

Table S13. Relative abundances of the taxa represented by the actual sequence variants derived from 16S rRNA gene amplicon library analysis of all mixed culture samples. Taxonomy is presented to genus-level resolution.

Taxonomy						Relative abundance of indicated taxon					
kingdom	phylum	class	order	family	genus	YCY-17 (H2)	YCY-18 (H2 + N2O)	YCY-19 (Acetate)	YCY-20 (Acetate + N2O)	YCY-21 (MeOH)	YCY-22 (MeOH + N2O)
d_Bacteria	p_Campylobacterota	c_Campylobacteria	o_Campylobacterales	f_Sulfurospirillaceae	g_Sulfurospirillum	0.005404085	0.274561404	0.000281326	0.000867364	0.024420045	0.607511258
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Citrobacter	0	0	0.097863801	0.354306343	0.001322264	0.000266199
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Sphingobacteriales	f_Lentimicrobiaceae	g_Lentimicrobium	0.001038073	0.005886839	0.222866145	0.015284355	0.00182439	0.000421482
d_Archaea	p_Halobacterota	c_Methanosarcinia	o_Methanosarciniales	f_Methanosarcinaceae	g_Methanomethylvoirans	9.16E-05	0	0	0	0.222073444	0.041260898
d_Archaea	p_Euryarchaeota	c_Methanobacteria	o_Methanobacteriales	f_Methanobacteriaceae	g_Methanobacterium	0.160412787	0.193107769	0.00011253	0	0	0
d_Archaea	p_Euryarchaeota	c_Methanobacteria	o_Methanobacteriales	f_Methanobacteriaceae	g_Methanobacterium	0.1367203	0.157539683	0.003469682	0.002742745	0.000435176	0.000221833
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Dethiosulfatibacteraceae	g_Dethiosulfatibacter	0.155069765	0.022911445	0	0	0	0
d_Archaea	p_Halobacterota	c_Methanosarcinia	o_Methanosarciniales	f_Methanosarcinaceae	g_Methanosarcina	0	0	0.131229018	0.150171129	0.001807652	0.000465849
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Rhodocyclaceae	g_uncultured	0.001343388	0.123830409	0.000262571	0.000328192	0.001138152	0.000532399
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Williamwhitmaniaceae	g_Blvii28_wastewater-sludge_group	0	0.000146199	0.05570247	0.008532983	0.121564624	0.004347923
d_Bacteria	p_Firmicutes	c_uncultured	o_uncultured	f_uncultured	g_uncultured	0.116783195	0.012949039	0.015116563	0.007431197	0.005958558	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_uncultured	0.112600372	0.04235589	0	9.38E-05	0	0
d_Bacteria	p_Spirochaetota	c_Spirochaetia	o_Spirochaetales	f_Spirochaetaceae	g_uncultured	0.000305316	0.000626566	0.066336578	0.069224999	0.107237305	0.063577275
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium_sensu_stricto_16	0.102311239	0.002694236	0	0	5.02E-05	0
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_Cloacimonadaceae	g_Candidatus_Cloacimonas	0	0	0	0	0.099270244	0.057476874
d_Bacteria	p_Firmicutes	c_Clostridia	o_Eubacteriales	f_Eubacteriaceae	g_Acetobacterium	0.000854884	0.001086048	0.000300081	0	0.000251063	0.0001331
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_ML635J-40_aquatic_group	g_ML635J-40_aquatic_group	0	0	0.081978282	0.056495851	0.001472902	0
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Syner-01	0.081213935	0.013011696	0.04624993	0.049134981	0	0
d_Bacteria	p_Desulfobacterota	c_Desulfobivriota	o_Desulfobivriales	f_Desulfobivriaceae	g_Desulfobivrio	0.00314475	0.013784461	0.004407434	0.048525482	0.078432029	0.007675414
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Paludibacteraceae	g_uncultured	0.077489085	0.001023392	0	0	0	0
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_Cloacimonadaceae	g_LNR_A2-18	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_uncultured	0	0	0	0.002391111	0.000719713	0.001242264
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_Cloacimonadaceae	g_W5	0	0	0	0	0.06423861	0.047472215
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_DMER64	0	0	0.000168795	7.03E-05	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Dysgonomonadaceae	g_Petrimonas	0.000244252	0.000355054	0.062041674	0.014323222	0.00222609	0.002218328
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Hungateiclostridiaceae	g_uncultured	0	0	0.058384441	0.006001219	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_uncultured	0	0	0.014910257	0.05462047	0.00020085	0
d_Bacteria	p_Armatimonadota	c_uncultured	o_uncultured	f_uncultured	g_uncultured	0	0	0	0	0.00169049	0.000798598
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_JGI-0000079-D21	0	0	0	0	0.053175108	0.01752479
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_uncultured	0	0	0	7.03E-05	0.000351488	0.000465849
d_Bacteria	p_Desulfobacterota	c_Desulfobivriota	o_Desulfobivriales	f_Desulfomicrobiaceae	g_Desulfomicrobium	0	0.000167084	0	0	0.010327051	0.04831518
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Dysgonomonadaceae	g_Proteiniphilum	0	0.000856307	0.042949043	0.006938909	0.000318013	0.015949777
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_U29-B03	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_S50_wastewater-sludge_group	0	0	0	0	0.043919258	0.00270636
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Thermovirga	0	0	0.012603387	0.042688359	0.000150638	0
d_Bacteria	p_Acidobacteriota	c_Holophagae	o_Holophagales	f_Holophagaceae	g_Holophagaceae	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium_sensu_stricto_7	0.009251061	0.040580618	0.001031527	0.001617516	0.009506913	0.001752479
d_Bacteria	p_Desulfobacterota	c_Desulfuromonadia	o_Geobacteriales	f_Geobacteriaceae	g_Trichlorobacter	0.000671694	0.03855472	0	0	0.000468651	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Bacteroidetes_vadinHA17	g_Bacteroidetes_vadinHA17	0	0	0	0	0.000184113	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_uncultured	6.11E-05	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Syntrophomonadia	o_Syntrophomonadales	f_Syntrophomonadaceae	g_uncultured	0	0	0.000300081	7.03E-05	0	0
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_W27	g_W27	0	0	0	0	0.037123824	0.027174516
d_Bacteria	p_Firmicutes	c_Incertae_Sedis	o_DTU014	f_DTU014	g_DTU014	0	0	0	0	0	0.000155283
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Williamwhitmaniaceae	g_Acetobacteroides	0	0	0	0	0	0
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Aminobacterium	0	0	0.003619723	0.011697689	0.000150638	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Anaerovoracaceae	g_Anaerovorax	0.01590694	0.001670844	0.014610176	0.00445403	0.026512235	0.002240511
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_dgA-11_gut_group	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Eubacteriales	f_Eubacteriaceae	g_Eubacterium	0	0	0	0	0	0
d_Archaea	p_Thermoplasmata	c_Thermoplasmata	o_Methanomassiliococcales	f_Methanomassiliococcaceae	g_Methanomassiliococcus	0	6.27E-05	0	0	0.020788003	0.006899
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Sedimentibacteraceae	g_Sedimentibacter	0.000274784	0.000814536	0	7.03E-05	0.000117163	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Sphingobacteriales	f_Lentimicrobiaceae	g_Lentimicrobiaceae	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_Longilinea	0	0	0	0	0	0.000110916
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Lactivibrio	0	0	0	0	0.003933318	0.002240511
d_Bacteria	p_Firmicutes	c_Clostridia	o_Christensenellales	f_Christensenellaceae	g_Christensenellaceae_R-7_group	0	0.001524645	0.006376714	0.006704487	0.007799685	0.000465849
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Gracilibacteraceae	g_Gracilibacter	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Peptostreptococcales-Tissierellales	g_Soehngenia	0.003633255	0.01566416	0.005026351	0.002156688	0	0
d_Archaea	p_Halobacterota	c_Methanosarcinia	o_Methanosarciniales	f_Methanosarcinaceae	g_Methanosarcina	0	0	0	0	0	0.000155283
d_Bacteria	p_Patescibacteria	c_Dojkabacteria	o_Dojkabacteria	f_Dojkabacteria	g_Dojkabacteria	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Pseudomonadaceae	g_Pseudomonas	0.000366379	0.000396825	0	0.000398518	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Dysgonomonadaceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Bacilli	o_Erysipelotrichales	f_Erysipelatoclostridiaceae	g_UCG-004	0	0	0	0	0	0
d_Archaea	p_Thermoplasmata	c_Thermoplasmata	o_Methanomassiliococcales	f_Methanomethylphilaceae	g_Candidatus_Methanogramnum	0	4.18E-05	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Prolixibacteraceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Coriobacteria	o.OPB41	f.OPB41	g.OPB41	0.000122126	0	0.002888276	0.01399503	8.37E-05	0
d_Bacteria	p_Caldatribacteriota	c_Caldatribacteriia	o_Caldatribacteriales	f_Caldatribacteriaceae	g_Candidatus_Caldatribacterium	0	0	0.00018755	0	0.000251063	0.000244016
d_Bacteria	p_Firmicutes	c_Desulfibacteriia	o_Desulfibacteriales	f_uncultured	g_uncultured	0.003633255	0.012719298	0.000918997	0.005063529	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptococcales	f_Peptococcaceae	g_uncultured	0.000305316	0.001086048	0.001913014	0.011978996	0.000602551	0
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_M5BL8	g_M5BL8	0	0	0.001669199	0.011721131	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Anaerovoracaceae	g_uncultured	0	6.27E-05	0.011665635	0.002414553	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_uncultured	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SBR1031	f_SBR1031	g_SBR1031	0	0	0	0	0.00033475	0.00054582
d_Bacteria	p_Acidobacteriota	c_Subgroup_22	o_Subgroup_22	f_Subgroup_22	g_Subgroup_22	0	0	0	0	0	0
d_Bacteria	p_Spirochaetota	c_Spirochaetia	o_Spirochaetales	f_Spirochaetaceae	g_Sphaerochaeta	0	0	0.010052702	0.003797646	0.000836876	0.000221833
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_009E01-B-SD-P15	g_009E01-B-SD-P15	0	0	0	0	0.005037994	0.009827192

d	Bacteria	p	Desulfobacterota	c	Syntrophia	o	Syntrophales	f	Smithellaceae	g	Smithella	0	0	0	0	0	0
d	Bacteria	p	Nitrospirota	c	Thermodesulfobionia	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0.003464667	0.009649726
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Selenomonadaceae	g	Propionispira	0	0	0	0	0	0
d	Bacteria	p	Bacteroidia	c	Bacteroidia	o	Bacteroidales	f	Rikenellaceae	g	Bact-08	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	Leptolinea	0	0	0	0	0.000786664	0.000155283
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Ruminococcaceae	g	Anaerofilum	0	0	0	0	0	0
d	Bacteria	p	Armatimonadota	c	Chthonomonadetes	o	Chthonomonadales	f	Chthonomonadales	g	Chthonomonadales	0	0	0	0	0.008569611	0.005168704
d	Bacteria	p	Latescibacterota	c	Latescibacteria	o	Latescibacterales	f	Latescibacteraceae	g	Candidatus Latescibacter	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Aminicenantia	o	Aminicenantales	f	Aminicenantales	g	Aminicenantales	0	0	0	0	0.000485388	0.001264447
d	Bacteria	p	Thermotogota	c	Thermotogae	o	Petrotogales	f	Petrotogaceae	g	AUTHM297	0	0	0	0	0.000368225	0.001685929
d	Bacteria	p	Desulfobacterota	c	Syntrophia	o	Syntrophales	f	Syntrophaceae	g	Syntrophus	0	0	0	0	0.0001339	0
d	Bacteria	p	Firmicutes	c	Thermoanaerobacteria	o	Thermoanaerobacterales	f	SRB2	g	SRB2	0.005404085	0.007790309	0	0	0	0
d	Bacteria	p	Thermotogota	c	Thermotogae	o	Kosmotogales	f	Kosmotogaceae	g	Mesotoga	0	0	0.005926593	0.007759389	0.000719713	0.000288383
d	Bacteria	p	Desulfobacterota	c	Syntrophia	o	Syntrophales	f	uncultured	g	uncultured	0	0	0	0	0.000150638	0.000643315
d	Bacteria	p	Firmicutes	c	Desulfobacteriia	o	Desulfobacteriales	f	Desulfobacteriales	g	Candidatus_Dichloromethanomonas	0	0	0.001369118	0.007571851	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Aeromonadales	f	Aeromonadaceae	g	Aeromonas	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Sporomusaceae	g	uncultured	0	0	0	0	0.007247347	0.001663746
d	Bacteria	p	Caldiseriata	c	Caldiseriata	o	Caldisericales	f	WCHB1-02	g	WCHB1-02	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Syntrophomonadia	o	Syntrophomonadales	f	Syntrophomonadaceae	g	Syntrophomonas	0	0	0	0	0.001154889	8.87E-05
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Acidaminococcales	f	Acidaminococcaceae	g	Acidaminococcus	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	Oscilibacter	0	0	0	0	0	0
d	Bacteria	p	Synergistota	c	Synergistia	o	Synergistales	f	Synergistaceae	g	EBM-39	0	0	0	0	0	0
d	Archaea	p	Halobacterota	c	Methanomicrobia	o	Methanomicrobiales	f	Methanoregulaceae	g	Methanoregula	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Lentisphaeria	o	Victivallales	f	GW2-44-16	g	GW2-44-16	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	NK4A214_group	0	0	0	0	0	0
d	Bacteria	p	Cloacimonadota	c	Cloacimonadia	o	Cloacimonadales	f	PBS-18	g	PBS-18	0	0	0	0	0	4.44E-05
d	Bacteria	p	Desulfobacterota	c	Desulfobionia	o	Desulfobioniales	f	Desulfobionaceae	g	Desulfocurvus	0	0	0.001012772	0.005086971	0	0
d	Bacteria	p	Cloacimonadota	c	Cloacimonadia	o	Cloacimonadales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	RBG-13-54-9	f	RBG-13-54-9	g	RBG-13-54-9	0	0	0	0	0	0
d	Bacteria	p	WPS-2	c	WPS-2	o	WPS-2	f	WPS-2	g	WPS-2	0	0	0.000543024	0	0	0
d	Bacteria	p	Bacteroidia	c	Bacteroidia	o	Bacteroidales	f	Muribaculaceae	g	Muribaculaceae	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Sporomusaceae	g	Pelosinus	0	0	0.000856307	0	0	0
d	Bacteria	p	Desulfobacterota	c	Syntrophorhabdia	o	Syntrophorhabdiales	f	Syntrophorhabdaceae	g	Syntrophorhabdus	0	0	0	0	0.0002678	0.000931698
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Pseudomonadales	f	Moraxellaceae	g	Acinetobacter	0	0	0	0	0	0
d	Archaea	p	Halobacterota	c	Methanomicrobia	o	Methanomicrobiales	f	Methanoregulaceae	g	Methanolinea	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Corynebacteriales	f	Mycobacteriaceae	g	Mycobacterium	0	0	0	0	0	0
d	Bacteria	p	Hydrogenedentes	c	Hydrogenedentia	o	Hydrogenedentiales	f	Hydrogenedentaceae	g	YC-Z55-LKJ63	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Acidaminococcales	f	Acidaminococcaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	WCHB1-81	o	WCHB1-81	f	WCHB1-81	g	WCHB1-81	9.38E-05	0.000140654	0.00020085	0.000354932	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	Flexilinea	0	0	0	0	6.70E-05	0
d	Archaea	p	Euryarchaeota	c	Methanobacteria	o	Methanobacteriales	f	Methanobacteriaceae	g	Methanosphaera	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Microgenomata	o	Candidatus_Woesebacteria	f	Candidatus_Woesebacteria	g	Candidatus_Woesebacteria	0	0	0	0	0	0
d	Bacteria	p	Bacteroidia	c	Kapabacteria	o	Kapabacteriales	f	Kapabacteriales	g	Kapabacteriales	0	0	0	0	0.000301275	0
d	Bacteria	p	Desulfobacterota	c	Syntrophobacteria	o	Syntrophobacteriales	f	Syntrophobacteraceae	g	Syntrophobacter	0	0	0	0	0	0.000266199
d	Archaea	p	Euryarchaeota	c	Methanobacteria	o	Methanobacteriales	f	Methanobacteriaceae	g	Methanobrevibacter	0	0	0	0	0	0
d	Bacteria	p	Caldiseriata	c	Caldiseriata	o	Caldisericales	f	LF045	g	LF045	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Desulfotomaculia	o	Desulfotomaculales	f	Desulfotomaculales	g	Pelotomaculum	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Micrococcales	f	Microbacteriaceae	g	Galbitalea	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	Anaerolineaceae	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Eubacteriales	f	Anaerofustaceae	g	Anaerofustis	0	0	0	0	0.003079704	0.000421482
d	Bacteria	p	Bacteroidia	c	SJA-28	o	SJA-28	f	SJA-28	g	SJA-28	0	0	0	0	0.001924815	6.65E-05
d	Bacteria	p	SAR324_clade(Mar	c	SAR324_clade(Marine_group	o	SAR324_clade(Marine_group_B)	f	SAR324_clade(Marine_group_B)	g	SAR324_clade(Marine_group_B)	0	0	0	0	0	0
d	Bacteria	p	Synergistota	c	Synergistia	o	Synergistales	f	Synergistaceae	g	uncultured	0.002869966	0.001315789	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Thermoleophilina	o	Gaiellales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridia	f	Hungateiclostridiaceae	g	Ruminiclostridium	0	0	0.000125313	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	Pelolinea	0	0	0	0	0.002644529	0.001020431
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridiales	f	Clostridiaceae	g	Proteiniclasticum	0.000366379	0.000355054	0	0	0.000351488	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcaceae	g	Romboutsia	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Acidobacteriata	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Syntrophomonadia	o	Syntrophomonadales	f	Syntrophomonadaceae	g	uncultured	0	0	0.000525141	0.000117211	0.00162354	0.000155283
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Christensenellales	f	Christensenellaceae	g	uncultured	0	0	0	0	0	0.000110916
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobia	o	Pedospaerales	f	Pedospaeraceae	g	ADurb_Bin063-1	0	0	0	0	0	0
d	Bacteria	p	Bacteroidia	c	Bacteroidia	o	Bacteroidales	f	Prolixibacteraceae	g	Meniscus	0	0	0	0	0	0
d	Bacteria	p	Zixibacteria	c	Zixibacteria	o	Zixibacteria	f	Zixibacteria	g	Zixibacteria	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	Intestinomonas	0	0.00234438	0.001218998	0	0	0.0001331
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridia UCG-014	f	Clostridia UCG-014	g	Clostridia UCG-014	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Hyphomicrobiaceae	g	Hyphomicrobium	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcales-Tissierellales	g	uncultured	0	0.00223185	0.000609499	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Sporomusaceae	g	Anaeromusa-Anaeromarcus	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Lachnospirales	f	Lachnospiraceae	g	Anaerostignum	0	0.002192982	0	0.000843921	0.000117163	4.44E-05
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Rhizobiales Incertae Sedis	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobia	o	Pedospaerales	f	Pedospaeraceae	g	Pedospaeraceae	0	0	0	0	0	0
d	Bacteria	p	Spirochaetota	c	Brachyspirae	o	Brachyspirales	f	Brachyspirales Incertae Sedis	g	Exilispira	0	0	0	0	0	0
d	Bacteria	p	Bacteroidia	c	Bacteroidia	o	Bacteroidales	f	Rikenellaceae	g	Alistipes	0	0.000206305	0.002133246	0	0	0.0001331
d	Bacteria	p	Campylobacterota	c	Campylobacteria	o	Campylobacteriales	f	Arcobacteraceae	g	Pseudarcobacter	0	0	0	0	0	0
d	Bacteria	p	Fermentibacterota	c	Fermentibacteria	o	Fermentibacterales	f	Fermentibacteraceae	g	Fermentibacteraceae	0	0	0	0	0	0
d	Bacteria	p	Thermotogota	c	Thermotogae	o	Petrotogales	f	Petrotogaceae	g	SC103	0	0	0	0	0	0
d	Bacteria	p	Bacteroidia	c	Bacteroidia	o	Bacteroidales	f	Dysgonomonadaceae	g	Fermentimonas	0	0	9.38E-05	0	0	0

d_Bacteria	p_Acidobacteriota	c_c5LKS83	o_c5LKS83	f_c5LKS83	g_c5LKS83	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Adurb.Bin180	f_Adurb.Bin180	g_Adurb.Bin180	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_Candidatus_Soleaeferrea	0	0	0	0	0	0
d_Archaea	p_Halobacterota	c_Methanomicrobia	o_Methanomicrobiales	f_Methanomicrobiaceae	g_Methanococcus	0	0	0.001650444	0.000351634	0	0
d_Bacteria	p_Elusimicrobiota	c_Endomicrobia	o_Endomicrobiales	f_Endomicrobiaceae	g_Endomicrobium	0.00037594	0	0	0	0.001238577	0.000510215
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_Bellilinea	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_D8A-2	o_D8A-2	f_D8A-2	g_D8A-2	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Hungateiclostridiaceae	g_HN-HF0106	0	0	0	0.000117211	0	0
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Aminomonas	0	0	0	0	0	0
d_Bacteria	p_Plantomycetota	c_Plantomycetes	o_Pirellulales	f_Pirellulaceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Rhodobacter	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium_sensu_stricto_1	0	0	0	0	0	0
d_Bacteria	p_Calditrichota	c_Calditrichia	o_Calditrichales	f_Calditrichaceae	g_Calditrichaceae	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Ignavibacteria	o_Ignavibacteriales	f_BSV40	g_BSV40	0	0	0	0	0	0
d_Bacteria	p_Patescibacteria	c_Berkelbacteria	o_Berkelbacteria	f_Berkelbacteria	g_Berkelbacteria	0	0	0	0	0	0
d_Bacteria	p_Firmicutes					0.00137392	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Actinobacteria	o_Micrococcales	f_Intrasporangiaceae	g_Ornithinibacter	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Acidovorax	0	0	0	0	0	0
d_Bacteria	p_Spirochaetota	c_V2072-189E03	o_V2072-189E03	f_V2072-189E03	g_V2072-189E03	0	0	0	0	0	0
d_Bacteria	p_Hydrogenedentes	c_Hydrogenedentia	o_Hydrogenedentiales	f_Hydrogenedensaceae	g_Hydrogenedensaceae	0	0.000206305	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_uncultured	f_uncultured	g_uncultured	0	0	0	0	0	0
d_Bacteria						0.000213721	8.35E-05	0	0	0.001322264	0.000754231
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia_vadinBB60_group	f_Clostridia_vadinBB60_group	g_Clostridia_vadinBB60_group	0	0	0	0	0	0
d_Bacteria	p_Patescibacteria					0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Thermotogota	c_Thermotogae	o_Thermotogales	f_Fervidobacteriaceae	g_Fervidobacterium	0	0	0	0	0	0.000399299
d_Bacteria	p_uncultured	c_uncultured	o_uncultured	f_uncultured	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Flavobacteriales	f_Flavobacteriaceae	g_Flavobacterium	0	0	0	0	0	0
d_Bacteria	p_Spirochaetota	c_Leptospirae	o_Leptospirales	f_Leptospiraceae	g_RBG-16-49-21	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Comamonadaceae	0	0	0	0	0	0
d_Bacteria	p_Latescibacterota	c_Latescibacterota	o_Latescibacterota	f_Latescibacterota	g_Latescibacterota	0	0	0	0	0	0
d_Bacteria	p_Patescibacteria	c_WWE3	o_WWE3	f_WWE3	g_WWE3	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Xanthobacteraceae	g_Xanthobacteraceae	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales	f_Anaerovoracaceae	g_[Eubacterium]_brachy_group	0	0	0	0	0.000251063	0.000110916
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Thioclava	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Tannerellaceae	g_Macellibacteroides	0	8.35E-05	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Hungateiclostridiaceae	g_Ercella	0	0	0.00018755	0	0	0
d_Bacteria	p_Acidobacteriota	c_Acidobacteriae	o_TSBb06	f_TSBb06	g_TSBb06	0	0	0	0	0.001121414	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Prevotellaceae	g_Prevotellaceae_UCG-004	0	0	0	0	0	0
d_Bacteria	p_Plantomycetota	c_Phycisphaerae	o_Phycisphaerales	f_AKAU3564_sediment_group	g_AKAU3564_sediment_group	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospiraceae	g_Oscillospiraceae	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Lautropia	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Bacilli	o_Acholeplasmatales	f_Acholeplasmataceae	g_Acholeplasma	0	0.000271512	0	0	0	0
d_Bacteria	p_Desulfobacterota	c_Syntrophobacteria	o_Syntrophobacteriales	f_Syntrophobacteraceae	g_Syntrophobacteraceae	0	0	0	0	0.001054464	0.000421482
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_SHA-4	g_SHA-4	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_Rikenellaceae	0	0.001002506	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_Anaerolinea	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Defluviimonas	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Chloroflexia	o_Thermomicrobiales	f_JG30-KF-CM45	g_JG30-KF-CM45	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Rhodoferrax	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Rhodocyclaceae	g_Dechlorobacter	0	0.000918964	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SJA-15	f_SJA-15	g_SJA-15	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Xanthobacteraceae	g_Bradyrhizobium	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Anaerolineales	f_Anaerolineaceae	g_Levilinea	0	0	0	0	0.000736451	0
d_Bacteria	p_Plantomycetota	c_Plantomycetes	o_Pirellulales	f_Pirellulaceae	g_Pir4_lineage	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Beijerinckiaceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Patescibacteria	c_Microgenomata	o_Candidatus_Pacebacteria	f_Candidatus_Pacebacteria	g_Candidatus_Pacebacteria	0	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Actinobacteria	o_Corynebacteriales	f_Nocardiaceae	g_Rhodococcus	0	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Actinobacteria	o_Micrococcales	f_Microbacteriaceae	g_Microbacterium	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Bacilli	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Turicibacter	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_[Eubacterium]_coprostanoligenes_group	g_[Eubacterium]_coprostanoligenes_group	0	0	0	0	0	0
d_Archaea	p_Thermoplasmata	c_Thermoplasmata	o_Methanomassiliococcales	f_Methanomassiliococaceae	g_uncultured	0	0	0	0	0.000167375	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Oscillospirales	g_Hydrogenoanaerobacterium	0	0.000730994	0	0	0.000164096	0
d_Bacteria	p_Cyanobacteria	c_Vampirivibrionia	o_Obscuribacteriales	f_Obscuribacteraceae	g_Candidatus_Obscuribacter	0	0	0	0	0	0
d_Bacteria	p_Sumerlaeota	c_Sumerlaeota	o_uncultured	f_uncultured	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Cloacimonadota	c_Cloacimonadia	o_Cloacimonadales	f_Cloacimonadaceae	g_Cloacimonadaceae	0.000710109	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Thermoleptophila	o_Solirubrobacteriales	f_67-14	g_67-14	0	0	0	0	0	0
d_Bacteria	p_Synergistota	c_Synergistia	o_Synergistales	f_Synergistaceae	g_Aminivibrio	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Hungateiclostridiaceae	g_Fastidiosipila	0	0	0.000675181	0.000586057	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Oscillospirales	f_Ruminococcaceae	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Verrucomicrobiota	c_Omnitrophia	o_Omnitrophales	f_Omnitrophaceae	g_Candidatus_Omnitrophus	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Paludibacteraceae	g_Paludibacter	0	0.000647452	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridia	f_Gracilibacteraceae	g_Gracilibacteraceae	0	0	0	0	0	0
d_Bacteria	p_Spirochaetota	c_Spirochaetia	o_Spirochaetales	f_Spirochaetaceae	g_Treponema	0	0	0	0	0	0
d_Bacteria	p_Actinobacteriota	c_Acidimicrobia	o_Microtrichiales	f_Illumatobacteraceae	g_CL500-29_marine_group	0	0	0	0	0	0
d_Bacteria	p_Plantomycetota	c_Pla3_lineage	o_Pla3_lineage	f_Pla3_lineage	g_Pla3_lineage	0	0	0	0	0	0
d_Bacteria	p_Desulfobacterota	c_Desulfobulbia	o_Desulfobulbales	f_Desulfobulbaceae	g_Desulfobulbus	0	0.000605681	0	0	0	0
d_Bacteria	p_Spirochaetota	c_Spirochaetia	o_Spirochaetales	f_Spirochaetaceae	g_Spirochaeta	0	0	0	0	0.00033475	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Devosiaceae	g_Devosia	0	0	0	0	0	0

d	Bacteria	p	Acidobacteriota	c	Acidobacteriae	o	Acidobacteriae	f	Acidobacteriae	g	Paludibaculum	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Novosphingobium	0	0	0	0	0	0
d	Archaea	p	Halobacterota	c	Methanomicrobia	o	Methanomicrobiales	f	Methanomicrobiaceae	g	Methanofollis	0	0.00011253	0	0	0	0
d	Bacteria	p	Nitrospirota	c	4-29-1	o	4-29-1	f	4-29-1	g	4-29-1	0	0	0	0.000552338	8.87E-05	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Caulobacterales	f	Hyphomonadaceae	g	Hirschia	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Vicinamibacteria	o	Vicinamibacterales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Dysgonomonadaceae	g	Dysgonomonadaceae	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	LD1-PA32	f	LD1-PA32	g	LD1-PA32	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcaceae	g	Acetanaerobium	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	UCG-002	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Phycisphaerae	o	Pla1_lineage	f	Pla1_lineage	g	Pla1_lineage	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Caulobacterales	f	Hyphomonadaceae	g	SW802	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhodobacteriales	f	Rhodobacteraceae	g	Amaricoccus	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Hyphomicrobiaceae	g	Pedomicrobium	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcaceae	g	Intestinibacter	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Kiritimatiellae	o	WCHB1-41	f	WCHB1-41	g	WCHB1-41	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Chitinophagales	f	Saprosiraceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Phycisphaerae	o	mle1-8	f	mle1-8	g	mle1-8	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Planctomycetales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Rhizobiaceae	g	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.000183189	0	0	0	0	0
d	Bacteria	p	Caldatibacteriota	c	JS1	o	JS1	f	JS1	g	JS1	0	0	7.50E-05	0.000421961	0	0
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobiae	o	Pedospaerales	f	Pedospaeraceae	g	DEV114	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	uncultured	g	uncultured	0.000417711	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae	g	Thauera	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	Chlamydiales	f	Parachlamydiaceae	g	Neochlamydia	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Sutterellaceae	g	AA99	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Enterobacteriales	f	Enterobacteriaceae	g	Escherichia-Shigella	0	0	0	0	0	0
d	Archaea	p	Halobacterota	c	Methanomicrobia	o	Methanomicrobiales	f	Methanospirillaceae	g	Methanospirillum	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Lentisphaeria	o	Victivallales	f	Victivallaceae	g	Victivallaceae	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Pleomorphomonadaceae	g	Pleomorphomonas	0	0	0	0	0	0
d	Bacteria	p	Sumerlaeota	c	Sumerlaeae	o	Sumerlaeae	f	Sumerlaeae	g	Sumerlaeae	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Marinilabiliaceae	g	[Cytophaga] xylanolytica_group	0.000396825	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	SB-5	g	SB-5	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Planctomycetales	f	Rubinisphaeraceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Lachnospirales	f	Lachnospiraceae	g	Lachnospiraceae_XPB1014_group	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Sporomusaceae	g	Sporomusa	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	Candidatus_Colwellbacteria	f	Candidatus_Colwellbacteria	g	Candidatus_Colwellbacteria	0	0	0	0	0	0
d	Bacteria	p	Caldisericata	c	Caldisericia	o	Caldisericales	f	TTA-B1	g	TTA-B1	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Xanthobacteraceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhodobacteriales	f	Rhodobacteraceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Barnesiellaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Bacilli	o	Izemoplasmatales	f	Izemoplasmataceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Devosiaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae	g	Dechloromonas	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Legionellales	f	Legionellaceae	g	Legionella	0	0	0	0	0	0
d	Bacteria	p	Armatimonadota	c	Fimbrimonadia	o	Fimbrimonadales	f	Fimbrimonadaceae	g	Fimbrimonadaceae	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Rikenellaceae	g	Rikenellaceae_RC9_gut_group	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Negativicutes	o	Veillonellales-Selenomonadales	f	Veillonellaceae	g	Megasphaera	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Bacilli	o	Lactobacillales	f	Carnobacteriaceae	g	Trichococcus	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	UCG-010	g	UCG-010	0	0	0	8.37E-05	0.000310566	0
d	Bacteria	p	Patescibacteria	c	Saccharimonadia	o	Saccharimonadales	f	Saccharimonadaceae	g	Saccharimonadales	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Comamonadaceae	g	Rhizobacter	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Caldilineales	f	Caldilineaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Desulfobacterota	c	uncultured	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Ruminococcaceae	g	Caproiciproducens	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Dehalococcoidia	o	FS117-23B-02	f	FS117-23B-02	g	FS117-23B-02	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Monoglobales	f	Monoglobaceae	g	Monoglobus	0	4.18E-05	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Planctomycetales	f	Rubinisphaeraceae	g	SH-PL14	0	0	0	0	0	0
d	Bacteria	p	Bdellovibrionota	c	Oligoflexia	o	O319-6G20	f	O319-6G20	g	O319-6G20	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	Chlamydiales	f	Parachlamydiaceae	g	Candidatus_Proteochlamydia	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Micropepsales	f	Micropepsaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	WS4	c	WS4	o	WS4	f	WS4	g	WS4	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	PeM15	f	PeM15	g	PeM15	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Chitinophagales	f	Chitinophagaceae	g	Ferruginibacter	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	Sporobacter	0	0	0	0.0002678	0.000266199	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	MSB-5E12	f	MSB-5E12	g	MSB-5E12	0	0	0	0.00020085	0.000266199	0
d	Bacteria	p	Acidobacteriota	c	Holophagae	o	Holophagales	f	Holophagaceae	g	Holophaga	0	0	0	0	0	0
d	Bacteria	p	Campylobacterota	c	Campylobacteria	o	Campylobacteriales	f	Arcobacteraceae	g	Arcobacter	0	0	0	0	0	0
d	Bacteria	p	Synergistota	c	Synergistia	o	Synergistales	f	Synergistaceae	g	Cloacibacillus	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Acidimicrobia	o	IMCC26256	f	IMCC26256	g	IMCC26256	0	0	0	0	0	0
d	Bacteria	p	Marinimicrobia (S)	c	Marinimicrobia (SAR406)	o	Marinimicrobia (SAR406 clade)	f	Marinimicrobia (SAR406 clade)	g	Marinimicrobia (SAR406 clade)	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Hyphomicrobiaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	ADurb.Bin120	0	0.00018755	0.000257865	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Rhizobiaceae	g	Mesorhizobium	0	0.00018797	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhodobacteriales	f	Rhodobacteraceae	g	Paracoccus	0	0	0	0	0	0
d	Bacteria	p	Fibrobacterota	c	Fibrobacteria	o	Fibrobacterales	f	Fibrobacteraceae	g	Fibrobacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Rhizobiaceae	g	uncultured	0	0	0	0	0	0

d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Xanthobacteraceae	g	Pseudorhodoplanes	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Christensenellales	f	Christensenellaceae			0	0	0	0	0	0
d	Bacteria	p	Caldiseriata	c	Caldiseriata	o	Caldiseriales	f	Caldiseriaceae	g	Caldisericum	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Syntrophomonadia	o	Syntrophomonadales	f	Syntrophomonadaceae	g	Pelospira	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	Candidatus_Nomurabacteria	f	Candidatus_Nomurabacteria	g	Candidatus_Nomurabacteria	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Pla4_lineage	o	Pla4_lineage	f	Pla4_lineage	g	Pla4_lineage	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Corynebacteriales	f	Nocardiaceae	g	Gordonia	0	0	0	0	0	0
d	Archaea	p	Euryarchaeota	c	Thermococci	o	Methanofastidiosales	f	Methanofastidiosaceae	g	Candidatus_Methanofastidiosum	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	Anaerolineae	o	Anaerolineales	f	Anaerolineaceae	g	Anaerolineaceae_UCG-001	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobiae	o	LD1-PB3	f	LD1-PB3	g	LD1-PB3	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Sphingopyxis	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Ignavibacteria	o	Ignavibacteriales	f	SR-FBR-L83	g	SR-FBR-L83	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae	g	Azospira	0.000213721	0.00018797	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Hyphomicrobiaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	SC1-84	g	SC1-84	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Propionibacteriales	f	Propionibacteriaceae	g	Brooklawnia	0	0	0	0	0	0
d	Bacteria	p	Campilobacterota	c	Campylobacteria	o	Campylobacterales	f	Sulfurimonadaceae	g	Sulfuricum	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridiales	f	Clostridiaceae	g	Youngiibacter	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	ABY1	o	Candidatus_Kerfeldbacteria	f	Candidatus_Kerfeldbacteria	g	Candidatus_Kerfeldbacteria	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Pirellulales	f	Pirellulaceae	g	Pirellula	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales					0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Microgenomata	o	Candidatus_Collierbacteria	f	Candidatus_Collierbacteria	g	Candidatus_Collierbacteria	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Phycisphaerae	o	CCM11a	f	CCM11a	g	CCM11a	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Isosphaerales	f	Isosphaeraeae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Ignavibacteria	o	Ignavibacteriales	f	Meliobacteraceae	g	IheB3-7	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridia	f	Hungateiclostridiaceae	g	Saccharofermentans	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Dongiales	f	Dongiaceae	g	Dongia	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae	g	Ferribacterium	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Holophagae	o	Holophagales	f	Holophagaceae			0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Acidimicrobia	o	Microtrichales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Desulfobacterota	c	Desulfuromonadia	o	Geobacterales	f	Geobacteraceae	g	Geobacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Bejerinckiaceae	g	Bosea	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Methyloligellaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Sphingosinicella	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Celvibrionales	f	Spongibacteraceae	g	BD1-7 clade	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia						0	0	0	0	0	0	
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Micrococcales	f	Microbacteriaceae	g	Parafrirogibacterium	0	0	0	0	0	0
d	Bacteria	p	Dependentiae	c	Babeliae	o	Babeliales	f	Babeliales	g	Babeliales	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridiales	f	Clostridiaceae	g	Sarcina	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Microgenomata	o	Candidatus_Shapirobacteria	f	Candidatus_Shapirobacteria	g	Candidatus_Shapirobacteria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae			0.000104428	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Limnochordia	o	Limnochordales	f	Limnochordaceae	g	Limnochordaceae	0	0	0.000164096	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcaceae	g	Peptoclostridium	0	0	0	0	0	0
d	Archaea	p	Crenarchaeota	c	Bathyrarchaeia	o	Bathyrarchaeia	f	Bathyrarchaeia	g	Bathyrarchaeia	0	0	0	0	0	0
d	Archaea	p	Euryarchaeota	c	Thermococci	o	Methanofastidiosales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Frankiales	f	Sporichthyaceae	g	Longivirga	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Micrococcales	f	Dermatophilaceae	g	Kineosphaera	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Bacteroidales_UCG-001	g	Bacteroidales_UCG-001	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Comamonadaceae	g	Sphaerotilus	0	0	0	0	0	0
d	Bacteria	p	Spirochaetota	c	MVP-15	o	MVP-15	f	MVP-15	g	MVP-15	0	0	0	0	0	0
d	Bacteria	p	Desulfobacterota	c	Desulfuromonadia	o	Desulfuromonadia	f	Desulfuromonadaceae	g		0.00015004	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Xanthomonadales	f	Xanthomonadaceae	g	Arenimonas	0	0	0	0	0	0
d	Bacteria	p	Methylomirabilota	c	Methylomirabilia	o	Methylomirabiales	f	Methylomirabilaceae	g	Sh7658-TzT-35	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Pirellulales	f	Pirellulaceae	g	Pir3_lineage	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Labraceae	g	Labrys	0	0	0	0	0	0
Unassigned														0.000140654	0	0	
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Micrococcales	f	Intrasporangiaceae	g	Tetrasphaera	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Lachnospirales	f	Lachnospiraceae	g		0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Phycisphaerae	o	MSB9	f	SG8-4	g	SG8-4	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Xanthobacteraceae	g	Alfia	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	Chlamydiales	f	Criblamydiaceae	g	Criblamydiaceae	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	M2PB4-65 termite group	g	M2PB4-65 termite group	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Desulfitobacteria	o	Desulfitobacteriales	f	Syntrophobotulaceae	g	Dehalobacter	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	Chlamydiales	f	Parachlamydiaceae			0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridiales	f	Clostridiaceae	g		0.000122126	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	Candidatus_Vogelbacteria	f	Candidatus_Vogelbacteria	g	Candidatus_Vogelbacteria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Rhodocyceae	g	Sulfuritalea	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Frankiales	f	Nakamurellaceae	g	Nakamurella	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Micrococcales	f	Microbacteriaceae	g	Leucobacter	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Ignavibacteria	o	Ignavibacteriales				0	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Caulobacterales	f	Hyphomonadaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Reyranelles	f	Reyranelleae	g	Reyranelle	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rickettsiales	f	Mitochondria	g	Mitochondria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Sphingobium	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Gammaproteobacteria_Incertae_Sedis	f	Unknown_Family	g	Acidibacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	R7C24	f	R7C24	g	R7C24	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Propionibacteriales	f	Propionibacteriaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Campilobacterota	c	Campylobacteria	o	Campylobacterales	f	Sulfurovum	g	Sulfurovum	0	0	0	0	0	0

d	Bacteria	p	Patescibacteria	c	Saccharimonadia	o	Saccharimonadales	f	LWQ8	g	LWQ8	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Acidobacteriae	o	GOUTB8	f	GOUTB8	g	GOUTB8	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Blastocatellia	o	DS-100	f	DS-100	g	DS-100	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Oscillospiraceae	g	Papillibacter	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	32-520	f	32-520	g	32-520	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Sphingomonas	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Comamonadaceae	g	Ottowia	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Lentisphaeria	o	Victivallales	f	vadinBE97	g	vadinBE97	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Prolibacteraceae	g	Mariniphaga	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Peptostreptococcales-Tissierellales	f	Peptostreptococcales-Tissierellales	g	W5053	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Caulobacterales	f	Hyphomonadaceae	g	Unknown Family	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Gammaproteobacteria Incertae Sed	f	Unknown Family	g	Candidatus Berkiella	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Acidobacteriae	o	Solibacterales	f	Solibacteraceae	g	Candidatus Solibacter	0	0	0	0.000100425	0	0
d	Bacteria	p	Desulfobacterota	c	Desulfobacterota	o	Desulfobacteriales	f	Desulfobacteriaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Propionibacteriales	f	Propionibacteriaceae	g	Propionicimonas	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	KD4-96	o	KD4-96	f	KD4-96	g	KD4-96	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	A0839	g	A0839	0	0	0	0	0	0
d	Bacteria	p	Sva0485	c	Sva0485	o	Sva0485	f	Sva0485	g	Sva0485	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Thermoanaerobaculia	o	Thermoanaerobaculales	f	Thermoanaerobaculaceae	g	Thermoanaerobaculum	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Acidimicrobia	o	Microtrichales	f	Jamiaceae	g	Jamia	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Acidimicrobia	o	Microtrichales	f	Microtrichaceae	g	IMC26207	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	ABY1	o	Candidatus_Falkowbacteria	f	Candidatus_Falkowbacteria	g	Candidatus_Falkowbacteria	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	Parcubacteria	f	Parcubacteria	g	Parcubacteria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	PLTA13	f	PLTA13	g	PLTA13	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Sphingobacteriales	f	AKYH767	g	AKYH767	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	SHA-26	o	SHA-26	f	SHA-26	g	SHA-26	0	0	0	0	0	0
d	Bacteria	p	Deinococota	c	Deinococci	o	Deinococcales	f	Deinococcaceae	g	Deinococcus	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	ABY1	o	Candidatus_Magasanikbacteria	f	Candidatus_Magasanikbacteria	g	Candidatus_Magasanikbacteria	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Parcubacteria	o	Parcubacteria	f	Parcubacteria	g	Parcubacteria	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Pirellulales	f	Pirellulaceae	g	Blastopirellula	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Planctomycetales	f	Schlesneriaceae	g	Planctopirius	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	Planctomycetales	f	Schlesneriaceae	g	Schlesneria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Holosporales	f	Holosporaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Nitrosomonadaceae	g	Ellin6067	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Methylococcales	f	Methylococcaceae	g	Methyloparacoccus	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobiae	o	Opitutales	f	Opitutaceae	g	Lacunisphaera	0	0	0	0	0	0
d	Bacteria	p	Cyanobacteria	c	Vampirivibronia	o	Obscuribacteriales	f	Obscuribacteraceae	g	Obscuribacteraceae	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Lentisphaeria	o	Oligosphaerales	f	Lenti-02	g	Lenti-02	0	0	0	0	0	0
d	Bacteria	p	Bdellovibrionota	c	Bdellovibrionia	o	Bdellovibrionales	f	Bdellovibrionaceae	g	Bdellovibrionia	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	BRH-c20a	o	BRH-c20a	f	BRH-c20a	g	BRH-c20a	0	0	0	0	0	0
d	Bacteria	p	Gemmatimonadota	c	MD2902-B12	o	MD2902-B12	f	MD2902-B12	g	MD2902-B12	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Thermoleophila	o	Gaiellales	f	Gaiellaceae	g	Gaiella	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Kryptonia	o	Kryptoniales	f	BSV26	g	BSV26	0	0	0	0	0	0
d	Bacteria	p	Dependentiae	c	Babeliae	o	Babeliales	f	Vermiphilaceae	g	Vermiphilaceae	0	0	0	0	0	0
d	Bacteria	p	NB1-j	c	NB1-j	o	NB1-j	f	NB1-j	g	NB1-j	0	0	0	0	0	0
d	Bacteria	p	Planctomycetota	c	Planctomycetes	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Sphingomonadales	f	Sphingomonadaceae	g	Polymorphobacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Competibacterales	f	Competibacteraceae	g	Candidatus Competibacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Diplorickeetsiales	f	Diplorickeetsiaceae	g	Rickettsiella	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Holophagae	o	Subgroup_7	f	Subgroup_7	g	Subgroup_7	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Actinobacteria	o	Propionibacteriales	f	Propionibacteriaceae	g	Propioniciclava	0	0	0	0	0	0
d	Bacteria	p	Bdellovibrionota	c	Bdellovibrionia	o	Bacteriovoracales	f	Bacteriovoracaceae	g	Peredibacter	0	0	0	0	0	0
d	Bacteria	p	Myxococota	c	Polyangia	o	Polyangiales	f	Polyangiaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhizobiales	f	Bejerinckiaceae	g	Bejerinckiaceae	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Rhodobacterales	f	Rhodobacteraceae	g	Roseobacter_clade_CHAB-I-5_lineage	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Aquaspirillaceae	g	Rivicola	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Xanthomonadales	f	Xanthomonadaceae	g	Pseudoxanthomonas	0	0	0	0	0	0
d	Bacteria	p	Chloroflexi	c	OLB14	o	OLB14	f	OLB14	g	OLB14	0	0	0	0	0	0
d	Bacteria	p	Patescibacteria	c	Microgenomata	o	Candidatus_Levybacteria	f	Candidatus_Levybacteria	g	Candidatus_Levybacteria	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Azospirillales	f	Inquilinaceae	g	Inquilinus	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Caulobacterales	f	Caulobacteraceae	g	Caulobacter	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Burkholderiales	f	Nitrosomonadaceae	g	Nitrosomonas	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Coxiellales	f	Coxiellaceae	g	Coxiella	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	uncultured	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Acidobacteriota	c	Subgroup_18	o	Subgroup_18	f	Subgroup_18	g	Subgroup_18	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	p-251-o5	g	p-251-o5	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Chitinophagales	f	uncultured	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Diplorickeetsiales	f	Diplorickeetsiaceae	g	uncultured	0	0	0	0	0	0
d	Archaea	p	Halobacterota	c	Methanomicrobia	o	Methanomicrobiales	f	Methanocorpusculaceae	g	Methanocorpusculum	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Oscillospirales	f	Ethanoliengenaceae	g	Acetanaerobacterium	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Alphaproteobacteria	o	Acetobacterales	f	Acetobacteraceae	g	Roseomonas	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Chlamydiae	o	Chlamydiales	f	cvE6	g	cvE6	0	0	0	0	0	0
d	Bacteria	p	Verrucomicrobiota	c	Verrucomicrobiae	o	Chthoniobacteriales	f	Terrimicrobiaceae	g	Terrimicrobium	0	0	0	0	0	0
d	Bacteria	p	Actinobacteriota	c	Thermoleophila	o	Solirubrobacteriales	f	Solirubrobacteraceae	g	Conexibacter	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Bacteroidales	f	Dysgonomonadaceae	g	uncultured	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Sphingobacteriales	f	S15A-MN91	g	S15A-MN91	0	0	0	0	0	0
d	Bacteria	p	Firmicutes	c	Clostridia	o	Clostridiales	f	Clostridiaceae	g	Clostridium_sensu_stricto_12	0	0	0	0	0	0
d	Bacteria	p	Proteobacteria	c	Gammaproteobacteria	o	Nitrosococcales	f	Nitrosococcaceae	g	CI75cm.2.12	0	0	0	0	0	0
d	Bacteria	p	Bacteroidota	c	Bacteroidia	o	Flavobacteriales	f	NS9_marine_group	g	NS9_marine_group	0	0	0	0	0	0

d_Bacteria	p_Fibrobacterota	c_Fibrobacteria	o_Fibrobacterales	f_Fibrobacterales	g_BBMC-4	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Peptostreptococcales-Tissierellales			0	0	0	0	0	0
d_Bacteria	p_Myxococcota	c_Polyangia	o_Haliangiales	f_Haliangiaceae	g_Haliangium	0	0	0	0	0	0
d_Bacteria	p_Patescibacteria	c_Microgenomatia	o_Microgenomatia	f_Microgenomatia	g_Microgenomatia	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Rhizobiales_Incertae_Sedis	g_Bauldia	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria				0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Prolixibacteraceae	g_Roseimarinus	0	0	0	0	0	0
d_Bacteria	p_Bacteroidota	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_SP3-e08	0	0	0	0	0	0
d_Bacteria	p_Bdellovibrionota	c_Oligoflexia	o_Oligoflexales	f_uncultured	g_uncultured	0	0	0	0	0	0
d_Bacteria	p_Calditrichota	c_Calditrichia	o_Calditrichales	f_Calditrichaceae	g_SM23-31	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Dehalococcoidia	o_Dehalococcoidales	f_Dehalococcoidaceae	g_Dehalogenimonas	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Clostridia	o_Lachnospirales	f_Lachnospiraceae	g_Epulopiscium	0	0	0	0	0	0
d_Bacteria	p_MBNT15	c_MBNT15	o_MBNT15	f_MBNT15	g_MBNT15	0	0	0	0	0	0
d_Bacteria	p_Myxococcota	c_bacteriap25	o_bacteriap25	f_bacteriap25	g_bacteriap25	0	0	0	0	0	0
d_Bacteria	p_Planctomycetota	c_Planctomycetes	o_Pirellulales	f_Pirellulaceae	g_Pir2_lineage	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae		0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales			0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Rhodanobacteraceae	g_Chiayivirga	0	0	0	0	0	0
d_Bacteria	p_Chloroflexi	c_Anaerolineae				0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Bacilli	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Erysipelothrix	0	0	0	0	0	0
d_Bacteria	p_Firmicutes	c_Negativicutes	o_Veillonellales-Selenomonadales	f_Veillonellaceae	g_Veillonella	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Burkholderiales	f_Hydrogenophilaceae	g_Thiobacillus	0	0	0	0	0	0
d_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Gammaproteobacteria_Incertae_Sedis	f_Unknown Family	g_Unknown Family	0	0	0	0	0	0
d_Bacteria	p_Verrucomicrobiota	c_Verrucomicrobiae	o_Pedosphaerales	f_Pedosphaeraceae		0	0	0	0	0	0