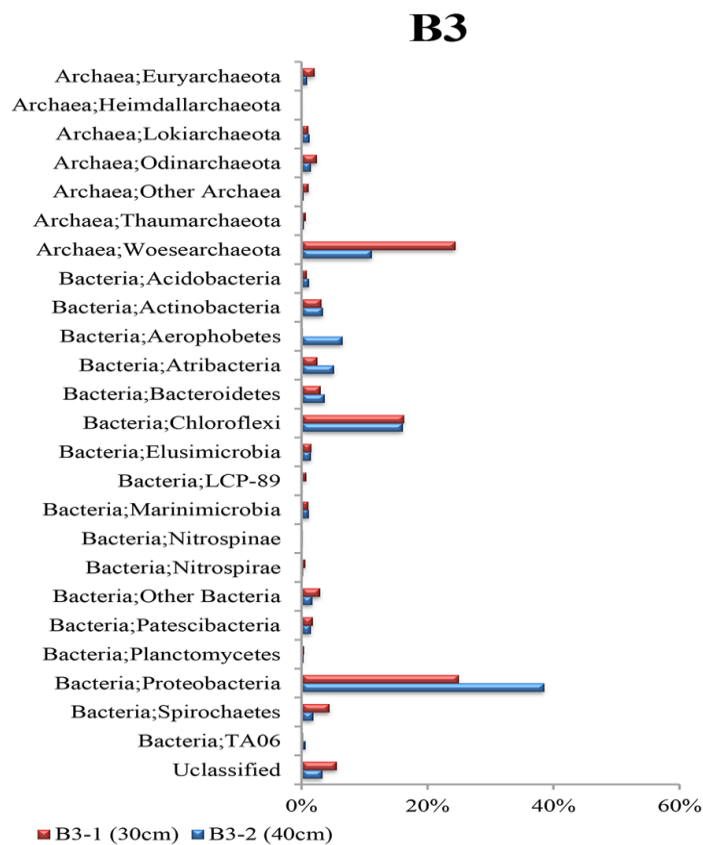
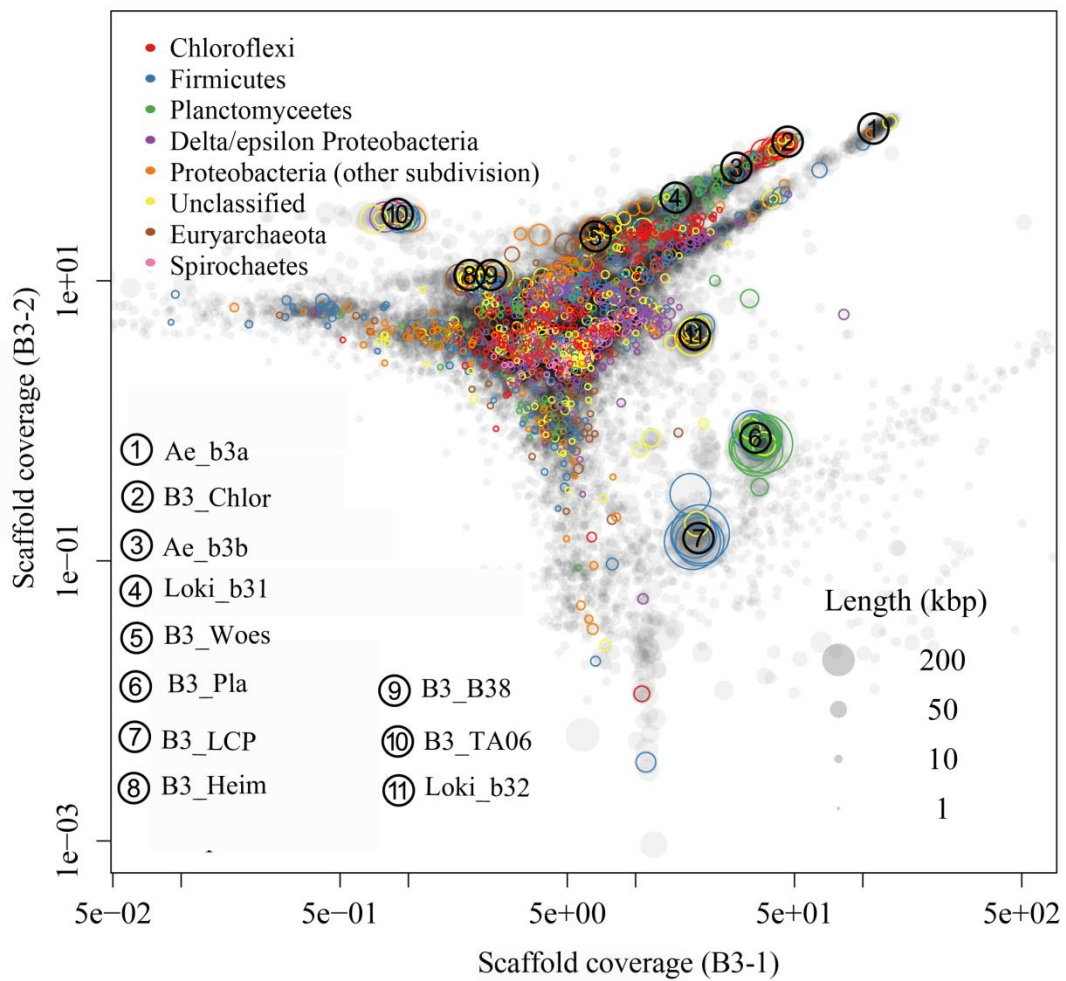
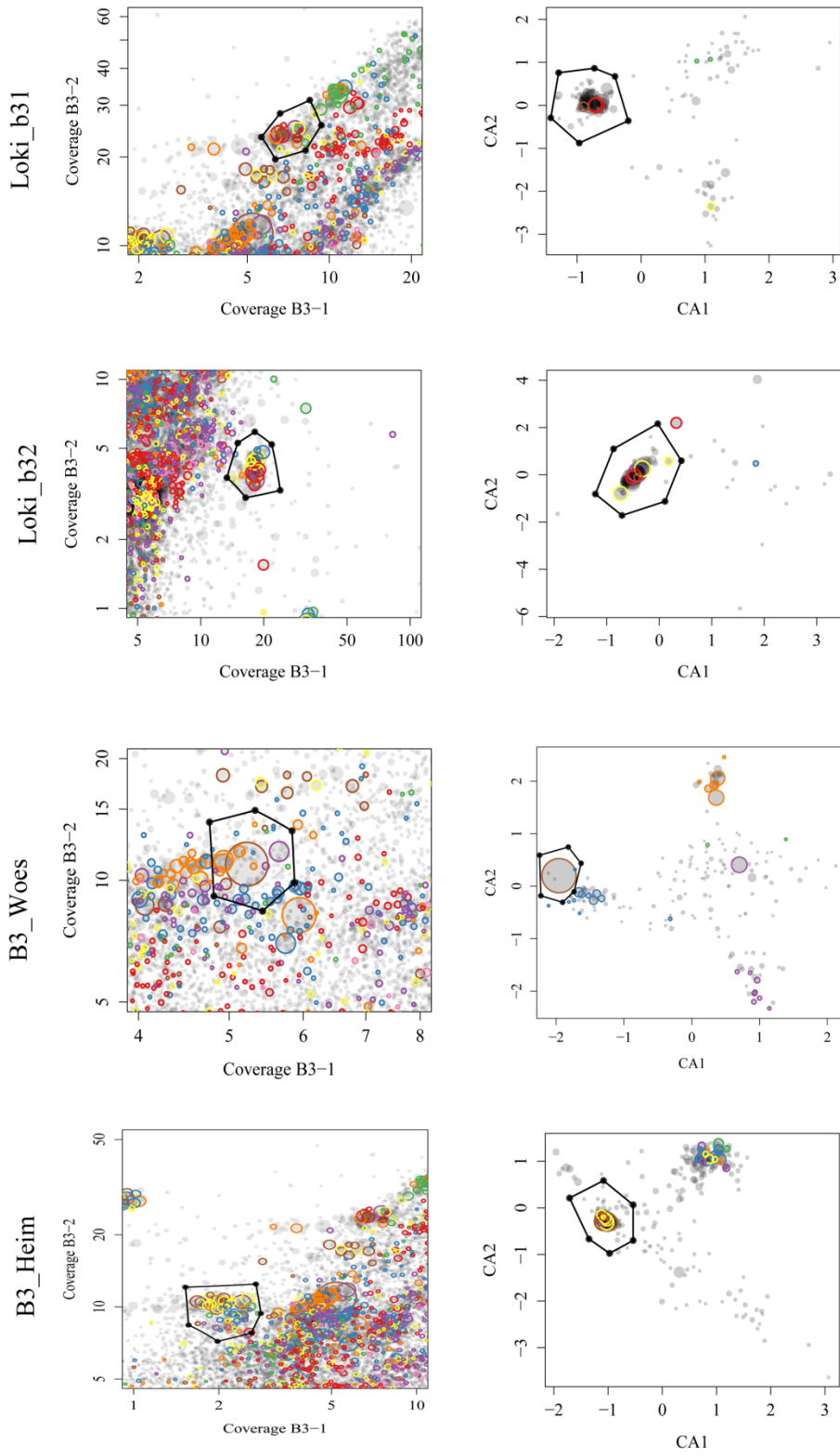


Figure S3. Genome binning based on coverage and tetranucleotide frequencies of the scaffolds of the B3 metagenomes. (A) metagenome-assembled genomes (MAGs) with different coverage levels in B3-1 and B3-2 were labeled with numbers. The coverage was determined by the recruitment of reads from B3-1 and B3-2 layers to the assembled scaffolds. Colors indicate a rough classification of different groups. (B) Archaeal scaffolds in the 2-D coverage plotting were pinpointed and were further separated based on correspondence analysis (CA) of tetranucleotide frequencies; (C) Bacterial scaffolds were located in the 2-D coverage plotting and further separated based on CA of tetranucleotide frequencies.

A



B



C

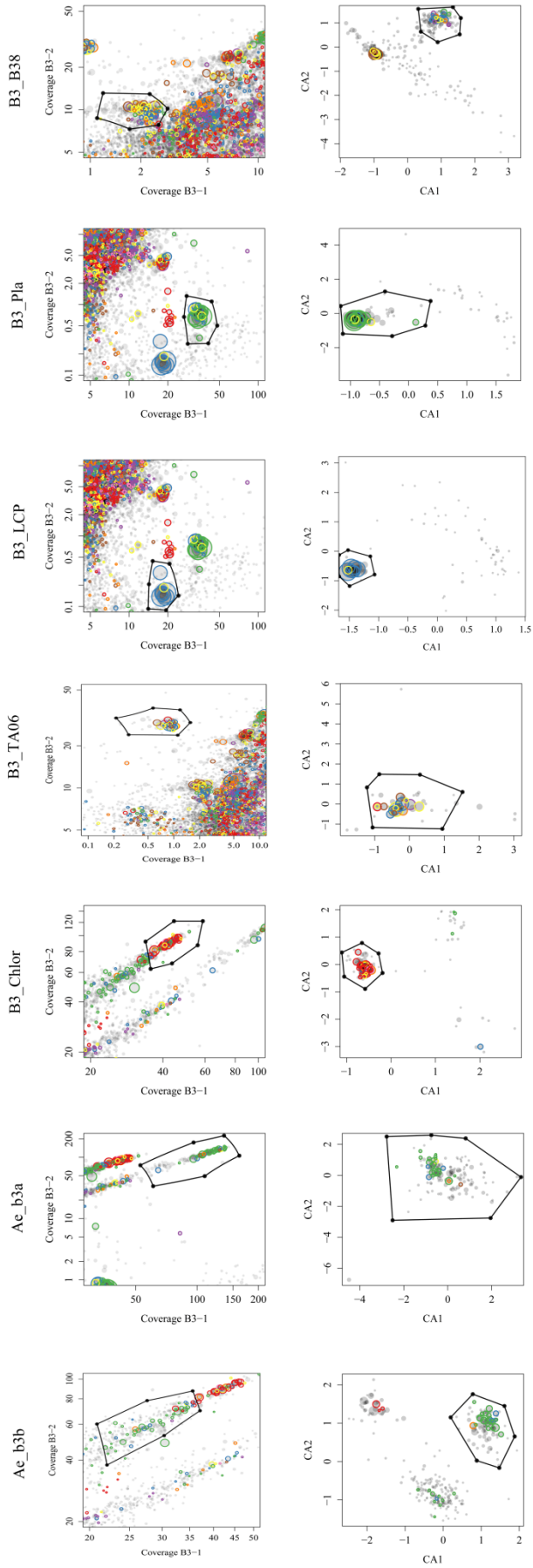


Figure S4. Relative abundance of metagenomic reads for each MAG in samples.

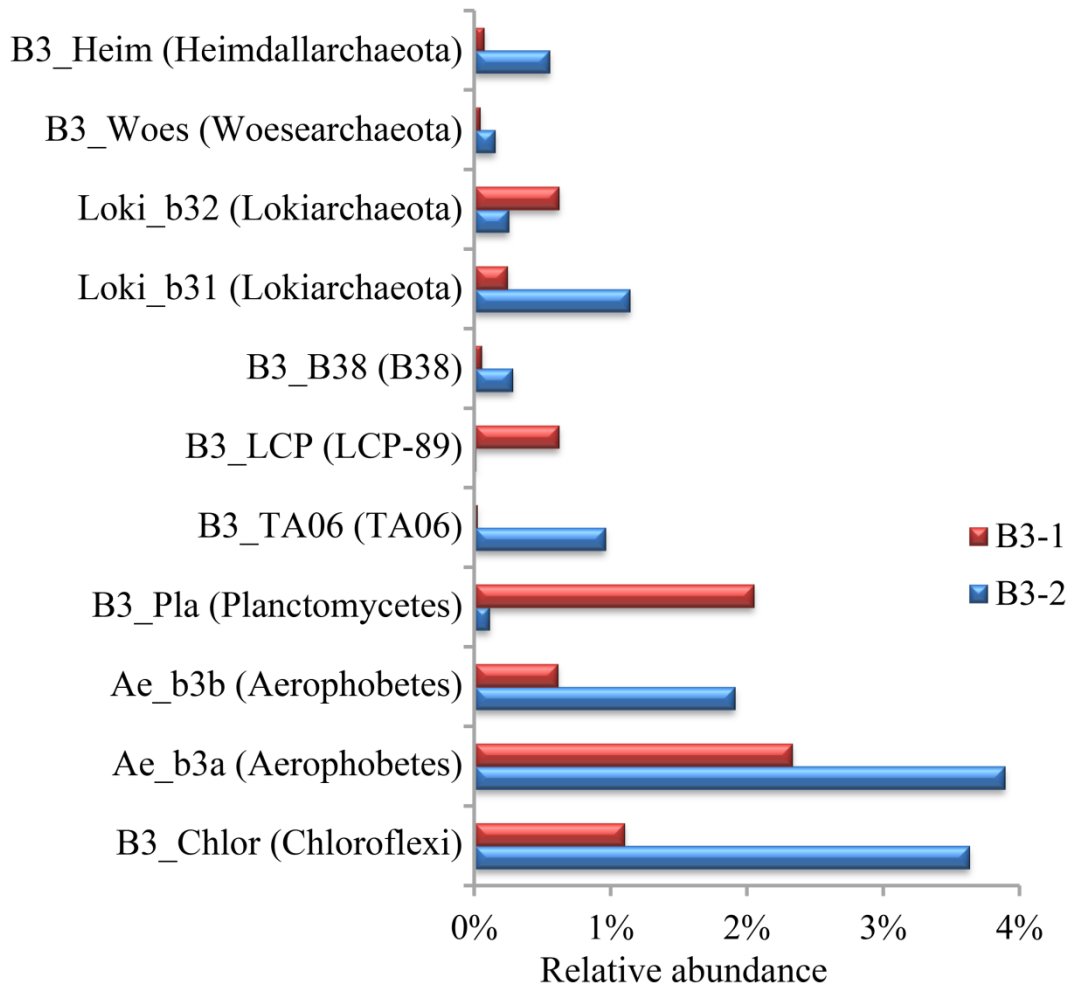


Figure S5. Phylogenetic analyses of 16S rRNA genes from bacterial MAGs (A) B38, (B) TA06 and (C) LCP-89 with relatives from different habitats. The tree was generated by raxmlGUI using maximum-likelihood method with GTRGAMMA model and 1000 replicates. Species detected in B3 are highlighted in red.

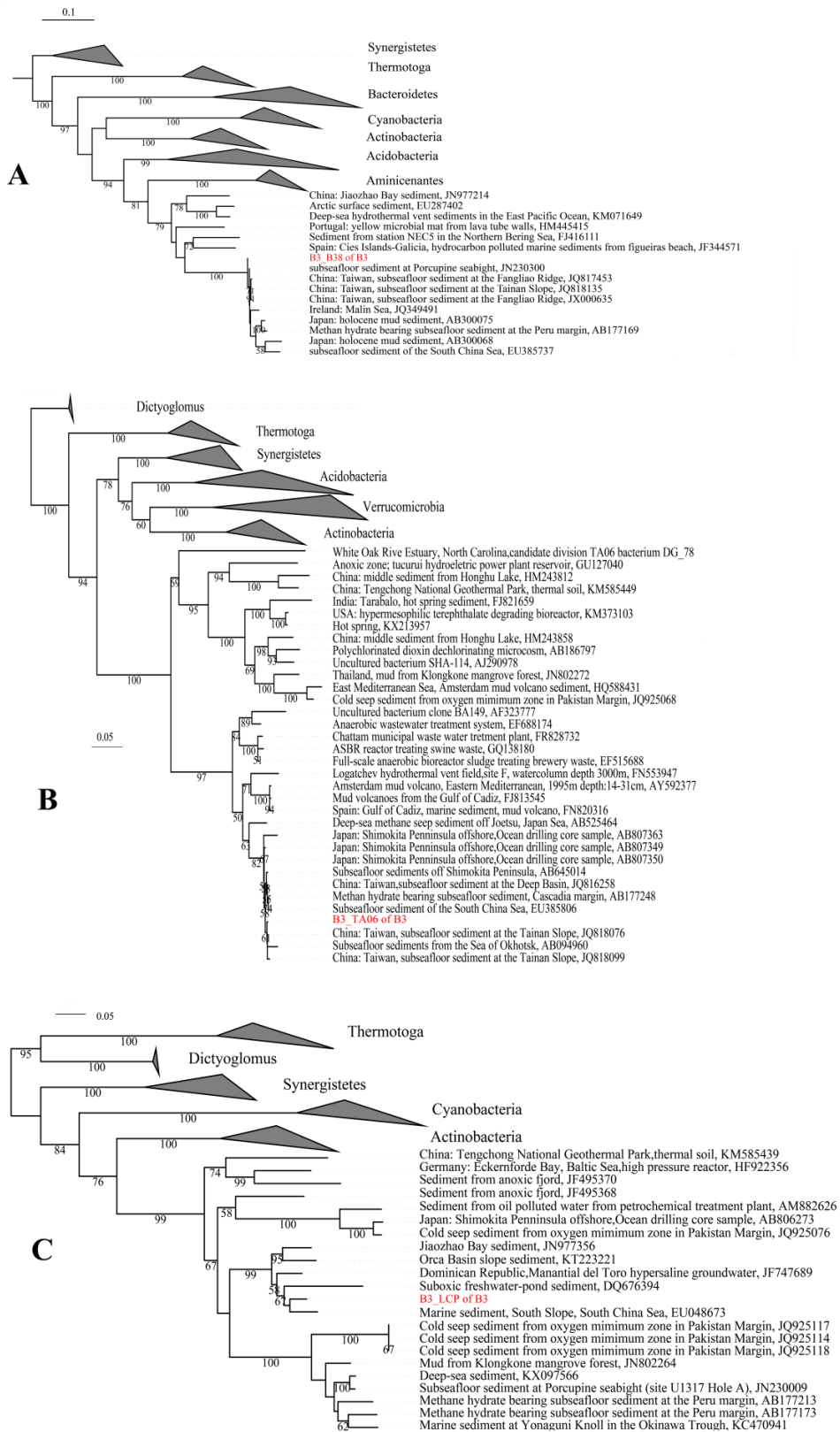


Figure S6. Phylogenetic analyses of 16S rRNA genes from archaeal MAGs (A) Lokiarchaeota and (B) Heimdallarchaeota with relatives from different habitats. The tree was generated by raxmlGUI using maximum-likelihood method with GTRGAMMA model and 1000 replicates. Species detected in B3 are highlighted in red.

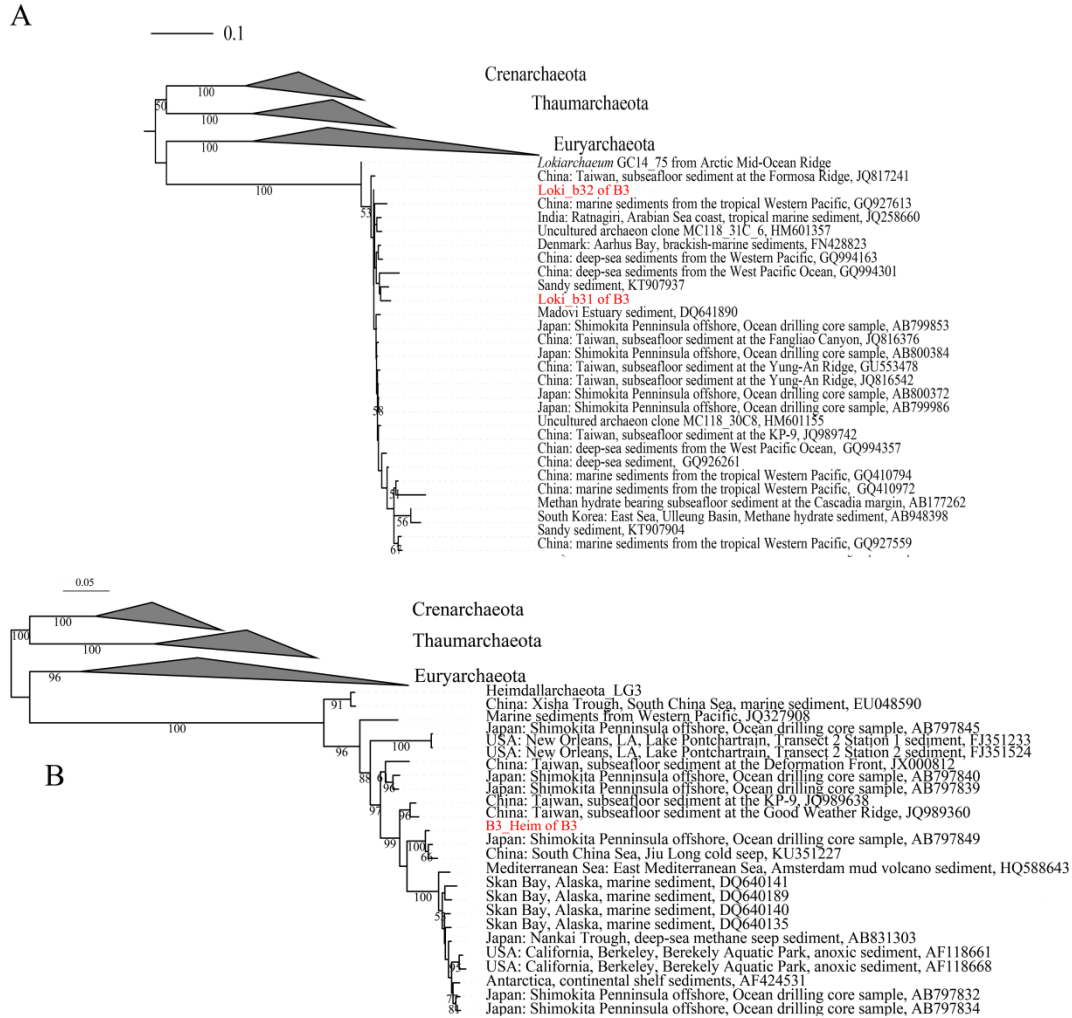


Figure S7. SECIS element (SECIS: selenocysteine insertion sequence) of MAGs (A) B3_B38 (B38) and (B) B3_LCP (LCP-89).

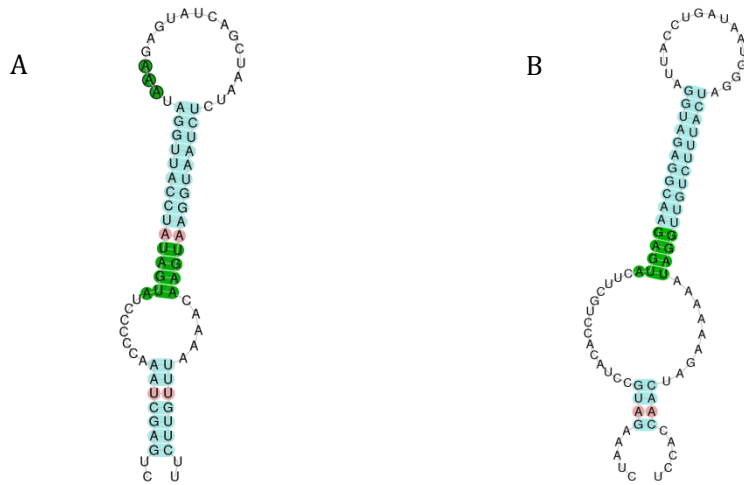


Figure S8. Phylogenetic analyses of B3_LCP DsrAB proteins in relation to other publicly available sequences generated using RAxML as part of the ARB software package. The closest BLAST in NCBI matches to Senitrabacteria were included in this phylogeny.

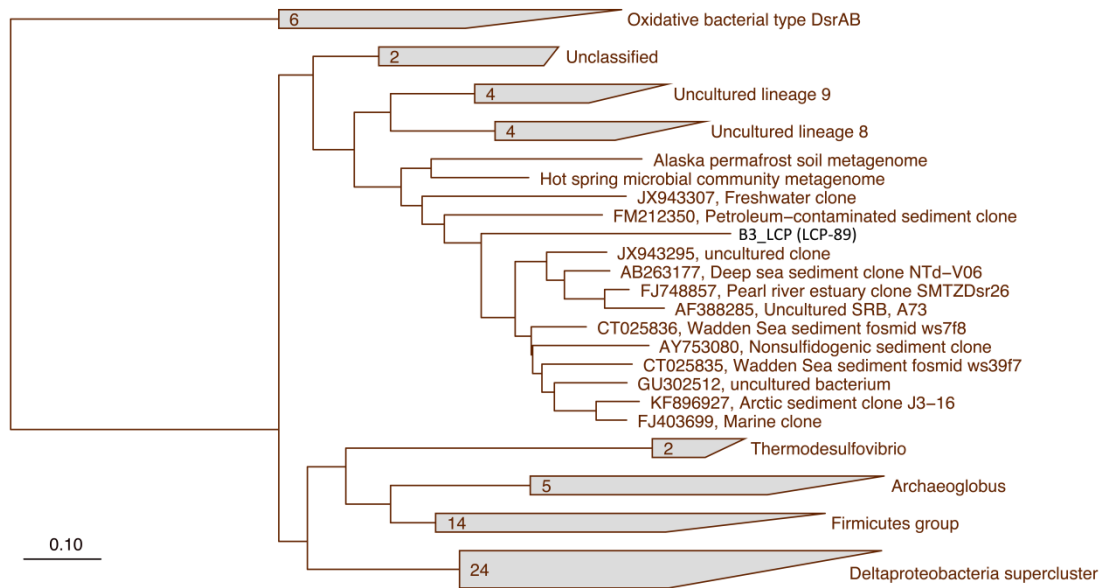


Figure S9. Peptidases predicted using MEROPS database.
 The family types of the peptidases are referred to http://merops.sanger.ac.uk/cgi-bin/family_index?type=P.

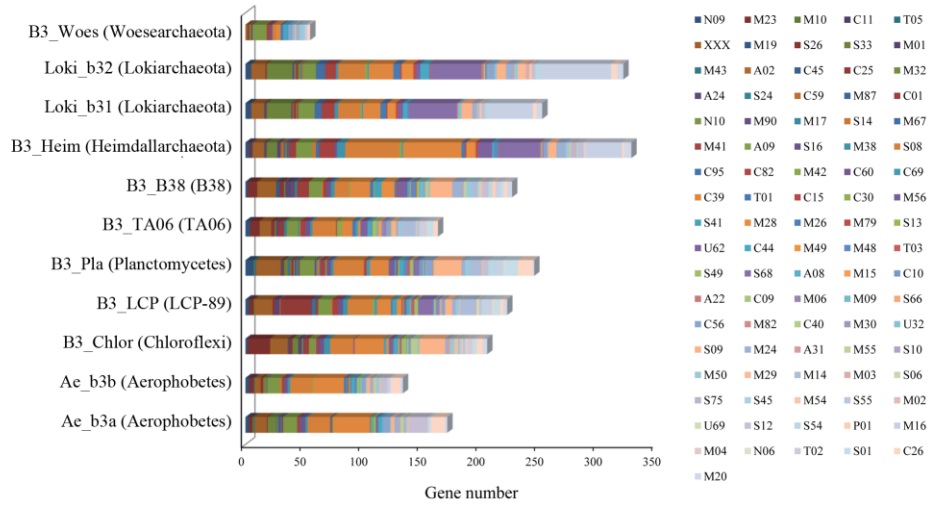


Figure S10. Schematic metabolisms of Lokiarchaeota (A) and Aerophobetes (B). Acc: acetyl-CoA carboxylase carboxyl transferase; FD_{ox} and FD_{red} : oxidized and reduced ferredoxin, respectively; Rnf complex: electron transport complex. Mrp: monovalent cation/proton antiporter; nirB: nitrite reductase (NADH) large subunit. The pathways with a red arrow are transcriptional active.

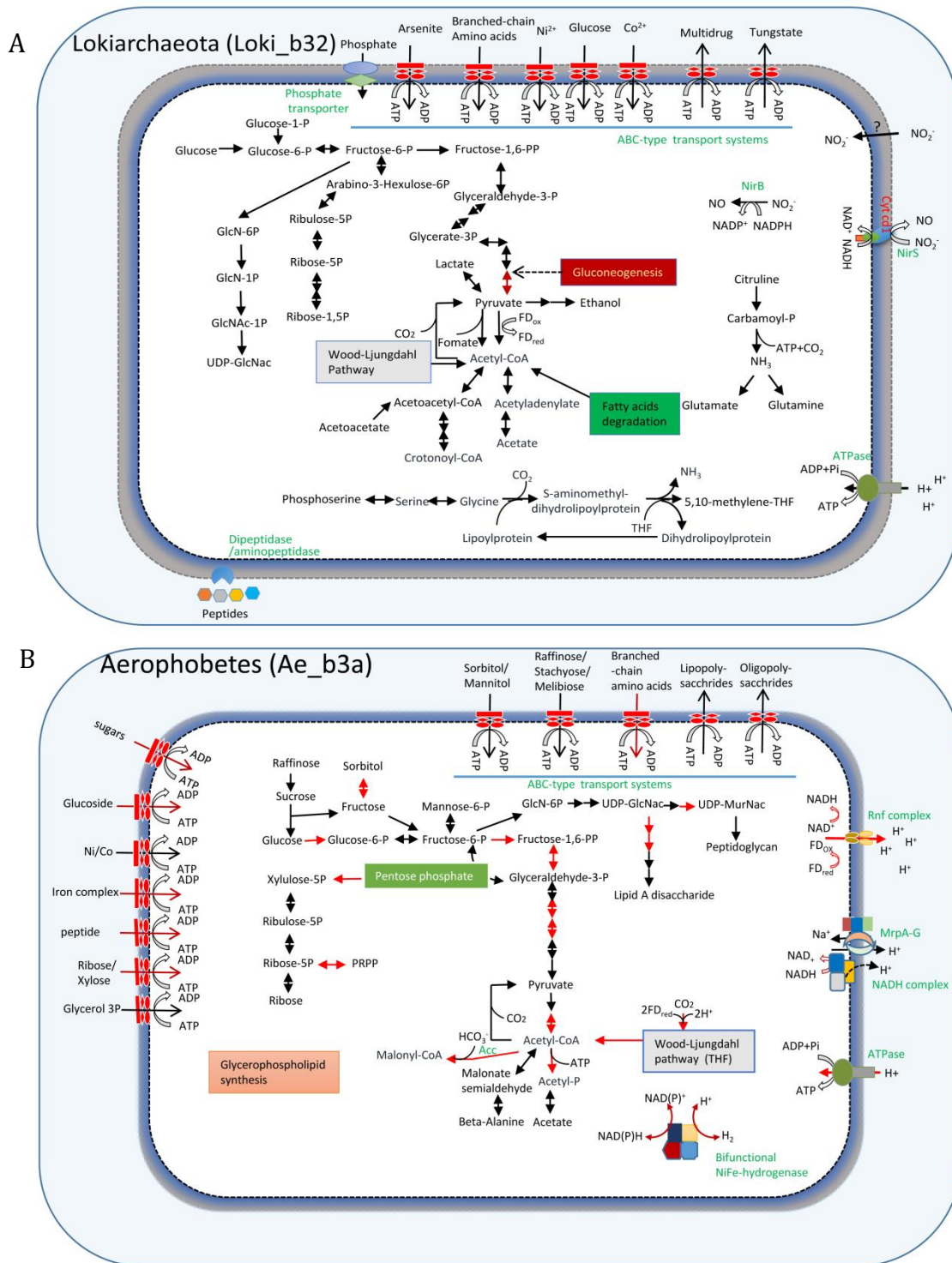
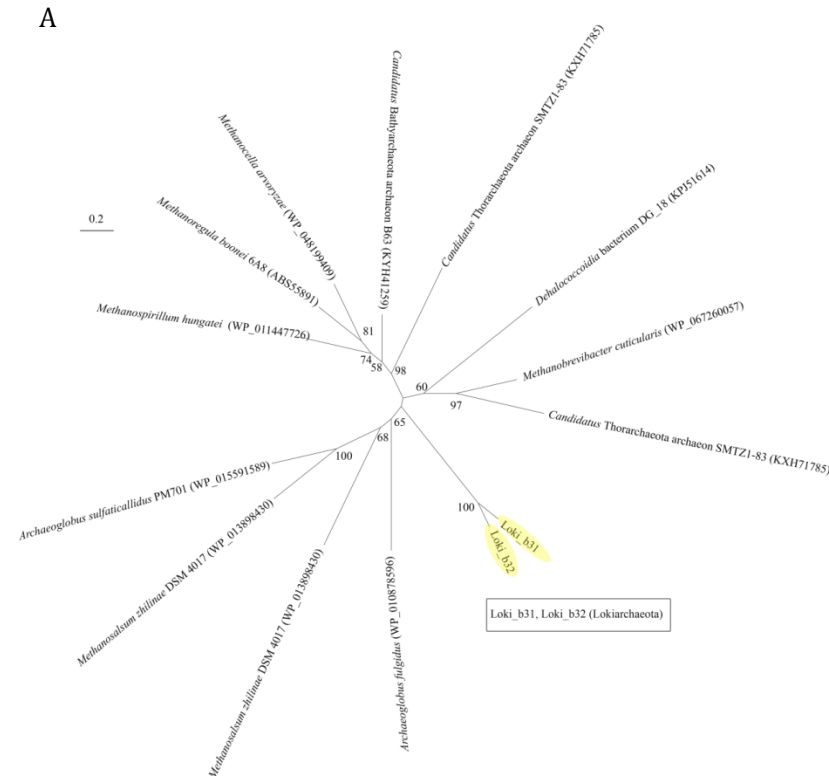


Figure S11. Phylogenetic tree based on (A) Acetyl-CoA decarboxylase/synthase complex subunit alpha/beta (AcsAB) and (B) Carbon monoxide CO dehydrogenase (Cdh) in Wood-Ljungdahl pathway. Using raxmlGUI, 1000 replicates and PROGTRGAMMA model, Bootstrap values >50% are shown. The AcsAB and Cdh genes from B3 are shaded in yellow.



B

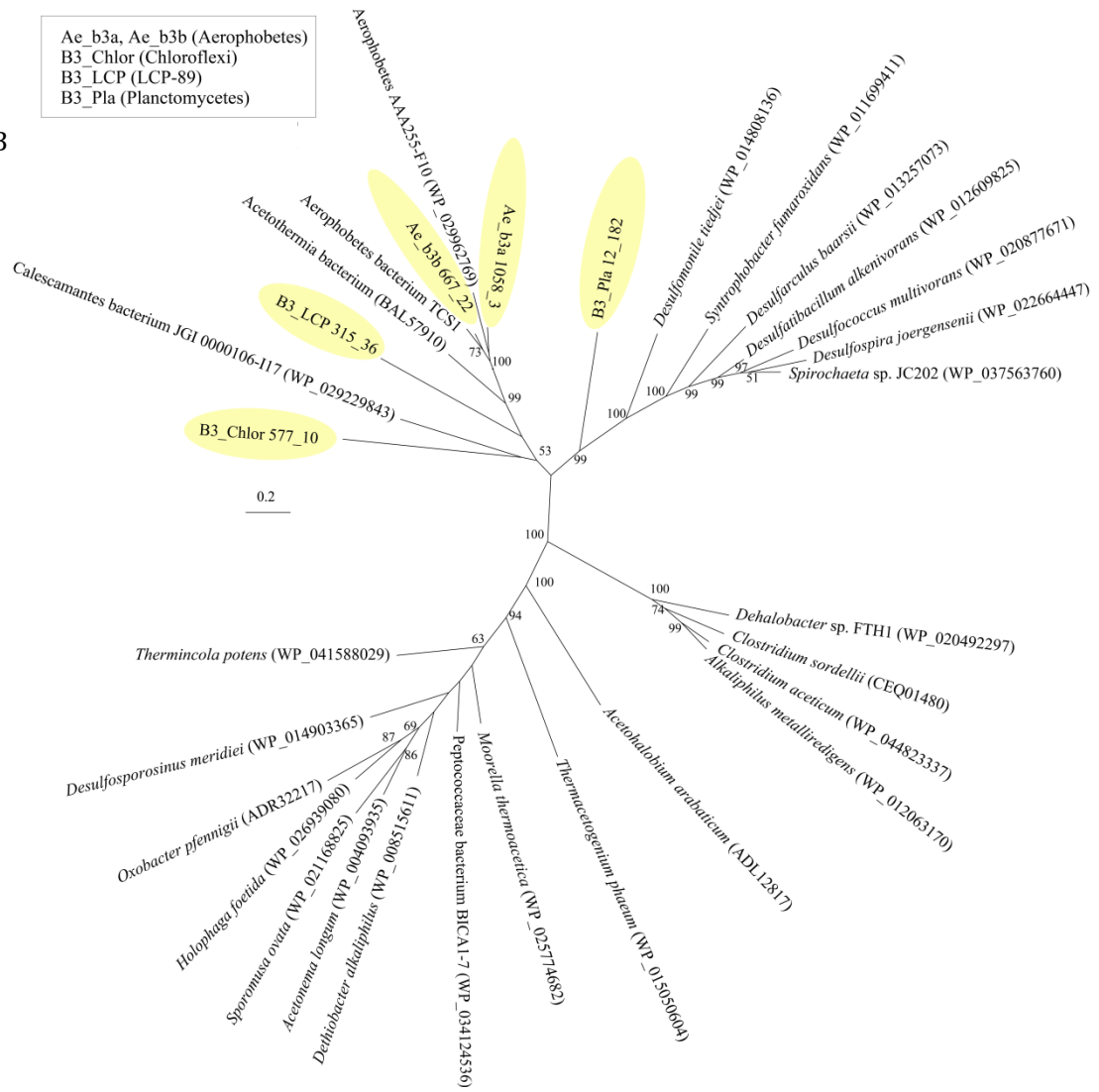
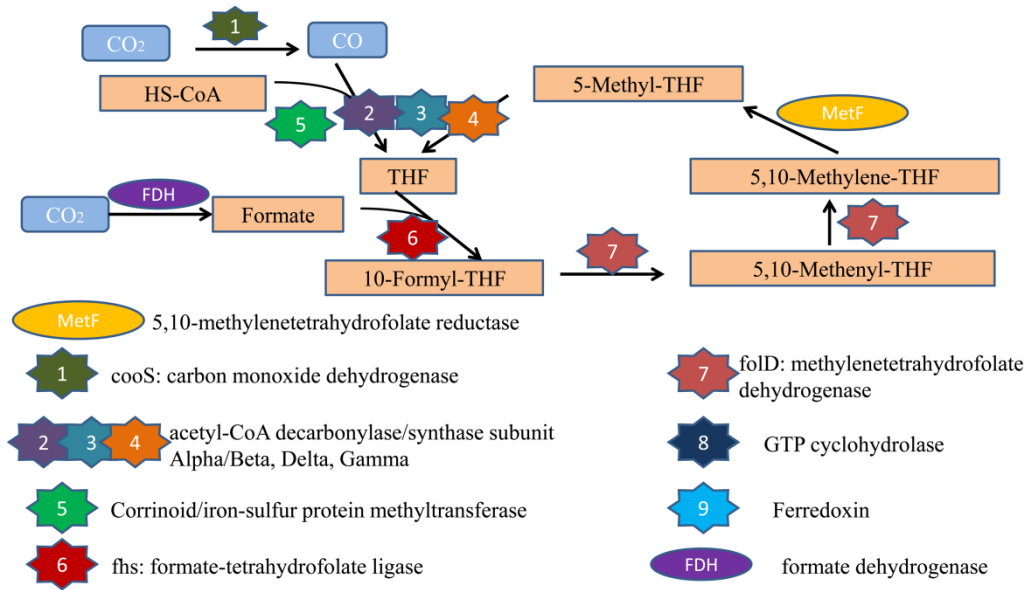
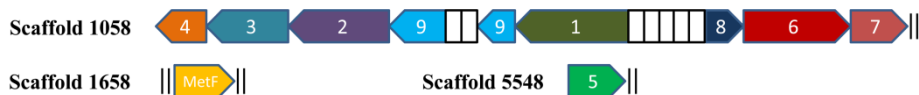


Figure S12. Organization of the genes involved in Wood-Ljungdahl (W-L) pathway. THF: tetrahydrofuran.



Ae_b3a(Aerophobetes):



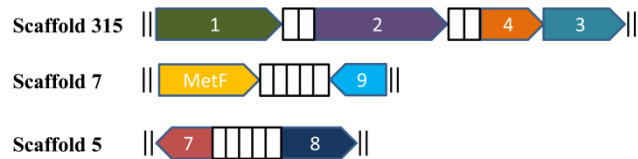
Ae_b3b (Aerophobetes) :



B3_Chlor (Chloroflexi) :



B3_LCP (LCP-89):



B3_Pla (Planctomycetes):

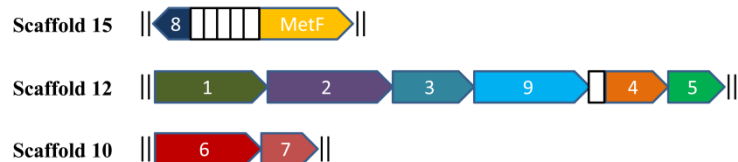


Figure S13. Read count for each MAGs of Metatranscriptome and Metagenome. (A) Percentage of transcripts assigned to B3 organisms in different layers. The transcriptome reads of clean Illumina data were aligned to CDSs of the B3 MAGs and were then summarized. (B) Percentage of metagenomic reads assigned to B3 MAGs in different layers.

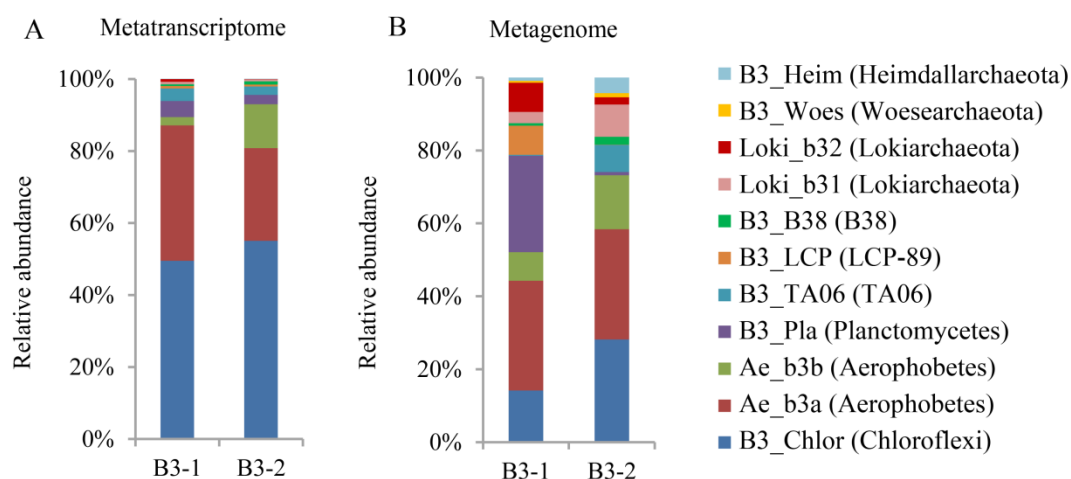


Figure S14. Genes of B3 MAGs expressed in metatranscriptome. Expression level of genes from MAGs reported in B3-1 and B3-2. The metatranscriptomic reads were selected for the 11 MAGs binned from the B3 metagenomes. The relative abundance of the genes was estimated by FPKM.

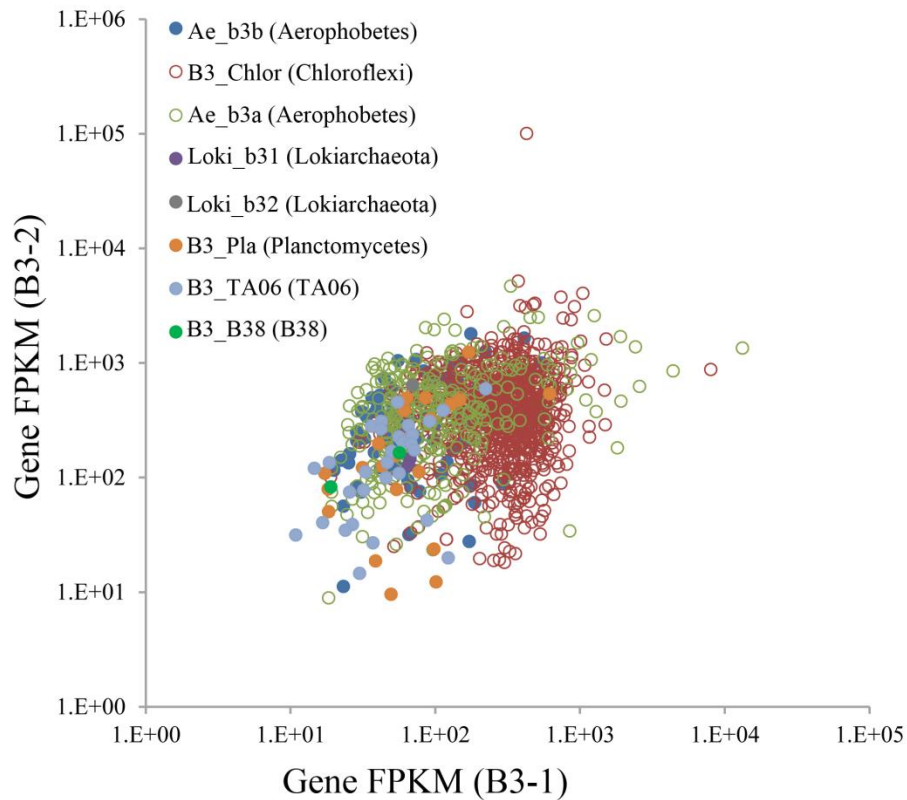


Table S1. Assembly statistics of B3 metagenomes.

	B3-1	B3-2
Raw data (Gbp)	12	15
Clean data (Gbp)	7.7	10.3
Total raw data (Gbp)	27	
Total clean data (Gbp)	18	
Assembly size (bp)	1,819,740,546	
N50 (bp)	837	
N90 (bp)	448	
Max length (bp)	1,000,545	
Average length (bp)	836	
Total of scaffolds	2,175,262	
Number of scaffolds >1Kbp	335,330	
Number of scaffolds >5Kbp	21,484	
Number of scaffolds >10Kbp	6,571	

Table S2. List of 24 conserved proteins in B3 and reference genomes.

	PF00164.22	PF00177.18	PF00189.17	PF00203.18	PF00237.16	PF00238.16	PF00252.15	PF00281.16	PF00297.19	PF00298.16	PF00318.17	PF00333.17	PF00347.20	PF00366.17	PF00380.16	PF00410.16	PF00411.16	PF00416.19	PF00466.17	PF00572.15	PF00573.19	PF00687.18	PF03719.12	PF03946.11
B3_Hades	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
B3_Woes	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
B3_Heim	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Loki_b31	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Loki_b32	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1
B3_Pla	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
B3_Chlor	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ae_b3a	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ae_b3b	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
B3_TA06	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
B3_B38	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
B3_LCP	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Nanoarchaeum_equitans_K in4_M_uid58009	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Synergistetes_bacterium_S GP1_uid197182	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Chlamydia_muridarum_Ni gg_uid57785	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Ignicoccus_hospitalis_KIN 4_I_uid58365	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Prosthecochloris_aestuarii_ DSM_271_uid58151	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Acidimicrobium_ferroxida ns_DSM_10331_uid59215	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Parachlamydia_acanthamoebae_ UV7_uid68335	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Elusimicrobium_minutum_ Pei191_uid58949	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Gloeobacter_JS_uid225602	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TA06_bacterium_DG_24	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Hyd24-12_bacterium_Ran_1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Bacteroides_CF50_uid222805	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Acholeplasma_laidlawii_P G_8A_uid58901	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Rhodothermus_marinus_DSM_4252_ uid41729	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Nostoc_PCC_7107_uid182932	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Gemmatimonas_aurantiaca_T_27_ uid58813	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Persephonella_marina_EX_HI_ uid58119	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Chloroflexus_aggregans_DSM_9485_ uid58621	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Brachyspira_hydrosentaria_e_WA1_ uid59291	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Eubacterium_eligens_ATC_C_27750_ uid59171	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Chlorobium_luteolum_DS_M_273_ uid58175	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Phycisphaera_mikurensis_NBRC_102666_ uid157331	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Mobiluncus_curtisii_ATCC_43063_ uid49695	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Nanoarchaeote_NstI_NstI	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1
Heimdallarchaeota LC_2	1	0	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
Streptobacillus_moniliformis_DSM_12112	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Hyd24-12_bacterium_Vib_1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Acidobacterium_MP5ACT_X9_uid50551	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Aquifex_aeolicus_VF5_uid57765	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Acaryochloris_marina_MB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Ae_b3a	1728_3	CE11	4.20	0.54	UDP-3-O-3-hydroxymyristoy
Ae_b3a	2584_10	CE10	4.08	0.55	peptidase S9
Ae_b3a	248_44	CE10	3.92	0.25	alpha/beta fold family hydrolase
Ae_b3a	2748_2	GH109	3.37	0.64	putative oxidoreductase
Ae_b3a	173_21	GH116	3.26	1.41	MULTISPECIES: hypothetical protein
Ae_b3a	11675_1	GH109	3.17	0.94	oxidoreductase
Ae_b3a	14454_1	CE9	2.34	0.27	N-acetylglucosamine-6-phosphate deacetylase
Ae_b3a	670_24	GT19	2.13	1.14	lipid-A-disaccharide synthase
Ae_b3a	782_32	GH127	2.01	0.23	arabinosidase
Ae_b3a	172_15	GT4	1.99	1.10	glycosyl transferase family 1
Ae_b3a	3453_10	GH94	1.89	3.73	N,N'-diacetylchitobiose phosphorylase
Ae_b3a	4566_4	GT2	1.85	0.51	glycosyl transferase
Ae_b3a	1428_9	GH120	1.63	1.16	parallel beta-helix repeat-containing protein, partial
Ae_b3a	297_13	GH109	1.62	3.38	oxidoreductase NAD-binding domain protein
Ae_b3a	172_13	GH130	0.69	0.42	glycosidase
Ae_b3a	5871_11	GH130	0.58	0.66	glycosidase
Chloroflexi					
B3_Chlor	504_4	GT83	2.29	0.71	conserved membrane protein of unknown function
B3_Chlor	92_28	GT83	1.95	0.63	glycosyl transferase family 39
B3_Chlor	150_56	GT4	1.26	5.31	putative glycosyltransferase
B3_Chlor	150_61	GT87	0.91	0.26	membrane protein
B3_Chlor	607_26	GT2	0.85	0.23	Glycosyltransferase
B3_Chlor	92_15	GT76	0.78	0.34	conserved hypothetical protein
B3_Chlor	100_57	CE1	0.75	0.18	3-oxoadipate enol-lactonase
B3_Chlor	143_67	GT2	0.67	0.17	glycosyl transferase
B3_Chlor	82_13	GT2	0.64	0.22	glycosyl transferase
B3_Chlor	100_78	GT83	0.60	0.82	membrane protein of unknown function
B3_Chlor	4446_12	GH65	0.60	0.63	Kojibiose phosphorylase
B3_Chlor	150_57	GT4	0.53	0.30	glycosyl transferase
B3_Chlor	63_23	CBM50	0.47	0.83	peptidoglycan-binding protein
B3_Chlor	2532_1	GT83	0.45	0.32	MULTISPECIES: glycosyl transferase family 39
B3_Chlor	308_39	GT4	0.45	0.12	MULTISPECIES: glycosyl transferase family 1
B3_Chlor	92_16	GT66	0.42	0.73	hypothetical conserved protein
B3_Chlor	92_10	GT87	0.42	0.33	hypothetical protein
B3_Chlor	6378_9	GT4	0.41	0.27	group 1 glycosyl transferase
B3_Chlor	143_63	GH3	0.39	0.30	glycosidase
B3_Chlor	4446_3	CE10	0.39	0.35	temperature sensitive supressor
B3_Chlor	150_64	GT83	0.39	0.28	hypothetical protein AMJ56_08725
B3_Chlor	63_26	CBM50	0.39	0.52	glycosyl hydrolase
B3_Chlor	92_32	GT83	0.35	0.22	Uncharacterized membrane protein
B3_Chlor	100_69	GT51	0.34	1.02	penicillin-binding protein 1C
B3_Chlor	150_62	GT83	0.33	0.39	glycosyl transferase family 39
B3_Chlor	220_10	CBM50	0.33	0.79	hypothetical protein Haur_2980
B3_Chlor	69_89	GT83	0.29	0.28	tetratricopeptide-repeat containing protein
B3_Chlor	150_66	GT39	0.29	0.16	hypothetical protein AMJ50_02015

B3_Chlor	100_54	CBM50	0.28	0.53	ErfK/YbiS/YcfS/YnhG family protein
B3_Chlor	485_15	GT4	0.28	0.23	MULTISPECIES: glycosyl transferase family 1
B3_Chlor	6378_1	GT83	0.28	5.01	Membrane protein-like protein
B3_Chlor	100_33	CE7	0.26	0.93	alpha/beta superfamily hydrolase
B3_Chlor	150_43	GH39	0.26	0.36	conserved hypothetical protein
B3_Chlor	360_43	GT39	0.26	0.88	NHL repeat containing protein
B3_Chlor	1486_20	GH23	0.25	0.53	lytic transglycosylase
B3_Chlor	100_14	CBM50	0.24	0.50	putative glycosyltransferase
B3_Chlor	308_40	GT4	0.24	0.23	glycosyl transferase family 1
B3_Chlor	63_25	CBM50	0.24	0.51	conserved exported protein of unknown function
B3_Chlor	150_63	GT83	0.24	1.02	Glycosyl transferase family 39
B3_Chlor	2278_9	GT2	0.23	0.45	succinoglycan biosynthesis protein exoa
B3_Chlor	2278_10	GT4	0.23	0.35	glycosyl transferase family 1
B3_Chlor	358_13	GH5	0.23	5.20	glycoside hydrolase
B3_Chlor	504_27	GH39	0.23	1.20	conserved protein of unknown function
B3_Chlor	864_18	GT83	0.23	0.80	hypothetical protein CLDAP_21560
B3_Chlor	948_13	CBM61	0.23	0.16	LysM domain-containing protein
B3_Chlor	864_36	GT83	0.23	0.52	PA14 domain protein
B3_Chlor	626_3	GT4	0.23	0.27	group 1 glycosyl transferase
B3_Chlor	340_37	GT51	0.23	0.86	penicillin-binding protein 1C
B3_Chlor	174_2	GT2	0.22	0.20	putative glycosyltransferase
B3_Chlor	308_44	GH2	0.22	3.37	beta-mannosidase
B3_Chlor	100_64	GT83	0.22	0.29	membrane protein of unknown function
B3_Chlor	150_67	GT39	0.22	1.41	glycosyl transferase family 39
B3_Chlor	143_41	GT39	0.21	2.99	membrane hypothetical protein
B3_Chlor	378_29	GH15	0.21	0.26	glycoside hydrolase family 15
B3_Chlor	2497_6	GT83	0.21	1.16	glycosyl transferase family 39
B3_Chlor	150_55	GT9	0.20	0.34	glycosyl transferase family 9
B3_Chlor	150_65	GT39	0.19	0.81	hypothetical protein AMJ56_08725
B3_Chlor	876_6	GT83	0.19	1.71	membrane protein-like protein
B3_Chlor	864_4	CBM50	0.19	0.22	putative peptidase
B3_Chlor	6132_6	GH74	0.18	0.38	hypothetical protein
B3_Chlor	785_29	GH3	0.18	0.41	beta-N-acetylhexosaminidase
B3_Chlor	150_44	GH18	0.16	1.13	exported protein of unknown function
B3_Chlor	580_5	CE10	0.16	0.30	peptidase, S9A/B/C family, catalytic domain protein
B3_Chlor	1378_8	CE1	0.16	0.12	alpha/beta hydrolase
B3_Chlor	92_3	CBM57	0.16	0.26	peptidase
B3_Chlor	220_30	GT83	0.16	0.51	dolichyl-phosphate-mannose-protein mannosyltransferase/ NHL repeat
B3_Chlor	220_11	CBM66	0.16	0.40	hypothetical protein AMJ85_00100
B3_Chlor	308_25	GH109	0.15	0.16	oxidoreductase domain protein
B3_Chlor	226_60	GT2	0.15	0.40	glucosaminyltransferase
B3_Chlor	308_41	GT4	0.14	0.59	glycosyl transferase group 1
B3_Chlor	487_35	GT39	0.13	0.34	putative membrane protein
B3_Chlor	220_31	GT83	0.13	1.24	MULTISPECIES: TIGR03663 family protein

B3_Chlor	536_17	AA6	0.12	0.06	nitric oxide synthase
B3_Chlor	876_5	GH39	0.12	0.80	conserved protein of unknown function
B3_Chlor	485_14	PL22	0.12	0.49	exported protein of unknown function
B3_Chlor	378_25	CBM32	0.10	0.16	coagulation factor 5/8 type domain-containing protein
B3_Chlor	876_13	CE4	0.10	0.20	polysaccharide deacetylase, partial
B3_Chlor	150_2	AA4	0.09	1.26	FAD-binding protein
B3_Chlor	92_54	GT28	0.08	0.30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase

*indicates (RNA FPKM)/ (DNA FPKM) in each layer.

Table S6. Microorganisms and 16S rRNA gene sequence accession numbers used for phylogenetic analysis

Accession number	Taxonomic group	Organism/clone name
JQ278807	Acetothermia	Uncultured bacterium clone fjc-63
FJ901734	Acetothermia	Uncultured Acetothermia bacterium clone LP5013
HE603999	Acetothermia	Uncultured bacterium clone Central-Bottom-cDNA_clone159
AY234418	Acidobacteria	Bacterium Ellin5001
AY234751	Acidobacteria	Bacterium Ellin6099
AY234723	Acidobacteria	Bacterium Ellin6071
AY234628	Actinobacteria	Bacterium Ellin5277
U30661	Actinobacteria	<i>Mycobacterium</i> sp. RJG11.135
AY234429	Actinobacteria	Bacterium Ellin5012
AB050206	Aenigmarchaeota	uncultured archaeon SAGMA-B
AB237753	Aenigmarchaeota	uncultured archaeon
AJ347789	Aenigmarchaeota	uncultured SA2 group euryarchaeote
DQ103684	Aenigmarchaeota	uncultured euryarchaeote
DQ133424	Aenigmarchaeota	uncultured Methanobacteriaceae archaeon
AB177139	Aerophobetes	Uncultured bacterium clone ODP1230B10.20
FJ873295	Aerophobetes	Uncultured bacterium clone boHTK-31
JSVS00000000	Aerophobetes	Aerophobetes bacterium TCS1
ASMN01000059	Aerophobetes	Aerophobetes bacterium SCGC AAA255-F10
ASMM01000001	Aerophobetes	Aerophobetes bacterium JGI 0000014-A15
FJ813562	Aminicenantes	Uncultured bacterium clone GoC_Bac_71_D0_C0_M1
AB177172	Aminicenantes	Uncultured bacterium clone ODP1230B20.28
AB177161	Aminicenantes	Uncultured bacterium clone ODP1230B18.23
AB015269	Atribacteria	uncultured Candidatus Atribacteria bacterium
AB189340	Atribacteria	Uncultured bacterium clone JT58-14
FJ873257	Atribacteria	Uncultured bacterium clone boHTK-28
JQ818135.1	B38	Uncultured bacterium clone MD-178-10-3261_T2-P_S2400
JX000635.1	B38	Uncultured bacterium clone ORI-934-08-P_S258-260_086B06
JN230300.1	B38	Uncultured bacterium clone 3H3M_69
AB177169.1	B38	Uncultured bacterium clone ODP1230B20.01
EU823302	Bacteroidetes	<i>Leeuwenhoekiella marinoflava</i> strain P7
L11703	Bacteroidetes	<i>Thermonema lapsum</i>
NR_042496	Bacteroidetes	<i>Flavobacterium johnsoniae</i> strain UW101
U05662	Calescamantes	Eubacteria EM 19

AF352537	Calescamantes	Uncultured bacterium clone BH81
AQST01000031	Calescamantes	Calescamantes bacterium SCGC AAA471-M6
CZVW01000013.1	Candidatus Kryptonina	Kryptonina bacterium JGI 23
LDXU01000006.1	Candidatus Kryptonina	<i>Thermokryptus mobilis</i>
X86447	Chloroflexi	<i>Herpetosiphon</i> sp.
AY395567	Chloroflexi	<i>Candidatus</i> Chlorothrix
FJ790638	Chloroflexi	Kallotenuales;AKIW781
FJ793156	Chloroflexi	Anaerolineaceae;uncultured
AB237730	Cloacimonetes	Uncultured bacterium clone HDBW-WB67
AB513440	Cloacimonetes	Uncultured bacterium clone TUT1989-U1
KJ881295	Cloacimonetes	Uncultured bacterium clone EGSB_20_2-21
AB009616	Crenarchaeota	<i>Thermoproteus</i> sp. IC-033
AB010957	Crenarchaeota	<i>Sulfolobus yangmingensis</i>
AB087499	Crenarchaeota	<i>Caldisphaera lagunensis</i>
AB109559	Crenarchaeota	<i>Aeropyrum camini</i>
DQ228594	Crenarchaeota	Uncultured archaeon
U40332	Cyanobacteria	<i>Microcystis viridis</i> NIES-102
EF174209	Cyanobacteria	Nostoc sp. 'Pannaria pallida cyanobiont' 2 Ch
AP011615	Cyanobacteria	<i>Arthrospira platensis</i> NIES-39
AB019734	Diapherotrites	Unidentified archaeon
AB019748	Diapherotrites	Unidentified archaeon
AB237755	Diapherotrites	Uncultured archaeon
AJ937874	Diapherotrites	Uncultured archaeon
NR_074876	Dictyoglomi	<i>Dictyoglomus thermophilum</i> strain H-6-12
CP001251	Dictyoglomi	<i>Dictyoglomus turgidum</i> DSM 6724
X69194	Dictyoglomi	<i>Dictyoglomus thermophilum</i> H-6-12
AB004575	Elusimicrobia	Uncultured bacterium clone TG13
AB034017	Elusimicrobia	Uncultured rumen bacterium 4C0d-3
JQ278784	Elusimicrobia	Uncultured bacterium clone fjc-39
AACY023249168	Euryarchaeota	Marine Group II;marine metagenome
AB004878	Euryarchaeota	<i>Haloterrigena turkmenica</i>
AB008853	Euryarchaeota	<i>Methanocalculus pumilus</i>
AB019758	Euryarchaeota	ANME-1a
AB019735	Euryarchaeota	Unidentified archaeon
AB034189	Euryarchaeota	Uncultured rumen methanogen
AB196288	Euryarchaeota	<i>Methanocella paludicola</i> SANAE
AB237756	Euryarchaeota	Uncultured archaeon
AJ347780	Euryarchaeota	Uncultured SA1 group euryarchaeote
AY234571	Gemmatimonadetes	Bacterium Ellin5220
AB015578	Gemmatimonadetes	Uncultured bacterium clone BD7-2
JQ311868	Gemmatimonadetes	Uncultured bacterium clone OTU80-64
JQ278764	Gracilibacteria	Uncultured bacterium clone fjc-16
JQ278776	Gracilibacteria	Uncultured bacterium clone fjc-31
JQ287266	Gracilibacteria	Uncultured bacterium clone 3M33_057
MDVS01000000	Heimdallarchaeota	Heimdallarchaeota LC_3
FN553950	Hyd24-12	Uncultured sediment bacterium clone 257-34
EF515519	Hyd24-12	Uncultured bacterium clone 29e09
EF515727	Hyd24-12	Uncultured bacterium clone 32g09
FJ813576	Latescibacteria	Uncultured bacterium clone GoC_Bac_161_D0_C0_M1
FJ813575	Latescibacteria	Uncultured bacterium clone GoC_Bac_163_D2_C0_M0

AB240493	Latescibacteria	Uncultured bacterium clone SRRT67
AB177213	LCP-89	Uncultured bacterium clone ODP1230B34.16
KC470941	LCP-89	Uncultured bacterium clone N_228
HF922356	LCP-89	Uncultured bacterium clone HP-Bac-F07
JYIM01000000	Lokiarchaeota	<i>Lokiarchaeum</i> GC14_75
DQ329861	OP11	Uncultured candidate division OP11 bacterium
HM856437	OP11	Uncultured candidate division OP11 bacterium
JN003058	OP11	Uncultured candidate division OP11 bacterium
AB015551	OP3	Uncultured bacterium clone BD3-9
JQ278816	OP3	Uncultured bacterium clone fjc-73
JQ278884	OP3	Uncultured bacterium clone hmx-282
JQ278939	Parcubacteria	Uncultured bacterium clone sf-17
JQ287076	Parcubacteria	Uncultured bacterium clone 3M23_041
JQ287225	Parcubacteria	Uncultured bacterium clone 3M33_009
FJ718986	Parvarchaeota	Uncultured archaeon
FJ810533	Parvarchaeota	Uncultured archaeon
FJ810536	Parvarchaeota	Uncultured archaeon
FJ810539	Parvarchaeota	Uncultured archaeon
FJ810527	Parvarchaeota	Uncultured archaeon
AY234714	Planctomycetes	Bacterium Ellin6062
AB015544	Planctomycetes	Uncultured bacterium clone BD2-16
AB015552	Planctomycetes	Uncultured bacterium clone BD3-11
JQ278972	Saccharibacteria	Uncultured candidate division TM7 bacterium clone sf-78
AB100499	Saccharibacteria	Uncultured candidate division TM7 bacterium clone Rs-045
FJ825446	Saccharibacteria	Uncultured bacterium clone 110_BE2_40
AB558582	Synergistetes	<i>Lactivibrio alcoholicus</i>
NR_043522	Synergistetes	<i>Thermovirga lienii</i> strain Cas60314
CM001377	Synergistetes	<i>Thermanaerovibrio velox</i> DSM 12556
FJ821659	TA06	Uncultured bacterium clone R15
AB186797	TA06	Uncultured bacterium clone TSBZ04
LJNI00000000	TA06	TA06_bacterium_DG_78
AY231458	Tenericutes	<i>Mesoplasma syrphidae</i>
U44771	Tenericutes	<i>Mycoplasma ovipneumoniae</i> ATCC 29419
AY257485	Tenericutes	<i>Acholeplasma pleciae</i>
AB050221	Thaumarchaeota	Soil Crenarchaeotic Group(SCG);uncultured archaeon SAGMA-P
AB050207	Thaumarchaeota	Marine Group I; uncultured archaeon SAGMA-C
AB050240	Thaumarchaeota	Uncultured archaeon SAGMA-10
AB050231	Thaumarchaeota	Uncultured archaeon SAGMA-Z
AF119127	Thaumarchaeota	Marine Group I;uncultured archaeon CRA8-11cm
AF227642	Thaumarchaeota	Uncultured crenarchaeote TRC23-30
KF954236	Thaumarchaeota	Marine Benthic Group A;uncultured thaumarchaeote
KJ810535	Thaumarchaeota	<i>Candidatus Nitrososphaera</i> sp. THUAOA
NR_102773	Thermotogae	<i>Thermosipho africanus</i> TCF52B strain TCF52B
NR_029163	Thermotogae	<i>Thermotoga maritima</i> strain MSB-8
NR_042373	Thermotogae	<i>Thermotoga naphthophila</i> strain RKU-10
NR_074833	Thermotogae	<i>Thermotoga thermarum</i> strain DSM 5069
NR_074951	Thermotogae	<i>Thermotoga lettingae</i> strain TMO
NR_074959	Thermotogae	<i>Thermotoga neapolitana</i> strain DSM 4359
LRSK01000239	Thorarchaeota	<i>Candidatus</i> Thorarchaeota archaeon SMTZ1-83
FJ351268	Thorarchaeota	Uncultured archaeon clone 060329_T2S2_S_T_SDP_038

FJ353523	Thorarchaeota	Uncultured archaeon clone Gctb_ML_097
AY234519	Verrucomicrobia	Bacterium Ellin5102
U60014	Verrucomicrobia	<i>Prostheco bacter debontii</i>
EF157839	Verrucomicrobia	<i>Lentimonas marisflavi</i>
CP010425.1	Woese archaeota	Archaeon GW2011_AR15
AACY020521239	Woese archaeota	Woese archaeota(DHVEG-6);marine metagenome
AACY023847387	Woese archaeota	Woese archaeota(DHVEG-6);marine metagenome
AB019750	Woese archaeota	Woese archaeota(DHVEG-6);unidentified archaeon
AB019749	Woese archaeota	Woese archaeota(DHVEG-6);unidentified archaeon
AB019751	Woese archaeota	Woese archaeota(DHVEG-6);unidentified archaeon
FJ792219	WS6	Uncultured bacterium clone SGYF454
AB243816	WS6	Uncultured bacterium clone Niigata-05
KC290428	WS6	Uncultured bacterium clone NY-28