



OTU	GS1A	%	PS1B	%	Taxonomy_Silva_132
otu0001	0	0	2	0.05	Bacteria;Acidobacteria;Acidobacteria_un;Acidobacteria_un;Acidobacteria_un;Acidobacteria_un;
otu0002	0	0	1	0.02	Bacteria;Acidobacteria;Acidobacteriia;Solibacterales;Solibacteraceae_(Subgroup_3);PAUC26f;
otu0003	49	0.82	5	0.12	Bacteria;Acidobacteria;Aminicenantia;Aminicenantales;Aminicenantales_fa;Aminicenantales_ge;
otu0004	1	0.02	7	0.17	Bacteria;Acidobacteria;AT-s3-28;AT-s3-28_or;AT-s3-28_fa;AT-s3-28_ge;
otu0005	1	0.02	0	0	Bacteria;Acidobacteria;Blastocatellia_(Subgroup_4);Blastocatellales;Blastocatellaceae;Blastocatella;
otu0006	0	0	2	0.05	Bacteria;Acidobacteria;Holophagae;Subgroup_7;Subgroup_7_fa;Subgroup_7_ge;
otu0007	1	0.02	0	0	Bacteria;Acidobacteria;ODP1230B23.02;ODP1230B23.02_or;ODP1230B23.02_fa;ODP1230B23.02_ge;
otu0008	1	0.02	15	0.36	Bacteria;Acidobacteria;Subgroup_17;Subgroup_17_or;Subgroup_17_fa;Subgroup_17_ge;
otu0009	9	0.15	41	0.99	Bacteria;Acidobacteria;Subgroup_21;Subgroup_21_or;Subgroup_21_fa;Subgroup_21_ge;
otu0010	5	0.08	50	1.21	Bacteria;Acidobacteria;Subgroup_22;Subgroup_22_or;Subgroup_22_fa;Subgroup_22_ge;
otu0011	2	0.03	11	0.27	Bacteria;Acidobacteria;Subgroup_26;Subgroup_26_or;Subgroup_26_fa;Subgroup_26_ge;
otu0012	0	0	1	0.02	Bacteria;Acidobacteria;Subgroup_5;Subgroup_5_or;Subgroup_5_fa;Subgroup_5_ge;
otu0013	1	0.02	13	0.32	Bacteria;Acidobacteria;Subgroup_6;Subgroup_6_or;Subgroup_6_fa;Subgroup_6_ge;
otu0014	0	0	1	0.02	Bacteria;Acidobacteria;Subgroup_6;Subgroup_6_un;Subgroup_6_un;Subgroup_6_un;
otu0015	8	0.13	30	0.73	Bacteria;Acidobacteria;Subgroup_9;Subgroup_9_or;Subgroup_9_fa;Subgroup_9_ge;
otu0016	8	0.13	0	0	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;B276-D12;
otu0017	9	0.15	81	1.96	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Subgroup_10;
otu0018	14	0.24	17	0.41	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Subgroup_23;
otu0019	0	0	1	0.02	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculaceae_un;
	109	1.83	278	6.74	
otu0020	4	0.07	8	0.19	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiia_un;Acidimicrobiia_un;Acidimicrobiia_un;
otu0021	2	0.03	2	0.05	Bacteria;Actinobacteria;Acidimicrobiia;Actinomarinales;Actinomarinales_un;Actinomarinales_un;
otu0022	104	1.75	78	1.89	Bacteria;Actinobacteria;Acidimicrobiia;Actinomarinales;uncultured;uncultured_ge;
otu0023	5	0.08	14	0.34	Bacteria;Actinobacteria;Acidimicrobiia;IMCC26256;IMCC26256_fa;IMCC26256_ge;
otu0024	0	0	3	0.07	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Ilumatobacteraceae;Ilumatobacter;
otu0025	0	0	14	0.34	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichaceae;IMCC26207;
otu0026	0	0	2	0.05	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichaceae;Microtrichaceae_un;
otu0027	0	0	42	1.02	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichaceae;Sva0996_marine_group;
otu0028	0	0	1	0.02	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichaceae;uncultured;
otu0029	0	0	10	0.24	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichales_un;Microtrichales_un;
otu0030	0	0	3	0.07	Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;uncultured;uncultured_ge;
otu0031	0	0	34	0.82	Bacteria;Actinobacteria;Actinobacteria;Actinobacteria_un;Actinobacteria_un;Actinobacteria_un;
otu0032	0	0	2	0.05	Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Mycobacteriaceae;Mycobacterium;
otu0033	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Nocardiaceae;Millsia;
otu0034	0	0	2	0.05	Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Nocardiaceae;Nocardia;
otu0035	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Frankiales;Frankiales_un;Frankiales_un;
otu0036	0	0	2	0.05	Bacteria;Actinobacteria;Actinobacteria;Frankiales;Geodermatophilaceae;Geodermatophilus;
otu0037	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Micrococcaceae_un;
otu0038	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Micromonosporales;Micromonosporaceae;Actinoplanes;
otu0039	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Micromonosporales;Micromonosporaceae;Micromonospora;
otu0040	0	0	2	0.05	Bacteria;Actinobacteria;Actinobacteria;PeM15;PeM15_fa;PeM15_ge;
otu0041	1	0.02	0	0	Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Nocardioideae;Nocardioide;
otu0042	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Propionibacteriaceae;Cutibacterium;
otu0043	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Propionibacteriaceae;Microclunatus;
otu0044	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Pseudonocardiales;Pseudonocardaceae;Actinomycetospora;
otu0045	0	0	5	0.12	Bacteria;Actinobacteria;Actinobacteria;Streptomycetales;Streptomycetaceae;Streptomyces;
otu0046	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Streptomycetales;Streptomycetaceae;Streptomycetaceae_un;
otu0047	0	0	1	0.02	Bacteria;Actinobacteria;Actinobacteria;Streptosporangiales;Streptosporangiaceae;Streptosporangiaceae_un;
otu0048	1	0.02	0	0	Bacteria;Actinobacteria;Actinobacteria;Streptosporangiales;Thermomonosporaceae;Actinoallomurus;
otu0049	1	0.02	8	0.19	Bacteria;Actinobacteria;Actinobacteria_un;Actinobacteria_un;Actinobacteria_un;Actinobacteria_un;
otu0050	1	0.02	5	0.12	Bacteria;Actinobacteria;Coriobacteriia;CG2-30-50-142;CG2-30-50-142_fa;CG2-30-50-142_ge;
otu0051	2	0.03	0	0	Bacteria;Actinobacteria;Coriobacteriia;FS118-23B-02;FS118-23B-02_fa;FS118-23B-02_ge;
otu0052	0	0	2	0.05	Bacteria;Actinobacteria;Coriobacteriia;OPB41;OPB41_fa;OPB41_ge;
otu0053	0	0	1	0.02	Bacteria;Actinobacteria;MB-A2-108;MB-A2-108_or;MB-A2-108_fa;MB-A2-108_ge;
otu0054	1	0.02	0	0	Bacteria;Actinobacteria;RBG-16-55-12;RBG-16-55-12_or;RBG-16-55-12_fa;RBG-16-55-12_ge;
otu0055	0	0	1	0.02	Bacteria;Actinobacteria;Rubrobacteria;Rubrobacteriales;Rubrobacteriaceae;Rubrobacter;
otu0056	0	0	1	0.02	Bacteria;Actinobacteria;Thermoleophilia;Gaiellales;Gaiellales_fa;Gaiellales_ge;
otu0057	3	0.05	4	0.1	Bacteria;Actinobacteria;Thermoleophilia;Gaiellales;Gaiellales_un;Gaiellales_un;
otu0058	1	0.02	24	0.58	Bacteria;Actinobacteria;Thermoleophilia;Gaiellales;uncultured;uncultured_ge;
otu0059	1	0.02	10	0.24	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacteriales;67-14;67-14_ge;
otu0060	1	0.02	1	0.02	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacteriales;Solirubrobacteraceae;Solirubrobacteraceae_un;
otu0061	1	0.02	0	0	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacteriales;Solirubrobacteriales_un;Solirubrobacteriales_un;
otu0062	0	0	6	0.15	Bacteria;Actinobacteria;Thermoleophilia;Thermoleophilia_un;Thermoleophilia_un;Thermoleophilia_un;
otu0063	0	0	2	0.05	Bacteria;Actinobacteria;WCHB1-81;WCHB1-81_or;WCHB1-81_fa;WCHB1-81_ge;
	129	2.17	299	7.25	
otu0064	0	0	1	0.02	Bacteria;Aegiribacteria;Aegiribacteria_cl;Aegiribacteria_or;Aegiribacteria_fa;Aegiribacteria_ge;
	0	0	1	0.02	
otu0065	0	0	1	0.02	Bacteria;AncK6;AncK6_cl;AncK6_or;AncK6_fa;AncK6_ge;
	0	0	1	0.02	
otu0066	1	0.02	1	0.02	Bacteria;Armatimonadetes;DG-56;DG-56_or;DG-56_fa;DG-56_ge;
otu0067	0	0	2	0.05	Bacteria;Armatimonadetes;Fimbriimonadia;Fimbriimonadales;Fimbriimonadaceae;Fimbriimonadaceae_ge;

otu0068	0	0	1	0.02	Bacteria;Armatimonadetes;Fimbriimonadia;Fimbriimonadales;Fimbriimonadaceae;Fimbriimonadaceae_un;
	1	0.02	4	0.1	
otu0069	3	0.05	0	0	Bacteria;Atribacteria;JS1;JS1_or;JS1_fa;JS1_ge;
	3	0.05	0	0	
otu0070	105	1.77	112	2.72	Bacteria;Bacteria_un;Bacteria_un;Bacteria_un;Bacteria_un;
	105	1.77	112	2.72	
otu0071	1	0.02	0	0	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidales_un;Bacteroidales_un;
otu0072	0	0	4	0.1	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidetes_BD2-2;Bacteroidetes_BD2-2_ge;
otu0073	0	0	6	0.15	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinifilaceae;Marinifilum;
otu0074	0	0	1	0.02	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiliaceae;Labilibacter;
otu0075	1	0.02	0	0	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinilabiliaceae;uncultured;
otu0076	0	0	1	0.02	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prolixibacteraceae;Prolixibacter;
otu0077	0	0	4	0.1	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidia_un;Bacteroidia_un;Bacteroidia_un;
otu0078	0	0	6	0.15	Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;Saprospiraceae;Saprospiraceae_un;
otu0079	0	0	13	0.32	Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;Saprospiraceae;uncultured;
otu0080	1	0.02	10	0.24	Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;uncultured;
otu0081	0	0	2	0.05	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomicaceae;Crocinitomicaceae_un;
otu0082	1	0.02	0	0	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomicaceae;Crocinitomix;
otu0083	0	0	3	0.07	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomicaceae;Salinirepens;
otu0084	0	0	3	0.07	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Actibacter;
otu0085	1	0.02	2	0.05	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Aquibacter;
otu0086	0	0	1	0.02	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Flavobacteriaceae_ge;
otu0087	3	0.05	8	0.19	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Flavobacteriaceae_un;
otu0088	2	0.03	3	0.07	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Lutibacter;
otu0089	0	0	3	0.07	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Lutimonas;
otu0090	0	0	5	0.12	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Robiginitalea;
otu0091	1011	17	0	0	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Salegentibacter;
otu0092	1	0.02	0	0	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Ulvibacter;
otu0093	0	0	9	0.22	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Zeaxanthinibacter;
otu0094	0	0	1	0.02	Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriales_un;Flavobacteriales_un;
otu0095	0	0	1	0.02	Bacteria;Bacteroidetes;Bacteroidia;Sphingobacteriales;AKYH767;AKYH767_ge;
otu0096	0	0	5	0.12	Bacteria;Bacteroidetes;Bacteroidia;Sphingobacteriales;Lentimicrobiaceae;Lentimicrobiaceae_ge;
otu0097	0	0	2	0.05	Bacteria;Bacteroidetes;Bacteroidia;Sphingobacteriales;Sphingobacteriales_un;Sphingobacteriales_un;
otu0098	0	0	1	0.02	Bacteria;Bacteroidetes;Ignavibacteria;Ignavibacteria_un;Ignavibacteria_un;Ignavibacteria_un;
otu0099	2	0.03	3	0.07	Bacteria;Bacteroidetes;Ignavibacteria;Ignavibacteriales;Ignavibacteriales_un;Ignavibacteriales_un;
otu0100	0	0	4	0.1	Bacteria;Bacteroidetes;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;lheB3-7;
otu0101	14	0.24	0	0	Bacteria;Bacteroidetes;Ignavibacteria;Ignavibacteriales;PHOS-HE36;PHOS-HE36_ge;
otu0102	1	0.02	3	0.07	Bacteria;Bacteroidetes;Ignavibacteria;Kryptoniales;BSV26;BSV26_ge;
otu0103	0	0	1	0.02	Bacteria;Bacteroidetes;Rhodothermia;Rhodothermales;Rhodothermaceae;Rhodothermaceae_un;
otu0104	0	0	7	0.17	Bacteria;Bacteroidetes;Rhodothermia;Rhodothermales;Rhodothermaceae;uncultured;
	1039	17.5	112	2.72	
otu0105	0	0	3	0.07	Bacteria;BRC1;BRC1_cl;BRC1_or;BRC1_fa;BRC1_ge;
	0	0	3	0.07	
otu0106	3	0.05	3	0.07	Bacteria;Calditrichaeota;Calditrichia;Calditrichales;Calditrichaceae;Calditrichaceae_ge;
otu0107	1	0.02	0	0	Bacteria;Calditrichaeota;Calditrichia;Calditrichales;Calditrichaceae;Calditrichaceae_un;
otu0108	3	0.05	0	0	Bacteria;Calditrichaeota;Calditrichia;Calditrichales;Calditrichaceae;Calorithrix;
otu0109	0	0	2	0.05	Bacteria;Calditrichaeota;Calditrichia;Calditrichales;Calditrichaceae;JdFR-76;
	7	0.12	5	0.12	
otu0110	2	0.03	0	0	Bacteria;Chlamydiae;LD1-PA32;LD1-PA32_or;LD1-PA32_fa;LD1-PA32_ge;
	2	0.03	0	0	
otu0111	0	0	1	0.02	Bacteria;Chloroflexi;Anaerolineae;1-20;1-20_fa;1-20_ge;
otu0112	9	0.15	0	0	Bacteria;Chloroflexi;Anaerolineae;ADurb.Bin180;ADurb.Bin180_fa;ADurb.Bin180_ge;
otu0113	9	0.15	3	0.07	Bacteria;Chloroflexi;Anaerolineae;Anaerolineae_un;Anaerolineae_un;Anaerolineae_un;
otu0114	8	0.13	6	0.15	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolineaceae_un;
otu0115	1	0.02	0	0	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;
otu0116	0	0	1	0.02	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;RBG-16-58-14;
otu0117	151	2.54	49	1.19	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;uncultured;
otu0118	9	0.15	27	0.65	Bacteria;Chloroflexi;Anaerolineae;Ardenticatenales;uncultured;uncultured_ge;
otu0119	0	0	19	0.46	Bacteria;Chloroflexi;Anaerolineae;Caldilineales;Caldilineaceae;uncultured;
otu0120	21	0.35	0	0	Bacteria;Chloroflexi;Anaerolineae;MSB-5B2;MSB-5B2_fa;MSB-5B2_ge;
otu0121	0	0	1	0.02	Bacteria;Chloroflexi;Anaerolineae;SBR1031;A4b;A4b_ge;
otu0122	6	0.1	18	0.44	Bacteria;Chloroflexi;Anaerolineae;SBR1031;SBR1031_fa;SBR1031_ge;
otu0123	1	0.02	0	0	Bacteria;Chloroflexi;Anaerolineae;Thermoflexales;Thermoflexaceae;Thermoflexus;
otu0124	18	0.3	5	0.12	Bacteria;Chloroflexi;Anaerolineae;uncultured;uncultured_fa;uncultured_ge;
otu0125	0	0	1	0.02	Bacteria;Chloroflexi;Chloroflexi_un;Chloroflexi_un;Chloroflexi_un;Chloroflexi_un;
otu0126	0	0	2	0.05	Bacteria;Chloroflexi;Chloroflexia;Thermomicrobiales;JG30-KF-CM45;JG30-KF-CM45_ge;
otu0127	1	0.02	0	0	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidales_Incertae_Sedis;Dehalobium;
otu0128	32	0.54	0	0	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidia_un;Dehalococcoidia_un;Dehalococcoidia_un;
otu0129	3	0.05	0	0	Bacteria;Chloroflexi;Dehalococcoidia;DscP2;DscP2_fa;DscP2_ge;
otu0130	3	0.05	1	0.02	Bacteria;Chloroflexi;Dehalococcoidia;FS117-23B-02;FS117-23B-02_fa;FS117-23B-02_ge;
otu0131	2	0.03	0	0	Bacteria;Chloroflexi;Dehalococcoidia;FW22;FW22_fa;FW22_ge;
otu0132	1	0.02	0	0	Bacteria;Chloroflexi;Dehalococcoidia;GIF3;GIF3_fa;GIF3_ge;

otu0133	9	0.15	0	0	Bacteria;Chloroflexi;Dehalococcoidia;GIF9;AB-539-J10;SCGC-AB-539-J10;
otu0134	3	0.05	0	0	Bacteria;Chloroflexi;Dehalococcoidia;H3_93;H3_93_fa;H3_93_ge;
otu0135	12	0.2	2	0.05	Bacteria;Chloroflexi;Dehalococcoidia;MSBL5;MSBL5_fa;MSBL5_ge;
otu0136	4	0.07	0	0	Bacteria;Chloroflexi;Dehalococcoidia;Napoli-4B-65;Napoli-4B-65_fa;Napoli-4B-65_ge;
otu0137	6	0.1	2	0.05	Bacteria;Chloroflexi;Dehalococcoidia;S085;S085_fa;S085_ge;
otu0138	4	0.07	0	0	Bacteria;Chloroflexi;Dehalococcoidia;Sh765B-AG-111;Sh765B-AG-111_fa;Sh765B-AG-111_ge;
otu0139	9	0.15	0	0	Bacteria;Chloroflexi;Dehalococcoidia;vadinBA26;vadinBA26_fa;vadinBA26_ge;
otu0140	5	0.08	1	0.02	Bacteria;Chloroflexi;JG30-KF-CM66;JG30-KF-CM66_or;JG30-KF-CM66_fa;JG30-KF-CM66_ge;
otu0141	1	0.02	42	1.02	Bacteria;Chloroflexi;KD4-96;KD4-96_or;KD4-96_fa;KD4-96_ge;
otu0142	0	0	2	0.05	Bacteria;Chloroflexi;Ktedonobacteria;MVP-21;MVP-21_fa;MVP-21_ge;
otu0143	0	0	2	0.05	Bacteria;Chloroflexi;TK17;TK17_or;TK17_fa;TK17_ge;
	328	5.52	185	4.48	
otu0144	5	0.08	0	0	Bacteria; CK-2C2-2 ;CK-2C2-2_cl;CK-2C2-2_or;CK-2C2-2_fa;CK-2C2-2_ge;
	5	0.08	0	0	
otu0145	0	0	8	0.19	Bacteria; Cyanobacteria ;Melainabacteria;Gastranaerophilales;Gastranaerophilales_fa;Gastranaerophilales_ge;
otu0146	0	0	7	0.17	Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobiaceae_un;
otu0147	1	0.02	38	0.92	Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium_PCC-6307;
otu0148	0	0	15	0.36	Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus_CC9902;
	1	0.02	68	1.65	
otu0149	5	0.08	21	0.51	Bacteria; Dadabacteria ;Dadabacteriia;Dadabacteriales;Dadabacteriales_fa;Dadabacteriales_ge;
	5	0.08	21	0.51	
otu0150	1	0.02	2	0.05	Bacteria; Deinococcus-Thermus ;Deinococci;Deinococcales;Trueperaceae;Truepera;
	1	0.02	2	0.05	
otu0151	2	0.03	1	0.02	Bacteria; Dependentiae ;Babeliae;Babeliales;Babeliaceae;Babeliaceae_ge;
otu0152	4	0.07	2	0.05	Bacteria;Dependentiae;Babeliae;Babeliales;Babeliales_fa;Babeliales_ge;
otu0153	7	0.12	11	0.27	Bacteria;Dependentiae;Babeliae;Babeliales;Babeliales_un;Babeliales_un;
otu0154	0	0	1	0.02	Bacteria;Dependentiae;Babeliae;Babeliales;UBA12409;UBA12409_ge;
otu0155	0	0	1	0.02	Bacteria;Dependentiae;Babeliae;Babeliales;UBA12411;UBA12411_ge;
otu0156	4	0.07	6	0.15	Bacteria;Dependentiae;Babeliae;Babeliales;Vermiphilaceae;Vermiphilaceae_ge;
	17	0.29	22	0.53	
otu0157	0	0	10	0.24	Bacteria; Epsilonbacteraota ;Campylobacteria;Campylobacteriales;Sulfurovaceae;Sulfurovum;
	0	0	10	0.24	
otu0158	1	0.02	0	0	Bacteria; Fibrobacteres ;Fibrobacteria;Fibrobacterales;TG3;TG3_ge;
	1	0.02	0	0	
otu0159	0	0	1	0.02	Bacteria; Firmicutes ;Bacilli;Bacillales;Alicyclobacillaceae;Effusibacillus;
otu0160	0	0	2	0.05	Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Tumebacillus;
otu0161	83	1.4	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Anaerobacillus;
otu0162	1	0.02	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Aquibacillus;
otu0163	13	0.22	3	0.07	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillaceae_un;
otu0164	141	2.37	66	1.6	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus;
otu0165	0	0	2	0.05	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Fictibacillus;
otu0166	15	0.25	3	0.07	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillales_un;Bacillales_un;
otu0167	0	0	2	0.05	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Ammoniphilus;
otu0168	0	0	1	0.02	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Cohnella;
otu0169	0	0	2	0.05	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillaceae_un;
otu0170	1	0.02	5	0.12	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;
otu0171	0	0	2	0.05	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Domibacillus;
otu0172	104	1.75	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Jeotgalibacillus;
otu0173	0	0	1	0.02	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Lysinibacillus;
otu0174	1430	24.1	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Paenisporosarcina;
otu0175	1	0.02	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Planococcaceae_ge;
otu0176	14	0.24	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Planococcaceae_un;
otu0177	155	2.61	0	0	Bacteria;Firmicutes;Bacilli;Bacillales;Sporolactobacillaceae;Salipaludibacillus;
otu0178	0	0	1	0.02	Bacteria;Firmicutes;Bacilli;Bacillales;Thermoactinomycetaceae;Shimazuella;
otu0179	1	0.02	0	0	Bacteria;Firmicutes;Bacilli;Bacilli_un;Bacilli_un;Bacilli_un;
otu0180	0	0	1	0.02	Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus;
otu0181	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;uncultured;
otu0182	0	0	14	0.34	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridiaceae_1_un;
otu0183	0	0	24	0.58	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_1;
otu0184	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_10;
otu0185	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_12;
otu0186	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_17;
otu0187	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_18;
otu0188	1	0.02	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_7;
otu0189	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_8;
otu0190	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Clostridium_sensu_stricto_9;
otu0191	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Fonticella;
otu0192	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;Oceanirhabdus;
otu0193	0	0	3	0.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_1;uncultured;
otu0194	1	0.02	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_4;Paramaledivibacter;
otu0195	0	0	4	0.1	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales_un;Clostridiales_un;
otu0196	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Defluviitaleaceae;Defluviitaleaceae_UCG-011;

otu0197	1	0.02	0	0	Bacteria;Firmicutes;Clostridia;Clostridiales;Family_XII;Family_XII_un;
otu0198	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Family_XVIII;uncultured;
otu0199	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Gracilibacteraceae;Lutispora;
otu0200	0	0	3	0.07	Bacteria;Firmicutes;Clostridia;Clostridiales;Heliobacteriaceae;Hydrogenispora;
otu0201	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Epulopiscium;
otu0202	1	0.02	8	0.19	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae_un;
otu0203	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnotalea;
otu0204	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Mobilitalea;
otu0205	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzrella_3;
otu0206	1	0.02	0	0	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Dehalobacterium;
otu0207	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Desulfurispora;
otu0208	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Peptococcaceae_un;
otu0209	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Paraclostridium;
otu0210	1	0.02	9	0.22	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Peptostreptococcaceae_un;
otu0211	0	0	18	0.44	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Romboutsia;
otu0212	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Sporacetigenium;
otu0213	1	0.02	0	0	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Tepidibacter;
otu0214	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Caproiciproducens;
otu0215	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium_1;
otu0216	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae_UCG-012;
otu0217	0	0	11	0.27	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae_un;
otu0218	0	0	1	0.02	Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;uncultured;
otu0219	0	0	2	0.05	Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;Syntrophomonadaceae_un;
otu0220	0	0	1	0.02	Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;ZOR0006;
otu0221	0	0	2	0.05	Bacteria;Firmicutes;Negativicutes;Selenomonadales;uncultured;uncultured_ge;
otu0222	0	0	1	0.02	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Veillonellaceae_un;
	1966	33.1	227	5.5	
otu0223	0	0	1	0.02	Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Cetobacterium;
otu0224	0	0	1	0.02	Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Psychrilyobacter;
	0	0	2	0.05	
otu0225	8	0.13	0	0	Bacteria;Gemmatimonadetes;AKAU4049;AKAU4049_or;AKAU4049_fa;AKAU4049_ge;
otu0226	3	0.05	11	0.27	Bacteria;Gemmatimonadetes;BD2-11_terrestrial_group;BD2-11_terrestrial_group_or;BD2-11_terrestrial_group_fa;BD2-11_terrestrial_group_ge;
otu0227	1	0.02	0	0	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonadaceae_un;
otu0228	5	0.08	9	0.22	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;uncultured;
otu0229	0	0	1	0.02	Bacteria;Gemmatimonadetes;Gemmatimonadetes_un;Gemmatimonadetes_un;Gemmatimonadetes_un;Gemmatimonadetes_un;
otu0230	3	0.05	0	0	Bacteria;Gemmatimonadetes;MD2902-B12;MD2902-B12_or;MD2902-B12_fa;MD2902-B12_ge;
otu0231	17	0.29	29	0.7	Bacteria;Gemmatimonadetes;PAUC43f_marine_benthic_group;PAUC43f_marine_benthic_group_or;PAUC43f_marine_benthic_group_fa;PAUC43f_marine_benthic_group_ge;
	37	0.62	50	1.21	
otu0232	3	0.05	0	0	Bacteria;GN01;GN01_cl;GN01_or;GN01_fa;GN01_ge;
	3	0.05	0	0	
otu0233	1	0.02	0	0	Bacteria;Halanaerobiaeota;Halanaerobia;Halanaerobiales;Halobacteroidaceae;Orenia;
otu0234	0	0	1	0.02	Bacteria;Halanaerobiaeota;Halanaerobia;Halanaerobiales;Halobacteroidaceae;uncultured;
	1	0.02	1	0.02	
otu0235	0	0	4	0.1	Bacteria;Hydrogenedentes;Hydrogenedentia;Hydrogenedentiales;Hydrogenedensaceae;Hydrogenedensaceae_ge;
	0	0	4	0.1	
otu0236	2	0.03	5	0.12	Bacteria;Kiritimatiella;Kiritimatiellae;Kiritimatiellales;Kiritimatiellaceae;R76-B128;
otu0237	2	0.03	3	0.07	Bacteria;Kiritimatiella;Kiritimatiellae;WCHB1-41;WCHB1-41_fa;WCHB1-41_ge;
	4	0.07	8	0.19	
otu0238	1	0.02	0	0	Bacteria;Latescibacteria;Latescibacteria;Latescibacteriales;Latescibacteraceae;Candidatus_Latescibacter;
otu0239	15	0.25	4	0.1	Bacteria;Latescibacteria;Latescibacteria;Latescibacteriales;Latescibacteraceae;Latescibacteraceae_ge;
otu0240	18	0.3	15	0.36	Bacteria;Latescibacteria;Latescibacteria_cl;Latescibacteria_or;Latescibacteria_fa;Latescibacteria_ge;
	34	0.57	19	0.46	
otu0241	0	0	1	0.02	Bacteria;Modulibacteria;Moduliflexia;Moduliflexales;Moduliflexaceae;Moduliflexaceae_ge;
	0	0	1	0.02	
otu0242	2	0.03	9	0.22	Bacteria;Nitrospinae;Nitrospina;Nitrospinales;Nitrospinaceae;Nitrospina;
otu0243	0	0	2	0.05	Bacteria;Nitrospinae;Nitrospina;Nitrospinales;Nitrospinaceae;Nitrospinaceae_un;
otu0244	5	0.08	2	0.05	Bacteria;Nitrospinae;P9X2b3D02;P9X2b3D02_or;P9X2b3D02_fa;P9X2b3D02_ge;
	7	0.12	13	0.32	
otu0245	1	0.02	0	0	Bacteria;Nitrospirae;4-29-1;4-29-1_or;4-29-1_fa;4-29-1_ge;
otu0246	0	0	30	0.73	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;
otu0247	3	0.05	0	0	Bacteria;Nitrospirae;Thermodesulfovibrionia;Magnetobacteriales;Magnetobacteriaceae;Magnetobacteriaceae_un;
otu0248	1	0.02	1	0.02	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrionaceae;
otu0249	7	0.12	1	0.02	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionia_un;Thermodesulfovibrionia_un;Thermodesulfovibrionia_un;
otu0250	49	0.82	37	0.9	Bacteria;Nitrospirae;Thermodesulfovibrionia;uncultured;uncultured_fa;uncultured_ge;
	61	1.03	69	1.67	
otu0251	7	0.12	1	0.02	Bacteria;Omnitrophicaeota;Omnitrophicaeota_cl;Omnitrophicaeota_or;Omnitrophicaeota_fa;Omnitrophicaeota_ge;
	7	0.12	1	0.02	
otu0252	3	0.05	0	0	Bacteria;Patescibacteria;ABY1;ABY1_un;ABY1_un;ABY1_un;
otu0253	1	0.02	0	0	Bacteria;Patescibacteria;ABY1;Candidatus_Falkowbacteria;Candidatus_Falkowbacteria_fa;Candidatus_Falkowbacteria_ge;
otu0254	1	0.02	1	0.02	Bacteria;Patescibacteria;ABY1;Candidatus_Kerfeldbacteria;Candidatus_Kerfeldbacteria_fa;Candidatus_Kerfeldbacteria_ge;

otu0255	3	0.05	0	0	Bacteria;Patescibacteria;ABY1;Candidatus_Komeilibacteria;Candidatus_Komeilibacteria_fa;Candidatus_Komeilibacteria_ge;
otu0256	1	0.02	0	0	Bacteria;Patescibacteria;ABY1;Candidatus_Uhrbacteria;Candidatus_Uhrbacteria_fa;Candidatus_Uhrbacteria_ge;
otu0257	2	0.03	8	0.19	Bacteria;Patescibacteria;Gracilibacteria;Candidatus_Peregrinibacteria;Candidatus_Peregrinibacteria_fa;Candidatus_Peregrinibacteria_ge;
otu0258	2	0.03	6	0.15	Bacteria;Patescibacteria;Gracilibacteria;Gracilibacteria_or;Gracilibacteria_fa;Gracilibacteria_ge;
otu0259	1	0.02	0	0	Bacteria;Patescibacteria;Microgenomatia;Candidatus_Chisholmbacteria;Candidatus_Chisholmbacteria_fa;Candidatus_Chisholmbacteria_ge;
otu0260	1	0.02	0	0	Bacteria;Patescibacteria;Microgenomatia;Candidatus_Curtissbacteria;Candidatus_Curtissbacteria_fa;Candidatus_Curtissbacteria_ge;
otu0261	1	0.02	0	0	Bacteria;Patescibacteria;Microgenomatia;Candidatus_Gottesmanbacteria;Candidatus_Gottesmanbacteria_fa;Candidatus_Gottesmanbacteria_ge;
otu0262	1	0.02	0	0	Bacteria;Patescibacteria;Microgenomatia;Candidatus_Woesebacteria;Candidatus_Woesebacteria_fa;Candidatus_Woesebacteria_ge;
otu0263	2	0.03	0	0	Bacteria;Patescibacteria;Microgenomatia;Candidatus_Woykebacteria;Candidatus_Woykebacteria_fa;Candidatus_Woykebacteria_ge;
otu0264	1	0.02	0	0	Bacteria;Patescibacteria;Microgenomatia;Microgenomatia_un;Microgenomatia_un;Microgenomatia_un;
otu0265	1	0.02	0	0	Bacteria;Patescibacteria;Parcubacteria;Candidatus_Campbellbacteria;Candidatus_Campbellbacteria_fa;Candidatus_Campbellbacteria_ge;
otu0266	0	0	2	0.05	Bacteria;Patescibacteria;Parcubacteria;Parcubacteria_un;Parcubacteria_un;Parcubacteria_un;
otu0267	1	0.02	6	0.15	Bacteria;Patescibacteria;Saccharimonadia;Saccharimonadales;Saccharimonadales_fa;Saccharimonadales_ge;
	22	0.37	23	0.56	
otu0268	0	0	1	0.02	Bacteria;Planctomycetes;BD7-11;BD7-11_or;BD7-11_fa;BD7-11_ge;
otu0269	0	0	1	0.02	Bacteria;Planctomycetes;Brocadia;Brocadiales;Scalinduae;Candidatus_Scalindua;
otu0270	2	0.03	23	0.56	Bacteria;Planctomycetes;OM190;OM190_or;OM190_fa;OM190_ge;
otu0271	3	0.05	5	0.12	Bacteria;Planctomycetes;Phycisphaerae;C86;C86_fa;C86_ge;
otu0272	1	0.02	3	0.07	Bacteria;Planctomycetes;Phycisphaerae;CCM11a;CCM11a_fa;CCM11a_ge;
otu0273	0	0	15	0.36	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;4572-13;4572-13_ge;
otu0274	0	0	1	0.02	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;L21-RPul-D3;L21-RPul-D3_ge;
otu0275	0	0	2	0.05	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;MSBL9_un;MSBL9_un;
otu0276	9	0.15	4	0.1	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;SG8-4;SG8-4_ge;
otu0277	0	0	1	0.02	Bacteria;Planctomycetes;Phycisphaerae;MSBL9;SM23-30;SM23-30_ge;
otu0278	3	0.05	0	0	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerae_un;Phycisphaerae_un;Phycisphaerae_un;
otu0279	1	0.02	2	0.05	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;AKAU3564_sediment_group;AKAU3564_sediment_group_ge;
otu0280	0	0	1	0.02	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaerae_un;Phycisphaerae_un;
otu0281	0	0	2	0.05	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaerae_un;Phycisphaerae_un;
otu0282	0	0	6	0.15	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaerae_un;Phycisphaerae_un;
otu0283	3	0.05	23	0.56	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaerae_un;Phycisphaerae_un;Phycisphaerae_un;
otu0284	0	0	2	0.05	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaerales_un;Phycisphaerales_un;
otu0285	0	0	1	0.02	Bacteria;Planctomycetes;Phycisphaerae;Pla1_lineage;Pla1_lineage_fa;Pla1_lineage_ge;
otu0286	0	0	10	0.24	Bacteria;Planctomycetes;Pla3_lineage;Pla3_lineage_or;Pla3_lineage_fa;Pla3_lineage_ge;
otu0287	0	0	1	0.02	Bacteria;Planctomycetes;Pla4_lineage;Pla4_lineage_or;Pla4_lineage_fa;Pla4_lineage_ge;
otu0288	3	0.05	55	1.33	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Blastopirellula;
otu0289	2	0.03	8	0.19	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Bythopirellula;
otu0290	23	0.39	41	0.99	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Pir4_lineage;
otu0291	0	0	3	0.07	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Pirellula;
otu0292	9	0.15	81	1.96	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Pirellulaceae_un;
otu0293	3	0.05	44	1.07	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Rhodopirellula;
otu0294	0	0	18	0.44	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Rubripirellula;
otu0295	2	0.03	7	0.17	Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;uncultured;
otu0296	0	0	4	0.1	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetacia_un;Planctomycetacia_un;Planctomycetacia_un;
otu0297	1	0.02	8	0.19	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gimesiaceae;uncultured;
otu0298	1	0.02	4	0.1	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetales_un;Planctomycetales_un;
otu0299	0	0	1	0.02	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Rubinisphaerae;Fuerstia;
otu0300	0	0	2	0.05	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Rubinisphaerae;uncultured;
otu0301	0	0	1	0.02	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;uncultured;uncultured_ge;
otu0302	1	0.02	0	0	Bacteria;Planctomycetes;Planctomycetacia;uncultured;uncultured_fa;uncultured_ge;
otu0303	1	0.02	4	0.1	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetacia_un;Planctomycetacia_un;Planctomycetacia_un;
otu0304	5	0.08	1	0.02	Bacteria;Planctomycetes;SPG12-343-353-B69;SPG12-343-353-B69_or;SPG12-343-353-B69_fa;SPG12-343-353-B69_ge;
otu0305	1	0.02	0	0	Bacteria;Planctomycetes;vadinHA49;vadinHA49_or;vadinHA49_fa;vadinHA49_ge;
	74	1.24	386	9.36	
otu0306	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;Acetobacteraceae_un;
otu0307	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_Incertae_Sedis;Unknown_Family;uncultured;
otu0308	21	0.35	100	2.42	Bacteria;Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_un;Alphaproteobacteria_un;Alphaproteobacteria_un;
otu0309	0	0	10	0.24	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacteriales;Parvularculaceae;uncultured;
otu0310	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Holosporales;Holosporaceae;Holosporaceae_un;
otu0311	1	0.02	0	0	Bacteria;Proteobacteria;Alphaproteobacteria;Micavibrionales;Micavibrionales_un;Micavibrionales_un;
otu0312	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;Parvibaculaceae;uncultured;
otu0313	0	0	6	0.15	Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;Parvibaculales_un;Parvibaculales_un;
otu0314	0	0	35	0.85	Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;PS1_clade;PS1_clade_ge;
otu0315	0	0	3	0.07	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Beijerinckiaceae_un;
otu0316	0	0	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Microvirga;
otu0317	2	0.03	102	2.47	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium;
otu0318	0	0	13	0.32	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobiaceae_un;
otu0319	0	0	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobium;
otu0320	87	1.46	12	0.29	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;uncultured;
otu0321	0	0	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;KF-JG30-B3;KF-JG30-B3_ge;
otu0322	4	0.07	106	2.57	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methyloligellaceae;Methyloceanibacter;
otu0323	31	0.52	16	0.39	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methyloligellaceae;Methyloligellaceae_un;
otu0324	9	0.15	6	0.15	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methyloligellaceae;uncultured;

otu0325	0	0	9	0.22	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Cohaesibacter;
otu0326	0	0	14	0.34	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Pseudahrensia;
otu0327	0	0	3	0.07	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobiaceae_un;
otu0328	0	0	13	0.32	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;uncultured;
otu0329	2	0.03	6	0.15	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales_Incertae_Sedis;Andersenella;
otu0330	0	0	13	0.32	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales_Incertae_Sedis;Bauldia;
otu0331	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales_Incertae_Sedis;Rhizobiales_Incertae_Sedis_un;
otu0332	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales_Incertae_Sedis;uncultured;
otu0333	5	0.08	33	0.8	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales_un;Rhizobiales_un;
otu0334	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Xanthobacteraceae_un;
otu0335	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Boseongicola;
otu0336	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Dinoroseobacter;
otu0337	0	0	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ketogulonigenium;
otu0338	254	4.27	0	0	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Oceanibulbus;
otu0339	25	0.42	0	0	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus;
otu0340	4	0.07	0	0	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Pelagimonas;
otu0341	66	1.11	19	0.46	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacteraceae_un;
otu0342	0	0	12	0.29	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ruegeria;
otu0343	68	1.14	0	0	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Sedimentitalea;
otu0344	0	0	25	0.61	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Silicimonas;
otu0345	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;uncultured;
otu0346	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Magnetospiraceae;uncultured;
otu0347	0	0	73	1.77	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Kiloniellaceae;Kiloniellaceae_un;
otu0348	0	0	4	0.1	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Kiloniellaceae;Limibacillus;
otu0349	3	0.05	118	2.86	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Kiloniellaceae;uncultured;
otu0350	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Rhodovibrionales_un;Rhodovibrionales_un;
otu0351	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;SAR11_clade;Clade_I;Clade_Ib;
otu0352	2	0.03	3	0.07	Bacteria;Proteobacteria;Alphaproteobacteria;Sneathiellales;Sneathiellaceae;AT-s3-44;
otu0353	0	0	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Altererythrobacter;
otu0354	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Erythrobacter;
otu0355	0	0	1	0.02	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium;
otu0356	0	0	3	0.07	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonadaceae_un;
otu0357	1	0.02	2	0.05	Bacteria;Proteobacteria;Alphaproteobacteria;uncultured;uncultured_fa;uncultured_ge;
otu0358	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Bacteriovoracaceae_un;
otu0359	1	0.02	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;Bradymonadales;Bradymonadales_fa;Bradymonadales_ge;
otu0360	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Bradymonadales;Bradymonadales_un;Bradymonadales_un;
otu0361	0	0	6	0.15	Bacteria;Proteobacteria;Deltaproteobacteria;Deltaproteobacteria_Incertae_Sedis;Unknown_Family;Deferrisoma;
otu0362	16	0.27	28	0.68	Bacteria;Proteobacteria;Deltaproteobacteria;Deltaproteobacteria_un;Deltaproteobacteria_un;Deltaproteobacteria_un;
otu0363	18	0.3	8	0.19	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfatiglan;
otu0364	0	0	5	0.12	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;uncultured;
otu0365	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Candidatus_Magnetomorum;
otu0366	14	0.24	10	0.24	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Desulfobacteraceae_un;
otu0367	0	0	8	0.19	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Desulfofrigus;
otu0368	0	0	4	0.1	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Desulfonema;
otu0369	0	0	2	0.05	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Desulfosarcina;
otu0370	23	0.39	5	0.12	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;SEEP-SRB1;
otu0371	11	0.19	28	0.68	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Sva0081_sediment_group;
otu0372	0	0	9	0.22	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;uncultured;
otu0373	1	0.02	17	0.41	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobulbaceae;Desulfobulbaceae_un;
otu0374	0	0	2	0.05	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobulbaceae;Desulfocapsa;
otu0375	0	0	3	0.07	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobulbaceae;Desulfopila;
otu0376	3	0.05	17	0.41	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobulbaceae;uncultured;
otu0377	0	0	2	0.05	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;
otu0378	0	0	10	0.24	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadales_un;Desulfuromonadales_un;
otu0379	0	0	8	0.19	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Sva1033;Sva1033_ge;
otu0380	11	0.19	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;DTB120;DTB120_fa;DTB120_ge;
otu0381	3	0.05	4	0.1	Bacteria;Proteobacteria;Deltaproteobacteria;MBNT15;MBNT15_fa;MBNT15_ge;
otu0382	2	0.03	3	0.07	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;bacteriap25;bacteriap25_ge;
otu0383	1	0.02	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Blfdi19;Blfdi19_ge;
otu0384	1	0.02	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Eel-36e1D6;Eel-36e1D6_ge;
otu0385	0	0	2	0.05	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Haliangiaceae;Haliangium;
otu0386	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;MidBa8;MidBa8_ge;
otu0387	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcales_un;Myxococcales_un;
otu0388	1	0.02	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;PS-B29;PS-B29_ge;
otu0389	50	0.84	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;uncultured;
otu0390	0	0	16	0.39	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;uncultured;
otu0391	0	0	3	0.07	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;UASB-TL25;UASB-TL25_ge;
otu0392	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;VHS-B4-70;VHS-B4-70_ge;
otu0393	31	0.52	98	2.38	Bacteria;Proteobacteria;Deltaproteobacteria;NB1-j;NB1-j_fa;NB1-j_ge;
otu0394	2	0.03	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;NKB15;NKB15_fa;NKB15_ge;
otu0395	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;0319-6G20;0319-6G20_ge;
otu0396	0	0	5	0.12	Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;Oligoflexaceae;uncultured;

otu0397	0	0	3	0.07	Bacteria;Proteobacteria;Deltaproteobacteria;SAR324_clade(Marine_group_B);SAR324_clade(Marine_group_B)_fa;SAR324_clade(M
otu0398	22	0.37	0	0	Bacteria;Proteobacteria;Deltaproteobacteria;Sva0485;Sva0485_fa;Sva0485_ge;
otu0399	0	0	17	0.41	Bacteria;Proteobacteria;Deltaproteobacteria;Sva0485;Sva0485_fa;Sva0485_ge;
otu0400	0	0	1	0.02	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;uncultured;
otu0401	40	0.67	49	1.19	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;uncultured;
otu0402	3	0.05	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;Alteromonadales;Marinobacteraceae;Marinobacter;
otu0403	0	0	34	0.82	Bacteria;Proteobacteria;Gammmaproteobacteria;Alteromonadales;Psychromonadaceae;Psychromonas;
otu0404	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Alteromonadales;Shewanellaceae;Ferrimonas;
otu0405	67	1.13	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;AT-s16;AT-s16_fa;AT-s16_ge;
otu0406	3	0.05	54	1.31	Bacteria;Proteobacteria;Gammmaproteobacteria;AT-s2-59;AT-s2-59_fa;AT-s2-59_ge;
otu0407	0	0	26	0.63	Bacteria;Proteobacteria;Gammmaproteobacteria;B2M28;B2M28_fa;B2M28_ge;
otu0408	6	0.1	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;BD7-8;BD7-8_fa;BD7-8_ge;
otu0409	0	0	5	0.12	Bacteria;Proteobacteria;Gammmaproteobacteria;Betaproteobacteriales;Nitrosomonadaceae;Nitrosomonadaceae_un;
otu0410	0	0	10	0.24	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Cellvibrionales_un;Cellvibrionales_un;
otu0411	0	0	7	0.17	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Haliaceae;Haliaceae_un;
otu0412	0	0	5	0.12	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Haliaceae;Halioglobus;
otu0413	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Haliaceae;OM60(NOR5)_clade;
otu0414	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Haliaceae;Parahalia;
otu0415	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Microbulbiferaceae;Microbulbifer;
otu0416	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Cellvibrionales;Spongiibacteraceae;BD1-7_clade;
otu0417	0	0	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;Chromatiales;Sedimenticolaceae;Sedimenticolaceae_un;
otu0418	1	0.02	34	0.82	Bacteria;Proteobacteria;Gammmaproteobacteria;Coxiellales;Coxiellaceae;Coxiella;
otu0419	0	0	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;EC3;EC3_fa;EC3_ge;
otu0420	0	0	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;Ectothiorhodospirales;Ectothiorhodospiraceae;Thiogranum;
otu0421	0	0	5	0.12	Bacteria;Proteobacteria;Gammmaproteobacteria;Ectothiorhodospirales;Thioalkalispiraceae;SS1-B-09-64;
otu0422	1	0.02	7	0.17	Bacteria;Proteobacteria;Gammmaproteobacteria;EPR3968-O8a-Bc78;EPR3968-O8a-Bc78_fa;EPR3968-O8a-Bc78_ge;
otu0423	0	0	4	0.1	Bacteria;Proteobacteria;Gammmaproteobacteria;EV818SWSAP88;EV818SWSAP88_fa;EV818SWSAP88_ge;
otu0424	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Gammmaproteobacteria_Incertae_Sedis;Unknown_Family;Candidatus_Berkiella;
otu0425	0	0	42	1.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Gammmaproteobacteria_Incertae_Sedis;Unknown_Family;uncultured;
otu0426	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Gammmaproteobacteria_Incertae_Sedis;Unknown_Family;Unknown_Family_ge;
otu0427	53	0.89	268	6.5	Bacteria;Proteobacteria;Gammmaproteobacteria;Gammmaproteobacteria_un;Gammmaproteobacteria_un;Gammmaproteobacteria_un;
otu0428	1	0.02	37	0.9	Bacteria;Proteobacteria;Gammmaproteobacteria;KI89A_clade;KI89A_clade_fa;KI89A_clade_ge;
otu0429	1	0.02	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;Legionellales;Legionellaceae;Legionella;
otu0430	0	0	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;Legionellales;Legionellaceae;Legionellaceae_un;
otu0431	0	0	4	0.1	Bacteria;Proteobacteria;Gammmaproteobacteria;Legionellales;Legionellaceae;uncultured;
otu0432	1	0.02	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;MBAE14;MBAE14_fa;MBAE14_ge;
otu0433	7	0.12	11	0.27	Bacteria;Proteobacteria;Gammmaproteobacteria;Nitrosococcales;Nitrosococcaceae;AqS1;
otu0434	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Nitrosococcales;Nitrosococcaceae;Cm1-21;
otu0435	0	0	2	0.05	Bacteria;Proteobacteria;Gammmaproteobacteria;Nitrosococcales;Nitrosococcaceae;FS142-36B-02;
otu0436	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Nitrosococcales;Nitrosococcaceae;MSB-1D1;
otu0437	1	0.02	12	0.29	Bacteria;Proteobacteria;Gammmaproteobacteria;Nitrosococcales;Nitrosococcaceae;Nitrosococcaceae_un;
otu0438	227	3.82	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;Alcanivoraceae;Alcanivorax;
otu0439	1	0.02	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;Halomonadaceae;Salinicola;
otu0440	536	9.02	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;Nitrincolaceae;Amphritea;
otu0441	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;Nitrincolaceae;Neptuniibacter;
otu0442	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;P13-46;P13-46_ge;
otu0443	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Oceanospirillales;Pseudohongiellaceae;Pseudohongiella;
otu0444	3	0.05	6	0.15	Bacteria;Proteobacteria;Gammmaproteobacteria;P0X4b2H11;P0X4b2H11_fa;P0X4b2H11_ge;
otu0445	0	0	17	0.41	Bacteria;Proteobacteria;Gammmaproteobacteria;Pltb-vmat-80;pltb-vmat-80_fa;pltb-vmat-80_ge;
otu0446	0	0	3	0.07	Bacteria;Proteobacteria;Gammmaproteobacteria;Steroidobacterales;Woeseiaceae;JTB255_marine_benthic_group;
otu0447	13	0.22	288	6.98	Bacteria;Proteobacteria;Gammmaproteobacteria;Steroidobacterales;Woeseiaceae;Woeseia;
otu0448	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Thiohalorhabdadales;Thiohalorhabdaceae;uncultured;
otu0449	0	0	13	0.32	Bacteria;Proteobacteria;Gammmaproteobacteria;UBA10353_marine_group;UBA10353_marine_group_fa;UBA10353_marine_group_g
otu0450	1	0.02	45	1.09	Bacteria;Proteobacteria;Gammmaproteobacteria;uncultured;uncultured_fa;uncultured_ge;
otu0451	164	2.76	0	0	Bacteria;Proteobacteria;Gammmaproteobacteria;Vibrionales;Vibrionaceae;Photobacterium;
otu0452	0	0	1	0.02	Bacteria;Proteobacteria;Gammmaproteobacteria;Vibrionales;Vibrionaceae;Vibrionaceae_un;
otu0453	11	0.19	29	0.7	Bacteria;Proteobacteria;Proteobacteria_un;Proteobacteria_un;Proteobacteria_un;Proteobacteria_un;
	1937	32.6	2172	52.7	
otu0454	1	0.02	4	0.1	Bacteria;Schekmanbacteria;Schekmanbacteria_cl;Schekmanbacteria_or;Schekmanbacteria_fa;Schekmanbacteria_ge;
	1	0.02	4	0.1	
otu0455	0	0	1	0.02	Bacteria;Spirochaetes;Leptospirae;Leptospirales;Leptospiraceae;uncultured;
otu0456	12	0.2	0	0	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta_2;
otu0457	1	0.02	1	0.02	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;uncultured;
	13	0.22	2	0.05	
otu0458	17	0.29	1	0.02	Bacteria;TA06;TA06_cl;TA06_or;TA06_fa;TA06_ge;
	17	0.29	1	0.02	
otu0459	1	0.02	5	0.12	Bacteria;Tenericutes;Mollicutes;Haloplasmatales;Haloplasmataceae;Haloplasma;
otu0460	1	0.02	5	0.12	Bacteria;Tenericutes;Mollicutes;Izimaplasmatales;Izimaplasmatales_fa;Izimaplasmatales_ge;
	2	0.03	10	0.24	
otu0461	0	0	1	0.02	Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Puniceicoccaceae;Cerasicoccus;
otu0462	0	0	1	0.02	Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Puniceicoccaceae;Verruc-01;
otu0463	0	0	1	0.02	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Rubritaleaceae;Persicirhabdus;

	0	0	3	0.07	
otu0464	0	0	1	0.02	Bacteria; WS1 ;WS1_cl;WS1_or;WS1_fa;WS1_ge;
	0	0	1	0.02	
otu0465	0	0	2	0.05	Bacteria; WS2 ;WS2_cl;WS2_or;WS2_fa;WS2_ge;
	0	0	2	0.05	
otu0466	4	0.07	2	0.05	Bacteria; Zixibacteria ;Zixibacteria_cl;Zixibacteria_or;Zixibacteria_fa;Zixibacteria_ge;
	4	0.07	2	0.05	
otu0467	1	0.02	1	0.02	unknown; unknown_un ;unknown_un;unknown_un;unknown_un;unknown_un;
	1	0.02	1	0.02	