

Landfill Leachate – 2021-06-24

Sample Overview

Site	Landfill Leachate
Date sampled	2021-06-24
Report type	Standard WW

qPCR Results

Test	Copy no.	%
bacF (Total Bacteria 1)	318327	100.0%
thau1 (Thauera Group 1)	5623	1.8%
thau2 (Thauera Group 2)	19474	6.1%

Bacteria

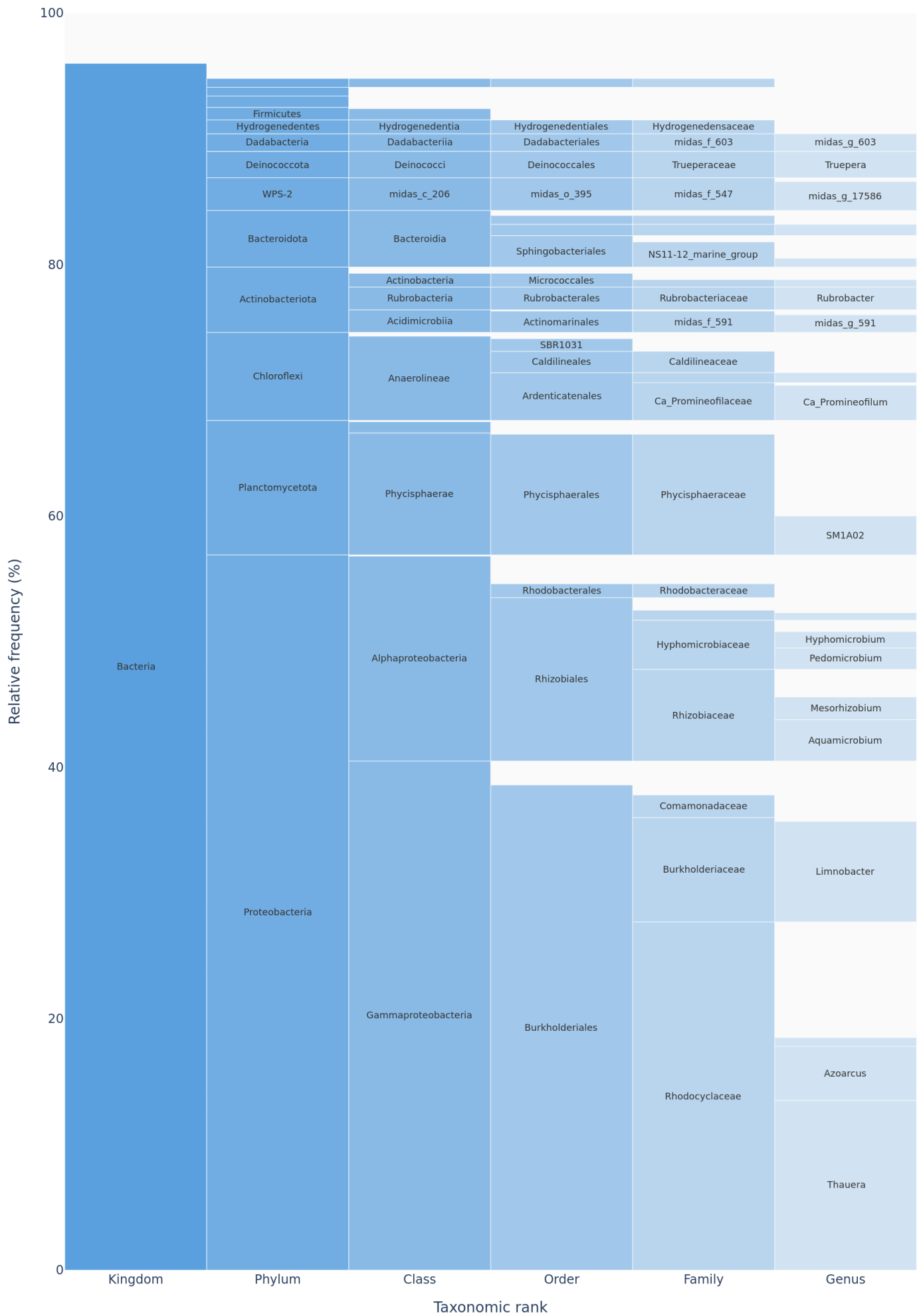
Kingdom	Phylum	Class	Order	Family	Genus	Rel. freq. %
Bacteria	—	—	—	—	—	0.4%
Bacteria	Abditibacteriota	Abditibacteria	Abditibacteriales	Abditibacteriaceae	Abditibacterium	0.1%
Bacteria	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	0.2%
Bacteria	Acidobacteriota	Acidobacteriae	Paludibaculum	midas_f_675	midas_g_42266	0.1%
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	—	0.4%
Bacteria	Actinobacteriota	—	—	—	—	0.5%
Bacteria	Actinobacteriota	Acidimicrobiia	Actinomarinales	midas_f_591	—	0.1%
Bacteria	Actinobacteriota	Acidimicrobiia	Actinomarinales	midas_f_591	midas_g_4688	0.2%
Bacteria	Actinobacteriota	Acidimicrobiia	Actinomarinales	midas_f_591	midas_g_591	1.4%
Bacteria	Actinobacteriota	Acidimicrobiia	IMCC26256	midas_f_2	—	0.1%
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Intrasporangiaceae	Tetrasphaera	0.6%
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	—	0.3%
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Galbitalea	0.1%
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Leucobacter	0.1%
Bacteria	Actinobacteriota	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	1.8%
Bacteria	Armatimonadota	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	—	0.1%
Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	—	0.1%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	—	—	0.1%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	—	0.1%
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Saprosiraceae	—	0.1%
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	—	0.6%
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	midas_g_48792	0.1%
Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Cryomorphaceae	Vicingus	0.9%
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	—	—	0.5%
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	NS11-12_marine_group	—	1.3%
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	NS11-12_marine_group	midas_g_50227	0.7%
Bacteria	Bdellovibrionota	Bdellovibrionia	Bacteriovoracales	Bacteriovoracaceae	—	0.2%
Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	—	0.2%
Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.1%
Bacteria	Bdellovibrionota	Oligoflexia	0319-6G20	—	—	0.1%
Bacteria	Bdellovibrionota	Oligoflexia	Oligoflexales	Oligoflexaceae	—	0.3%
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	—	0.1%
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	midas_g_50073	0.1%

Kingdom	Phylum	Class	Order	Family	Genus	Rel. freq. %
Bacteria	Chloroflexi	Anaerolineae	Ardenticatenales	Ca_Promineofilaceae	—	0.2%
Bacteria	Chloroflexi	Anaerolineae	Ardenticatenales	Ca_Promineofilaceae	Ca_Promineofilum	2.8%
Bacteria	Chloroflexi	Anaerolineae	Ardenticatenales	midas_f_39435	midas_g_39435	0.8%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	—	0.4%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	Litorilinea	0.2%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	midas_g_13853	0.1%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	midas_g_2138	0.3%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	midas_g_2582	0.5%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	midas_g_4907	0.1%
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	midas_g_7167	0.1%
Bacteria	Chloroflexi	Anaerolineae	SBR1031	A4b	—	0.2%
Bacteria	Chloroflexi	Anaerolineae	SBR1031	A4b	midas_g_25102	0.1%
Bacteria	Chloroflexi	Anaerolineae	SBR1031	A4b	midas_g_8129	0.1%
Bacteria	Chloroflexi	Anaerolineae	SBR1031	midas_f_1469	midas_g_2178	0.2%
Bacteria	Chloroflexi	Anaerolineae	SBR1031	midas_f_184	midas_g_184	0.4%
Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	midas_g_1212	0.2%
Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	midas_g_882	0.1%
Bacteria	Dadabacteria	Dadabacteriia	Dadabacteriales	midas_f_603	midas_g_603	1.4%
Bacteria	Deinococcota	Deinococci	Deinococcales	Trueperaceae	Truepera	2.1%
Bacteria	Desulfobacterota	Desulfuromonadia	PB19	midas_f_1334	midas_g_49245	0.1%
Bacteria	Firmicutes	—	—	—	—	0.1%
Bacteria	Firmicutes	Bacilli	—	—	—	0.6%
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.1%
Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Paenibacillus	0.2%
Bacteria	Gemmatimonadota	BD2-11_terrestrial_group	midas_o_58609	midas_f_58609	—	0.1%
Bacteria	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	—	0.4%
Bacteria	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	midas_g_1166	0.1%
Bacteria	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	midas_g_49324	0.1%
Bacteria	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	midas_g_6621	0.5%
Bacteria	Nitrospirota	Nitrospiria	Nitrospirales	Nitrospiraceae	Nitrospira	0.2%
Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	—	—	0.1%
Bacteria	Patescibacteria	midas_c_34838	midas_o_34838	midas_f_52344	midas_g_52344	0.1%
Bacteria	Planctomycetota	BD7-11	midas_o_17905	midas_f_17905	—	0.1%
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	—	6.0%
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SM1A02	3.1%
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	midas_g_36898	0.5%

Kingdom	Phylum	Class	Order	Family	Genus	Rel. freq. %
Bacteria	Planctomycetota	Phycisphaerae	mle1-8	midas_f_1686	—	0.1%
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	—	0.1%
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	midas_g_9516	0.1%
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	—	0.3%
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Blastopirellula	0.1%
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pir4_lineage	0.1%
Bacteria	Planctomycetota	Planctomycetes	Planctomycetales	Rubinisphaeraceae	Planctomicrobium	0.1%
Bacteria	Planctomycetota	Planctomycetes	midas_o_1071	midas_f_1071	midas_g_29742	0.1%
Bacteria	Proteobacteria	—	—	—	—	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	—	—	—	0.4%
Bacteria	Proteobacteria	Alphaproteobacteria	Kiloniellales	Fodinicurvataceae	midas_g_34634	0.2%
Bacteria	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	—	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Micavibrionales	midas_f_25039	midas_g_31560	0.2%
Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Ca_Odysella	0.4%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	—	—	0.6%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Amb-16S-1323	midas_g_27435	0.2%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	—	0.9%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	1.3%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	1.7%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	—	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	midas_g_11150	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	—	1.7%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aminobacter	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aquamicrobium	3.3%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	1.8%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Pseudaminobacter	0.4%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	—	0.2%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	midas_g_1919	0.6%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	—	0.3%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	0.4%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.3%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	midas_f_7641	midas_g_83775	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	—	0.1%
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.3%
Bacteria	Proteobacteria	Alphaproteobacteria	Tistrellales	Geminicoccaceae	midas_g_5706	0.4%

Kingdom	Phylum	Class	Order	Family	Genus	Rel. freq. %
Bacteria	Proteobacteria	Gammaproteobacteria	—	—	—	0.3%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	—	—	0.4%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	—	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	—	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Lautropia	0.2%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnobacter	8.0%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	—	0.6%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.5%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Ottowia	0.2%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Type_1701	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	midas_g_81	0.4%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosomonas	0.2%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	—	8.2%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Azoarcus	4.3%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Denitromonas	0.4%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Thauera	13.5%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Zoogloea	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	midas_g_26	0.7%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	midas_g_9719	0.5%
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	TRA3-20	midas_g_3776	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Alteromonadaceae	Rheinheimera	0.1%
Bacteria	Proteobacteria	Gammaproteobacteria	Francisellales	Francisellaceae	Francisella	0.2%
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.4%
Bacteria	Proteobacteria	Gammaproteobacteria	Steroidobacterales	Woeseiaceae	JTB255_marine_benthic_group	0.5%
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	—	0.3%
Bacteria	Proteobacteria	Gammaproteobacteria	midas_o_26	midas_f_116	midas_g_37891	0.1%
Bacteria	Sumerlaeota	Sumerlaeia	Sumerlaeales	Sumerlaeaceae	—	0.6%
Bacteria	Sumerlaeota	Sumerlaeia	Sumerlaeales	Sumerlaeaceae	Sumerlaea	0.1%
Bacteria	WPS-2	midas_c_206	midas_o_395	midas_f_547	—	0.3%
Bacteria	WPS-2	midas_c_206	midas_o_395	midas_f_547	midas_g_17586	2.3%

Relative frequencies may not sum to 100% due to rounding and low-abundance filtering (< 0.10%). Filtered cumulative relative frequency: 5.32%.



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