The following supplement accompanies the article

Microbial community assembly in marine sediments

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Table S1: Identities of the ranked taxonomic groups shown in the depth distribution (Figure 4).

The taxonomic classification of 16S rRNA gene sequence reads were based on the Silva database version 123 [Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner FO (2013) The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Acids Res. 41 (D1): D590- D596]

Rank Number	Domain	Phylum	Class
[1]	Bacteria	Proteobacteria	Alphaproteobacteria
[2]	Bacteria	Firmicutes	Clostridia
[3]	Bacteria	Actinobacteria	Actinobacteria
[4]	Bacteria	Firmicutes	Bacilli
[5]	Bacteria	Proteobacteria	Gammaproteobacteria
[6]	Bacteria	Bacteria unclassified	Bacteria unclassified
[7]	Bacteria	Planctomycetes	Phycisphaerae
[8]	Bacteria	Proteobacteria	Deltaproteobacteria
[9]	Archaea	Euryarchaeota	Thermoplasmata
[10]	Bacteria	Chloroflexi	Dehalococcoidia
[11]	Archaea	Lokiarchaeota (MBG-B)	Unclassified
[12]	Bacteria	Acidobacteria	Acidobacteria
[13]	Bacteria	Aminicenantes	Unclassified
[14]	Bacteria	Actinobacteria	OPB41
[15]	Archaea	Bathy archaeota (Miscellaneous Crenarchaeotic Group	Unclassified
[16]	Bacteria	Bacteroidetes	Cytophagia
[17]	Bacteria	Chloroflexi	Unclassified
[18]	Bacteria	Chloroflexi	Anaerolineae
[19]	Archaea	Unclassified	Unclassified
[20]	Bacteria	Proteobacteria	Unclassified
[21]	Bacteria	Planctomycetes	Planctomycetacia
[22]	Bacteria	Atribacteria	Unclassified
[23]	Bacteria	Nitrospirae	Nitrospira
[24]	Archaea	Thaumarchaeota	Marine Group I
[25]	Bacteria	Bacteroidetes	Flavobacteriia
[26]	Archaea	Archaea unclassified	Unclassified
[27]	Bacteria	Actinobacteria	Acidimicrobiia
[28]	Bacteria	Parcubacteria	Unclassified
[29]	Bacteria	Planctomycetes	Unclassified
[30]	Bacteria	Spirochaetae	Spirochaetes
[31]	Bacteria	Aerophobetes	Unclassified

[32]	Bacteria	Gemmatimonadetes	Gemmatimonadetes
[33]	Archaea	Thaumarchaeota	Group C3
[34]	Bacteria	Bacteroidetes	Unclassified
[35]	Bacteria	Bacteroidetes	Bacteroidia
[36]	Bacteria	TA06	Unclassified
[37]	Bacteria	Bacteroidetes	Sphingobacteriia
[38]	Bacteria	Candidate division OP3	Unclassified
[39]	Bacteria	Deferribacteres	Deferribacteres Incertae Sedis
[40]	Archaea	Euryarchaeota	Methanomicrobia
[41]	Bacteria	Bacteroidetes	Bacteroidetes BD2-2
[42]	Bacteria	Chlamydiae	Chlamydiae
[43]	Bacteria	Marinimicrobia (SAR406 clade)	Unclassified
[44]	Bacteria	Planctomycetes	vadinHA49
[45]	Bacteria	Chlorobi	Ignavibacteria
[46]	Bacteria	Latescibacteria	Latescibacteria Incertae Sedis
[47]	Bacteria	Latescibacteria	Unclassified
[48]	Bacteria	Proteobacteria	Betaproteobacteria
[49]	Bacteria	TM6	Unclassified
[50]	Bacteria	Hydrogenedentes	Unclassified
[51]	Bacteria	Acidobacteria	Holophagae
[52]	Bacteria	Gracilibacteria	Unclassified
[53]	Archaea	Marine Hydrothermal Vent Group(MHVG)	Unclassified
[54]	Bacteria	Chloroflexi	MSB-5B2
[55]	Bacteria	Proteobacteria	Epsilonproteobacteria
[56]	Bacteria	Actinobacteria	Unclassified
[57]	Bacteria	Chloroflexi	S085
[58]	Bacteria	Verrucomicrobia	Spartobacteria
[59]	Bacteria	Chloroflexi	Thermoflexia
[60]	Bacteria	Lentisphaerae	WCHB1-41
[61]	Bacteria	Acidobacteria	Subgroup 22
[62]	Bacteria	Planctomycetes	Pla4 lineage
[63]	Bacteria	Lentisphaerae	Unclassified
[64]	Eukaryota	Eukaryota unclassified	Unclassified
[65]	Bacteria	Chloroflexi	Ardenticatenia
[66]	Bacteria	Chloroflexi	KD4-96
[67]	Bacteria	Fibrobacteres	Fibrobacteria
[68]	Bacteria	Cyanobacteria	Chloroplast
[69]	Bacteria	Planctomycetes	OM190
[70]	Bacteria	Elusimicrobia	Elusimicrobia
[71]	Archaea	Thaumarchaeota	Unclassified
[72]	Bacteria	LCP-89	Unclassified
[73]	Bacteria	JL-ETNP-Z39	Unclassified
[74]	Bacteria	Verrucomicrobia	Verrucomicrobiae
[75]	Bacteria	Acetothermia	Unclassified
[76]	Bacteria	Actinobacteria	Thermoleophilia
[77]	Bacteria	Kazan-3B-09	Unclassified
[78]	Bacteria	Planctomycetes	Pla3 lineage
[79]	Bacteria	Chloroflexi	Caldilineae
[80]	Bacteria	Bacteroidetes	SB-5
[81]	Bacteria	Chlorobi	Chlorobia
[82]	Bacteria	Planctomycetes	MBMPE71
[83]	Bacteria	Planctomycetes	MD2896-B258
[84]	Bacteria	Hyd24-12	Unclassified
[85]	Bacteria	Microgenomates	Unclassified

[86]	Bacteria	Verrucomicrobia	OPB35 soil group
[87]	Bacteria	Acidobacteria	Subgroup 26
[88]	Bacteria	Omnitrophica	NPL-UPA2
[89]	Bacteria	Cyanobacteria	Cyanobacteria
[90]	Bacteria	LD1-PA38	Unclassified
[91]	Bacteria	Bacteroidetes	Bacteroidetes vadinHA17
[92]	Bacteria	Chloroflexi	JG30-KF-CM66
[93]	Bacteria	Bacteroidetes	Bacteroidetes VC2.1 Bac22
[94]	Archaea	Thaumarchaeota	Soil Crenarchaeotic Group (SCG)
[95]	Bacteria	GOUTA4	Unclassified
[96]	Bacteria	Acidobacteria	Unclassified
[97]	Bacteria	Chloroflexi	SAR202 clade
[98]	Bacteria	Fusobacteria	Fusobacteriia
[99]	Bacteria	Verrucomicrobia	Opitutae
[100]	Bacteria	PAUC34f	Unclassified
[101]	Archaea	Aenigmarchaeota	Unclassified
[102]	Archaea	Ancient Archaeal Group(AAG)	Unclassified
[103]	Bacteria	Cyanobacteria	Melainabacteria
[104]	Bacteria	Verrucomicrobia	Unclassified
[105]	Bacteria	Firmicutes	Unclassified
[106]	Archaea	Euryarchaeota	Unclassified
[107]	Bacteria	Lentisphaerae	R76-B128
[108]	Bacteria	Tenericutes	Mollicutes
[109]	Archaea	Aenigmarchaeota	Deep Sea Euryarchaeotic Group (DSEG)
[110]	Archaea	Aigarchaeota	Terrestrial Hot Spring Gp (THSCG)
[111]	Bacteria	Armatimonadetes	Unclassified
[112]	Bacteria	Parcubacteria	Parcubacteria Incertae Sedis
[113]	Bacteria	SHA-109	Unclassified
[114]	Bacteria	Proteobacteria	Proteobacteria Incertae Sedis
[115]	Archaea	Aenigmarchaeota	Aenigmarchaeota Incertae Sedis
[116]	Bacteria	Cloacimonetes	MSBL8
[117]	Archaea	Thaumarchaeota	Marine Benthic Group A
[118]	Bacteria	Candidate division SR1	Unclassified
[119]	Bacteria	Lentisphaerae	Oligosphaeria
[120]	Bacteria	Omnitrophica	Unclassified
[121]	Bacteria	Proteobacteria	SC3-20
[122]	Bacteria	Firmicutes	Negativicutes
[123]	Bacteria	Planctomycetes	BD7-11
[124]	Bacteria	Proteobacteria	SPOTSOCT00m83
[125]	Bacteria	Proteobacteria	TA18
[126]	Bacteria	Verrucomicrobia	S-BQ2-57 soil group
[127]	Bacteria	Lentisphaerae	LD1-PA34
[128]	Bacteria	WCHB1-60	Unclassified
[129]	Bacteria	Cloacimonetes	Unclassified
[130]	Bacteria	Actinobacteria	MB-A2-108
[131]	Bacteria	Chloroflexi	KZNMV-5-B42
[132]	Bacteria	Lentisphaerae	LD1-PB3
[133]	Bacteria	Chloroflexi	Thermomicrobia
[134]	Bacteria	Saccharibacteria	Unclassified
[135]	Bacteria	Cyanobacteria	ML635J-21
[136]	Bacteria	Lentisphaerae	c5LKS8
[137]	Archaea	Thaumarchaeota	AK8

[138]	Bacteria	Proteobacteria	JTB23
[139]	Bacteria	Actinobacteria	Coriobacteriia
[140]	Bacteria	Chloroflexi	TK10
[141]	Bacteria	Lentisphaerae	Lentisphaeria
[142]	Bacteria	Proteobacteria	Milano-WF1B-44
[143]	Bacteria	Omnitrophica	Omnitrophica Incertae Sedis
[144]	Archaea	SM1K20	Unclassified
[145]	Bacteria	Lentisphaerae	DEV055
[146]	Archaea	Euryarchaeota	Methanobacteria
[147]	Bacteria	Chloroflexi	Gitt-GS-136
[148]	Bacteria	Actinobacteria	Rubrobacteria
[149]	Bacteria	Lentisphaerae	MSBL3
[150]	Bacteria	Cyanobacteria	Unclassified
[151]	Bacteria	Proteobacteria	pItb-vmat-80
[152]	Bacteria	Lentisphaerae	BS5
[153]	Bacteria	Proteobacteria	MACA-EFT26
[154]	Bacteria	Firmicutes	Erysipelotrichia
[155]	Bacteria	OC31	Unclassified
[156]	Archaea	Aigarchaeota	Unclassified
[157]	Archaea	Miscellaneous Euryarchaeotic Group (MEG)	Unclassified
[158]	Bacteria	SM2F11	Unclassified
[159]	Archaea	Thaumarchaeota	AK59
[160]	Bacteria	Firmicutes	OPB54
[161]	Bacteria	Planctomycetes	028H05-P-BN-P5
[162]	Bacteria	Proteobacteria	ARKDMS-49
[163]	Bacteria	Thermotogae	Thermotogae
[164]	Eukaryota	Opisthokonta	Nucletmycea
[165]	Bacteria	Lentisphaerae	PBS-III-20
[166]	Bacteria	Planctomycetes	SGST604
[167]	Bacteria	Proteobacteria	AEGEAN-245
[168]	Eukaryota	SAR	Stramenopiles
[169]	Archaea	Thaumarchaeota	pMC2A209
[170]	Bacteria	Aquificae	Aquificae
[171]	Bacteria	Lentisphaerae	113B434
[172]	Bacteria	Lentisphaerae	B01R017
[173]	Bacteria	Verrucomicrobia	Verrucomicrobia Incertae Sedis
[174]	Archaea	Diapherotrites	Diapherotrites Incertae Sedis
[175]	Bacteria	Chloroflexi	Ktedonobacteria
[176]	Bacteria	Deferribacteres	Deferribacteres
[177]	Bacteria	Verrucomicrobia	Arctic97B-4 marine group
[178]	Archaea	Crenarchaeota	Thermoprotei
[179]	Archaea	Euryarchaeota	Archaeoglobi
[180]	Archaea	Euryarchaeota	Halobacteria
[181]	Archaea	Euryarchaeota	Thermococci
[182]	Bacteria	Cloacimonetes	MSBL2
[183]	Bacteria	Lentisphaerae	SS1-B-03-39
[184]	Bacteria	Lentisphaerae	WCHB1-25
[185]	Bacteria	Proteobacteria	Skagenf62
[186]	Eukaryota	Archaeplastida	Chloroplastida
[187]	Archaea	Diapherotrites	Diapherotrites unclassified
[188]	Archaea	Thaumarchaeota	South African Gold Mine Gp 1 (SAGMCG-1)
[189]	Bacteria	Lentisphaerae	Lentisphaerae RFP12 gut group
[190]	Bacteria	Proteobacteria	Zetaproteobacteria

[191]	Eukaryota	Opisthokonta	Holozoa
[192]	Archaea	Nanoarchaeota	Nanoarchaeota Incertae Sedis
[193]	Archaea	Parvarchaeota	Parvarchaeota Incertae Sedis
[194]	Bacteria	Acetothermia	Unknown Class
[195]	Bacteria	Armatimonadetes	Armatimonadia
[196]	Bacteria	Lentisphaerae	ML1228J-2
[197]	Bacteria	Synergistetes	Synergistia

Table S2: Taxnomic identities of OTUs that persist across depth intervals (Figure 7B-D).

The taxonomic classification of 16S rRNA gene sequence reads were based on the Silva database version 123 [Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner FO (2013) The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Acids Res. 41 (D1): D590- D596]

Figure 7B – Aarhus Bay

Rank Number	Classification
1	Archaea;Lokiarchaeota;
2	Bacteria;Atribacteria;
3	Archaea;Bathyarchaeota;
4	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
5	Archaea;Lokiarchaeota;
6	Bacteria;Aerophobetes;
7	Archaea;Hadesarchaea;
8	Archaea;Thaumarchaeota;Marine Group I;
9	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
10	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
11	Archaea;Lokiarchaeota;
12	Archaea;
13	Archaea;Bathyarchaeota;
14	Bacteria;Chloroflexi;Dehalococcoidia;
15	Bacteria;Aerophobetes;
16	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
17	Bacteria;Acetothermia;
18	Archaea;Bathyarchaeota;
19	Bacteria;Aminicenantes;
20	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
21	Archaea;Thaumarchaeota;Group C3;
22	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
23	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
24	Unclassified;
25	Archaea;Lokiarchaeota;

26	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
27	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
28	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
29	Archaea;Thaumarchaeota;Marine Group I;
30	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
31	Archaea;Thaumarchaeota;Group C3;
32	Archaea;Thaumarchaeota;Marine Group I;
33	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
34	Bacteria;Planctomycetes;MBMPE71;
35	Bacteria;Actinobacteria;OPB41;
36	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;uncultured;
37	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
38	Archaea;Thaumarchaeota;Group C3;
39	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
40	Archaea;Bathyarchaeota;
41	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
42	Archaea;Bathyarchaeota;
43	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
44	Archaea;Thaumarchaeota;Marine Group I;
45	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
46	Archaea;Marine Hydrothermal Vent Group(MHVG);
47	Bacteria;Chloroflexi;Dehalococcoidia;
48	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
49	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
50	Unclassified;
51	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
52	Bacteria;Atribacteria;
53	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
54	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
55	Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaet a 2;
56	Bacteria;Aerophobetes;
57	Bacteria;Elusimicrobia;Elusimicrobia;4-29;
58	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
59	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
60	Archaea;Marine Hydrothermal Vent Group(MHVG);
61	Archaea;Lokiarchaeota;
62	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
63	Archaea;Thaumarchaeota;Group C3;
64	Bacteria;Omnitrophica;
65	Archaea;Thaumarchaeota;Group C3;
66	Unclassified;

67	Archaea;Lokiarchaeota;
68	Unclassified;
69	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales; Desulfobacteraceae;SEEP-SRB1;
70	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
71	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
72	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
73	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae; uncultured;
74	Archaea;Lokiarchaeota;
75	Bacteria;Firmicutes;Clostridia;Halanaerobiales;ODP1230B8.23;
76	Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae; Candidatus Scalindua;
77	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
78	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
79	Bacteria;Omnitrophica;
80	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
81	Archaea;Bathyarchaeota;
82	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
83	Archaea;Hadesarchaea;
84	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
85	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
86	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
87	Archaea;Marine Hydrothermal Vent Group(MHVG);
88	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
89	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
90	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
91	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
92	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales; Syntrophobacteraceae;uncultured;
93	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
94	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
95	Bacteria;Chloroflexi;Dehalococcoidia;
96	Bacteria;Chloroflexi;Dehalococcoidia;
97	Bacteria;Chloroflexi;S085;
98	Bacteria;TM6 (Dependentiae);
99	Bacteria;Chloroflexi;Dehalococcoidia;
100	Bacteria;Chloroflexi;Dehalococcoidia;
101	Bacteria;Chloroflexi;Dehalococcoidia;
102	Bacteria;Chloroflexi;Dehalococcoidia;
103	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales; Rhodospirillaceae;uncultured;

104	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
105	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
106	Bacteria;Omnitrophica;
107	Archaea;
108	Archaea;Thaumarchaeota;Marine Group I;
109	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;

Figure 7C – China Sea

Rank Number	Classification
1	Archaea;Lokiarchaeota;
2	Bacteria;Atribacteria;
3	Archaea;Bathyarchaeota;
4	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
5	Archaea;Lokiarchaeota;
6	Bacteria;Aerophobetes;
7	Archaea;Hadesarchaea;
8	Archaea;Thaumarchaeota;Marine Group I;
9	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
10	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
11	Archaea;Lokiarchaeota;
12	Archaea;
13	Archaea;Bathyarchaeota;
14	Bacteria;Chloroflexi;Dehalococcoidia;
15	Bacteria;Aerophobetes;
16	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
17	Bacteria;Acetothermia;
18	Archaea;Bathyarchaeota;
19	Bacteria;Aminicenantes;
20	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
21	Archaea;Thaumarchaeota;Group C3;
22	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
23	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
24	Unclassified;
25	Archaea;Lokiarchaeota;
26	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
27	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
28	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
29	Archaea;Thaumarchaeota;Marine Group I;
30	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;

31	Archaea;Thaumarchaeota;Group C3;
32	Archaea;Thaumarchaeota;Marine Group I;
33	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
34	Bacteria;Planctomycetes;MBMPE71;
35	Bacteria;Actinobacteria;OPB41;
36	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;uncultured;
37	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
38	Archaea;Thaumarchaeota;Group C3;
39	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
40	Archaea;Bathyarchaeota;
41	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
42	Archaea;Bathyarchaeota;
43	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
44	Archaea;Thaumarchaeota;Marine Group I;
45	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
46	Archaea;Marine Hydrothermal Vent Group(MHVG);
47	Bacteria;Chloroflexi;Dehalococcoidia;
48	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
49	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
50	Unclassified;
51	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
52	Bacteria;Atribacteria;
53	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
54	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
55	Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;Spirochaet a 2;
56	Bacteria;Aerophobetes;
57	Bacteria;Elusimicrobia;Elusimicrobia;4-29;
58	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
59	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
60	Archaea;Marine Hydrothermal Vent Group(MHVG);
61	Archaea;Lokiarchaeota;
62	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;
63	Archaea;Thaumarchaeota;Group C3;
64	Bacteria;Omnitrophica;
65	Archaea;Thaumarchaeota;Group C3;
66	Unclassified;
67	Archaea;Lokiarchaeota;
68	Unclassified;
69	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales; Desulfobacteraceae;SEEP-SRB1;
70	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;

71	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
72	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
73	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae; uncultured;
74	Archaea;Lokiarchaeota;
75	Bacteria;Firmicutes;Clostridia;Halanaerobiales;ODP1230B8.23;
76	Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae; Candidatus Scalindua;
77	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
78	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
79	Bacteria;Omnitrophica;
80	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
81	Archaea;Bathyarchaeota;
82	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
83	Archaea;Hadesarchaea;
84	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
85	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
86	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
87	Archaea;Marine Hydrothermal Vent Group(MHVG);
88	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
89	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
90	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
91	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
92	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales; Syntrophobacteraceae;uncultured;
93	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
94	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
95	Bacteria;Chloroflexi;Dehalococcoidia;
96	Bacteria;Chloroflexi;Dehalococcoidia;
97	Bacteria;Chloroflexi;S085;
98	Bacteria;TM6 (Dependentiae);
99	Bacteria;Chloroflexi;Dehalococcoidia;
100	Bacteria;Chloroflexi;Dehalococcoidia;
101	Bacteria;Chloroflexi;Dehalococcoidia;
102	Bacteria;Chloroflexi;Dehalococcoidia;
103	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales; Rhodospirillaceae;uncultured;
104	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
105	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
106	Bacteria;Omnitrophica;
107	Archaea;
108	Archaea;Thaumarchaeota;Marine Group I;
109	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;

110	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
111	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae; uncultured;
112	Unclassified;
113	Archaea;Thaumarchaeota;Marine Group I;
114	Archaea;Bathyarchaeota;
115	Archaea;Bathyarchaeota;
116	Archaea;Bathyarchaeota;
117	Archaea;Bathyarchaeota;
118	Unclassified;
119	Unclassified;
120	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
121	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
122	Bacteria;Marinimicrobia (SAR406 clade);
123	Bacteria;Chloroflexi;Dehalococcoidia;Napoli-4B-65;
124	Bacteria;Elusimicrobia;Elusimicrobia;MD2896-B235;
125	Unclassified;
126	Bacteria;Chloroflexi;SBR2076;
127	Archaea;Bathyarchaeota;
128	Archaea;Bathyarchaeota;
129	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
130	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
131	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;uncultured;
132	Archaea;Hadesarchaea;
133	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
134	Archaea;Lokiarchaeota;
135	Archaea;Bathyarchaeota;
136	Bacteria;Firmicutes;Clostridia;Halanaerobiales;ODP1230B8.23;
137	Bacteria;Omnitrophica;
138	Archaea;Marine Hydrothermal Vent Group(MHVG);
139	Bacteria;Aerophobetes;
140	Archaea;
141	Bacteria;AC1;
142	Bacteria;Chloroflexi;Dehalococcoidia;Napoli-4B-65;
143	Unclassified;
144	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
145	Archaea;Bathyarchaeota;
146	Unclassified;
147	Unclassified;
148	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae; Desulfatiglans;
149	Archaea;Bathyarchaeota;
150	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae; Coxiella;

151	Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae; Spirochaeta 2;
152	Bacteria;Chloroflexi;Dehalococcoidia;
153	Archaea;Lokiarchaeota;
154	Archaea;Bathyarchaeota;
155	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
156	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
157	Archaea;Bathyarchaeota;
158	Unclassified;
159	Unclassified;
160	Bacteria;Chloroflexi;Dehalococcoidia;
161	Bacteria;Planctomycetes;Pla3 lineage;
162	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Benthic Group D and DHVEG-1;
163	Unclassified;
164	Bacteria;Chloroflexi;Dehalococcoidia;
165	Bacteria;BRC1;
166	Bacteria;Planctomycetes;MBMPE71;
167	Bacteria;Deferribacteres;Deferribacteres Incertae Sedis;Unknown Order;Unknown Family;Caldithrix;
168	Bacteria;RBG-1 (Zixibacteria);
169	Bacteria;Proteobacteria;Deltaproteobacteria;Sva0485;
170	Archaea;Thaumarchaeota;Marine Group I;
171	Bacteria;Chloroflexi;Dehalococcoidia;
172	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
173	Archaea;Thaumarchaeota;Marine Group I;Unknown Order;Unknown Family;Candidatus Nitrosopumilus;
174	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
175	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;
176	Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Mycobacteriaceae; Mycobacterium;
177	Archaea;Bathyarchaeota;
178	Bacteria;Proteobacteria;Gammaproteobacteria;Sva0071;
179	Bacteria;WS1;
180	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;
181	Bacteria;Chloroflexi;Dehalococcoidia;
182	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
183	Archaea;Bathyarchaeota;
184	Bacteria;Deferribacteres;Deferribacteres Incertae Sedis;Unknown Order;Unknown Family;Caldithrix;
185	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;Planctomyces;
186	Bacteria;Planctomycetes;Planctomycetacia;Brocadiales;Brocadiaceae; Candidatus Scalindua;
187	Archaea;Thaumarchaeota;Marine Benthic Group A;
188	Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae;uncultured;
189	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;ANT06-05;

190	Bacteria;Firmicutes;Clostridia;Halanaerobiales;ODP1230B8.23;
191	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;
192	Archaea;Bathyarchaeota;
193	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;
194	Unclassified;
195	Bacteria;Bacteroidetes;Bacteroidetes BD2-2;
196	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;
197	Bacteria;Spirochaetae;Spirochaetes;Spirochaetales;Spirochaetaceae; Spirochaeta 2;
198	Bacteria;Bacteroidetes;SB-5;
199	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;Pir4 lineage;
200	Archaea;Bathyarchaeota;
201	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales; Planctomycetaceae;Pir4 lineage;
202	Archaea;Lokiarchaeota;
203	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;
204	Archaea;Thaumarchaeota;Soil Crenarchaeotic Group(SCG);
205	Bacteria;Bacteroidetes;Bacteroidetes BD2-2;
206	Unclassified;
207	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae; uncultured;
208	Archaea;Bathyarchaeota;

Figure 7D – Nankai Trough

Rank Number	Classification
1	Bacteria;Atribacteria;
2	Bacteria;Atribacteria;
3	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
4	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
5	Bacteria;Actinobacteria;OPB41;
6	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;
7	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;
8	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;