

Supplementary Materials

Supporting methods

Sequence comparison to DNA isolation kit blank and drilling fluid (For Costa Rica sediment samples)

Because DNA concentrations were very low in many of the sediment samples, and PCR tests indicated that in a few of the samples, if present at all, DNA may not be in high enough amounts to overcome the “background” DNA from the DNA extraction kits, a representative DNA extraction kit blank was sequenced along with all other samples. To remove any signal from the extraction kit in all samples, as well as to remove any samples whose genuine DNA was not in high enough abundance to overcome the extraction kit background, sequence results from the SILVA pipeline were processed initially as follows: 1. Classification of reads was examined at the “fully expanded” taxonomic depth from the SILVA pipeline output, and all lineages present in the extraction blank in any amount were flagged. 2. To account for sequencing error in classification, further lineages were added to the flagged ones by going up in taxonomic level to “order” and flagging every sequence identified as being from the same order as any sequence present in the extraction blank. There were a few cases where the taxonomy of sequences in the extraction blank did not go down as far as the level of “order”, and for those, the most specific level identified above order was used to assess any further matches. For example, if the sequence was classified down to “class,” then any remaining sequences in that class would also be removed. Those cases were: Bacteria/Cyanobacteria/Chloroplast (for which no other matches to 'chloroplast' were found within Cyanobacteria sequences, and hence no additional sequences removed); Eukaryota/Archaeplastida/Chloroplastida/Charophyta/Phragmoplastophyta/Streptophyta/Embryophyta/Tracheophyta/Spermatophyta/Magnoliophyta (For which several additional lineages within Magnoliophyta were identified and removed); and Eukaryota/Opisthokonta/Holozoa/Metazoa (Animalia)/Eumetazoa/Bilateria/Chordata/Vertebrata/Gnathostomata/Euteleostomi/Tetrapoda/Mammalia (For which no other matches to class mammalia were found and hence no additional sequences removed). 3. All flagged lineages were then removed from every sample. 4. Finally, after the removal of those lineages, the deepest sample from site 1378 and the deepest sample from site 1379 were found to have lost the majority of their sequences (84% and 86% losses, respectively) and were thus eliminated from further analysis. All other samples retained 77% or greater of their original sequences at this stage. The number of sequences for each sample before and after this process is shown in Table S1.

An additional concern of sediment samples with low biomass is the interference of contaminating microorganisms present in the drilling fluid used to obtain the samples, particularly for deeper samples obtained using extended core barrel coring technology. Hence, sequences were further parsed via comparison to sequences observed in a sample of the drilling fluid used during IODP Expedition 334. Classifications of sequence reads from the drilling fluid were examined at the “fully expanded” taxonomic depth from the SILVA pipeline output (Table S2). When combined sequences of a given taxonomic “order” found in the drilling mud totaled to more than 0.35% of the total sequences in the drill mud, all sequences from every sediment sample in the same “order” were removed. The cutoff of 0.35% was chosen in an attempt to process the samples in a way that most accurately reflected what we felt to be genuine drill fluid contaminants, allowing for removal of the maximum amount of suspected contaminant lineages while still preserving sequences which appeared to be genuine deep sea lineages. In addition to those removals, sequences classified as candidate phylum SBR1093 and Proteobacteria Candidate Group SPOTSOCT00m83 were not able to be classified down to “order” level, but totaled above 0.35% and were thus also removed from all samples. Some Gammaproteobacteria sequences were not able to be further classified, and though totaling more than 0.35%, were not removed from other samples, as many Gammaproteobacteria exist in subseafloor sediments from lineages not present in drill fluid, and would be incorrectly removed. After this processing, one additional sample was found to have lost the majority of its sequences and was thus removed from further analysis (1379 494 mbsf, 91% loss). All other samples

had 73% or greater of their original sequences remaining. The number of sequences before and after this process is shown in Table S1.

Sequencing of additional samples for primer validation

All 3 supplemental samples used for primer validation testing were sequenced with 454 Life Sciences Technology. Metagenomic sequencing of the Dead Sea water sample was performed on a Roche 454 Genome Sequencer FLX sequencing system (454 Life Sciences) with Titanium chemistry as previously described (Rhodes et al., 2010). Metagenomic sequencing of the anaerobic digester and Pacific Ocean seawater samples was carried out by the Pennsylvania State University Center for Comparative Genomics and Bioinformatics on ¼ of a picotiter plate on a Roche 454 Genome Sequencer FLX+ sequencing system with Titanium Chemistry (454 Life Sciences) as described (Poinar et al., 2006). For Pacific Ocean seawater sample, due to limited yield, DNA was first amplified via multiple displacement amplification with a REPLI-g midi kit (Qiagen Inc.), according to the manufacturer's instructions, except for using a shortened extension time of only 3 hours. The amplified DNA was then digested with S1 nuclease (1U/mL) for 30 minutes at 37°C to remove single-stranded DNA. Product from this amplification was visible when run on a 1% agarose gel, and the corresponding negative control showed no product.

Table S1. Sample Information. .

Sample Name (In Text)	1378 2.88 mbsf	1378 32.29 mbsf	1378 63.82 mbsf	1378 93.98 mbsf	1378 124.78 mbsf	1378 158.24 mbsf	1378 240.90 mbsf
IODP Designation	334 U1378B 1H-2	334 U1378B 4H-6	334 U1378B 8H-2	334 U1378B 11H-3	334 U1378B 16H-3	334 U1378B 20X-5	334 U1378B 30X-2
# Seqs. (Original)	43961	11157	6795	9013	10782	12764	20253
# Seqs. (After E.Blank)	43795	11099	6429	8691	9621	12482	19996
# Seqs. (After Drill Mud)	43765	11098	6415	8682	9598	11610	19763
(Continued)							
Sample Name (In Text)	1378 329.1 mbsf	1378 402.27 mbsf	1379 2.90 mbsf	1379 22.08 mbsf	1379 45.38 mbsf	1379 67.28 mbsf	1379 89.38 mbsf
IODP Designation	334 U1378B 40X-4	334 U1378B 50X-2	334 U137C1H-2	334 U1379C 3H-4	334 U1379C 7H-2	334 U1379C 11H-3	334 U1379C 16H-2
# Seqs. (Original)	10422	8837	26479	49504	20003	9139	13869
# Seqs. (After E.Blank)	8051	1372	26418	49479	19882	8858	13470
# Seqs. (After Drill Mud)	7595	*	26411	49479	19878	8825	13462
(Continued)							
Sample Name (In Text)	1379 115.07 mbsf	1379 211.53 mbsf	1379 496.38 mbsf	1379 636.37 mbsf	E.Blank	Drill Fluid	
IODP Designation	334 U1379C 20X-3	334 U1379C 30X-2	334 U1379C 60X-4	334 U1379C 75X-4	/	/	
# Seqs. (Original)	14040	16400	13542	10144	8812	12106	

# Seqs. (After E.Blank)	13968	15539	11614	1389	0	10830
# Seqs. (After Drill Mud)	13961	15524	1258	*	0	0

* = Sample was deleted after E.Blank analysis and not further processed. Abbreviations: (mbsf) = Meters Below Seafloor, (Seqs.) = Sequences, (E. Blank) = DNA Extraction Kit Blank.

Table S2. Correlations.

	1378 Correlations	1379 Correlations
Archaea		
Bathyarchaeota	SO4(.984**),NH4(-.830*)	pH(.766*),Li(-.812*)
Lokiarchaeota	Depth(-.868**),Salinity(.871**), NH4(-.827*),K(.780*),Mg(.847**), Br(-.888**),B(.877**)	Salinity(.861*),pH(-.755*), Mg(.939**),Si(.773*),B(.833*)
Bacteria		
Planctomycetes	NH4(-.753*),Sr(.733*)	Salinity(.956**),SO4(.955**),Mg(.794*)
Deltaproteobacteria	Depth(-.874**),Salinity(.865**), NH4(-.719*),K(.918**),Mg(.881**), Br(-.944**),B(.739*)	Mg(.774*),Si(.770*),Li(.948**),B(.758*)
Aerophobetes	Li(-.799*)	Depth(.897**),NH4(.759*),Br(.871*)
Elusimicrobia	pH(.710*),NH4(.774*),B(-.777*), Sr(-.726*)	No Correlations
Atribacteria	NH4(.725*)	No Correlations
Depth	Salinity(-.986**),NH4(.782*), K(-.920**),Mg(-.982**),Br(.927**), B(-.769*),Ba(.903**)	NH4(.942**),K(-.926**),Br(.991**)

Stars indicate statistical significance. Two stars is very significant, one star is significant.

Table S3. Drilling Fluid Composition.

Classification	Number of Sequences
Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Halobacteriaceae;Halogramnum;	8
Archaea;Thaumarchaeota;Marine Group I;	4
Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;	12
Bacteria;Acidobacteria;Solibacteres;Solibacterales;Solibacteraceae(Subgroup3); PAUC26f;	1
Bacteria;Acidobacteria;Subgroup 22;	3
Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Acidimicrobiaceae;Illumatobacter;	1
Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;	2
Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;OM1 clade;Candidatus Actinomarina;	13
Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Sva0996 marine group;	3
Bacteria;Actinobacteria;Actinobacteria;Pseudonocardiales;Pseudonocardiaceae; Saccharopolyspora;	3
Bacteria;Actinobacteria;Actinobacteria;Pseudonocardiales;Pseudonocardiaceae; Tamarichabitans;	3
Bacteria;Bacteroidetes;Bacteroidetes Incertae Sedis;Order III;uncultured;	2
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;	6
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Carboxylicivirga;	33
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Marinifilum;	89

Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;Marinilabilia;	9
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiaceae;uncultured;	13
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prolixibacteraceae; Mangrovibacterium;	108
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prolixibacteraceae;Sunxiuqinia;	20
Bacteria;Bacteroidetes;Bacteroidia;BacteroidiaIncertaeSedis;Draconibacteriaceae; Draconibacterium;	812
Bacteria;Bacteroidetes;Bacteroidia;BacteroidiaIncertaeSedis;Draconibacteriaceae; Tangfeifania;	104
Bacteria;Bacteroidetes;Bacteroidia;BacteroidiaIncertaeSedis;Draconibacteriaceae; uncultured;	45
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;NS10mar ine group;	12
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae;uncultur ed;	1
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Areniba cter;	4
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Croceital ea;	1
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Formosa ;	1
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gramell a;	20
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Maribact er;	1
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Muricau da;	155
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae; Pseudofulvibacter;	3
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae; Robiginitalea;	21
Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae; Tenacibaculum;	16
Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;	13
Bacteria;Chloroflexi;Ardenticatenia;uncultured;	5
Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;uncultured;	6
Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Prochlorococcus;	7
Bacteria;Cyanobacteria;Cyanobacteria;SubsectionI;FamilyI;Synechococcus;	33
Bacteria;Deinococcus- Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera;	3
Bacteria;Elusimicrobia;Elusimicrobia;Lineage IV;	2
Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Leptotrichiaceae;uncultured;	10
Bacteria;Gemmatimonadetes;BD2-11 terrestrial group;	3
Bacteria;Nitrospinae;Nitrospina;Nitrospinales;Nitrospinaceae;Nitrospina;	24
Bacteria;Nitrospirae;Nitrospira;Nitrospirales;0319-6A21;	1
Bacteria;PAUC34f;	2
Bacteria;Planctomycetes;Phycisphaerae;CCM11a;	2
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae; Pir4 lineage;	6
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae; uncultured;	5

Bacteria;Proteobacteria;ARKICE-90;	2
Bacteria;Proteobacteria;Alphaproteobacteria;4-Org1-14;	6
Bacteria;Proteobacteria;Alphaproteobacteria;Alphaproteobacteria Incertae Sedis;Unknown Family;Eilatimonas;	2
Bacteria;Proteobacteria;Alphaproteobacteria;Alphaproteobacteria Incertae Sedis;Unknown Family;uncultured;	13
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; Brevundimonas;	3
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;	2
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Gemmobacter;	7
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Halovulum;	29
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Hasllibacter;	1
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Jannaschia;	6
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Leisingera;	610
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Litorisediminicola;	1
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Loktanella;	8
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Lutimaribacter;	2
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Mamelella;	17
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Marinovum;	10
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Maritimibacter;	174
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Oceaniovalibus;	16
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Roseinatronobacter;	8
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Roseivivax;	1
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Roseobacter clade CHAB-I-5 lineage;	13
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Roseovarius;	27
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Ruegeria;	49
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Seohaecicola;	37
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Sulfitobacter;	5
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Thalassobius;	3
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Thalassococcus;	24

Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Tropicibacter;	6
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Tropicimonas;	7
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; uncultured;	4380
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae; Magnetovibrio;	1
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae; Pelagibius;	3
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae; uncultured;	69
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;T9d;	15
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;	4
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 1;	15
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade;Surface 2;	1
Bacteria;Proteobacteria;Alphaproteobacteria;ss1-B-07-44;	3
Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilac eae; Tepidiphilus;	1
Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadacea e; Nitrosomonas;	3
Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae; Denitromonas;	42
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae ; Peredibacter;	11
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae ; uncultured;	3
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteracea e; Desulfobacter;	13
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteracea e; uncultured;	1
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;	18
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae; Desulfobulbus;	3
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae; Desulfopila;	2
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiac eae;Desulfomicrobium;	2
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionac eae;Desulfovibrio;	35
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales; Desulfuromonadaceae;Desulfuromonas;	2
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales; Desulfuromonadaceae;Pelobacter;	11
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Sva1033;	2
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae; Sandaracinus;	10
Bacteria;Proteobacteria;Gammaproteobacteria;	66
Bacteria;Proteobacteria;Gammaproteobacteria;34P16;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae; Aeromonas;	7

Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae; Zobellella;	6
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae; uncultured;	186
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae; Alteromonas;	13
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae; Marinobacter;	758
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae; Salinimonas;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Ferrimonadaceae; Ferrimonas;	9
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Idiomarinae; Idiomarina;	9
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales; Pseudoalteromonadaceae;Pseudoalteromonas;	4
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;	5
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales; Cellvibrionaceae;Marinimicrobium;	97
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae; Pseudomaricurvus;	6
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae; uncultured;	28
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Haliea;	7
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae; OM60(NOR5) clade;	6
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Parahal iea;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae; Pseudohalieu;	4
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;C1- B045;	357
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae; Porticoccus;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospirac eae; Thioalkalispira;	32
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospirac eae; Thioalkalivibrio;	17
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospirac eae; uncultured;	15
Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Granulosicoccaceae; Granulosicoccus;	11
Bacteria;Proteobacteria;Gammaproteobacteria;F9P41300-M23;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis; Unknown Family;Sedimenticola;	79
Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis; Unknown Family;Thiohalophilus;	78
Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis; Unknown Family;Thiohalorhabdus;	4
Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria Incertae Sedis; Unknown Family;Thiopfundum;	1

Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoraceae; Kangiella;	99
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae; Halomonas;	3
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;MBAE14;	55
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;OM182 clade;	2
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Marinobacterium;	137
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Marinomonas;	16
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Motiliproteus;	3
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Neptuniibacter;	461
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Neptunomonas;	1
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Oceanospirillum;	10
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae; Pseudohongiella;	25
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SAR86 clade;	11
Bacteria;Proteobacteria;Gammaproteobacteria;PYR10d3;	5
Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae; Oceanococcus;	5
Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae; Salinisphaera;	9
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae; Cycloclasticus;	106
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae; Thiomicrospira;	15
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae; uncultured;	9
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio;	463
Bacteria;Proteobacteria;Gammaproteobacteria;WN-HWB-116;	5
Bacteria;Proteobacteria;Gammaproteobacteria;uncultured;	2
Bacteria;Proteobacteria;Proteobacteria Incertae Sedis;Unknown Order; Unknown Family;Candidatus Tenderia;	4
Bacteria;Proteobacteria;SPOTSOCT00m83;	58
Bacteria;SBR1093;	63
Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaeta 2;	26
Bacteria;Verrucomicrobia;OPB35 soil group;	1
Bacteria;Verrucomicrobia;Opitutae;Puniceicoccales;Puniceicoccaceae;Puniceicoccus;	19
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;	6
Eukaryota;Opisthokonta;Holozoa;Metazoa (Animalia);Eumetazoa;Bilateria;Arthropoda;Crustacea;Maxillopoda;Copepoda; Calanoida;	2
Eukaryota;Opisthokonta;Holozoa;Metazoa (Animalia);Eumetazoa;Ctenophora;Typhlocoela;Cydippida;	4
Total	10830