

Taxonomy Summary. Current Level:

		Total	G1	G2
Legend	Taxonomy	%	%	%
	Unclassified;Other	0.5%	0.7%	0.3%
p	Acidobacteria;Other	0.1%	0.2%	0.1%
p	Acidobacteria;c Acidobacteriia	2.3%	1.7%	2.8%
p	Acidobacteria;c Blastocatellia-(Subgroup-4)	9.6%	5.6%	13.6%
p	Acidobacteria;c Holophagae	0.3%	0.4%	0.3%
p	Acidobacteria;c Subgroup-11	0.1%	0.1%	0.1%
p	Acidobacteria;c Subgroup-15	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-17	0.2%	0.2%	0.1%
p	Acidobacteria;c Subgroup-18	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-20	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-22	0.3%	0.4%	0.2%
p	Acidobacteria;c Subgroup-25	0.1%	0.1%	0.1%
p	Acidobacteria;c Subgroup-5	0.4%	0.4%	0.4%
p	Acidobacteria;c Subgroup-6	6.6%	7.4%	5.7%
p	Acidobacteria;c Subgroup-9	0.0%	0.0%	0.0%
p	Actinobacteria;Other	0.0%	0.0%	0.1%
p	Actinobacteria;c 0319-7L14	0.1%	0.1%	0.1%
p	Actinobacteria;c Acidimicrobiia	2.8%	3.3%	2.2%
p	Actinobacteria;c Actinobacteria	13.4%	14.1%	12.7%
p	Actinobacteria;c MB-A2-108	0.7%	0.8%	0.5%
p	Actinobacteria;c Nitriliruptoria	0.0%	0.0%	0.0%
p	Actinobacteria;c Rubrobacteria	0.1%	0.0%	0.1%
p	Actinobacteria;c Thermoleophilia	1.2%	1.3%	1.1%
p	Armatimonadetes;c Fimbriimonadia	0.0%	0.0%	0.0%
p	BRC1;Other	0.0%	0.0%	0.0%
p	BRC1;c uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c Bacteroidia	11.8%	14.6%	9.0%
p	Bacteroidetes;c Ignavibacteria	0.2%	0.2%	0.1%
p	Chloroflexi;Other	0.0%	0.0%	0.0%
p	Chloroflexi;c AD3	0.0%	0.0%	0.0%
p	Chloroflexi;c Anaerolineae	2.0%	1.6%	2.4%
p	Chloroflexi;c Chloroflexia	1.7%	0.8%	2.6%
p	Chloroflexi;c Dehalococcoidia	0.4%	0.5%	0.3%
p	Chloroflexi;c Gitt-GS-136	0.3%	0.4%	0.1%
p	Chloroflexi;c JG30-KF-CM66	0.1%	0.2%	0.1%
p	Chloroflexi;c KD4-96	0.7%	0.9%	0.5%
p	Chloroflexi;c Ktedonobacteria	0.1%	0.0%	0.1%
p	Chloroflexi;c OLB14	0.1%	0.1%	0.1%
p	Chloroflexi;c P2-11E	0.2%	0.1%	0.2%
p	Chloroflexi;c TK10	0.3%	0.3%	0.3%
p	Dadabacteria;c Dadabacteriia	0.0%	0.0%	0.0%
p	Dependentiae;c Babeliae	0.1%	0.1%	0.0%
p	Elusimicrobia;c Elusimicrobia	0.0%	0.0%	0.0%
p	Elusimicrobia;c Lineage-IIa	0.1%	0.1%	0.0%
p	Elusimicrobia;c Lineage-IIb	0.0%	0.0%	0.0%
p	Entotheonellaeota;c Entotheonellia	0.1%	0.1%	0.1%
p	Euryarchaeota;c Methanomicrobia	0.0%	0.0%	0.0%
p	Euryarchaeota;c Thermoplasmata	1.8%	0.9%	2.8%
p	Firmicutes;c Bacilli	2.9%	0.9%	4.8%
p	Firmicutes;c Clostridia	0.0%	0.0%	0.0%
p	GAL15;c uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c AKAU4049	0.2%	0.3%	0.0%
p	Gemmatimonadetes;c BD2-11-terrestrial-group	0.1%	0.2%	0.0%
p	Gemmatimonadetes;c Gemmatimonadetes	2.6%	2.5%	2.8%
p	Gemmatimonadetes;c Longimicrobia	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c S0134-terrestrial-group	0.5%	0.5%	0.5%
p	Hydrogenedentes;c Hydrogenedentia	0.0%	0.0%	0.0%
p	Latescibacteria;Other	0.3%	0.4%	0.1%
p	Latescibacteria;c Latescibacteria	0.2%	0.3%	0.0%
p	Latescibacteria;c uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c uncultured-Fibrobacteres-bacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c uncultured-Pelobacter-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c uncultured-bacterium	0.4%	0.5%	0.3%
p	Latescibacteria;c uncultured-prokaryote	0.0%	0.0%	0.0%
p	Latescibacteria;c uncultured-proteobacterium	0.0%	0.0%	0.0%

p	Latescibacteria;c	uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaea	0.1%	0.1%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia	0.2%	0.4%	0.1%
p	Nitrospirae;c	Nitrospira	0.5%	0.4%	0.7%
p	Patescibacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1	0.1%	0.0%	0.1%
p	Patescibacteria;c	Berkelbacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Microgenomatia	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria	0.1%	0.1%	0.2%
p	Patescibacteria;c	Saccharimonadia	0.5%	0.4%	0.6%
p	Patescibacteria;c	WWE3	0.0%	0.0%	0.0%
p	Planctomycetes;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	BD7-11	0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae	1.7%	1.4%	2.1%
p	Planctomycetes;c	Pla3-lineage	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage	0.1%	0.1%	0.1%
p	Planctomycetes;c	Planctomycetacia	0.4%	0.4%	0.5%
p	Proteobacteria;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria	10.3%	11.1%	9.5%
p	Proteobacteria;c	Deltaproteobacteria	2.7%	2.8%	2.6%
p	Proteobacteria;c	Gammaproteobacteria	8.7%	10.8%	6.6%
p	Rokubacteria;c	NC10	1.2%	1.6%	0.9%
p	Thaumarchaeota;c	Group-1.1c	0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria	1.3%	1.3%	1.3%
p	Verrucomicrobia;c	Verrucomicrobiae	6.1%	5.5%	6.8%
p	WPS-2;Other		0.0%	0.0%	0.0%
p	Zixibacteria;Other		0.0%	0.0%	0.0%
p	Zixibacteria;c	uncultured-bacterium	0.0%	0.0%	0.0%

Taxonomy Summary. Current Level:

		Total	G1	G2
Legend	Taxonomy	%	%	%
	Unclassified;Other;Other	0.5%	0.7%	0.3%
p	Acidobacteria;Other;Other	0.1%	0.2%	0.1%
p	Acidobacteria;c Acidobacteriia;o Acidobacteriales	0.3%	0.2%	0.4%
p	Acidobacteria;c Acidobacteriia;o Solibacterales	1.8%	1.4%	2.3%
p	Acidobacteria;c Acidobacteriia;o Subgroup-12	0.0%	0.0%	0.0%
p	Acidobacteria;c Acidobacteriia;o Subgroup-13	0.0%	0.0%	0.0%
p	Acidobacteria;c Acidobacteriia;o Subgroup-2	0.1%	0.2%	0.1%
p	Acidobacteria;c Blastocatellia-(Subgroup-4);Other	2.6%	1.6%	3.6%
p	Acidobacteria;c Blastocatellia-(Subgroup-4);o 11-24	0.4%	0.4%	0.4%
p	Acidobacteria;c Blastocatellia-(Subgroup-4);o Blastocatellales	0.7%	0.5%	0.9%
p	Acidobacteria;c Blastocatellia-(Subgroup-4);o DS-100	0.0%	0.0%	0.0%
p	Acidobacteria;c Blastocatellia-(Subgroup-4);o Elev-16S-573	5.9%	3.1%	8.7%
p	Acidobacteria;c Holophagae;o Holophagales	0.0%	0.0%	0.0%
p	Acidobacteria;c Holophagae;o Subgroup-7	0.3%	0.4%	0.3%
p	Acidobacteria;c Subgroup-11;Other	0.1%	0.1%	0.1%
p	Acidobacteria;c Subgroup-11;o uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-15;Other	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-15;o uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-17;Other	0.1%	0.1%	0.0%
p	Acidobacteria;c Subgroup-17;o uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-17;o uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-17;o uncultured-bacterium	0.1%	0.1%	0.0%
p	Acidobacteria;c Subgroup-18;Other	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-18;o uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-20;o uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-22;Other	0.1%	0.1%	0.1%
p	Acidobacteria;c Subgroup-22;o uncultured-Acidobacterium-sp.	0.0%	0.1%	0.0%
p	Acidobacteria;c Subgroup-22;o uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c Subgroup-25;Other	0.0%	0.1%	0.0%
p	Acidobacteria;c Subgroup-25;o uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-25;o uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-25;o uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-5;Other	0.0%	0.0%	0.0%
p	Acidobacteria;c Subgroup-5;o uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%

p	Acidobacteria;c	Subgroup-5;o	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-5;o	uncultured-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Subgroup-6;Other		5.4%	6.2%	4.6%
p	Acidobacteria;c	Subgroup-6;o	Acidobacteria-bacterium-WX90	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	Unknown-Order	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteriales-bacterium	0.1%	0.1%	0.1%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Holophagae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-bacterium	0.8%	0.9%	0.8%
p	Acidobacteria;c	Subgroup-6;o	uncultured-beta-proteobacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-9;Other		0.0%	0.0%	0.0%
p	Actinobacteria;Other;Other			0.0%	0.0%	0.1%
p	Actinobacteria;c	0319-7L14;Other		0.0%	0.0%	0.1%
p	Actinobacteria;c	0319-7L14;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;Other		0.3%	0.3%	0.3%
p	Actinobacteria;c	Acidimicrobiia;o	Acidimicrobiales	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	Actinomarinales	0.7%	1.3%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256	0.5%	0.5%	0.4%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales	0.8%	0.8%	0.7%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured	0.5%	0.3%	0.8%
p	Actinobacteria;c	Actinobacteria;Other		0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales	1.4%	0.7%	2.2%
p	Actinobacteria;c	Actinobacteria;o	Frankiales	0.2%	0.1%	0.2%
p	Actinobacteria;c	Actinobacteria;o	Glycomycetales	1.0%	1.9%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Kineosporiales	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales	0.6%	0.8%	0.5%
p	Actinobacteria;c	Actinobacteria;o	Micromonosporales	0.5%	0.5%	0.5%
p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales	1.6%	1.6%	1.5%
p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales	0.3%	0.2%	0.4%
p	Actinobacteria;c	Actinobacteria;o	Streptomycetales	7.6%	8.0%	7.3%
p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales	0.1%	0.2%	0.0%
p	Actinobacteria;c	MB-A2-108;Other		0.1%	0.1%	0.1%
p	Actinobacteria;c	MB-A2-108;o	uncultured-actinobacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium	0.6%	0.7%	0.4%
p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium-contig00016	0.0%	0.0%	0.0%
p	Actinobacteria;c	Nitriliruptoria;o	Euzebyales	0.0%	0.0%	0.0%
p	Actinobacteria;c	Rubrobacteria;o	Rubrobacterales	0.1%	0.0%	0.1%
p	Actinobacteria;c	Thermoleophilia;Other		0.1%	0.1%	0.1%
p	Actinobacteria;c	Thermoleophilia;o	Gaiellales	0.6%	0.7%	0.6%
p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales	0.5%	0.5%	0.4%
p	Actinobacteria;c	Thermoleophilia;o	uncultured	0.0%	0.0%	0.0%
p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales	0.0%	0.0%	0.0%
p	BRC1;Other;Other			0.0%	0.0%	0.0%
p	BRC1;c	uncultured-bacterium;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Bacteroidetes-VC2.1-Bac22	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales	8.4%	11.3%	5.4%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales	2.1%	2.1%	2.2%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales	0.4%	0.2%	0.5%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales	0.9%	1.0%	0.9%
p	Bacteroidetes;c	Ignavibacteria;o	Ignavibacteriales	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales	0.1%	0.1%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56	0.1%	0.0%	0.1%
p	Bacteroidetes;c	Ignavibacteria;o	SJA-28	0.0%	0.1%	0.0%
p	Chloroflexi;Other;Other			0.0%	0.0%	0.0%
p	Chloroflexi;c	AD3;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales	1.2%	0.9%	1.5%
p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales	0.2%	0.1%	0.2%
p	Chloroflexi;c	Anaerolineae;o	Caldilineales	0.0%	0.0%	0.1%
p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9	0.1%	0.1%	0.1%
p	Chloroflexi;c	Anaerolineae;o	SBR1031	0.4%	0.4%	0.5%
p	Chloroflexi;c	Anaerolineae;o	uncultured-Bellilinea-sp.	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Chloroflexales	1.2%	0.4%	2.0%
p	Chloroflexi;c	Chloroflexia;o	Kallotenuales	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales	0.5%	0.4%	0.6%

p	Chloroflexi;c	Dehalococcoidia;o	S085	0.4%	0.5%	0.3%
p	Chloroflexi;c	Gitt-GS-136;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	Gitt-GS-136;o	uncultured-bacterium	0.3%	0.4%	0.1%
p	Chloroflexi;c	JG30-KF-CM66;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	JG30-KF-CM66;o	uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	JG30-KF-CM66;o	uncultured-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	KD4-96;Other		0.2%	0.3%	0.1%
p	Chloroflexi;c	KD4-96;o	uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	KD4-96;o	uncultured-bacterium	0.4%	0.5%	0.3%
p	Chloroflexi;c	Ktedonobacteria;o	C0119	0.0%	0.0%	0.0%
p	Chloroflexi;c	Ktedonobacteria;o	Ktedonobacterales	0.0%	0.0%	0.1%
p	Chloroflexi;c	OLB14;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	OLB14;o	uncultured-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	OLB14;o	uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	P2-11E;o	uncultured-bacterium	0.2%	0.1%	0.2%
p	Chloroflexi;c	TK10;Other		0.2%	0.2%	0.2%
p	Chloroflexi;c	TK10;o	uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.1%
p	Chloroflexi;c	TK10;o	uncultured-bacterium	0.0%	0.1%	0.0%
p	Dadabacteria;c	Dadabacteria;o	Dadabacterales	0.0%	0.0%	0.0%
p	Dependentiae;c	Babeliae;o	Babeliales	0.1%	0.1%	0.0%
p	Elusimicrobia;c	Elusimicrobia;o	MVP-88	0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIa;Other		0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIa;o	uncultured-bacterium	0.0%	0.1%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Entotheonellaeota;c	Entotheonellia;o	Entotheonellales	0.1%	0.1%	0.1%
p	Euryarchaeota;c	Methanomicrobia;o	Methanosarcinales	0.0%	0.0%	0.0%
p	Euryarchaeota;c	Thermoplasmata;Other		0.1%	0.1%	0.1%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II	1.3%	0.7%	1.8%
p	Euryarchaeota;c	Thermoplasmata;o	Methanomassiliococcales	0.5%	0.0%	0.9%
p	Euryarchaeota;c	Thermoplasmata;o	uncultured	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales	2.9%	0.9%	4.8%
p	Firmicutes;c	Clostridia;o	Clostridiales	0.0%	0.0%	0.0%
p	GAL15;c	uncultured-bacterium;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	AKAU4049;Other		0.2%	0.3%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;Other		0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium	0.0%	0.1%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales	2.6%	2.5%	2.8%
p	Gemmatimonadetes;c	Longimicrobia;o	Longimicrobiales	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;Other		0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium	0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-bacterium	0.2%	0.2%	0.2%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales	0.0%	0.0%	0.0%
p	Latescibacteria;Other;Other			0.3%	0.4%	0.1%
p	Latescibacteria;c	Latescibacteria;o	Latescibacterales	0.2%	0.3%	0.0%
p	Latescibacteria;c	uncultured-Acidobacterium-sp.;o	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Fibrobacteres-bacterium;o	uncultured-Fibrobacteres-bacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Pelobacter-sp.;o	uncultured-Pelobacter-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-bacterium;o	uncultured-bacterium	0.4%	0.5%	0.3%
p	Latescibacteria;c	uncultured-prokaryote;o	uncultured-prokaryote	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-proteobacterium;o	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-soil-bacterium;o	uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Aenigmarchaeales	0.1%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Deep-Sea-Euryarchaeotic-Group(DSEG)	0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;Other		0.1%	0.2%	0.1%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15	0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9	0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7	0.1%	0.1%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	uncultured-euryarchaeote	0.0%	0.0%	0.0%
p	Nitrospirae;c	Nitrospira;o	Nitrospirales	0.5%	0.4%	0.7%
p	Patescibacteria;Other;Other			0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;o	Candidatus-Kuenenbacteria	0.0%	0.0%	0.1%
p	Patescibacteria;c	ABY1;o	Candidatus-Magasanikbacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;o	Candidatus-Uhrbacteria	0.0%	0.0%	0.0%

p	Patescibacteria;c	Berkelbacteria;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria;o	Candidatus-Abawacabacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria;o	Candidatus-Peribacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Microgenomatia;o	Candidatus-Woesebacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Azambacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Kaiserbacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Nomurabacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Terrybacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Yanofskybacteria	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	GWA2-38-13b	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Saccharimonadia;o	Saccharimonadales	0.5%	0.4%	0.6%
p	Patescibacteria;c	WWE3;Other		0.0%	0.0%	0.0%
p	Planctomycetes;Other;Other			0.0%	0.0%	0.0%
p	Planctomycetes;c	BD7-11;o	uncultured-Planctomycetales-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	BD7-11;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;o	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;Other		0.2%	0.2%	0.2%
p	Planctomycetes;c	Phycisphaerae;o	CCM11a	0.2%	0.2%	0.2%
p	Planctomycetes;c	Phycisphaerae;o	Phycisphaerales	0.1%	0.1%	0.1%
p	Planctomycetes;c	Phycisphaerae;o	Pla1-lineage	0.0%	0.1%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales	1.1%	0.8%	1.4%
p	Planctomycetes;c	Phycisphaerae;o	mle1-8	0.1%	0.0%	0.1%
p	Planctomycetes;c	Pla3-lineage;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o	uncultured-prokaryote	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o	Gemmatales	0.2%	0.1%	0.2%
p	Planctomycetes;c	Planctomycetacia;o	Pirellulales	0.2%	0.2%	0.2%
p	Planctomycetes;c	Planctomycetacia;o	Planctomycetales	0.1%	0.1%	0.1%
p	Planctomycetes;c	Planctomycetacia;o	uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;Other;Other			0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;Other		1.8%	1.7%	2.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Azospirillales	0.1%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales	0.3%	0.4%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o	Elsterales	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Holospirales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Micropepsales	0.1%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Reyranellales	0.2%	0.3%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales	5.3%	5.8%	4.9%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodobacterales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodovibrionales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sneathiellales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales	1.9%	2.3%	1.6%
p	Proteobacteria;c	Alphaproteobacteria;o	Tistrellales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured	0.4%	0.4%	0.4%
p	Proteobacteria;c	Deltaproteobacteria;Other		0.2%	0.3%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Bdellovibrionales	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfarcucales	0.2%	0.1%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15	0.1%	0.1%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales	1.5%	1.7%	1.4%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j	0.4%	0.5%	0.3%
p	Proteobacteria;c	Deltaproteobacteria;o	Oligoflexales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	RCP2-54	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	SAR324-clade(Marine-group-B)	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Syntrophobacterales	0.1%	0.0%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;Other		0.5%	0.6%	0.4%
p	Proteobacteria;c	Gammaproteobacteria;o	Acidiferrobacterales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Aeromonadales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales	4.5%	4.3%	4.8%
p	Proteobacteria;c	Gammaproteobacteria;o	CCD24	0.2%	0.3%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Diploricetisiales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	EPR3968-O8a-Bc78	0.0%	0.0%	0.0%

p	Proteobacteria;c	Gammaproteobacteria;o	Enterobacteriales	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Gammaproteobacteria-Incertae-Sedis	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	JG36-GS-52	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	KI89A-clade	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13	0.7%	1.3%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales	0.5%	0.8%	0.2%
p	Proteobacteria;c	Gammaproteobacteria;o	R7C24	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales	0.1%	0.0%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacteriales	1.4%	2.0%	0.7%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales	0.8%	1.4%	0.1%
p	Rokubacteria;c	NC10;o	Rokubacteriales	1.2%	1.6%	0.9%
p	Thaumarchaeota;c	Group-1.1c;Other		0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosopumilales	0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales	1.3%	1.3%	1.3%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosotaleales	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;Other		0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacteriales	2.1%	1.3%	2.8%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Methylacidiphilales	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Opitutales	1.4%	2.5%	0.3%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales	2.6%	1.6%	3.6%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales	0.1%	0.1%	0.1%
p	WPS-2;Other;Other			0.0%	0.0%	0.0%
p	Zixibacteria;Other;Other			0.0%	0.0%	0.0%
p	Zixibacteria;c	uncultured-bacterium;o	uncultured-bacterium	0.0%	0.0%	0.0%

Taxonomy Summary. Current Level:

Legend	Taxonomy				Total	G1	G2
					%	%	%
	Unclassified;Other;Other;Other				0.5%	0.7%	0.3%
p	Acidobacteria;Other;Other;Other				0.1%	0.2%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;Other		0.1%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Acidobacteriaceae-(Subgroup-1)	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Koribacteraceae	0.1%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured	0.2%	0.1%	0.2%
p	Acidobacteria;c	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3)	1.8%	1.4%	2.3%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-12;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-13;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;Other		0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-bacterium	0.1%	0.1%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-forest-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);Other;Other			2.6%	1.6%	3.6%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;Other		0.1%	0.0%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae	0.7%	0.5%	0.9%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;Other		0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;Other		5.1%	2.3%	8.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-bacterium	0.7%	0.8%	0.7%
p	Acidobacteria;c	Holophagae;o	Holophagales;f	Holophagaceae	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;Other		0.2%	0.2%	0.2%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c	Subgroup-11;Other;Other			0.1%	0.1%	0.1%
p	Acidobacteria;c	Subgroup-11;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-15;Other;Other			0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-15;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;Other;Other			0.1%	0.1%	0.0%

p	Acidobacteria;c	Subgroup-17;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;o	uncultured-Acidobacteriales-bacterium;f	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;o	uncultured-bacterium;f	uncultured-bacterium	0.1%	0.1%	0.0%
p	Acidobacteria;c	Subgroup-18;Other;Other			0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-18;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-20;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-22;Other;Other			0.1%	0.1%	0.1%
p	Acidobacteria;c	Subgroup-22;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.	0.0%	0.1%	0.0%
p	Acidobacteria;c	Subgroup-22;o	uncultured-bacterium;f	uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c	Subgroup-25;Other;Other			0.0%	0.1%	0.0%
p	Acidobacteria;c	Subgroup-25;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-25;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-25;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-5;Other;Other			0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-5;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Subgroup-5;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-5;o	uncultured-bacterium;f	uncultured-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Subgroup-6;Other;Other			5.4%	6.2%	4.6%
p	Acidobacteria;c	Subgroup-6;o	Acidobacteria-bacterium-WX90;f	Acidobacteria-bacterium-WX90	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	Unknown-Order;f	Unknown-Family	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteriaceae-bacterium;f	uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteriales-bacterium;f	uncultured-Acidobacteriales-bacterium	0.1%	0.1%	0.1%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-Holophagae-bacterium;f	uncultured-Holophagae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-bacterium;f	uncultured-bacterium	0.8%	0.9%	0.8%
p	Acidobacteria;c	Subgroup-6;o	uncultured-beta-proteobacterium;f	uncultured-beta-proteobacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-6;o	uncultured-proteobacterium;f	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-9;Other;Other			0.0%	0.0%	0.0%
p	Actinobacteria;Other;Other;Other				0.0%	0.0%	0.1%
p	Actinobacteria;c	0319-7L14;Other;Other			0.0%	0.0%	0.1%
p	Actinobacteria;c	0319-7L14;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;Other;Other			0.3%	0.3%	0.3%
p	Actinobacteria;c	Acidimicrobiia;o	Acidimicrobiales;f	Acidimicrobiaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	Actinomarinales;f	uncultured	0.7%	1.3%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;Other		0.4%	0.4%	0.3%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-Acidimicrobiales-bacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-Acidimicrobiidae-bacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-actinobacterium	0.0%	0.0%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-organism	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;Other		0.1%	0.1%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Iamiaceae	0.2%	0.2%	0.2%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Illumatobacteraceae	0.2%	0.3%	0.2%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Microtrichaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	uncultured	0.2%	0.2%	0.2%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured;Other		0.3%	0.2%	0.5%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-Acidimicrobiidae-bacterium	0.0%	0.0%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-actinobacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-bacterium	0.1%	0.0%	0.1%
p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-soil-bacterium	0.0%	0.0%	0.1%
p	Actinobacteria;c	Actinobacteria;Other;Other			0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Mycobacteriaceae	0.3%	0.1%	0.5%
p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae	1.1%	0.5%	1.7%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Cryptosporangiaceae	0.1%	0.0%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Frankiaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae	0.0%	0.0%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Nakamurellaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Sporichthyaceae	0.0%	0.0%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	uncultured	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Glycomycetales;f	Glycomycetaceae	1.0%	1.9%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Kineosporiales;f	Kineosporiaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;Other		0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Cellulomonadaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Demequinaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Intrasporangiaceae	0.1%	0.1%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae	0.1%	0.2%	0.1%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae	0.2%	0.0%	0.3%
p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae	0.3%	0.5%	0.0%

p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae	0.5%	0.5%	0.5%
p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioideaceae	1.6%	1.6%	1.5%
p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Propionibacteriaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae	0.3%	0.2%	0.4%
p	Actinobacteria;c	Actinobacteria;o	Streptomycetales;f	Streptomycetaceae	7.6%	8.0%	7.3%
p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae	0.1%	0.2%	0.0%
p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Thermomonosporaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	MB-A2-108;Other;Other			0.1%	0.1%	0.1%
p	Actinobacteria;c	MB-A2-108;o	uncultured-actinobacterium;f	uncultured-actinobacterium	0.0%	0.0%	0.0%
p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium;f	uncultured-bacterium	0.6%	0.7%	0.4%
p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium-contig00016;f	uncultured-bacterium-contig00016	0.0%	0.0%	0.0%
p	Actinobacteria;c	Nitrilriuptoria;o	Euzebyales;f	Euzebyaceae	0.0%	0.0%	0.0%
p	Actinobacteria;c	Rubrobacteria;o	Rubrobacterales;f	Rubrobacteriaceae	0.1%	0.0%	0.1%
p	Actinobacteria;c	Thermoleophilia;Other;Other			0.1%	0.1%	0.1%
p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;Other		0.0%	0.0%	0.0%
p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured	0.6%	0.7%	0.6%
p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f	67-14	0.3%	0.4%	0.2%
p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f	Solirubrobacteraceae	0.2%	0.2%	0.2%
p	Actinobacteria;c	Thermoleophilia;o	uncultured;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales;f	Fimbriimonadaceae	0.0%	0.0%	0.0%
p	BRC1;Other;Other;Other				0.0%	0.0%	0.0%
p	BRC1;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;Other;Other			0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Bacteroidetes-VC2.1-Bac22;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	37-13	0.1%	0.1%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae	8.0%	11.0%	5.1%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Saprospiraceae	0.3%	0.2%	0.3%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	uncultured	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Cytophagaceae	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Hymenobacteraceae	0.1%	0.0%	0.2%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae	2.0%	2.0%	2.0%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Spirosomaceae	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Flavobacteriaceae	0.3%	0.1%	0.5%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	NS9-marine-group	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	AKYH767	0.3%	0.2%	0.3%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	NS11-12-marine-group	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae	0.3%	0.5%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	env.OPS-17	0.3%	0.2%	0.4%
p	Bacteroidetes;c	Ignavibacteria;o	Ignavibacteriales;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales;f	BSV26	0.1%	0.1%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-#0319-6E22	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-KF-JG30-B11	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	SJA-28;f	uncultured-bacterium	0.0%	0.1%	0.0%
p	Chloroflexi;Other;Other;Other				0.0%	0.0%	0.0%
p	Chloroflexi;c	AD3;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;Other;Other			0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae	1.2%	0.9%	1.5%
p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured	0.2%	0.1%	0.2%
p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae	0.0%	0.0%	0.1%
p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;Other		0.0%	0.0%	0.1%
p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;f	uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;f	uncultured-sludge-bacterium-A31	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	SBR1031;Other		0.1%	0.2%	0.0%
p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b	0.3%	0.2%	0.4%
p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	uncultured-Bellilinea-sp.;f	uncultured-Bellilinea-sp.	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Chloroflexaceae	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Herpetosiphonaceae	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Roseiflexaceae	1.2%	0.4%	2.0%
p	Chloroflexi;c	Chloroflexia;o	Kallotenuales;f	AKIW781	0.0%	0.0%	0.0%
p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	AKYG1722	0.1%	0.1%	0.2%

p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	JG30-KF-CM45	0.3%	0.2%	0.4%
p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	Thermomicrobiaceae	0.0%	0.0%	0.0%
p	Chloroflexi;c	Dehalococcoidia;o	S085;Other		0.2%	0.3%	0.1%
p	Chloroflexi;c	Dehalococcoidia;o	S085;f	uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Dehalococcoidia;o	S085;f	uncultured-bacterium	0.1%	0.2%	0.1%
p	Chloroflexi;c	Dehalococcoidia;o	S085;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Gitt-GS-136;Other;Other			0.0%	0.0%	0.0%
p	Chloroflexi;c	Gitt-GS-136;o	uncultured-bacterium;f	uncultured-bacterium	0.3%	0.4%	0.1%
p	Chloroflexi;c	JG30-KF-CM66;Other;Other			0.0%	0.0%	0.0%
p	Chloroflexi;c	JG30-KF-CM66;o	uncultured-Chloroflexi-bacterium;f	uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	JG30-KF-CM66;o	uncultured-bacterium;f	uncultured-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	KD4-96;Other;Other			0.2%	0.3%	0.1%
p	Chloroflexi;c	KD4-96;o	uncultured-Chloroflexi-bacterium;f	uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	KD4-96;o	uncultured-bacterium;f	uncultured-bacterium	0.4%	0.5%	0.3%
p	Chloroflexi;c	Ktedonobacteria;o	C0119;Other		0.0%	0.0%	0.0%
p	Chloroflexi;c	Ktedonobacteria;o	C0119;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Ktedonobacteria;o	Ktedonobacterales;f	Ktedonobacteraceae	0.0%	0.0%	0.1%
p	Chloroflexi;c	OLB14;Other;Other			0.0%	0.0%	0.0%
p	Chloroflexi;c	OLB14;o	uncultured-bacterium;f	uncultured-bacterium	0.1%	0.1%	0.1%
p	Chloroflexi;c	OLB14;o	uncultured-gamma-proteobacterium;f	uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	P2-11E;o	uncultured-bacterium;f	uncultured-bacterium	0.2%	0.1%	0.2%
p	Chloroflexi;c	TK10;Other;Other			0.2%	0.2%	0.2%
p	Chloroflexi;c	TK10;o	uncultured-Chloroflexi-bacterium;f	uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.1%
p	Chloroflexi;c	TK10;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.1%	0.0%
p	Dadabacteria;c	Dadabacteria;i;o	Dadabacterales;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Dependentiae;c	Babeliae;o	Babeliales;Other		0.0%	0.0%	0.0%
p	Dependentiae;c	Babeliae;o	Babeliales;f	Babeliaceae	0.0%	0.0%	0.0%
p	Dependentiae;c	Babeliae;o	Babeliales;f	Vermiphilaceae	0.0%	0.0%	0.0%
p	Elusimicrobia;c	Elusimicrobia;o	MVP-88;Other		0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIa;Other;Other			0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIa;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.1%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Entotheonella;c	Entotheonella;o	Entotheonellales;f	Entotheonellaceae	0.1%	0.1%	0.1%
p	Euryarchaeota;c	Methanomicrobia;o	Methanosarcinales;f	Methanosarcinaceae	0.0%	0.0%	0.0%
p	Euryarchaeota;c	Thermoplasmata;Other;Other			0.1%	0.1%	0.1%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;Other		0.2%	0.1%	0.2%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;f	uncultured-archaeon	1.1%	0.6%	1.6%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;f	uncultured-haloarchaeon	0.0%	0.0%	0.0%
p	Euryarchaeota;c	Thermoplasmata;o	Methanomassiliicoccales;f	uncultured	0.5%	0.0%	0.9%
p	Euryarchaeota;c	Thermoplasmata;o	uncultured;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae	2.7%	0.8%	4.6%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae	0.2%	0.1%	0.3%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Thermoactinomycetaceae	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Clostridiaceae-1	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Heliobacteriaceae	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Peptostreptococcaceae	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Ruminococcaceae	0.0%	0.0%	0.0%
p	GAL15;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	AKAU4049;Other;Other			0.2%	0.3%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;Other;Other			0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium	0.0%	0.1%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae	2.6%	2.5%	2.8%
p	Gemmatimonadetes;c	Longimicrobia;o	Longimicrobiales;f	Longimicrobiaceae	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;Other;Other			0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium	0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium	0.2%	0.2%	0.2%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales;f	Hydrogenedensaceae	0.0%	0.0%	0.0%
p	Latescibacteria;Other;Other;Other				0.3%	0.4%	0.1%
p	Latescibacteria;c	Latescibacteria;o	Latescibacterales;f	Latescibacteraceae	0.2%	0.3%	0.0%
p	Latescibacteria;c	uncultured-Acidobacterium-sp.;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%

p	Latescibacteria;c	uncultured-Fibrobacteres-bacterium;o	uncultured-Fibrobacteres-bacterium;f	uncultured-Fibrobacteres-bacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Pelobacter-sp.;o	uncultured-Pelobacter-sp.;f	uncultured-Pelobacter-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium	0.4%	0.5%	0.3%
p	Latescibacteria;c	uncultured-prokaryote;o	uncultured-prokaryote;f	uncultured-prokaryote	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-proteobacterium;o	uncultured-proteobacterium;f	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-soil-bacterium;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Aenigmarchaeales;Other		0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Aenigmarchaeales;f	uncultured-archaeon	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Deep-Sea-Euryarchaeotic-Group(DSEG);Other		0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;Other;Other			0.1%	0.2%	0.1%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;f	Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15	0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;f	Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9	0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;f	Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7	0.1%	0.1%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;o	uncultured-euryarchaeote;f	uncultured-euryarchaeote	0.0%	0.0%	0.0%
p	Nitrospirae;c	Nitrospira;o	Nitrospirales;f	Nitrospiraceae	0.5%	0.4%	0.7%
p	Patescibacteria;Other;Other;Other				0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;Other;Other			0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;o	Candidatus-Kuenenbacteria;f	uncultured-bacterium	0.0%	0.0%	0.1%
p	Patescibacteria;c	ABY1;o	Candidatus-Magasanikbacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;o	Candidatus-Magasanikbacteria;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	ABY1;o	Candidatus-Uhrbacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Berkelbacteria;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria;o	Candidatus-Abawacabacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria;o	Candidatus-Abawacabacteria;f	Candidatus-Abawacabacteria-bacterium-RBG_16_42_10	0.0%	0.0%	0.0%
p	Patescibacteria;c	Gracilibacteria;o	Candidatus-Peribacteria;f	Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20	0.0%	0.0%	0.0%
p	Patescibacteria;c	Microgenomatia;o	Candidatus-Woesebacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;Other;Other			0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Azambacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Azambacteria;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Kaiserbacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Nomurabacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Terrybacteria;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Yanofskybacteria;Other		0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Yanofskybacteria;f	Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Yanofskybacteria;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	Candidatus-Yanofskybacteria;f	uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	GWA2-38-13b;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	GWA2-38-13b;f	uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Parcubacteria;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Patescibacteria;c	Saccharimonadia;o	Saccharimonadales;Other		0.2%	0.2%	0.3%
p	Patescibacteria;c	Saccharimonadia;o	Saccharimonadales;f	Saccharimonadaceae	0.1%	0.0%	0.2%
p	Patescibacteria;c	Saccharimonadia;o	Saccharimonadales;f	uncultured-Candidatus-Saccharibacteria-bacterium	0.0%	0.0%	0.1%
p	Patescibacteria;c	Saccharimonadia;o	Saccharimonadales;f	uncultured-bacterium	0.1%	0.1%	0.1%
p	Patescibacteria;c	WWE3;Other;Other			0.0%	0.0%	0.0%
p	Planctomycetes;Other;Other;Other				0.0%	0.0%	0.0%
p	Planctomycetes;c	BD7-11;o	uncultured-Planctomycetales-bacterium;f	uncultured-Planctomycetales-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	BD7-11;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;Other;Other			0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	OM190;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;Other;Other			0.2%	0.2%	0.2%
p	Planctomycetes;c	Phycisphaerae;o	CCM11a;Other		0.1%	0.0%	0.1%
p	Planctomycetes;c	Phycisphaerae;o	CCM11a;f	uncultured-Planctomycetia-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	CCM11a;f	uncultured-bacterium	0.1%	0.2%	0.1%
p	Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;f	Phycisphaeraceae	0.1%	0.1%	0.1%
p	Planctomycetes;c	Phycisphaerae;o	Pla1-lineage;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Pla1-lineage;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	CPla-3-termite-group	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	Tepidisphaeraceae	0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	WD2101-soil-group	1.1%	0.8%	1.4%
p	Planctomycetes;c	Phycisphaerae;o	mle1-8;Other		0.0%	0.0%	0.0%
p	Planctomycetes;c	Phycisphaerae;o	mle1-8;f	uncultured-bacterium	0.1%	0.0%	0.1%

p	Planctomycetes;c	Pla3-lineage;Other;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;Other;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o uncultured-bacterium;f uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o uncultured-prokaryote;f uncultured-prokaryote	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Gemmatales;f Gemmataceae	0.2%	0.1%	0.2%
p	Planctomycetes;c	Planctomycetacia;o Pirellulales;f Pirellulaceae	0.2%	0.2%	0.2%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f Rubinisphaeraceae	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f Schlesneriaceae	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f uncultured	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o uncultured;f uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;Other;Other;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;Other;Other	1.8%	1.7%	2.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f Azospirillaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f Inquilinaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f uncultured	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Caulobacteraceae	0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Hyphomonadaceae	0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Parvularculaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f Elsteraceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f uncultured	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Holosporales;f Holosporaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Micropepsales;f Micropepsaceae	0.1%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Reyranelles;f Reyranelaceae	0.2%	0.3%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;Other	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f A0839	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Amb-16S-1323	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Beijerinckiaceae	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f D05-2	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Devosiaceae	0.2%	0.3%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Hyphomicrobiaceae	0.3%	0.6%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f KF-JG30-B3	0.8%	0.7%	0.9%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Labraceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Methyloiligellaceae	0.4%	0.4%	0.4%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiaceae	0.7%	0.9%	0.5%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiales-Incertae-Sedis	0.3%	0.2%	0.3%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhodomicrobiaceae -	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Xanthobacteraceae	2.3%	2.5%	2.2%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f uncultured	0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhodobacterales;f Rhodobacteraceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhodospirillales;f Rhodospirillaceae	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhodospirillales;f uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhodovibrionales;f Fodinicurvataceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Sneathiellales;f Sneathiellaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Sphingomonadales;f Sphingomonadaceae	1.9%	2.3%	1.6%
p	Proteobacteria;c	Alphaproteobacteria;o Tistrellales;f Geminicoccaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;Other	0.2%	0.2%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-Acetobacteraceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-Rhodospirillaceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-Rhodospirillales-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-Stella-sp.	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o uncultured;f uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;Other;Other	0.2%	0.3%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o Bdellovibrionales;f Bdellovibrionaceae	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Desulfarculales;f Desulfarculaceae	0.2%	0.1%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o Desulfuromonadales;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Desulfuromonadales;f Geobacteraceae	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o MBNT15;Other	0.1%	0.0%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o MBNT15;f uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o MBNT15;f uncultured-proteobacterium	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;Other	0.1%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f Archangiaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f B1rii41	0.2%	0.2%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f Blfdi19	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f Eel-36e1D6	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f Haliangiaceae	0.3%	0.4%	0.3%
p	Proteobacteria;c	Deltaproteobacteria;o Myxococcales;f Nannocystaceae	0.0%	0.0%	0.0%

p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	P3OB-42	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Phaselicystidaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae	0.1%	0.1%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	UASB-TL25	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Vulгатibacteraceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25	0.6%	0.7%	0.6%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	mle1-27	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-Green-Bay-ferromanganous-micronodule-bacterium-MND4	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-bacterium	0.3%	0.4%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Oligoflexales;f	Oligoflexaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	RCP2-54;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	RCP2-54;f	uncultured-prokaryote	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	SAR324-clade(Marine-group-B);f	bacterium-enrichment-culture-clone-B30(2011)	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Syntrophobacteriales;f	Syntrophaceae	0.1%	0.0%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;Other;Other			0.5%	0.6%	0.4%
p	Proteobacteria;c	Gammaproteobacteria;o	Acidiferrobacterales;f	Acidiferrobacteraceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Aeromonadales;f	Aeromonadaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;Other		1.7%	1.4%	2.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	A21b	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	B1-7BS	0.1%	0.1%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae	1.1%	1.3%	0.8%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Chromobacteriaceae	0.1%	0.1%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Rhodocyclaceae	0.3%	0.2%	0.5%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	SC-I-84	0.6%	0.5%	0.6%
p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	TRA3-20	0.7%	0.7%	0.7%
p	Proteobacteria;c	Gammaproteobacteria;o	CCD24;f	uncultured-bacterium	0.2%	0.3%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;f	Haliaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Diplorickettsiales;f	Diplorickettsiaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	EPR3968-O8a-Bc78;f	uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Enterobacteriales;f	Enterobacteriaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Gammaproteobacteria-Incertae-Sedis;f	Unknown-Family	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	JG36-GS-52;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	KI89A-clade;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;f	uncultured-bacterium	0.7%	1.2%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;f	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae	0.0%	0.1%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae	0.4%	0.7%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;f	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;f	Solimonadaceae	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacterales;f	Steroidobacteraceae	1.4%	2.0%	0.7%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae	0.0%	0.0%	0.1%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae	0.7%	1.4%	0.1%
p	Rokubacteria;c	NC10;o	Rokubacteriales;Other		0.0%	0.0%	0.0%
p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-Gram-positive-bacterium	0.1%	0.1%	0.0%
p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-bacterium	1.2%	1.5%	0.8%
p	Thaumarchaeota;c	Group-1.1c;Other;Other			0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosopumilales;f	Nitrosopumilaceae	0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae	1.3%	1.3%	1.3%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosotaleales;f	Nitrosotaleaceae	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;Other;Other			0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;Other		0.1%	0.1%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae	1.9%	1.0%	2.7%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Xiphinematobacteraceae	0.2%	0.3%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Methylacidiphilales;f	Methylacidiphilaceae	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Opitutales;f	Opitutaceae	1.4%	2.5%	0.3%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae	2.6%	1.6%	3.6%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;Other		0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Akkermansiaceae	0.0%	0.0%	0.0%

p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Rubritaleaceae	0.1%	0.1%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae	0.0%	0.0%	0.0%
p	WPS-2;Other;Other;Other				0.0%	0.0%	0.0%
p	Zixibacteria;Other;Other;Other				0.0%	0.0%	0.0%
p	Zixibacteria;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium	0.0%	0.0%	0.0%

Taxonomy Summary. Current Level:

Legend	Taxonomy				Total %	G1 %	G2 %
	Unclassified;Other;Other;Other;Other				0.5%	0.7%	0.3%
p	Acidobacteria;Other;Other;Other;Other				0.1%	0.2%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;Other;Other		0.1%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Acidobacteriaceae-(Subgroup-1);g uncultured	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Koribacteraceae;g Candidatus-Koribacter	0.1%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;Other	0.1%	0.1%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);Other	0.0%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);g Candidatus-Solibacter	1.8%	1.4%	2.2%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-12;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-13;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;Other;Other		0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-forest-soil-bacterium;g uncultured-forest-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);Other;Other;Other			2.6%	1.6%	3.6%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;Other;Other		0.1%	0.0%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteriales-bacterium;g uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-bacterium;g uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;Other	0.2%	0.1%	0.4%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g Blastocatella	0.1%	0.1%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g Stenotrophobacter	0.1%	0.0%	0.1%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g uncultured	0.3%	0.3%	0.3%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;Other;Other		0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;Other;Other		5.1%	2.3%	8.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-bacterium;g uncultured-bacterium	0.7%	0.8%	0.7%
p	Acidobacteria;c	Holophagae;o	Holophagales;f	Holophagaceae;g Geothrix	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;Other;Other		0.2%	0.2%	0.2%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteriales-bacterium;g uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-Acidobacterium-sp.;g uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-bacterium;g uncultured-bacterium	0.1%	0.2%	0.1%
p	Acidobacteria;c	Subgroup-11;Other;Other;Other			0.1%	0.1%	0.1%
p	Acidobacteria;c	Subgroup-11;o	uncultured-bacterium;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-15;Other;Other;Other			0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-15;o	uncultured-bacterium;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;Other;Other;Other			0.1%	0.1%	0.0%
p	Acidobacteria;c	Subgroup-17;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;o	uncultured-Acidobacteriales-bacterium;f	uncultured-Acidobacteriales-bacterium;g uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-17;o	uncultured-bacterium;f	uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.0%
p	Acidobacteria;c	Subgroup-18;Other;Other;Other			0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-18;o	uncultured-bacterium;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-20;o	uncultured-bacterium;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Subgroup-22;Other;Other;Other			0.1%	0.1%	0.1%

	p Acidobacteria;c Acidobacterium-sp.	Subgroup-22;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.;g	uncultured-	0.0%	0.1%	0.0%
	p Acidobacteria;c	Subgroup-22;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.1%	0.2%	0.1%
	p Acidobacteria;c	Subgroup-25;Other;Other;Other				0.0%	0.1%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium	Subgroup-25;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium;g	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-25;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-25;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-5;Other;Other;Other				0.0%	0.0%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium	Subgroup-5;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium;g	uncultured-	0.2%	0.2%	0.2%
	p Acidobacteria;c Acidobacterium-sp.	Subgroup-5;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.;g	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-5;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.2%	0.2%	0.2%
	p Acidobacteria;c	Subgroup-6;Other;Other;Other				5.4%	6.2%	4.6%
	p Acidobacteria;c bacterium-WX90	Subgroup-6;o	Acidobacteria-bacterium-WX90;f	Acidobacteria-bacterium-WX90;g	Acidobacteria-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-6;o	Unknown-Order;f	Unknown-Family;g	Luteitalea	0.0%	0.0%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium	Subgroup-6;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium;g	uncultured-	0.2%	0.2%	0.2%
	p Acidobacteria;c	Subgroup-6;o	uncultured-Acidobacteriaceae-bacterium;f	uncultured-Acidobacteriaceae-bacterium;g	uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;g uncultured-Acidobacteriales-bacterium	Subgroup-6;o	uncultured-Acidobacteriales-bacterium;f	uncultured-Acidobacteriales-bacterium;g	uncultured-Acidobacteriales-bacterium	0.1%	0.1%	0.1%
	p Acidobacteria;c Acidobacterium-sp.	Subgroup-6;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.;g	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c Holophagae-bacterium	Subgroup-6;o	uncultured-Holophagae-bacterium;f	uncultured-Holophagae-bacterium;g	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-6;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.8%	0.9%	0.8%
	p Acidobacteria;c proteobacterium	Subgroup-6;o	uncultured-beta-proteobacterium;f	uncultured-beta-proteobacterium;g	uncultured-beta-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-6;o	uncultured-proteobacterium;f	uncultured-proteobacterium;g	uncultured-proteobacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-9;Other;Other;Other				0.0%	0.0%	0.0%
	p Actinobacteria;Other;Other;Other;Other					0.0%	0.0%	0.1%
	p Actinobacteria;c	0319-7L14;Other;Other;Other				0.0%	0.0%	0.1%
	p Actinobacteria;c	0319-7L14;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;Other;Other;Other				0.3%	0.3%	0.3%
	p Actinobacteria;c	Acidimicrobiia;o	Acidimicrobiales;f	Acidimicrobiaceae;g	uncultured	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Actinomarinales;f	uncultured;Other		0.1%	0.1%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Actinomarinales;f	uncultured;g	uncultured-Actinomycetales-bacterium	0.6%	1.2%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	Actinomarinales;f	uncultured;g	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	IMCC26256;Other;Other			0.4%	0.4%	0.3%
	p Actinobacteria;c bacterium	Acidimicrobiia;o	IMCC26256;f	uncultured-Acidimicrobiales-bacterium;g	uncultured-Acidimicrobiales-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c bacterium	Acidimicrobiia;o	IMCC26256;f	uncultured-Acidimicrobiidae-bacterium;g	uncultured-Acidimicrobiidae-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-actinobacterium;g	uncultured-actinobacterium	0.0%	0.0%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	IMCC26256;f	uncultured-organism;g	uncultured-organism	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;Other;Other			0.1%	0.1%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Iamiaceae;g	Iamia	0.2%	0.2%	0.2%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Ilumatobacteraceae;Other		0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Ilumatobacteraceae;g	Ilumatobacter	0.1%	0.1%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Ilumatobacteraceae;g	uncultured	0.1%	0.2%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Ilumatobacteraceae;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Microtrichaceae;g	uncultured	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	uncultured;Other		0.1%	0.1%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	uncultured;g	uncultured-bacterium	0.1%	0.1%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	uncultured;Other;Other			0.3%	0.2%	0.5%
	p Actinobacteria;c bacterium	Acidimicrobiia;o	uncultured;f	uncultured-Acidimicrobiidae-bacterium;g	uncultured-Acidimicrobiidae-bacterium	0.0%	0.0%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-actinobacterium;g	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-bacterium;g	uncultured-bacterium	0.1%	0.0%	0.1%
	p Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.0%	0.1%
	p Actinobacteria;c	Actinobacteria;Other;Other;Other				0.0%	0.0%	0.0%
	p Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Mycobacteriaceae;g	Mycobacterium	0.3%	0.1%	0.5%
	p Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia	0.9%	0.5%	1.4%
	p Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Rhodococcus	0.2%	0.1%	0.3%
	p Actinobacteria;c	Actinobacteria;o	Frankiales;f	Cryptosporangiaceae;g	Cryptosporangium	0.0%	0.0%	0.0%
	p Actinobacteria;c	Actinobacteria;o	Frankiales;f	Cryptosporangiaceae;g	Fodinicola	0.0%	0.0%	0.1%
	p Actinobacteria;c	Actinobacteria;o	Frankiales;f	Frankiaceae;g	Frankia	0.0%	0.0%	0.0%

	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;g Blastococcus	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;g Geodermatophilus	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Nakamurellaceae;g Nakamurella	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Sporichthyaceae;g Sporichthya	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Sporichthyaceae;g uncultured	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	uncultured;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	uncultured;g uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Glycomycetales;f	Glycomycetaceae;g Glycomyces	1.0%	1.9%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Glycomycetales;f	Glycomycetaceae;g uncultured	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Kineosporiales;f	Kineosporiaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;Other;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Cellulomonadaceae;g Cellulomonas	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Demequinaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Intrasporangiaceae;Other	0.1%	0.1%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g Agromyces	0.1%	0.2%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g Leifsonia	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g Microbacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae;g Arthrobacter	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae;g Pseudarthrobacter	0.1%	0.0%	0.2%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae;g Cellulosimicrobium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae;g Promicromonospora	0.3%	0.5%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;Other	0.2%	0.2%	0.3%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Actinoplanes	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Dactylosporangium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Krasilnikovia	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Luedemannella	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Micromonospora	0.2%	0.2%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Phytomonospora	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g Stackebrandtia	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g uncultured	0.1%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;Other	0.3%	0.2%	0.3%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g Actinopolymorpha	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g Aeromicrobium	0.0%	0.1%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g Kribbella	0.7%	0.9%	0.5%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g Marmoricola	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g Nocardioides	0.5%	0.4%	0.7%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Propionibacteriaceae;g Microlunatus	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Propionibacteriaceae;g uncultured	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;Other	0.1%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;g Actinophytocola	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;g Allokutzneria	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;g Amycolatopsis	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;g Crossiella	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardaceae;g Pseudonocardia	0.1%	0.1%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Streptomycetales;f	Streptomycetaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptomycetales;f	Streptomycetaceae;g Streptomyces	7.6%	8.0%	7.3%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;g Nonomuraea	0.1%	0.2%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;g uncultured	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Thermomonosporaceae;Other	0.0%	0.0%	0.0%
	p	Actinobacteria;c		MB-A2-108;Other;Other;Other		0.1%	0.1%	0.1%
	p	Actinobacteria;c		MB-A2-108;o uncultured-actinobacterium;f uncultured-actinobacterium;g uncultured-actinobacterium		0.0%	0.0%	0.0%
	p	Actinobacteria;c		MB-A2-108;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium		0.6%	0.7%	0.4%
	p	Actinobacteria;c		MB-A2-108;o uncultured-bacterium-contig00016;f uncultured-bacterium-contig00016;g uncultured-bacterium-contig00016		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Nitriliruptoria;o	Euzebyales;f Euzebyaceae;g uncultured		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Rubrobacteria;o	Rubrobacterales;f Rubrobacteriaceae;g Rubrobacter		0.1%	0.0%	0.1%
	p	Actinobacteria;c		Thermoleophilia;Other;Other;Other		0.1%	0.1%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;Other;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f uncultured;Other		0.2%	0.2%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f uncultured;g uncultured-Gaiella-sp.		0.1%	0.1%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f uncultured;g uncultured-Rubrobacteria-bacterium		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f uncultured;g uncultured-actinobacterium		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f uncultured;g uncultured-bacterium		0.4%	0.4%	0.3%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f 67-14;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f 67-14;g uncultured-actinobacterium		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f 67-14;g uncultured-bacterium		0.3%	0.3%	0.2%

p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f	Solirubrobacteraceae;g	Conexibacter	0.0%	0.0%	0.0%
p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacterales;f	Solirubrobacteraceae;g	Solirubrobacter	0.2%	0.2%	0.2%
p	Actinobacteria;c	Thermoleophilia;o	uncultured;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales;f	Fimbriimonadaceae;Other		0.0%	0.0%	0.0%
p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales;f	Fimbriimonadaceae;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	BRC1;Other;Other;Other;Other					0.0%	0.0%	0.0%
p	BRC1;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;Other;Other;Other				0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Bacteroidetes-VC2.1-Bac22;Other;Other			0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;Other;Other			0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	37-13;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	37-13;g	uncultured-bacterium	0.0%	0.1%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;Other		0.4%	0.4%	0.5%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga	2.4%	4.8%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Dinghuibacter	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Ferruginibacter	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Filimonas	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavihumibacter	0.3%	0.5%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter	0.4%	0.2%	0.6%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavitalea	0.2%	0.3%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niabella	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niastella	0.8%	1.2%	0.4%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niveitalea	0.0%	0.1%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Parafilimonas	0.1%	0.1%	0.2%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Terrimonas	1.4%	2.3%	0.5%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured	1.9%	1.2%	2.6%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Saprospiraceae;g	uncultured	0.3%	0.2%	0.3%
p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	uncultured;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Cytophagaceae;g	Sporocytophaga	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Hymenobacteraceae;g	Adhaeribacter	0.1%	0.0%	0.2%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;Other		0.3%	0.1%	0.4%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	Ohtaekwangia	1.0%	1.3%	0.7%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured	0.7%	0.7%	0.8%
p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Spirosomaceae;g	Dyadobacter	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae;g	Fluviicola	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Flavobacteriaceae;g	Flavobacterium	0.3%	0.1%	0.5%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	NS9-marine-group;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	NS9-marine-group;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;Other;Other			0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	AKYH767;Other		0.1%	0.1%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	AKYH767;g	uncultured-bacterium	0.2%	0.2%	0.2%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	NS11-12-marine-group;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;Other		0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Olivibacter	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Pedobacter	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Solitalea	0.1%	0.2%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Sphingobacterium	0.2%	0.3%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	uncultured	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	env.OPS-17;Other		0.1%	0.1%	0.1%
p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	env.OPS-17;g	uncultured-bacterium	0.2%	0.1%	0.3%
p	Bacteroidetes;c	Ignavibacteria;o	Ignavibacteriales;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales;f	BSV26;Other		0.1%	0.1%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales;f	BSV26;g	uncultured-Chlorobi-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;Other;Other			0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-#0319-6E22;g	uncultured-bacterium-#0319-6E22	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-KF-JG30-B11;g	uncultured-bacterium-KF-JG30-B11	0.0%	0.0%	0.0%
p	Bacteroidetes;c	Ignavibacteria;o	SJA-28;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.1%	0.0%
p	Chloroflexi;Other;Other;Other;Other					0.0%	0.0%	0.0%
p	Chloroflexi;c	AD3;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;Other;Other;Other				0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;Other		0.3%	0.3%	0.4%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	Anaerolinea	0.0%	0.0%	0.0%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	Longilinea	0.4%	0.2%	0.7%
p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured	0.4%	0.4%	0.4%
p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;Other		0.1%	0.0%	0.1%
p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;g	uncultured-Litorilinea-sp.	0.1%	0.1%	0.2%
p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;g	uncultured-prokaryote	0.0%	0.0%	0.0%

p Chloroflexi;c Anaerolineae;o Caldilineales;f Caldilineaceae;g Litorilinea	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o Caldilineales;f Caldilineaceae;g uncultured	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o RBG-13-54-9;Other;Other	0.0%	0.0%	0.1%
p Chloroflexi;c Anaerolineae;o RBG-13-54-9;f uncultured-Caldilineaceae-bacterium;g uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o RBG-13-54-9;f uncultured-sludge-bacterium-A31;g uncultured-sludge-bacterium-A31	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;Other;Other	0.1%	0.2%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;Other	0.0%	0.0%	0.1%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;g uncultured-Caldilineales-bacterium	0.1%	0.0%	0.1%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;g uncultured-bacterium	0.1%	0.1%	0.2%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;g uncultured-sludge-bacterium-H8	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;g uncultured-sludge-bacterium-S14	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f A4b;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f uncultured-Caldilineaceae-bacterium;g uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o SBR1031;f uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Anaerolineae;o uncultured-Bellilinea-sp.;f uncultured-Bellilinea-sp.;g uncultured-Bellilinea-sp.	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;Other;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;f Chloroflexaceae;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;f Chloroflexaceae;g Candidatus-Chloroploca	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;f Herpetosiphonaceae;g Herpetosiphon	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;f Roseiflexaceae;g Roseiflexus	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Chloroflexales;f Roseiflexaceae;g uncultured	1.2%	0.4%	2.0%
p Chloroflexi;c Chloroflexia;o Kallotenuales;f AKIW781;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Kallotenuales;f AKIW781;g uncultured-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f AKYG1722;Other	0.0%	0.1%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f AKYG1722;g uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f AKYG1722;g uncultured-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f AKYG1722;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;Other	0.2%	0.2%	0.3%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-bacterium	0.1%	0.1%	0.1%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f Thermomicrobiaceae;g Nitrolancea	0.0%	0.0%	0.0%
p Chloroflexi;c Dehalococcoidia;o S085;Other;Other	0.2%	0.3%	0.1%
p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.2%	0.1%
p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Gitt-GS-136;Other;Other;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Gitt-GS-136;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.3%	0.4%	0.1%
p Chloroflexi;c JG30-KF-CM66;Other;Other;Other	0.0%	0.0%	0.0%
p Chloroflexi;c JG30-KF-CM66;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c JG30-KF-CM66;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.1%
p Chloroflexi;c KD4-96;Other;Other;Other	0.2%	0.3%	0.1%
p Chloroflexi;c KD4-96;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
p Chloroflexi;c KD4-96;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.4%	0.5%	0.3%
p Chloroflexi;c Ktedonobacteria;o C0119;Other;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Ktedonobacteria;o C0119;f uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;Other	0.0%	0.0%	0.0%
p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;g Thermosporothrix	0.0%	0.0%	0.0%
p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;g uncultured	0.0%	0.0%	0.0%
p Chloroflexi;c OLB14;Other;Other;Other	0.0%	0.0%	0.0%
p Chloroflexi;c OLB14;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.1%
p Chloroflexi;c OLB14;o uncultured-gamma-proteobacterium;f uncultured-gamma-proteobacterium;g uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
p Chloroflexi;c P2-11E;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.2%	0.1%	0.2%
p Chloroflexi;c TK10;Other;Other;Other	0.2%	0.2%	0.2%
p Chloroflexi;c TK10;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.1%
p Chloroflexi;c TK10;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.1%	0.0%
p Dadabacteria;c Dadabacteriaia;o Dadabacterales;f uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Dependuntiae;c Babeliae;o Babeliales;Other;Other	0.0%	0.0%	0.0%
p Dependuntiae;c Babeliae;o Babeliales;f Babeliaceae;g uncultured-bacterium	0.0%	0.0%	0.0%
p Dependuntiae;c Babeliae;o Babeliales;f Vermiphilaceae;Other	0.0%	0.0%	0.0%
p Dependuntiae;c Babeliae;o Babeliales;f Vermiphilaceae;g uncultured-bacterium	0.0%	0.0%	0.0%
p Elusimicrobia;c Elusimicrobia;o MVP-88;Other;Other	0.0%	0.0%	0.0%
p Elusimicrobia;c Lineage-IIa;Other;Other;Other	0.0%	0.0%	0.0%

p	Elusimicrobia;c	Lineage-IIa;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.1%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Elusimicrobia;c	Lineage-IIb;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Entotheonellaeota;c	Entotheonellia;o	Entotheonellales;f	Entotheonellaceae;Other		0.0%	0.0%	0.0%
p	Entotheonellaeota;c	Entotheonellia;o	Entotheonellales;f	Entotheonellaceae;g	Candidatus-Entotheonella	0.0%	0.0%	0.0%
p	Entotheonellaeota;c	Entotheonellia;o	Entotheonellales;f	Entotheonellaceae;g	uncultured-bacterium	0.0%	0.1%	0.0%
p	Euryarchaeota;c	Methanomicrobia;o	Methanosarcinales;f	Methanosarcinaceae;g	Methanosarcina	0.0%	0.0%	0.0%
p	Euryarchaeota;c	Thermoplasmata;Other;Other;Other				0.1%	0.1%	0.1%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;Other;Other			0.2%	0.1%	0.2%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;f	uncultured-archaeon;g	uncultured-archaeon	1.1%	0.6%	1.6%
p	Euryarchaeota;c	Thermoplasmata;o	Marine-Group-II;f	uncultured-haloarchaeon;g	uncultured-haloarchaeon	0.0%	0.0%	0.0%
p	Euryarchaeota;c	Thermoplasmata;o	Methanomassiliicoccales;f	uncultured;g	uncultured-archaeon	0.5%	0.0%	0.9%
p	Euryarchaeota;c	Thermoplasmata;o	uncultured;Other;Other			0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus	2.6%	0.8%	4.5%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Fictibacillus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Brevibacillus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Oxalophagus	0.1%	0.0%	0.2%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Paenibacillus	0.1%	0.1%	0.1%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Thermobacillus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Domibacillus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Lysinibacillus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Sporosarcina	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Thermoactinomycetaceae;g	Shimazuella	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Clostridiaceae-1;g	Clostridium-sensu-stricto-1	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Heliobacteriaceae;g	Hydrogenispora	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Peptostreptococcaceae;g	Sporacetigenium	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Ruminococcaceae;g	Ruminococcus-2	0.0%	0.0%	0.0%
p	GAL15;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	AKAU4049;Other;Other;Other				0.2%	0.3%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;Other;Other;Other				0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium;g	uncultured-Gemmatimonadales-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium;g	uncultured-Gemmatimonadetes-bacterium	0.0%	0.1%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;Other		0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatimonas	0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatirosa	0.1%	0.0%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured	2.2%	2.2%	2.3%
p	Gemmatimonadetes;c	Longimicrobia;o	Longimicrobiales;f	Longimicrobiaceae;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;Other;Other;Other				0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium;g	uncultured-Gemmatimonadales-bacterium	0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium;g	uncultured-Gemmatimonadetes-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.2%	0.2%	0.2%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales;f	Hydrogenedensaceae;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales;f	Hydrogenedensaceae;g	uncultured-bacterium-SJP-3	0.0%	0.0%	0.0%
p	Latescibacteria;Other;Other;Other;Other					0.3%	0.4%	0.1%
p	Latescibacteria;c	Latescibacteria;o	Latescibacterales;f	Latescibacteraceae;Other		0.0%	0.0%	0.0%
p	Latescibacteria;c	Latescibacteria;o	Latescibacterales;f	Latescibacteraceae;g	uncultured-bacterium	0.1%	0.2%	0.0%
p	Latescibacteria;c	uncultured-Acidobacterium-sp.;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.;g	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Fibrobacteres-bacterium;o	uncultured-Fibrobacteres-bacterium;f	uncultured-Fibrobacteres-bacterium;g	uncultured-Fibrobacteres-bacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Pelobacter-sp.;o	uncultured-Pelobacter-sp.;f	uncultured-Pelobacter-sp.;g	uncultured-Pelobacter-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.4%	0.5%	0.3%
p	Latescibacteria;c	uncultured-prokaryote;o	uncultured-prokaryote;f	uncultured-prokaryote;g	uncultured-prokaryote	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-proteobacterium;o	uncultured-proteobacterium;f	uncultured-proteobacterium;g	uncultured-proteobacterium	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-soil-bacterium;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Aenigmarchaeales;Other;Other			0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Aenigmarchaeales;f	uncultured-archaeon;g	uncultured-archaeon	0.0%	0.1%	0.0%
p	Nanoarchaeaeota;c	Nanohaloarchaeia;o	Deep-Sea-Euryarchaeotic-Group(DSEG);Other;Other			0.0%	0.0%	0.0%
p	Nanoarchaeaeota;c	Woesearchaeia;Other;Other;Other				0.1%	0.2%	0.1%

p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;f Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;g Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;f Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;g Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;f Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;g Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7	0.1%	0.1%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o uncultured-euryarchaeote;f uncultured-euryarchaeote;g uncultured-euryarchaeote	0.0%	0.0%	0.0%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira	0.5%	0.4%	0.7%
p Patescibacteria;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Kuenenbacteria;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.1%
p Patescibacteria;c ABY1;o Candidatus-Magasanikbacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Magasanikbacteria;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Uhrbacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Berkelbacteria;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Abawacabacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Abawacabacteria;f Candidatus-Abawacabacteria-bacterium-RBG_16_42_10;g Candidatus-Abawacabacteria-bacterium-RBG_16_42_10	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Peribacteria;f Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20;g Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20	0.0%	0.0%	0.0%
p Patescibacteria;c Microgenomatia;o Candidatus-Woesebacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Azambacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Azambacteria;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Kaiserbacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Nomurabacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Terrybacteria;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19;g Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f uncultured-deep-sea-bacterium;g uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o GWA2-38-13b;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o GWA2-38-13b;f uncultured-deep-sea-bacterium;g uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Saccharimonadia;o Saccharimonadales;Other;Other	0.2%	0.2%	0.3%
p Patescibacteria;c Saccharimonadia;o Saccharimonadales;f Saccharimonadaceae;g uncultured-bacterium	0.1%	0.0%	0.2%
p Patescibacteria;c Saccharimonadia;o Saccharimonadales;f uncultured-Candidatus-Saccharibacteria-bacterium;g uncultured-Candidatus-Saccharibacteria-bacterium	0.0%	0.0%	0.1%
p Patescibacteria;c Saccharimonadia;o Saccharimonadales;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.1%
p Patescibacteria;c WWE3;Other;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;c BD7-11;o uncultured-Planctomycetales-bacterium;f uncultured-Planctomycetales-bacterium;g uncultured-Planctomycetales-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c BD7-11;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c OM190;Other;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;c OM190;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c OM190;o uncultured-soil-bacterium;f uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;Other;Other;Other	0.2%	0.2%	0.2%
p Planctomycetes;c Phycisphaerae;o CCM11a;Other;Other	0.1%	0.0%	0.1%
p Planctomycetes;c Phycisphaerae;o CCM11a;f uncultured-Planctomycetia-bacterium;g uncultured-Planctomycetia-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o CCM11a;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.2%	0.1%
p Planctomycetes;c Phycisphaerae;o Phycisphaerales;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Phycisphaerales;f Phycisphaeraceae;Other	0.0%	0.0%	0.1%
p Planctomycetes;c Phycisphaerae;o Phycisphaerales;f Phycisphaeraceae;g uncultured	0.1%	0.1%	0.1%
p Planctomycetes;c Phycisphaerae;o Pla1-lineage;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Pla1-lineage;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f CPla-3-termite-group;Other	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f CPla-3-termite-group;g uncultured-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f CPla-3-termite-group;g uncultured-soil-bacterium-PBS-22	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f Tepidisphaeraceae;g uncultured-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f WD2101-soil-group;Other	0.4%	0.2%	0.6%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f WD2101-soil-group;g uncultured-bacterium	0.6%	0.5%	0.7%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f WD2101-soil-group;g uncultured-planctomycete	0.0%	0.0%	0.1%
p Planctomycetes;c Phycisphaerae;o Tepidisphaerales;f WD2101-soil-group;g uncultured-soil-bacterium	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o mle1-8;Other;Other	0.0%	0.0%	0.0%
p Planctomycetes;c Phycisphaerae;o mle1-8;f uncultured-bacterium;g uncultured-bacterium	0.1%	0.0%	0.1%
p Planctomycetes;c Pla3-lineage;Other;Other;Other	0.0%	0.0%	0.0%

p	Planctomycetes;c	Pla4-lineage;Other;Other;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Pla4-lineage;o uncultured-prokaryote;f uncultured-prokaryote;g uncultured-prokaryote	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Gemmatales;f Gemmataceae;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Gemmatales;f Gemmataceae;g Fimbrioglobus	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Gemmatales;f Gemmataceae;g Gemmata	0.1%	0.1%	0.1%
p	Planctomycetes;c	Planctomycetacia;o Gemmatales;f Gemmataceae;g uncultured	0.1%	0.0%	0.1%
p	Planctomycetes;c	Planctomycetacia;o Pirellulales;f Pirellulaceae;Other	0.0%	0.0%	0.1%
p	Planctomycetes;c	Planctomycetacia;o Pirellulales;f Pirellulaceae;g Bythopirellula	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Pirellulales;f Pirellulaceae;g Pirellula	0.1%	0.1%	0.1%
p	Planctomycetes;c	Planctomycetacia;o Pirellulales;f Pirellulaceae;g uncultured	0.1%	0.0%	0.1%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;Other;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f Rubinisphaeraceae;g Planctomicrobium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f Schlesneriaceae;g Planctopirus	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f uncultured;Other	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f uncultured;g uncultured-Planctomyces-sp.	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o Planctomycetales;f uncultured;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Planctomycetes;c	Planctomycetacia;o uncultured;f uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;Other;Other;Other;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;Other;Other;Other	1.8%	1.7%	2.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f Azospirillaceae;g Azospirillum	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f Inquilinaceae;g Inquilinus	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Azospirillales;f uncultured;g uncultured-bacterium	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;Other;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Caulobacteraceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Caulobacteraceae;g Brevundimonas	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Caulobacteraceae;g Phenyllobacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Caulobacteraceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Hyphomonadaceae;g Hirschia	0.1%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Hyphomonadaceae;g uncultured	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Caulobacterales;f Parvularculaceae;g Amphiplicatus	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f Elsteraceae;g Lacibacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f uncultured;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f uncultured;g uncultured-Acetobacteraceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f uncultured;g uncultured-alpha-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Elsterales;f uncultured;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Holosporales;f Holosporaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Micropepsales;f Micropepsaceae;g uncultured	0.1%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Reyranellales;f Reyranellaceae;g Reyranella	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Reyranellales;f Reyranellaceae;g uncultured	0.1%	0.2%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;Other;Other	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f A0839;g uncultured-bacterium	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Amb-16S-1323;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Beijerinckiaceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Beijerinckiaceae;g Bosea	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Beijerinckiaceae;g Microvirga	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f D05-2;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Devosiaceae;Other	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Devosiaceae;g Devosia	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Devosiaceae;g uncultured	0.1%	0.2%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Hyphomicrobiaceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Hyphomicrobiaceae;g Hyphomicrobium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Hyphomicrobiaceae;g Pedomicrobium	0.3%	0.5%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Hyphomicrobiaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f KF-JG30-B3;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f KF-JG30-B3;g uncultured-bacterium	0.8%	0.7%	0.9%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Labraceae;g Labrys	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Methylobacteriaceae;Other	0.0%	0.1%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Methylobacteriaceae;g uncultured	0.3%	0.3%	0.3%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiaceae;Other	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiaceae;g Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.3%	0.2%	0.3%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiaceae;g Ensifer	0.3%	0.5%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiaceae;g Mesorhizobium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiales-Incertae-Sedis;g Bauldia	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhizobiales-Incertae-Sedis;g uncultured	0.2%	0.2%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o Rhizobiales;f Rhodomicrobiaceae;g Rhodomicrobium	0.0%	0.0%	0.0%

p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;Other	1.0%	1.0%	1.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g Ancylobacter	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g Bradyrhizobium	0.5%	0.5%	0.4%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g Pseudolabrys	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g Rhodoplanes	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g uncultured	0.7%	0.7%	0.6%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;g uncultured-Rhizobiales-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;g uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodobacterales;f	Rhodobacteraceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodobacterales;f	Rhodobacteraceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	Rhodospirillaceae;g uncultured	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	uncultured;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	uncultured;g uncultured-Rhodospirillaceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodovibrionales;f	Fodinicurvataceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sneathiellales;f	Sneathiellaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;Other	0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g Altererythrobacter	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g Novosphingobium	0.2%	0.3%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g Sphingobium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g Sphingomonas	1.3%	1.6%	1.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Tistrellales;f	Geminicoccaceae;g Candidatus-Alysiosphaera	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Tistrellales;f	Geminicoccaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;Other;Other		0.2%	0.2%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Acetobacteraceae-bacterium;g uncultured-Acetobacteraceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Rhodospirillaceae-bacterium;g uncultured-Rhodospirillaceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Rhodospirillales-bacterium;g uncultured-Rhodospirillales-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Stella-sp.;g uncultured-Stella-sp.	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-bacterium;g uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-soil-bacterium;g uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;Other;Other;Other			0.2%	0.3%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Bdellovibrionales;f	Bdellovibrionaceae;g Bdellovibrio	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfarculales;f	Desulfarculaceae;g uncultured	0.2%	0.1%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;Other;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;f	Geobacteraceae;g Geobacter	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;Other;Other		0.1%	0.0%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;f	uncultured-bacterium;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;f	uncultured-proteobacterium;g uncultured-proteobacterium	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;Other;Other		0.1%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Archangiaceae;g Anaeromyxobacter	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	BIrii41;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	BIrii41;g uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Blfdi19;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Blfdi19;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Eel-36e1D6;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g Haliangium	0.3%	0.4%	0.3%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g Nannocystis	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	P3OB-42;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	P3OB-42;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Phaselicytidaceae;g Phaselicystis	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;Other	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;g Pajaroellobacter	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;g Polyangium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g Sandaracinus	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g uncultured	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	UASB-TL25;g uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Vulgatibacteraceae;g Vulgatibacter	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;Other	0.5%	0.5%	0.5%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g uncultured-delta-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g uncultured-proteobacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g uncultured-soil-bacterium	0.1%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g unidentified	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	mle1-27;Other	0.0%	0.0%	0.0%

	p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	mle1-27;g	uncultured-delta-proteobacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	uncultured;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	uncultured;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-Green-Bay-ferromanganous-micronodule-bacterium-MND4;g	uncultured-Green-Bay-ferromanganous-micronodule-bacterium-MND4	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-bacterium;g	uncultured-bacterium	0.3%	0.4%	0.2%
	p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-proteobacterium;g	uncultured-proteobacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	Oligoflexales;f	Oligoflexaceae;g	Oligoflexus	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	RCP2-54;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	RCP2-54;f	uncultured-prokaryote;g	uncultured-prokaryote	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	SAR324-clade(Marine-group-B);f	bacterium-enrichment-culture-clone-B30(2011);g	bacterium-enrichment-culture-clone-B30(2011)	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Deltaproteobacteria;o	Syntrophobacterales;f	Syntrophaceae;g	uncultured	0.1%	0.0%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;Other;Other				0.5%	0.6%	0.4%
	p	Proteobacteria;c	Gammaproteobacteria;o	Acidiferrobacterales;f	Acidiferrobacteraceae;g	Sulfurifustis	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Aeromonadales;f	Aeromonadaceae;g	Aeromonas	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;Other;Other			1.7%	1.4%	2.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	A21b;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	A21b;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	B1-7BS;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	B1-7BS;g	uncultured-bacterium	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;Other		0.2%	0.2%	0.3%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Bordetella	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Burkholderia-Caballeronia-Paraburkholderia	0.0%	0.0%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Comamonas	0.1%	0.1%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Cupriavidus	0.4%	0.7%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Hydrogenophaga	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Massilia	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Noviherbaspirillum	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Ramlibacter	0.2%	0.2%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Rhizobacter	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Sphaerotilus	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	Variovorax	0.1%	0.1%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Burkholderiaceae;g	uncultured	0.1%	0.0%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Chromobacteriaceae;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Chromobacteriaceae;g	Paludibacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Rhodocyclaceae;Other		0.3%	0.1%	0.4%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Rhodocyclaceae;g	Azoarcus	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	Rhodocyclaceae;g	Thauera	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	SC-I-84;Other		0.3%	0.3%	0.2%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	SC-I-84;g	uncultured-bacterium	0.2%	0.1%	0.2%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	SC-I-84;g	uncultured-beta-proteobacterium	0.1%	0.1%	0.2%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	TRA3-20;Other		0.6%	0.7%	0.5%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	TRA3-20;g	uncultured-bacterium	0.1%	0.1%	0.2%
	p	Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacteriales;f	TRA3-20;g	uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	CCD24;f	uncultured-bacterium;g	uncultured-bacterium	0.2%	0.3%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;f	Haliaceae;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Diplorickettsiales;f	Diplorickettsiaceae;g	Aquicella	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	EPR3968-O8a-Bc78;f	uncultured-gamma-proteobacterium;g	uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Enterobacteriales;f	Enterobacteriaceae;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Enterobacteriales;f	Enterobacteriaceae;g	Pantoea	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Gammaproteobacteria-Incertae-Sedis;f	Unknown-Family;g	uncultured	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	JG36-GS-52;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	KI89A-clade;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;f	uncultured-bacterium;g	uncultured-bacterium	0.7%	1.2%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	PLTA13;f	uncultured-proteobacterium;g	uncultured-proteobacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	Acinetobacter	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	uncultured	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Azotobacter	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas	0.4%	0.7%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;Other;Other			0.0%	0.0%	0.0%

p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;Other;Other			0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;f	Solimonadaceae;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacterales;f	Steroidobacteraceae;g	uncultured	1.4%	2.0%	0.7%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	Dokdonella	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	Dyella	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	uncultured	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Arenimonas	0.1%	0.1%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Luteimonas	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Lysobacter	0.6%	1.2%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Pseudoxanthomonas	0.0%	0.1%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Stenotrophomonas	0.0%	0.0%	0.0%
p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Thermomonas	0.0%	0.0%	0.0%
p	Rokubacteria;c	NC10;o	Rokubacteriales;Other;Other			0.0%	0.0%	0.0%
p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-Gram-positive-bacterium;g	uncultured-Gram-positive-bacterium	0.1%	0.1%	0.0%
p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-bacterium;g	uncultured-bacterium	1.2%	1.5%	0.8%
p	Thaumarchaeota;c	Group-1.1c;Other;Other;Other				0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosopumilales;f	Nitrosopumilaceae;g	Candidatus-Nitrosotenuis	0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;Other		0.5%	0.5%	0.5%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	Candidatus-Nitrocosmicus	0.1%	0.1%	0.1%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	Candidatus-Nitrososphaera	0.4%	0.4%	0.4%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	uncultured-archaeon	0.3%	0.3%	0.2%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	uncultured-bacterium	0.0%	0.0%	0.0%
p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosotaleales;f	Nitrosotaleaceae;g	uncultured-archaeon	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;Other;Other;Other				0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;Other;Other			0.1%	0.1%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;Other		0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;g	Candidatus-Udaeobacter	1.9%	1.0%	2.7%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Xiphinematobacteraceae;g	Candidatus-Xiphinematobacter	0.2%	0.3%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Methylocidiphilales;f	Methylocidiphilaceae;g	uncultured	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Opitutales;f	Opitutaceae;Other		1.2%	2.3%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Opitutales;f	Opitutaceae;g	Lacunisphaera	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Opitutales;f	Opitutaceae;g	Opitutus	0.1%	0.1%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae;Other		1.1%	0.6%	1.5%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae;g	uncultured-Verrucomicrobia-bacterium	0.0%	0.0%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae;g	uncultured-bacterium	1.1%	0.7%	1.5%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae;g	uncultured-soil-bacterium	0.3%	0.2%	0.4%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Pedosphaerales;f	Pedosphaeraceae;g	uncultured-subdivision-3-bacterium	0.1%	0.0%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;Other;Other			0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Akkermansiaceae;g	Akkermansia	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Rubritaleaceae;g	Luteolibacter	0.1%	0.1%	0.1%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;Other		0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;g	Verrucomicrobium	0.0%	0.0%	0.0%
p	Verrucomicrobia;c	Verrucomicrobiae;o	Verrucomicrobiales;f	Verrucomicrobiaceae;g	uncultured	0.0%	0.0%	0.0%
p	WPS-2;Other;Other;Other;Other					0.0%	0.0%	0.0%
p	Zixibacteria;Other;Other;Other;Other					0.0%	0.0%	0.0%
p	Zixibacteria;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium	0.0%	0.0%	0.0%

Taxonomy Summary. Current Level:

						Total	G1	G2	
Legend	Taxonomy					%	%	%	
	Unclassified;Other;Other;Other;Other;Other					0.5%	0.7%	0.3%	
p	Acidobacteria;Other;Other;Other;Other;Other					0.1%	0.2%	0.1%	
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;Other;Other;Other			0.1%	0.0%	0.1%	
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Acidobacteriaceae-(Subgroup-1);g	uncultured;s	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Koribacteraceae;g	Candidatus-Koribacter;Other	0.0%	0.0%	0.0%	
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	Koribacteraceae;g	Candidatus-Koribacter;s	uncultured-bacterium	0.1%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;Other;Other		0.1%	0.1%	0.1%	
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g	uncultured-Acidobacteria-bacterium;s	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.1%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g	uncultured-Acidobacteriaceae-bacterium;s	uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Acidobacteriales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Acidobacteria;c	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);Other;Other		0.0%	0.0%	0.1%	
p	Acidobacteria;c	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);g	Candidatus-Solibacter;Other	0.9%	0.6%	1.3%	

	p Acidobacteria;c Acidobacteria-bacterium	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);g	Candidatus-Solibacter;s	uncultured-	0.3%	0.3%	0.3%
	p Acidobacteria;c Acidobacteriales-bacterium	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);g	Candidatus-Solibacter;s	uncultured-	0.2%	0.2%	0.2%
	p Acidobacteria;c bacterium	Acidobacteriia;o	Solibacterales;f	Solibacteraceae-(Subgroup-3);g	Candidatus-Solibacter;s	uncultured-	0.3%	0.3%	0.4%
	p Acidobacteria;c	Acidobacteriia;o	Subgroup-12;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;s	Acidobacteriia;o	Subgroup-13;f	uncultured-Acidobacteria-bacterium;g	uncultured-Acidobacteria-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Acidobacteriia;o	Subgroup-2;Other;Other;Other				0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;s	Acidobacteriia;o	Subgroup-2;f	uncultured-Acidobacteria-bacterium;g	uncultured-Acidobacteria-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Acidobacteriia;o	Subgroup-2;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.0%
	p Acidobacteria;c bacterium;s	Acidobacteriia;o	Subgroup-2;f	uncultured-forest-soil-bacterium;g	uncultured-forest-soil-	uncultured-forest-soil-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Acidobacteriia;o	Subgroup-2;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);Other;Other;Other;Other					2.6%	1.6%	3.6%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	11-24;Other;Other;Other				0.1%	0.0%	0.1%
	p Acidobacteria;c bacterium;s	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteria-bacterium;g	uncultured-Acidobacteria-	uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
	p Acidobacteria;c Acidobacteriales-bacterium;s	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-Acidobacteriales-bacterium;g	uncultured-	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Blastocatellia-(Subgroup-4);o	11-24;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.2%	0.1%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;Other;Other			0.2%	0.1%	0.4%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	Blastocatella;Other		0.0%	0.0%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	Blastocatella;s	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	Blastocatella;s	uncultured-bacterium	0.1%	0.0%	0.1%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	Stenotrophobacter;Other		0.0%	0.0%	0.1%
	p Acidobacteria;c bacterium	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	Stenotrophobacter;s	uncultured-	0.0%	0.0%	0.0%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	uncultured;s	uncultured-	0.3%	0.3%	0.3%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Blastocatellales;f	Blastocatellaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	DS-100;Other;Other;Other				0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;s	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-Acidobacteria-bacterium;g	uncultured-Acidobacteria-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Blastocatellia-(Subgroup-4);o	DS-100;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Blastocatellia-(Subgroup-4);o	Elev-16S-573;Other;Other;Other				5.1%	2.3%	8.0%
	p Acidobacteria;c Acidobacteria-bacterium;s	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-Acidobacteria-bacterium;g	uncultured-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;s	Blastocatellia-(Subgroup-4);o	Elev-16S-573;f	uncultured-bacterium;g	uncultured-	uncultured-bacterium	0.7%	0.8%	0.7%
	p Acidobacteria;c	Holophagae;o	Holophagales;f	Holophagaceae;g	Geothrix;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Holophagae;o	Subgroup-7;Other;Other;Other				0.2%	0.2%	0.2%
	p Acidobacteria;c bacterium;s	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteria-bacterium;g	uncultured-Acidobacteria-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium;s	Holophagae;o	Subgroup-7;f	uncultured-Acidobacteriales-bacterium;g	uncultured-Acidobacteriales-	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c sp;s	Holophagae;o	Subgroup-7;f	uncultured-Acidobacterium-sp.;g	uncultured-Acidobacterium-	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
	p Acidobacteria;c	Holophagae;o	Subgroup-7;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.2%	0.1%
	p Acidobacteria;c	Subgroup-11;Other;Other;Other;Other					0.1%	0.1%	0.1%
	p Acidobacteria;c bacterium	Subgroup-11;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-15;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Subgroup-15;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-17;Other;Other;Other;Other					0.1%	0.1%	0.0%
	p Acidobacteria;c Acidobacteria-bacterium;s	Subgroup-17;o	uncultured-Acidobacteria-bacterium;f	uncultured-Acidobacteria-bacterium;g	uncultured-	uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c	Subgroup-17;o	uncultured-Acidobacteriales-bacterium;f	uncultured-Acidobacteriales-	uncultured-Acidobacteriales-	uncultured-Acidobacteriales-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Subgroup-17;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.0%
	p Acidobacteria;c	Subgroup-18;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Acidobacteria;c bacterium	Subgroup-18;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%

	p Acidobacteria;c Subgroup-20;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-22;Other;Other;Other;Other	0.1%	0.1%	0.1%
	p Acidobacteria;c Subgroup-22;o uncultured-Acidobacterium-sp.;f uncultured-Acidobacterium-sp.;g uncultured-Acidobacterium-sp.;s uncultured-Acidobacterium-sp.	0.0%	0.1%	0.0%
	p Acidobacteria;c Subgroup-22;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.1%	0.2%	0.1%
	p Acidobacteria;c Subgroup-25;Other;Other;Other;Other	0.0%	0.1%	0.0%
	p Acidobacteria;c Subgroup-25;o uncultured-Acidobacteria-bacterium;f uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium;s uncultured-Acidobacteria-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-25;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-25;o uncultured-soil-bacterium;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-5;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-5;o uncultured-Acidobacteria-bacterium;f uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium;s uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
	p Acidobacteria;c Subgroup-5;o uncultured-Acidobacterium-sp.;f uncultured-Acidobacterium-sp.;g uncultured-Acidobacterium-sp.;s uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-5;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.2%	0.2%	0.2%
	p Acidobacteria;c Subgroup-6;Other;Other;Other;Other	5.4%	6.2%	4.6%
	p Acidobacteria;c Subgroup-6;o Acidobacteria-bacterium-WX90;f Acidobacteria-bacterium-WX90;g Acidobacteria-bacterium-WX90;s Acidobacteria-bacterium-WX90	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o Unknown-Order;f Unknown-Family;g Luteitalea;Other	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o Unknown-Order;f Unknown-Family;g Luteitalea;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o uncultured-Acidobacteria-bacterium;f uncultured-Acidobacteria-bacterium;g uncultured-Acidobacteria-bacterium;s uncultured-Acidobacteria-bacterium	0.2%	0.2%	0.2%
	p Acidobacteria;c Subgroup-6;o uncultured-Acidobacteriaceae-bacterium;f uncultured-Acidobacteriaceae-bacterium;g uncultured-Acidobacteriaceae-bacterium;s uncultured-Acidobacteriaceae-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o uncultured-Acidobacteriales-bacterium;f uncultured-Acidobacteriales-bacterium;g uncultured-Acidobacteriales-bacterium;s uncultured-Acidobacteriales-bacterium	0.1%	0.1%	0.1%
	p Acidobacteria;c Subgroup-6;o uncultured-Acidobacterium-sp.;f uncultured-Acidobacterium-sp.;g uncultured-Acidobacterium-sp.;s uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o uncultured-Holophagae-bacterium;f uncultured-Holophagae-bacterium;g uncultured-Holophagae-bacterium;s uncultured-Holophagae-bacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.8%	0.9%	0.8%
	p Acidobacteria;c Subgroup-6;o uncultured-beta-proteobacterium;f uncultured-beta-proteobacterium;g uncultured-beta-proteobacterium;s uncultured-beta-proteobacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-6;o uncultured-proteobacterium;f uncultured-proteobacterium;g uncultured-proteobacterium;s uncultured-proteobacterium	0.0%	0.0%	0.0%
	p Acidobacteria;c Subgroup-9;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Actinobacteria;Other;Other;Other;Other;Other	0.0%	0.0%	0.1%
	p Actinobacteria;c 0319-7L14;Other;Other;Other;Other	0.0%	0.0%	0.1%
	p Actinobacteria;c 0319-7L14;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;Other;Other;Other;Other	0.3%	0.3%	0.3%
	p Actinobacteria;c Acidimicrobiia;o Acidimicrobiales;f Acidimicrobiaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o Actinomarinales;f uncultured;Other;Other	0.1%	0.1%	0.0%
	p Actinobacteria;c Acidimicrobiia;o Actinomarinales;f uncultured;g uncultured-Actinomycetales-bacterium;s uncultured-Actinomycetales-bacterium	0.6%	1.2%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Actinomarinales;f uncultured;g uncultured-actinobacterium;s uncultured-actinobacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;Other;Other;Other	0.4%	0.4%	0.3%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;f uncultured-Acidimicrobiales-bacterium;g uncultured-Acidimicrobiales-bacterium;s uncultured-Acidimicrobiales-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;f uncultured-Acidimicrobidae-bacterium;g uncultured-Acidimicrobidae-bacterium;s uncultured-Acidimicrobidae-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;f uncultured-actinobacterium;g uncultured-actinobacterium;s uncultured-actinobacterium	0.0%	0.0%	0.1%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o IMCC26256;f uncultured-organism;g uncultured-organism;s uncultured-organism	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;Other;Other;Other	0.1%	0.1%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Iamiaceae;g Iamia;Other	0.1%	0.1%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Iamiaceae;g Iamia;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Ilumatobacteraceae;Other;Other	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Ilumatobacteraceae;g Ilumatobacter;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Ilumatobacteraceae;g uncultured;Other	0.0%	0.0%	0.0%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Ilumatobacteraceae;g uncultured;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Actinobacteria;c Acidimicrobiia;o Microtrichales;f Ilumatobacteraceae;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%

	p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	Microtrichaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	uncultured;Other;Other			0.1%	0.1%	0.1%
	p	Actinobacteria;c	Acidimicrobiia;o	Microtrichales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
	p	Actinobacteria;c	Acidimicrobiia;o	uncultured;Other;Other;Other				0.3%	0.2%	0.5%
	p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-Acidimicrobidae-bacterium;g	uncultured-Acidimicrobidae-bacterium;s	uncultured-Acidimicrobidae-bacterium	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-actinobacterium;g	uncultured-actinobacterium;s	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.0%	0.1%
	p	Actinobacteria;c	Acidimicrobiia;o	uncultured;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Mycobacteriaceae;g	Mycobacterium;Other		0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Mycobacteriaceae;g	Mycobacterium;s	uncultured-bacterium	0.3%	0.1%	0.4%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia;s	Nocardia-niigatensis	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia;s	Nocardia-pseudovaccinii-NBRC-100343	0.9%	0.4%	1.3%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia;s	Nocardia-sp.-HBUD30303	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Nocardia;s	Nocardia-sp.-HBUM-79084	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Rhodococcus;Other		0.2%	0.1%	0.3%
	p	Actinobacteria;c	Actinobacteria;o	Corynebacteriales;f	Nocardiaceae;g	Rhodococcus;s	Rhodococcus-ruber	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Cryptosporangiaceae;g	Cryptosporangium;s	Cryptosporangium-aurantiacum	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Cryptosporangiaceae;g	Fodinicola;s	uncultured-bacterium	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Frankiaceae;g	Frankia;s	Frankia-sp.	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;g	Blastococcus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Geodermatophilaceae;g	Geodermatophilus;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Nakamurellaceae;g	Nakamurella;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Sporichthyaceae;g	Sporichthya;s	Sporichthya-polymorpha-DSM-43042	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	Sporichthyaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	uncultured;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Frankiales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Glycomycetales;f	Glycomycetaceae;g	Glycomyces;Other		1.0%	1.9%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Glycomycetales;f	Glycomycetaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Kineosporiales;f	Kineosporiaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;Other;Other;Other				0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Cellulomonadaceae;g	Cellulomonas;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Demequinaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Intrasporangiaceae;Other;Other			0.1%	0.1%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g	Agromyces;Other		0.1%	0.1%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g	Agromyces;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g	Leifsonia;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Microbacteriaceae;g	Microbacterium;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae;g	Arthrobacter;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae;g	Arthrobacter;s	Arthrobacter-crystallopoietes	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Micrococcaceae;g	Pseudarthrobacter;Other		0.1%	0.0%	0.2%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae;g	Cellulosimicrobium;s	Cellulosimicrobium-cellulans	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae;g	Promicromonospora;Other		0.1%	0.3%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micrococcales;f	Promicromonosporaceae;g	Promicromonospora;s	Cellulomonas-sp.-ZYG2	0.1%	0.2%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;Other;Other			0.2%	0.2%	0.3%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Actinoplanes;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Dactylosporangium;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Krasilnikovia;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Luedemannella;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Luedemannella;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Micromonospora;Other		0.2%	0.2%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Phytomonospora;s	Phytomonospora-endophytica	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	Stackebrandtia;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Micromonosporales;f	Micromonosporaceae;g	uncultured;s	uncultured-bacterium	0.1%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;Other;Other			0.3%	0.2%	0.3%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Actinopolymorpha;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Aeromicrobium;s	uncultured-bacterium	0.0%	0.1%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Kribbella;s	uncultured-bacterium	0.7%	0.9%	0.5%

	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Marmoricola;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Nocardioides;Other		0.5%	0.3%	0.6%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Nocardioides;s	uncultured-Nocardioides-sp.	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Nocardioides;s	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Nocardioides;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Nocardioidaceae;g	Nocardioides;s	uncultured-organism	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Propionibacteriaceae;g	Microclunatus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Propionibacteriales;f	Propionibacteriaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;Other;Other			0.1%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Actinophytocola;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Actinophytocola;s	actinobacterium-	0.0%	0.0%	0.0%
	ND2ZKDS4									
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Allokutzneria;s	Allokutzneria-multivorans	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Amycolatopsis;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Crossiella;s	uncultured-bacterium	0.0%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Pseudonocardia;Other		0.1%	0.0%	0.1%
	p	Actinobacteria;c	Actinobacteria;o	Pseudonocardiales;f	Pseudonocardiaceae;g	Pseudonocardia;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptomycetales;f	Streptomycetaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptomycetales;f	Streptomycetaceae;g	Streptomyces;Other		7.6%	8.0%	7.3%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;g	Nonomuraea;s	uncultured-bacterium	0.1%	0.2%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Streptosporangiaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Actinobacteria;o	Streptosporangiales;f	Thermomonosporaceae;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	MB-A2-108;Other;Other;Other;Other					0.1%	0.1%	0.1%
	p	Actinobacteria;c	MB-A2-108;o	uncultured-actinobacterium;f	uncultured-actinobacterium;g	uncultured-actinobacterium;s	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.6%	0.7%	0.4%
	p	Actinobacteria;c	MB-A2-108;o	uncultured-bacterium-contig00016;f	uncultured-bacterium-contig00016;g	uncultured-bacterium-contig00016;s	uncultured-bacterium-contig00016	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Nitriliruptoria;o	Euzebyales;f	Euzebyaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Rubrobacteria;o	Rubrobacteriales;f	Rubrobacteriaceae;g	Rubrobacter;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Rubrobacteria;o	Rubrobacteriales;f	Rubrobacteriaceae;g	Rubrobacter;s	uncultured-Actinomycetales-bacterium	0.1%	0.0%	0.1%
	p	Actinobacteria;c	Rubrobacteria;o	Rubrobacteriales;f	Rubrobacteriaceae;g	Rubrobacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;Other;Other;Other;Other					0.1%	0.1%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;Other;Other;Other				0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured;Other;Other			0.2%	0.2%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured;g	uncultured-Gaiella-sp.;s	uncultured-Gaiella-sp.	0.1%	0.1%	0.1%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured;g	uncultured-Rubrobacteria-bacterium;s	uncultured-Rubrobacteria-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured;g	uncultured-actinobacterium;s	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Gaiellales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.4%	0.4%	0.3%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	67-14;Other;Other			0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	67-14;g	uncultured-actinobacterium;s	uncultured-actinobacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	67-14;g	uncultured-bacterium;s	uncultured-bacterium	0.3%	0.3%	0.2%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	Solirubrobacteraceae;g	Conexibacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	Solirubrobacteraceae;g	Solirubrobacter;Other		0.0%	0.0%	0.0%
	p	Actinobacteria;c	Thermoleophilia;o	Solirubrobacteriales;f	Solirubrobacteraceae;g	Solirubrobacter;s	uncultured-bacterium	0.2%	0.2%	0.2%
	p	Actinobacteria;c	Thermoleophilia;o	uncultured;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales;f	Fimbriimonadaceae;Other;Other			0.0%	0.0%	0.0%
	p	Armatimonadetes;c	Fimbriimonadia;o	Fimbriimonadales;f	Fimbriimonadaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	BRC1;Other;Other;Other;Other;Other							0.0%	0.0%
	p	BRC1;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Bacteroidetes-VC2.1-Bac22;Other;Other;Other						0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;Other;Other;Other						0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	37-13;Other;Other			0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	37-13;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;Other;Other			0.4%	0.4%	0.5%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga;Other		2.3%	4.6%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga;s	Chitinophaga-rupis	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga;s	Chitinophaga-sp.-A5I53	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga;s	uncultured-Flexibacter-sp.	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Chitinophaga;s	uncultured-bacterium	0.1%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Dinghuibacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Ferruginibacter;Other		0.0%	0.0%	0.0%

	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Filimonas;s bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c NBRC-106054	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavihumibacter;s Flavihumibacter-petaseus-	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavihumibacter;s uncultured-bacterium	0.3%	0.5%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter;Other	0.1%	0.1%	0.2%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter;s Flavisolibacter-sp.-LCS9	0.0%	0.0%	0.0%
	p	Bacteroidetes;c bacterium	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter;s uncultured-Bacteroidetes-	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter;s uncultured-Flavisolibacter-sp.	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavisolibacter;s uncultured-bacterium	0.2%	0.2%	0.3%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Flavitalea;s uncultured-bacterium	0.2%	0.3%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niabella;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niabella;s Niabella-sp.-UI6	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niabella;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niastella;Other	0.2%	0.2%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niastella;s uncultured-Niastella-sp.	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niastella;s uncultured-bacterium	0.6%	0.9%	0.3%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Niveitalea;s Niveitalea-solisilvae	0.0%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Parafilimonas;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Parafilimonas;s uncultured-bacterium	0.1%	0.1%	0.2%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Terrimonas;Other	0.2%	0.3%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Terrimonas;s uncultured-Bacteroidetes-bacterium	0.0%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	Terrimonas;s uncultured-bacterium	1.1%	1.9%	0.3%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;Other	1.5%	0.9%	2.2%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s estrogen-degrading-bacterium-KC2	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s uncultured-Bacteroidetes-bacterium	0.1%	0.1%	0.1%
	p	Bacteroidetes;c bacterium	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s uncultured-Chitinophagaceae-	0.1%	0.1%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s uncultured-bacterium	0.1%	0.1%	0.2%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Chitinophagaceae;g	uncultured;s uncultured-soil-bacterium	0.0%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Saprospiraceae;g	uncultured;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Saprospiraceae;g	uncultured;s uncultured-Bacteroidetes-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	Saprospiraceae;g	uncultured;s uncultured-bacterium	0.2%	0.2%	0.2%
	p	Bacteroidetes;c	Bacteroidia;o	Chitinophagales;f	uncultured;g	uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Cytophagaceae;g	Sporocytophaga;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Hymenobacteraceae;g	Adhaeribacter;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Hymenobacteraceae;g	Adhaeribacter;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Hymenobacteraceae;g	Adhaeribacter;s uncultured-soil-bacterium	0.1%	0.0%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;Other;Other		0.3%	0.1%	0.4%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	Ohtaekwangia;Other	0.1%	0.0%	0.2%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	Ohtaekwangia;s Globodera-pallida	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	Ohtaekwangia;s uncultured-bacterium	0.9%	1.3%	0.5%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;Other	0.4%	0.3%	0.6%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;s uncultured-Flexibacter-sp.	0.0%	0.0%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;s uncultured-Ohtaekwangia-sp.	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;s uncultured-Sphingobacteriales-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;s uncultured-bacterium	0.2%	0.3%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Microscillaceae;g	uncultured;s uncultured-soil-bacterium	0.1%	0.0%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Cytophagales;f	Spirosomaceae;g	Dyadobacter;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae;Other;Other		0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae;g	Fluviicola;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Crocinitomicaceae;g	Fluviicola;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Flavobacteriaceae;g	Flavobacterium;Other	0.3%	0.1%	0.4%
	p	Bacteroidetes;c bacterium	Bacteroidia;o	Flavobacteriales;f	Flavobacteriaceae;g	Flavobacterium;s uncultured-Bacteroidetes-	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	Flavobacteriaceae;g	Flavobacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	NS9-marine-group;Other;Other		0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Flavobacteriales;f	NS9-marine-group;g	uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;Other;Other;Other			0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	AKYH767;Other;Other		0.1%	0.1%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	AKYH767;g	uncultured-bacterium;s uncultured-bacterium	0.2%	0.2%	0.2%
	p	Bacteroidetes;c bacterium	Bacteroidia;o	Sphingobacteriales;f	NS11-12-marine-group;g	uncultured-bacterium;s uncultured-	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;Other;Other		0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Olivibacter;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Pedobacter;Other	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Solitalea;Other	0.0%	0.1%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Solitalea;s Solitalea-canadensis	0.1%	0.1%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	Sphingobacterium;Other	0.2%	0.3%	0.0%

	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	Sphingobacteriaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	env.OPS-17;Other;Other			0.1%	0.1%	0.1%
	p	Bacteroidetes;c	Bacteroidia;o	Sphingobacteriales;f	env.OPS-17;g	uncultured-bacterium;s	uncultured-bacterium	0.2%	0.1%	0.3%
	p	Bacteroidetes;c	Ignavibacteria;o	Ignavibacteriales;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales;f	BSV26;Other;Other			0.1%	0.1%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	Kryptoniales;f	BSV26;g	uncultured-Chlorobi-bacterium;s	uncultured-Chlorobi-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	OPB56;Other;Other;Other				0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-#0319-6E22;g	uncultured-bacterium-#0319-6E22;s	uncultured-bacterium-#0319-6E22	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	OPB56;f	uncultured-bacterium-KF-JG30-B11;g	uncultured-bacterium-KF-JG30-B11;s	uncultured-bacterium-KF-JG30-B11	0.0%	0.0%	0.0%
	p	Bacteroidetes;c	Ignavibacteria;o	SJA-28;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.1%	0.0%
	p	Chloroflexi;Other;Other;Other;Other						0.0%	0.0%	0.0%
	p	Chloroflexi;c	AD3;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;Other;Other			0.3%	0.3%	0.4%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	Anaerolinea;Other		0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	Longilinea;s	uncultured-Chloroflexi-bacterium	0.4%	0.2%	0.7%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured;Other		0.3%	0.3%	0.3%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured;s	uncultured-Anaerolineae-bacterium	0.0%	0.0%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured;s	uncultured-Bellilinea-sp.	0.1%	0.1%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured;s	uncultured-sludge-bacterium-H39	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Anaerolineales;f	Anaerolineaceae;g	uncultured;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;Other;Other			0.1%	0.0%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;g	uncultured-Litorilinea-sp.;s	uncultured-Litorilinea-sp.	0.1%	0.1%	0.2%
	p	Chloroflexi;c	Anaerolineae;o	Ardenticatenales;f	uncultured;g	uncultured-prokaryote;s	uncultured-prokaryote	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	Litorilinea;Other		0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	Litorilinea;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	Litorilinea;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	uncultured;s	Chloroflexi-bacterium-ET1	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	Caldilineales;f	Caldilineaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;Other;Other;Other				0.0%	0.0%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;f	uncultured-Caldilineaceae-bacterium;g	uncultured-Caldilineaceae-bacterium;s	uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	RBG-13-54-9;f	uncultured-sludge-bacterium-A31;g	uncultured-sludge-bacterium-A31;s	uncultured-sludge-bacterium-A31	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;Other;Other;Other				0.1%	0.2%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;Other;Other			0.0%	0.0%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;g	uncultured-Caldilineales-bacterium;s	uncultured-Caldilineales-bacterium	0.1%	0.0%	0.1%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.2%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;g	uncultured-sludge-bacterium-H8;s	uncultured-sludge-bacterium-H8	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;g	uncultured-sludge-bacterium-S14;s	uncultured-sludge-bacterium-S14	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	A4b;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-Caldilineaceae-bacterium;g	uncultured-Caldilineaceae-bacterium;s	uncultured-Caldilineaceae-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	SBR1031;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Anaerolineae;o	uncultured-Bellilinea-sp.;f	uncultured-Bellilinea-sp.;g	uncultured-Bellilinea-sp.;s	uncultured-Bellilinea-sp.	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;Other;Other;Other				0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Chloroflexaceae;Other;Other			0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Chloroflexaceae;g	Candidatus-Chloroploca;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Herpetosiphonaceae;g	Herpetosiphon;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Roseiflexaceae;g	Roseiflexus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Roseiflexaceae;g	uncultured;Other		0.2%	0.1%	0.3%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Roseiflexaceae;g	uncultured;s	uncultured-bacterium	1.0%	0.3%	1.7%
	p	Chloroflexi;c	Chloroflexia;o	Chloroflexales;f	Roseiflexaceae;g	uncultured;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Kallotenuales;f	AKIW781;Other;Other			0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Kallotenuales;f	AKIW781;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	AKYG1722;Other;Other			0.0%	0.1%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	AKYG1722;g	uncultured-Chloroflexi-bacterium;s	uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
	p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	AKYG1722;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	AKYG1722;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Chloroflexi;c	Chloroflexia;o	Thermomicrobiales;f	JG30-KF-CM45;Other;Other			0.2%	0.2%	0.3%

	p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-Chloroflexi-bacterium;s uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-bacterium;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f JG30-KF-CM45;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Chloroflexia;o Thermomicrobiales;f Thermomicrobiaceae;g Nitrolancea;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Dehalococcoidia;o S085;Other;Other;Other	0.2%	0.3%	0.1%
	p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium;s uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.1%	0.2%	0.1%
	p Chloroflexi;c Dehalococcoidia;o S085;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Gitt-GS-136;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c Gitt-GS-136;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.3%	0.4%	0.1%
	p Chloroflexi;c JG30-KF-CM66;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c JG30-KF-CM66;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium;s uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c JG30-KF-CM66;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Chloroflexi;c KD4-96;Other;Other;Other;Other	0.2%	0.3%	0.1%
	p Chloroflexi;c KD4-96;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium;s uncultured-Chloroflexi-bacterium	0.1%	0.1%	0.1%
	p Chloroflexi;c KD4-96;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.4%	0.5%	0.3%
	p Chloroflexi;c Ktedonobacteria;o C0119;Other;Other;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c Ktedonobacteria;o C0119;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;Other;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;g Thermosporothrix;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c Ktedonobacteria;o Ktedonobacterales;f Ktedonobacteraceae;g uncultured;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c OLB14;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Chloroflexi;c OLB14;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.1%	0.1%	0.1%
	p Chloroflexi;c OLB14;o uncultured-gamma-proteobacterium;f uncultured-gamma-proteobacterium;g uncultured-gamma-proteobacterium;s uncultured-gamma-proteobacterium	0.0%	0.0%	0.0%
	p Chloroflexi;c P2-11E;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.2%	0.1%	0.2%
	p Chloroflexi;c TK10;Other;Other;Other;Other	0.2%	0.2%	0.2%
	p Chloroflexi;c TK10;o uncultured-Chloroflexi-bacterium;f uncultured-Chloroflexi-bacterium;g uncultured-Chloroflexi-bacterium;s uncultured-Chloroflexi-bacterium	0.0%	0.0%	0.1%
	p Chloroflexi;c TK10;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.1%	0.0%
	p Dadabacteria;c Dadabacteriia;o Dadabacterales;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Dependitiae;c Babeliae;o Babeliales;Other;Other;Other	0.0%	0.0%	0.0%
	p Dependitiae;c Babeliae;o Babeliales;f Babeliaceae;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Dependitiae;c Babeliae;o Babeliales;f Vermiphilaceae;Other;Other	0.0%	0.0%	0.0%
	p Dependitiae;c Babeliae;o Babeliales;f Vermiphilaceae;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Elusimicrobia;c Elusimicrobia;o MVP-88;Other;Other;Other	0.0%	0.0%	0.0%
	p Elusimicrobia;c Lineage-IIa;Other;Other;Other;Other	0.0%	0.0%	0.0%
	p Elusimicrobia;c Lineage-IIa;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.1%	0.0%
	p Elusimicrobia;c Lineage-IIb;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p Elusimicrobia;c Lineage-IIb;o uncultured-soil-bacterium;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Entothaeonellaeota;c Entothaeonellia;o Entothaeonellales;f Entothaeonellaceae;Other;Other	0.0%	0.0%	0.0%
	p Entothaeonellaeota;c Entothaeonellia;o Entothaeonellales;f Entothaeonellaceae;g Candidatus-Entothaeonella;Other	0.0%	0.0%	0.0%
	p Entothaeonellaeota;c Entothaeonellia;o Entothaeonellales;f Entothaeonellaceae;g Candidatus-Entothaeonella;s uncultured-delta-proteobacterium	0.0%	0.0%	0.0%
	p Entothaeonellaeota;c Entothaeonellia;o Entothaeonellales;f Entothaeonellaceae;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.1%	0.0%
	p Euryarchaeota;c Methanomicrobia;o Methanosarcinales;f Methanosarcinaceae;g Methanosarcina;s uncultured-archaeon	0.0%	0.0%	0.0%
	p Euryarchaeota;c Thermoplasmata;Other;Other;Other;Other	0.1%	0.1%	0.1%
	p Euryarchaeota;c Thermoplasmata;o Marine-Group-II;Other;Other;Other	0.2%	0.1%	0.2%
	p Euryarchaeota;c Thermoplasmata;o Marine-Group-II;f uncultured-archaeon;g uncultured-archaeon;s uncultured-archaeon	1.1%	0.6%	1.6%
	p Euryarchaeota;c Thermoplasmata;o Marine-Group-II;f uncultured-haloarchaeon;g uncultured-haloarchaeon;s uncultured-haloarchaeon	0.0%	0.0%	0.0%
	p Euryarchaeota;c Thermoplasmata;o Methanomassiliicoccales;f uncultured;g uncultured-archaeon;s uncultured-archaeon	0.5%	0.0%	0.9%
	p Euryarchaeota;c Thermoplasmata;o uncultured;Other;Other;Other	0.0%	0.0%	0.0%
	p Firmicutes;c Bacilli;o Bacillales;f Bacillaceae;Other;Other	0.0%	0.0%	0.0%
	p Firmicutes;c Bacilli;o Bacillales;f Bacillaceae;g Bacillus;Other	0.2%	0.1%	0.4%
	p Firmicutes;c Bacilli;o Bacillales;f Bacillaceae;g Bacillus;s Bacillus-acidiceler	0.0%	0.0%	0.0%

p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	Bacillus-aryabhatai	0.1%	0.1%	0.1%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	Bacillus-drentensis	1.4%	0.2%	2.6%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	Bacillus-funiculus	0.8%	0.2%	1.3%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	Bacillus-pumilus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	Bacillus-simplex	0.0%	0.1%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Bacillus;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Bacillaceae;g	Fictibacillus;s	Fictibacillus-barbaricus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Brevibacillus;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Oxalophagus;Other		0.1%	0.0%	0.2%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Paenibacillus;Other		0.1%	0.1%	0.1%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Paenibacillaceae;g	Thermobacillus;s	Thermobacillus-xylanilyticus	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Domibacillus;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Lysinibacillus;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Planococcaceae;g	Sporosarcina;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Firmicutes;c	Bacilli;o	Bacillales;f	Thermoactinomycetaceae;g	Shimazuella;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Clostridiaceae-1;g	Clostridium-sensu-stricto-1;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Heliobacteriaceae;g	Hydrogenispora;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Peptostreptococcaceae;g	Sporacetigenium;Other		0.0%	0.0%	0.0%
p	Firmicutes;c	Clostridia;o	Clostridiales;f	Ruminococcaceae;g	Ruminococcus-2;s	uncultured-Papillibacter-sp.	0.0%	0.0%	0.0%
p	GAL15;c	uncultured-bacterium;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	AKAU4049;Other;Other;Other;Other					0.2%	0.3%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;Other;Other;Other;Other					0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium;g	uncultured-Gemmatimonadales-bacterium;s	uncultured-Gemmatimonadales-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium;g	uncultured-Gemmatimonadetes-bacterium;s	uncultured-Gemmatimonadetes-bacterium	0.0%	0.1%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	BD2-11-terrestrial-group;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;Other;Other			0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatimonas;Other		0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatimonas;s	uncultured-Gemmatimonadaceae-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatimonas;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	Gemmatirosa;s	uncultured-bacterium	0.1%	0.0%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;Other		0.8%	0.9%	0.8%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-Gemmatimonadales-bacterium	0.5%	0.6%	0.5%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-Gemmatimonadetes-bacterium	0.1%	0.0%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-Gemmatimonas-sp.	0.1%	0.0%	0.1%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-bacterium	0.5%	0.3%	0.8%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-low-G+C-Gram-positive-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	Gemmatimonadetes;o	Gemmatimonadales;f	Gemmatimonadaceae;g	uncultured;s	uncultured-proteobacterium	0.2%	0.4%	0.0%
p	Gemmatimonadetes;c	Longimicrobia;o	Longimicrobiales;f	Longimicrobiaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;Other;Other;Other;Other					0.1%	0.1%	0.1%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadales-bacterium;f	uncultured-Gemmatimonadales-bacterium;g	uncultured-Gemmatimonadales-bacterium;s	uncultured-Gemmatimonadales-bacterium	0.2%	0.2%	0.2%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-Gemmatimonadetes-bacterium;f	uncultured-Gemmatimonadetes-bacterium;g	uncultured-Gemmatimonadetes-bacterium;s	uncultured-Gemmatimonadetes-bacterium	0.0%	0.0%	0.0%
p	Gemmatimonadetes;c	S0134-terrestrial-group;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.2%	0.2%	0.2%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales;f	Hydrogenedensaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Hydrogenedentes;c	Hydrogenedentia;o	Hydrogenedentiales;f	Hydrogenedensaceae;g	uncultured-bacterium-SJP-3;s	uncultured-bacterium-SJP-3	0.0%	0.0%	0.0%
p	Latescibacteria;Other;Other;Other;Other;Other						0.3%	0.4%	0.1%
p	Latescibacteria;c	Latescibacteria;o	Latescibacteriales;f	Latescibacteraceae;Other;Other			0.0%	0.0%	0.0%
p	Latescibacteria;c	Latescibacteria;o	Latescibacteriales;f	Latescibacteraceae;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.2%	0.0%
p	Latescibacteria;c	uncultured-Acidobacterium-sp.;o	uncultured-Acidobacterium-sp.;f	uncultured-Acidobacterium-sp.;g	uncultured-Acidobacterium-sp.;s	uncultured-Acidobacterium-sp.	0.0%	0.0%	0.0%
p	Latescibacteria;c	uncultured-Fibrobacteres-bacterium;o	uncultured-Fibrobacteres-bacterium;f	uncultured-Fibrobacteres-bacterium;g	uncultured-Fibrobacteres-bacterium;s	uncultured-Fibrobacteres-bacterium	0.0%	0.0%	0.0%

p Latescibacteria;c uncultured-Pelobacter-sp.;o uncultured-Pelobacter-sp.;f uncultured-Pelobacter-sp.;g uncultured-Pelobacter-sp.;s uncultured-Pelobacter-sp.	0.0%	0.0%	0.0%
p Latescibacteria;c uncultured-bacterium;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.4%	0.5%	0.3%
p Latescibacteria;c uncultured-prokaryote;o uncultured-prokaryote;f uncultured-prokaryote;g uncultured-prokaryote;s uncultured-prokaryote	0.0%	0.0%	0.0%
p Latescibacteria;c uncultured-proteobacterium;o uncultured-proteobacterium;f uncultured-proteobacterium;g uncultured-proteobacterium;s uncultured-proteobacterium	0.0%	0.0%	0.0%
p Latescibacteria;c uncultured-soil-bacterium;o uncultured-soil-bacterium;f uncultured-soil-bacterium;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.0%	0.1%	0.0%
p Nanoarchaeaeota;c Nanohaloarchaeia;o Aenigmarchaeales;Other;Other;Other	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Nanohaloarchaeia;o Aenigmarchaeales;f uncultured-archaeon;g uncultured-archaeon;s uncultured-archaeon	0.0%	0.1%	0.0%
p Nanoarchaeaeota;c Nanohaloarchaeia;o Deep-Sea-Euryarchaeotic-Group(DSEG);Other;Other;Other	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;Other;Other;Other;Other	0.1%	0.2%	0.1%
p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;f Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;g Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15;s Candidatus-Amesbacteria-bacterium-GW2011_GWC1_47_15	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;f Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;g Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9;s Candidatus-Pacearchaeota-archaeon-RBG_19FT_COMBO_34_9	0.0%	0.0%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;f Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;g Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7;s Candidatus-Staskawiczbacteria-bacterium-RIFOXYA2_FULL_32_7	0.1%	0.1%	0.0%
p Nanoarchaeaeota;c Woesearchaeia;o uncultured-euryarchaeote;f uncultured-euryarchaeote;g uncultured-euryarchaeote;s uncultured-euryarchaeote	0.0%	0.0%	0.0%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira;Other	0.4%	0.3%	0.5%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira;s uncultured-Nitrospira-sp.	0.1%	0.0%	0.1%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira;s uncultured-Nitrospiraceae-bacterium	0.0%	0.0%	0.0%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira;s uncultured-bacterium	0.0%	0.0%	0.0%
p Nitrospirae;c Nitrospira;o Nitrospirales;f Nitrospiraceae;g Nitrospira;s uncultured-soil-bacterium	0.0%	0.0%	0.1%
p Patescibacteria;Other;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Kuenenbacteria;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.1%
p Patescibacteria;c ABY1;o Candidatus-Magasanikbacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Magasanikbacteria;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c ABY1;o Candidatus-Uhrbacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Berkelbacteria;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Abawacabacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Abawacabacteria;f Candidatus-Abawacabacteria-bacterium-RBG_16_42_10;g Candidatus-Abawacabacteria-bacterium-RBG_16_42_10;s Candidatus-Abawacabacteria-bacterium-RBG_16_42_10	0.0%	0.0%	0.0%
p Patescibacteria;c Gracilibacteria;o Candidatus-Peribacteria;f Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20;g Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20;s Candidatus-Peribacteria-bacterium-RIFCSPHIGHO2_02_FULL_53_20	0.0%	0.0%	0.0%
p Patescibacteria;c Microgenomatia;o Candidatus-Woesebacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Azambacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Azambacteria;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Kaiserbacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Nomurabacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Terrybacteria;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;Other;Other;Other	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19;g Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19;s Candidatus-Yanofskybacteria-bacterium-RIFCSPHIGHO2_02_FULL_46_19	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o Candidatus-Yanofskybacteria;f uncultured-deep-sea-bacterium;g uncultured-deep-sea-bacterium;s uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o GWA2-38-13b;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o GWA2-38-13b;f uncultured-deep-sea-bacterium;g uncultured-deep-sea-bacterium;s uncultured-deep-sea-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Parcubacteria;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
p Patescibacteria;c Saccharimonadia;o Saccharimonadales;Other;Other;Other	0.2%	0.2%	0.3%

	p Patescibacteria;c bacterium	Saccharimonadia;o	Saccharimonadales;f	Saccharimonadaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.0%	0.2%
	p Patescibacteria;c bacterium;g	Saccharimonadia;o	Saccharimonadales;f	uncultured-Candidatus-Saccharibacteria-bacterium;s	uncultured-Candidatus-Saccharibacteria-bacterium	uncultured-Candidatus-Saccharibacteria-bacterium	0.0%	0.0%	0.1%
	p Patescibacteria;c bacterium	Saccharimonadia;o	Saccharimonadales;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
	p Patescibacteria;c	WWE3;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Planctomycetes;Other;Other;Other;Other;Other						0.0%	0.0%	0.0%
	p Planctomycetes;c	BD7-11;o	uncultured-Planctomycetales-bacterium;f	uncultured-Planctomycetales-bacterium;g	uncultured-Planctomycetales-bacterium;s	uncultured-Planctomycetales-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	BD7-11;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	OM190;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Planctomycetes;c	OM190;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	OM190;o	uncultured-soil-bacterium;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;Other;Other;Other;Other					0.2%	0.2%	0.2%
	p Planctomycetes;c	Phycisphaerae;o	CCM11a;Other;Other;Other				0.1%	0.0%	0.1%
	p Planctomycetes;c	Phycisphaerae;o	CCM11a;f	uncultured-Planctomycetia-bacterium;g	uncultured-Planctomycetia-bacterium;s	uncultured-Planctomycetia-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	CCM11a;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.2%	0.1%
	p Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;Other;Other;Other				0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;f	Phycisphaeraeaceae;Other;Other			0.0%	0.0%	0.1%
	p Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;f	Phycisphaeraeaceae;g	uncultured;Other		0.1%	0.1%	0.1%
	p Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;f	Phycisphaeraeaceae;g	uncultured;s	uncultured-Bacteroidetes-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Phycisphaerales;f	Phycisphaeraeaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Pla1-lineage;Other;Other;Other				0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Pla1-lineage;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	CPla-3-termite-group;Other;Other			0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	CPla-3-termite-group;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	CPla-3-termite-group;g	uncultured-soil-bacterium-PBS-22;s	uncultured-soil-bacterium-PBS-22	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	Tepidisphaeraeaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	WD2101-soil-group;Other;Other			0.4%	0.2%	0.6%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	WD2101-soil-group;g	uncultured-bacterium;s	uncultured-bacterium	0.6%	0.5%	0.7%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	WD2101-soil-group;g	uncultured-planctomycete;s	uncultured-planctomycete	0.0%	0.0%	0.1%
	p Planctomycetes;c	Phycisphaerae;o	Tepidisphaerales;f	WD2101-soil-group;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	mle1-8;Other;Other;Other				0.0%	0.0%	0.0%
	p Planctomycetes;c	Phycisphaerae;o	mle1-8;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.0%	0.1%
	p Planctomycetes;c	Pla3-lineage;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Planctomycetes;c	Pla4-lineage;Other;Other;Other;Other					0.0%	0.0%	0.0%
	p Planctomycetes;c	Pla4-lineage;o	uncultured-bacterium;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Pla4-lineage;o	uncultured-prokaryote;f	uncultured-prokaryote;g	uncultured-prokaryote;s	uncultured-prokaryote	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;Other;Other			0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	Fimbrioglobus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	Gemmata;Other		0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	Gemmata;s	uncultured-Gemmata-sp.	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	Gemmata;s	uncultured-bacterium	0.1%	0.0%	0.1%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	uncultured;s	uncultured-Planctomycetia-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	uncultured;s	uncultured-prokaryote	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Gemmatales;f	Gemmataceae;g	uncultured;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;Other;Other			0.0%	0.0%	0.1%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	Bythopirellula;Other		0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	Pirellula;Other		0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	Pirellula;s	uncultured-bacterium	0.1%	0.1%	0.1%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	Pirellula;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	uncultured;s	uncultured-Pasteuria-sp.	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Pirellulales;f	Pirellulaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Planctomycetales;Other;Other;Other				0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Planctomycetales;f	Rubinisphaeraeaceae;g	Planctomicrobium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Planctomycetes;c	Planctomycetacia;o	Planctomycetales;f	Schlesneriaceae;g	Planctopirus;Other		0.0%	0.0%	0.0%

	p	Planctomycetes;c	Planctomycetacia;o	Planctomycetales;f	uncultured;Other;Other	0.0%	0.0%	0.0%
	p	Planctomycetes;c Planctomyces-sp.	Planctomycetacia;o	Planctomycetales;f	uncultured;g uncultured-Planctomyces-sp.;s uncultured-	0.0%	0.0%	0.0%
	p	Planctomycetes;c	Planctomycetacia;o	Planctomycetales;f	uncultured;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Planctomycetes;c	Planctomycetacia;o	uncultured;f	uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;Other;Other;Other;Other;Other				0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;Other;Other;Other;Other			1.8%	1.7%	2.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Azospirillales;f	Azospirillaceae;g Azospirillum;s uncultured-Azospirillum-sp.	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Azospirillales;f	Inquilinaceae;g Inquilinus;s Inquilinus-limosus	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Azospirillales;f	uncultured;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.1%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;Other;Other;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;Other;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;g Brevundimonas;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;g Phenyllobacterium;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;g Phenyllobacterium;s uncultured-bacterium	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;g uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c proteobacterium	Alphaproteobacteria;o	Caulobacterales;f	Caulobacteraceae;g uncultured;s uncultured-alpha-	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Hyphomonadaceae;g Hirschia;s uncultured-bacterium	0.1%	0.1%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Hyphomonadaceae;g uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Hyphomonadaceae;g uncultured;s uncultured-bacterium	0.0%	0.1%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Caulobacterales;f	Parvularculaceae;g Amphiplicatus;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Elsterales;f	Elsteraceae;g Lacibacterium;s Lacibacterium-aquatile	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Elsterales;f	uncultured;Other;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Elsterales;f	uncultured;g uncultured-Acetobacteraceae-bacterium;s uncultured-Acetobacteraceae-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c proteobacterium	Alphaproteobacteria;o	Elsterales;f	uncultured;g uncultured-alpha-proteobacterium;s uncultured-alpha-	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Elsterales;f	uncultured;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Holosporales;f	Holosporaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Micropepsales;f	Micropepsaceae;g uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Micropepsales;f	Micropepsaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Micropepsales;f	Micropepsaceae;g uncultured;s uncultured-proteobacterium	0.1%	0.0%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Reyranellales;f	Reyranellaceae;g Reyranella;s uncultured-bacterium	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Reyranellales;f	Reyranellaceae;g uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Reyranellales;f	Reyranellaceae;g uncultured;s uncultured-bacterium	0.1%	0.2%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Reyranellales;f	Reyranellaceae;g uncultured;s uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;Other;Other;Other		0.0%	0.1%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	A0839;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Amb-16S-1323;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Beijerinckiaceae;Other;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Beijerinckiaceae;g Bosea;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Beijerinckiaceae;g Microvirga;s Microvirga-massiliensis	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Beijerinckiaceae;g Microvirga;s uncultured-bacterium	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	D05-2;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Devosiaceae;Other;Other	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Devosiaceae;g Devosia;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Devosiaceae;g uncultured;s uncultured-bacterium	0.1%	0.2%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Hyphomicrobiaceae;Other;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Hyphomicrobiaceae;g Hyphomicrobium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Hyphomicrobiaceae;g Pedomicrobium;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Hyphomicrobiaceae;g Pedomicrobium;s uncultured-bacterium	0.3%	0.5%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Hyphomicrobiaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	KF-JG30-B3;Other;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	KF-JG30-B3;g uncultured-bacterium;s uncultured-bacterium	0.8%	0.7%	0.9%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Labraceae;g Labrys;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Labraceae;g Labrys;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Methylobacteriaceae;Other;Other	0.0%	0.1%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Methylobacteriaceae;g uncultured;Other	0.3%	0.3%	0.3%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Methylobacteriaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiaceae;Other;Other	0.1%	0.1%	0.1%
	p	Proteobacteria;c Rhizobium;Other	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiaceae;g Allorhizobium-Neorhizobium-Pararhizobium-	0.0%	0.0%	0.0%
	p	Proteobacteria;c Rhizobium;s Rhizobium-etli	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiaceae;g Allorhizobium-Neorhizobium-Pararhizobium-	0.3%	0.2%	0.3%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiaceae;g Ensifer;s Ensifer-adhaerens	0.3%	0.5%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiaceae;g Mesorhizobium;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiales-Incertae-Sedis;g Bauldia;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiales-Incertae-Sedis;g Bauldia;s uncultured-bacterium	0.1%	0.1%	0.1%
	p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiales-Incertae-Sedis;g uncultured;Other	0.0%	0.0%	0.0%

p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhizobiales-Incertae-Sedis;g	uncultured;s	uncultured-bacterium	0.2%	0.1%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Rhodomicrobiaceae;g	Rhodomicrobium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;Other;Other			1.0%	1.0%	1.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	Ancylobacter;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	Bradyrhizobium;Other		0.5%	0.5%	0.4%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	Pseudolabrys;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	Rhodoplanes;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	uncultured;Other		0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	Xanthobacteraceae;g	uncultured;s	uncultured-bacterium	0.6%	0.6%	0.6%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;Other;Other			0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;g	uncultured-Rhizobiales-bacterium;s	uncultured-Rhizobiales-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhizobiales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodobacterales;f	Rhodobacteraceae;Other;Other			0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodobacterales;f	Rhodobacteraceae;g	uncultured;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	Rhodospirillaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	uncultured;Other;Other			0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodospirillales;f	uncultured;g	uncultured-Rhodospirillaceae-bacterium;s	uncultured-Rhodospirillaceae-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Rhodovibrionales;f	Fodinicurvataceae;g	uncultured;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sneathiellales;f	Sneathiellaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;Other;Other			0.1%	0.2%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Altererythrobacter;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Altererythrobacter;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Novosphingobium;Other		0.2%	0.3%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Novosphingobium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Sphingobium;s	Sphingobium-sp.-YL23	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Sphingomonas;Other		1.3%	1.6%	1.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	Sphingomonas;s	uncultured-Sphingomonas-sp.	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	uncultured;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Sphingomonadales;f	Sphingomonadaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Tistrellales;f	Geminicoccaceae;g	Candidatus-Alysiosphaera;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	Tistrellales;f	Geminicoccaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;Other;Other;Other				0.2%	0.2%	0.2%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Acetobacteraceae-bacterium;g	uncultured-Acetobacteraceae-bacterium		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Rhodospirillaceae-bacterium;g	uncultured-Rhodospirillaceae-bacterium		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Rhodospirillales-bacterium;g	uncultured-Rhodospirillales-bacterium		0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-Stella-sp.;g	uncultured-Stella-sp.;s	uncultured-Stella-sp.-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Alphaproteobacteria;o	uncultured;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-bacterium	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;Other;Other;Other;Other					0.2%	0.3%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	Bdellovibrionales;f	Bdellovibrionaceae;g	Bdellovibrio;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Bdellovibrionales;f	Bdellovibrionaceae;g	Bdellovibrio;s	Bdellovibrionales-bacterium-RBG_16_40_8	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Bdellovibrionales;f	Bdellovibrionaceae;g	Bdellovibrio;s	uncultured-bacterium	0.0%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfarculales;f	Desulfarculaceae;g	uncultured;Other		0.1%	0.1%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfarculales;f	Desulfarculaceae;g	uncultured;s	uncultured-Desulfuromonadales-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfarculales;f	Desulfarculaceae;g	uncultured;s	uncultured-bacterium	0.1%	0.1%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;Other;Other;Other				0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;f	Geobacteraceae;g	Geobacter;Other		0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;f	Geobacteraceae;g	Geobacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Desulfuromonadales;f	Geobacteraceae;g	Geobacter;s	uncultured-delta-proteobacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;Other;Other;Other				0.1%	0.0%	0.2%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	MBNT15;f	uncultured-proteobacterium;g	uncultured-proteobacterium;s	uncultured-proteobacterium	0.0%	0.0%	0.1%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;Other;Other;Other				0.1%	0.1%	0.0%
p	Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Archangiaceae;g	Anaeromyxobacter;Other		0.0%	0.0%	0.0%

	p Proteobacteria;c Anaeromyxobacter-sp.	Deltaproteobacteria;o	Myxococcales;f	Archangiaceae;g	Anaeromyxobacter;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Archangiaceae;g	Anaeromyxobacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c proteobacterium	Deltaproteobacteria;o	Myxococcales;f	Archangiaceae;g	Anaeromyxobacter;s	uncultured-delta-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	BIrii41;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	BIrii41;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Blfdi19;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Blfdi19;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Eel-36e1D6;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;Other		0.2%	0.2%	0.2%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;s	delta-proteobacterium-LWH25	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;s	uncultured-Kofleriaceae-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;s	uncultured-Nannocystineae-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;s	uncultured-bacterium	0.0%	0.1%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Haliangiaceae;g	Haliangium;s	uncultured-prokaryote	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g	Nannocystis;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g	Nannocystis;s	Nannocystis-pusilla	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g	Nannocystis;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Nannocystaceae;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	P3OB-42;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	P3OB-42;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Phaselicystidaceae;g	Phaselicystis;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Phaselicystidaceae;g	Phaselicystis;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;g	Pajaroellobacter;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;g	Pajaroellobacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Polyangiaceae;g	Polyangium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	Sandaracinus;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	Sandaracinus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	uncultured;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	uncultured;s	delta-proteobacterium-LX33	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	uncultured;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Sandaracinaceae;g	uncultured;s	uncultured-soil-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	UASB-TL25;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Vulgatibacteraceae;g	Vulgatibacter;s	uncultured-Hyalangium-sp.	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	Vulgatibacteraceae;g	Vulgatibacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;Other;Other			0.5%	0.5%	0.5%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g	uncultured-delta-proteobacterium;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c proteobacterium	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g	uncultured-proteobacterium;s	uncultured-	0.1%	0.1%	0.1%
	p Proteobacteria;c bacterium	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g	uncultured-soil-bacterium;s	uncultured-soil-	0.1%	0.1%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	bacteriap25;g	unidentified;s	unidentified	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	mle1-27;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c proteobacterium	Deltaproteobacteria;o	Myxococcales;f	mle1-27;g	uncultured-delta-proteobacterium;s	uncultured-delta-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	uncultured;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Myxococcales;f	uncultured;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	NB1-j;Other;Other;Other				0.0%	0.0%	0.0%
	p Proteobacteria;c MND4;g	Deltaproteobacteria;o	NB1-j;f	uncultured-Green-Bay-ferromanganous-micronodule-bacterium-MND4;s	uncultured-Green-Bay-ferromanganous-micronodule-bacterium-MND4		0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	NB1-j;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.3%	0.4%	0.2%
	p Proteobacteria;c proteobacterium	Deltaproteobacteria;o	NB1-j;f	uncultured-proteobacterium;g	uncultured-proteobacterium;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Deltaproteobacteria;o	NB1-j;f	uncultured-soil-bacterium;g	uncultured-soil-bacterium;s	uncultured-soil-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Oligoflexales;f	Oligoflexaceae;g	Oligoflexus;s	uncultured-Desulfocurvus-sp.	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	RCP2-54;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c prokaryote	Deltaproteobacteria;o	RCP2-54;f	uncultured-prokaryote;g	uncultured-prokaryote;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	SAR324-clade(Marine-group-B);f	bacterium-enrichment-culture-clone-B30(2011);g	bacterium-enrichment-culture-clone-B30(2011);s	bacterium-enrichment-culture-clone-B30(2011)	0.0%	0.0%	0.0%
	p Proteobacteria;c	Deltaproteobacteria;o	Syntrophobacterales;f	Syntrophaceae;g	uncultured;Other		0.0%	0.0%	0.0%

	p Proteobacteria;c bacterium	Deltaproteobacteria;o	Syntrophobacterales;f	Syntrophaceae;g	uncultured;s	uncultured-Myxococcales-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;Other;Other;Other;Other					0.5%	0.6%	0.4%
	p Proteobacteria;c	Gammaproteobacteria;o	Acidiferrobacterales;f	Acidiferrobacteraceae;g	Sulfurifustis;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	Acidiferrobacterales;f	Acidiferrobacteraceae;g	Sulfurifustis;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Aeromonadales;f	Aeromonadaceae;g	Aeromonas;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;Other;Other;Other				1.7%	1.4%	2.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	A21b;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	A21b;g	uncultured-bacterium;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	B1-7BS;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	B1-7BS;g	uncultured-bacterium;s	uncultured-bacterium	0.1%	0.1%	0.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;Other;Other			0.2%	0.2%	0.3%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Bordetella;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c Paraburkholderia;Other	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Burkholderia-Caballeronia-		0.0%	0.0%	0.1%
	p Proteobacteria;c prokaryote	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Comamonas;s	uncultured-	0.1%	0.1%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Cupriavidus;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Cupriavidus;s	Cupriavidus-necator	0.4%	0.7%	0.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Cupriavidus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Hydrogenophaga;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Massilia;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Noviherbaspirillum;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Ramlibacter;Other		0.1%	0.2%	0.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Ramlibacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Rhizobacter;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Rhizobacter;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Sphaerotilus;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c Burkholderiales-bacterium	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Sphaerotilus;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	Variovorax;Other		0.1%	0.1%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Burkholderiaceae;g	uncultured;Other		0.1%	0.0%	0.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Chromobacteriaceae;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Chromobacteriaceae;g	Paludibacterium;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Rhodocyclaceae;Other;Other			0.3%	0.1%	0.4%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Rhodocyclaceae;g	Azoarcus;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Rhodocyclaceae;g	Thauera;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	Rhodocyclaceae;g	Thauera;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	SC-I-84;Other;Other			0.3%	0.3%	0.2%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	SC-I-84;g	uncultured-bacterium;s	uncultured-bacterium	0.2%	0.1%	0.2%
	p Proteobacteria;c proteobacterium;s	Gammaproteobacteria;o	Betaproteobacterales;f	SC-I-84;g	uncultured-beta-	proteobacterium	0.1%	0.1%	0.2%
	p Proteobacteria;c	Gammaproteobacteria;o	Betaproteobacterales;f	TRA3-20;Other;Other			0.6%	0.7%	0.5%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	Betaproteobacterales;f	TRA3-20;g	uncultured-bacterium;s	uncultured-	0.1%	0.1%	0.2%
	p Proteobacteria;c proteobacterium;s	Gammaproteobacteria;o	Betaproteobacterales;f	TRA3-20;g	uncultured-gamma-	proteobacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	CCD24;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.2%	0.3%	0.1%
	p Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;Other;Other;Other				0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Cellvibrionales;f	Haliaceae;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Diplorickettsiales;f	Diplorickettsiaceae;g	Aquicella;s	uncultured-bacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c proteobacterium;s	Gammaproteobacteria;o	EPR3968-O8a-Bc78;f	uncultured-gamma-proteobacterium;g	uncultured-gamma-	proteobacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Enterobacterales;f	Enterobacteriaceae;Other;Other			0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Enterobacterales;f	Enterobacteriaceae;g	Pantoea;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	Gammaproteobacteria-Incertae-Sedis;f	Unknown-Family;g	uncultured;Other		0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	JG36-GS-52;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	JG36-TzT-191;Other;Other;Other				0.0%	0.0%	0.0%
	p Proteobacteria;c bacterium	Gammaproteobacteria;o	JG36-TzT-191;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-	0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	KI89A-clade;Other;Other;Other				0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	PLTA13;Other;Other;Other				0.0%	0.0%	0.0%
	p Proteobacteria;c	Gammaproteobacteria;o	PLTA13;f	uncultured-bacterium;g	uncultured-bacterium;s	uncultured-bacterium	0.7%	1.2%	0.1%
	p Proteobacteria;c proteobacterium;s	Gammaproteobacteria;o	PLTA13;f	uncultured-proteobacterium;g	uncultured-	proteobacterium	0.0%	0.0%	0.0%
	p Proteobacteria;c calcoaceticus	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	Acinetobacter;s	Acinetobacter-	0.0%	0.0%	0.0%

	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Moraxellaceae;g	uncultured;s gamma-proteobacterium-Y-134	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;Other;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Azotobacter;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas;Other	0.3%	0.5%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas;s Pseudomonas-citronellolis	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas;s Pseudomonas-plecoglossida	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas;s Pseudomonas-resinovorans	0.0%	0.1%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Pseudomonadales;f	Pseudomonadaceae;g	Pseudomonas;s Pseudomonas-sp.-enrichment-culture-clone-HSL33	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;Other;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	R7C24;f	uncultured-bacterium;g	uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;Other;Other;Other			0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Salinisphaerales;f	Solimonadaceae;Other;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacterales;f	Steroidobacteraceae;g	uncultured;Other	0.9%	1.3%	0.5%
	p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacterales;f	Steroidobacteraceae;g	uncultured;s uncultured-bacterium	0.4%	0.6%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Steroidobacterales;f	Steroidobacteraceae;g	uncultured;s uncultured-gamma-proteobacterium	0.1%	0.2%	0.1%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;Other;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	Dokdonella;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	Dyella;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	Dyella;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	uncultured;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	uncultured;s uncultured-Xanthomonadaceae-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Rhodanobacteraceae;g	uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;Other;Other		0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Arenimonas;s uncultured-bacterium	0.1%	0.1%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Luteimonas;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Lysobacter;Other	0.2%	0.4%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Lysobacter;s uncultured-bacterium	0.4%	0.8%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Pseudoxanthomonas;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Pseudoxanthomonas;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Stenotrophomonas;Other	0.0%	0.0%	0.0%
	p	Proteobacteria;c	Gammaproteobacteria;o	Xanthomonadales;f	Xanthomonadaceae;g	Thermomonas;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Rokubacteria;c	NC10;o	Rokubacteriales;Other;Other;Other			0.0%	0.0%	0.0%
	p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-Gram-positive-bacterium;g	uncultured-Gram-positive-bacterium;s uncultured-Gram-positive-bacterium	0.1%	0.1%	0.0%
	p	Rokubacteria;c	NC10;o	Rokubacteriales;f	uncultured-bacterium;g	uncultured-bacterium;s uncultured-bacterium	1.2%	1.5%	0.8%
	p	Thaumarchaeota;c	Group-1.1c;Other;Other;Other;Other				0.0%	0.0%	0.0%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosopumilales;f	Nitrosopumilaceae;g	Candidatus-Nitrosotenuis;s uncultured-archaeon	0.0%	0.0%	0.0%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;Other;Other		0.5%	0.5%	0.5%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	Candidatus-Nitrocosmicus;s uncultured-archaeon	0.1%	0.1%	0.1%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	Candidatus-Nitrososphaera;Other	0.4%	0.4%	0.4%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	Candidatus-Nitrososphaera;s uncultured-archaeon	0.1%	0.0%	0.1%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	uncultured-archaeon;s uncultured-archaeon	0.3%	0.3%	0.2%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrososphaerales;f	Nitrososphaeraceae;g	uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%
	p	Thaumarchaeota;c	Nitrososphaeria;o	Nitrosotaleales;f	Nitrosotaleaceae;g	uncultured-archaeon;s uncultured-archaeon	0.0%	0.0%	0.0%
	p	Verrucomicrobia;c	Verrucomicrobiae;Other;Other;Other;Other				0.0%	0.0%	0.0%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;Other;Other;Other			0.1%	0.1%	0.1%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;Other;Other		0.0%	0.0%	0.0%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;g	Candidatus-Udaeobacter;Other	0.5%	0.3%	0.7%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;g	Candidatus-Udaeobacter;s uncultured-Spartobacteria-bacterium	0.0%	0.0%	0.0%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Chthoniobacteraceae;g	Candidatus-Udaeobacter;s uncultured-bacterium	1.3%	0.7%	1.9%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Xiphinematobacteraceae;g	Candidatus-Xiphinematobacter;Other	0.0%	0.0%	0.0%
	p	Verrucomicrobia;c	Verrucomicrobiae;o	Chthoniobacterales;f	Xiphinematobacteraceae;g	Candidatus-Xiphinematobacter;s uncultured-Verrucomicrobia-bacterium	0.0%	0.0%	0.0%

p Verrucomicrobia;c Verrucomicrobiae;o Chthoniobacterales;f Xiphinematobacteraceae;g Candidatus-Xiphinematobacter;s uncultured-bacterium	0.2%	0.3%	0.1%
p Verrucomicrobia;c Verrucomicrobiae;o Methyacidiphilales;f Methyacidiphilaceae;g uncultured;s candidate-division-WWE3-bacterium-RIFCSPLOWO2_01_FULL_53_14	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Opitutales;f Opitutaceae;Other;Other	1.2%	2.3%	0.1%
p Verrucomicrobia;c Verrucomicrobiae;o Opitutales;f Opitutaceae;g Lacunisphaera;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Opitutales;f Opitutaceae;g Lacunisphaera;s Opitutus-sp.	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Opitutales;f Opitutaceae;g Lacunisphaera;s uncultured-bacterium	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Opitutales;f Opitutaceae;g Opitutus;s uncultured-bacterium	0.1%	0.1%	0.1%
p Verrucomicrobia;c Verrucomicrobiae;o Pedosphaerales;f Pedosphaeraceae;Other;Other	1.1%	0.6%	1.5%
p Verrucomicrobia;c Verrucomicrobiae;o Pedosphaerales;f Pedosphaeraceae;g uncultured-Verrucomicrobia-bacterium;s uncultured-Verrucomicrobia-bacterium	0.0%	0.0%	0.1%
p Verrucomicrobia;c Verrucomicrobiae;o Pedosphaerales;f Pedosphaeraceae;g uncultured-bacterium;s uncultured-bacterium	1.1%	0.7%	1.5%
p Verrucomicrobia;c Verrucomicrobiae;o Pedosphaerales;f Pedosphaeraceae;g uncultured-soil-bacterium;s uncultured-soil-bacterium	0.3%	0.2%	0.4%
p Verrucomicrobia;c Verrucomicrobiae;o Pedosphaerales;f Pedosphaeraceae;g uncultured-subdivision-3-bacterium;s uncultured-subdivision-3-bacterium	0.1%	0.0%	0.1%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;Other;Other;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Akkermansiaceae;g Akkermansia;s uncultured-bacterium	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Rubritaleaceae;g Luteolibacter;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Rubritaleaceae;g Luteolibacter;s Haloferula-sp.-BvORR071	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Rubritaleaceae;g Luteolibacter;s uncultured-Verrucomicrobia-bacterium	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Rubritaleaceae;g Luteolibacter;s uncultured-bacterium	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Verrucomicrobiaceae;Other;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Verrucomicrobiaceae;g Verrucomicrobium;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Verrucomicrobiaceae;g uncultured;Other	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Verrucomicrobiaceae;g uncultured;s uncultured-Verrucomicrobia-bacterium	0.0%	0.0%	0.0%
p Verrucomicrobia;c Verrucomicrobiae;o Verrucomicrobiales;f Verrucomicrobiaceae;g uncultured;s uncultured-bacterium	0.0%	0.0%	0.0%
p WPS-2;Other;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Zixibacteria;Other;Other;Other;Other;Other	0.0%	0.0%	0.0%
p Zixibacteria;c uncultured-bacterium;o uncultured-bacterium;f uncultured-bacterium;g uncultured-bacterium;s uncultured-bacterium	0.0%	0.0%	0.0%