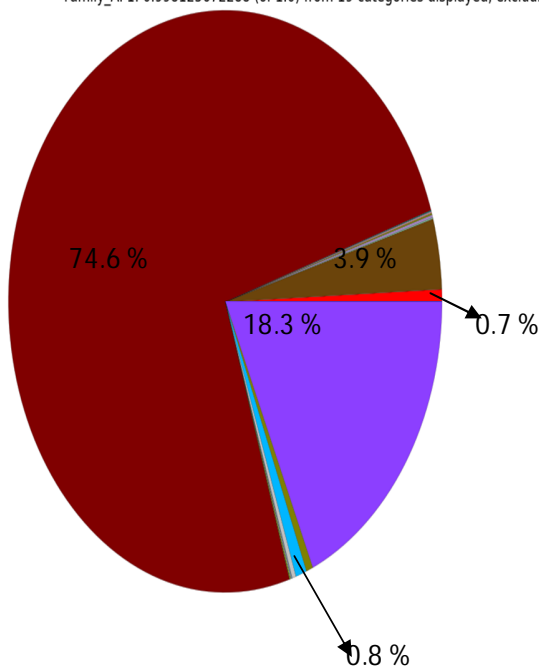


Family_AP1: 0.998125672288 (of 1.0) from 19 categories displayed, excluding 0.00187432771189 from 42 categories ('All Other Categories')

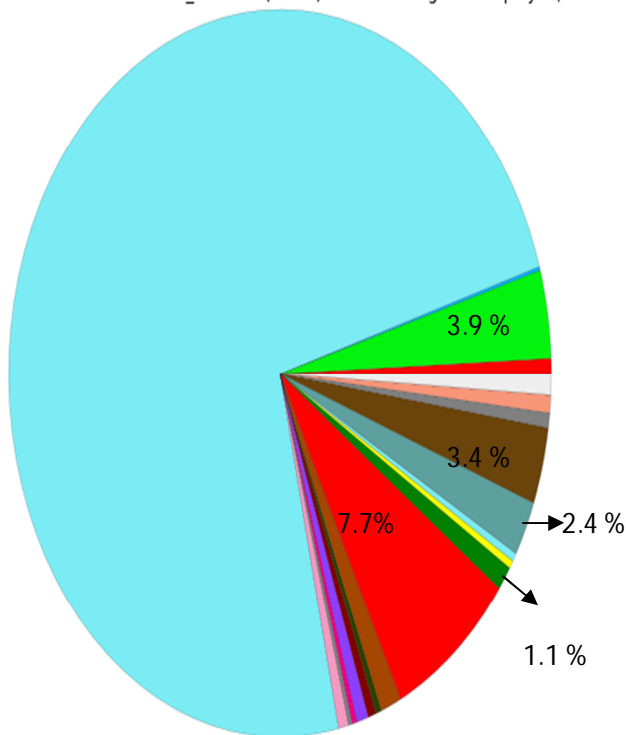


Total Legend	Taxonomy Family level	Sample %
	Unassigned;Other;Other;Other;Other	0.7%
	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_EB1017	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae	0.0%
	k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_	0.0%
	k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Conexibacteraceae	0.0%
	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae	3.9%
	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae	0.0%
	k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae	0.0%
	k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae	0.0%
	k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_[Roseiflexales];f_[Kouleothrixaceae]	0.0%
	k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_YS2;f_	0.0%
	k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae	0.1%
	k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae	0.2%
	k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_Pseudanabaenaceae	0.0%
	k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Synechococcales;f_Synechococcaceae	0.0%
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae	0.0%

k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae	74.6%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Planctomycetales;f_Planctomycetaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradvrrhizobiaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae	0.1%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophilales;f_Methylophilaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae	0.3%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfarculales;f_Desulfarculaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae	0.8%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Spirobacillales;f_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae	0.5%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae	18.3%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae	0.0%
k_Bacteria;p_TM6;c_SJA-4;o_ ;f_	0.0%
k_Bacteria;p_TM7;c_TM7-1;o_ ;f_	0.0%
k_Bacteria;p_Tenericutes;c_CK-1C4-19;o_ ;f_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae	0.0%
k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae]	0.0%

Fig. VIII.A.1. Taxonomy at family level (Top 5 families shown in Pie diagram).

Genus_API: 1.0 (of 1.0) from 20 categories displayed, including 0.00947320311525 from 94 categories ('All Other Categories')



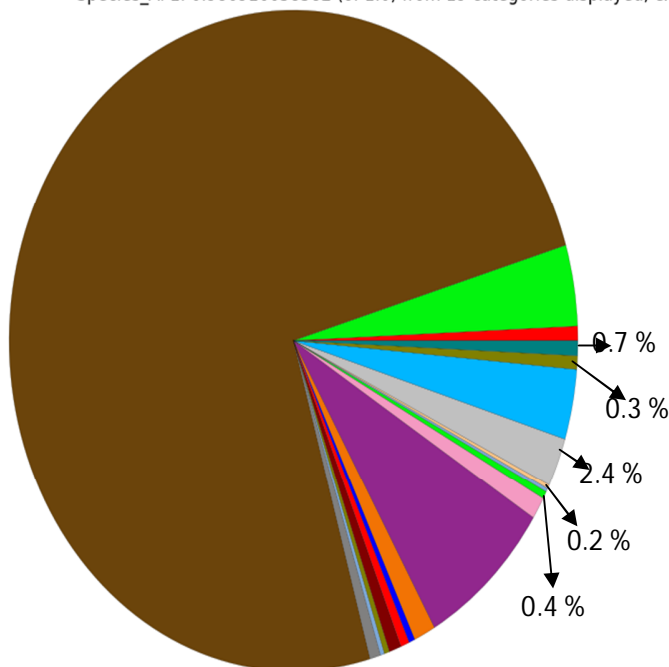
Total Legend	Taxonomy Genus level	Sample %
Unassigned;Other;Other;Other;Other;Other	Other	0.7%
k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_EB1017;g_	EB1017	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_;	g_	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_	g_	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Curtobacterium	Curtobacterium	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter	Leucobacter	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter	Arthrobacter	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Micrococcus	Micrococcus	0.0%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium	Mycobacterium	0.0%
k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Solirubrobacteriales;f_;	g_	0.0%
k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Solirubrobacteriales;f_Conexibacteraceae;g_	g_	0.0%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	Bacteroides	3.9%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella	Prevotella	0.0%
k_Bacteria;p_Bacteroidetes;c_Sphingobacteria;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium	Sphingobacterium	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae;g_	g_	0.0%
k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae;g_Caldilinea	Caldilinea	0.0%
k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_[Roseiflexales];f_[Kouleothrixaceae];g_	g_	0.0%
k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_YS2;f_;	g_	0.0%
k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;Other	Other	0.0%
k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;g_	g_	0.1%

k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;g_	0.2%
k_Bacteria;p_Cyanobacteria;c_Synechococcophycidae;o_Pseudanabaenales;f_Pseudanabaenaceae;g_	0.0%
k_Bacteria;p_Cyanobacteria;c_Synechococcophycidae;o_Synechococcales;f_Synechococcaceae;g_Synechococcus	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Vagococcus	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus	0.0%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;Other	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_SMB53	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;Other	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_	73.7%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Anaeromusa	0.6%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Anaerovibrio	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Pelosinus	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_vadinHB04	0.2%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Gemmatales;f_Gemmataceae;g_	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Gemmatales;f_Isosphaeraceae;g_	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Pirellulales;f_Pirellulaceae;g_	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Pirellulales;f_Pirellulaceae;g_A17	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Pirellulales;f_Pirellulaceae;g_Pirellula	0.0%
k_Bacteria;p_Plantomycetes;c_Plantomycetia;o_Plantomycetales;f_Plantomycetaceae;g_Plantomyces	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Pseudochrobactrum	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Devesia	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Methylosinus	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Phyllobacterium	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacteriales;f_Rhodobacteraceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacteriales;f_Rhodobacteraceae;g_Anaerospora	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacteriales;f_Rhodobacteraceae;g_Paracoccus	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacteriales;f_Rhodobacteraceae;g_Rhodobacter	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseococcus	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	0.1%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Zymomonas	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Delftia	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Limnochabans	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Methylbium	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Cupriavidus	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophilales;f_Methylophilaceae;g_Methylotenera	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Microvirgula	0.3%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfurculales;f_Desulfurculaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila	0.1%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0.7%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Spirobacillales;f_g_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_	0.5%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;Other	0.3%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_	1.2%

k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Citrobacter	7.7%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Cronobacter	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Edwardsiella	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter	1.1%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Erwinia	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia	0.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	0.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Kluyvera	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Morganella	2.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Proteus	3.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Providencia	0.7%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Salmonella	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia	0.8%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Trabulsiella	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas	0.0%
k_Bacteria;p_TM6;c_SJA-4;o_ ;f_ ;g_	0.0%
k_Bacteria;p_TM7;c_TM7-1;o_ ;f_ ;g_	0.0%
k_Bacteria;p_Tenericutes;c_CK-1C4-19;o_ ;f_ ;g_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Luteolibacter	0.0%
k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_	0.0%
k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_Candidatus Xiphinematobacter	0.0%
k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_OR-59	0.0%

Fig. VIII.A.2. Taxonomy at genus level.

Species_AP1: 0.986916638582 (of 1.0) from 19 categories displayed, excluding 0.0130833614175 from 110 categories ('All Other Categories')



Total Legend	Taxonomy species level	Sample %
	Unassigned;Other;Other;Other;Other;Other;Other;Other	0.7%
	k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_EB1017;g_:_s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_:_g_:_s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_:_s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Curtobacterium;s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter;s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter;s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Micrococcus;s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium;s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Solirubrobacteriales;f_:_g_:_s_	0.0%
	k_Bacteria;p_Actinobacteria;c_Thermoleophilla;o_Solirubrobacteriales;f_Conexibacteraceae;g_:_s_	0.0%
	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_	3.9%
	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s_copri	0.0%
	k_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium;s_multivorum	0.0%
	k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae;g_:_s_	0.0%
	k_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;f_Caldilineaceae;g_Caldilinea;s_	0.0%
	k_Bacteria;p_Chloroflexi;c_Chloroflexi;o_Roseiflexales;f_Kouleothrixaceae;g_:_s_	0.0%
	k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_YS2;f_:_g_:_s_	0.0%
	k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;Other;Other	0.0%
	k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;g_:_s_	0.1%
	k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;g_:_s_	0.2%
	k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_Pseudanabaenaceae;g_:_s_	0.0%
	k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Synechococcales;f_Synechococcaceae;g_Synechococcus;s_	0.0%
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus;s_	0.0%
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Vagococcus;s_	0.0%
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_	0.0%
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_	0.0%
	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;Other;Other	0.0%
	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_:_s_	0.0%
	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;Other	0.0%
	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;s_	0.1%

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;s_intestinale	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;s_neonatale	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_SMB53;s_	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus;s_	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_s_	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_s_	0.1%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;Other;Other	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_s_	73.7%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Anaeromusa;s_	0.6%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Anaerovibrio;s_	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Pelosinus;s_	0.0%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_vadinHB04;s_	0.2%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata;s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_A17;s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_Pirellula;s_	0.0%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Planctomycetales;f_Planctomycetaceae;g_Planctomyces;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;Other;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Pseudochrobactrum;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Devosia;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Methylosinus;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Phyllobacterium;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Anaerospora;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseococcus;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_echinoides	0.1%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Zymomonas;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;Other;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Delftia;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Limnohabitans;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Methylibium;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Cupriavidus;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophilales;f_Methylophilaceae;g_Methylotenera;s_mobilis	0.0%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Microvirgula;s_aerodentrificans	0.3%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfurculales;f_Desulfurculaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila;s_	0.1%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio;s_	0.7%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Spirobacillales;f_g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;Other;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_s_	0.5%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;Other;Other	0.3%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_s_	1.2%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Citrobacter;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Citrobacter;s_	7.6%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Cronobacter;s_dublinensis	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Edwardsiella;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter;Other	1.1%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter;s_cloacae	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter;s_hormaechei	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Erwinia;Other	0.0%

k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia;s_coli	0.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella;s_	0.2%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella;s_oxytoca	0.2%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Kluyvera;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Morganella;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Morganella;s_	0.1%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Morganella;s_morganii	2.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Proteus;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Proteus;s_	3.4%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Providencia;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Providencia;s_	0.7%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Salmonella;s_enterica	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia;s_	0.1%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia;s_marcescens	0.7%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Serratia;s_ureilytica	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Trabulsiella;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Trabulsiella;s_farmeri	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_s_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella;s_	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas;Other	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas;s_stutzeri	0.0%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas;s_	0.0%
k_Bacteria;p_TM6;c_SJA-4;o_f_g_s_	0.0%
k_Bacteria;p_TM7;c_TM7-1;o_f_g_s_	0.0%
k_Bacteria;p_Tenericutes;c_CK-1C4-19;o_f_g_s_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_s_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Luteolibacter;s_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacteriales;f_Chthoniobacteraceae;g_s_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacteriales;f_Chthoniobacteraceae;g_Candidatus Xiphinematobacter;s_	0.0%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacteriales;f_Chthoniobacteraceae;g_OR-59;s_	0.0%

Fig. VIII.A.3. Taxonomy at species level.

Consensus Lineage	API	#OTU ID
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Bilophila;s__	111	denovo280
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio;s__	122	denovo585
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo735
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__morganii	102	denovo873
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo1230
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo1482
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	112	denovo1547
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__oxytoca	100	denovo1906
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__morganii	100	denovo2041
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__	100	denovo2220
Unassigned	100	denovo2771
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo3055
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo3126
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo3853
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae	100	denovo4448
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus;s__	100	denovo4831
Unassigned	100	denovo4916
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__s__	100	denovo4938
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__	100	denovo5012
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter	100	denovo5049
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__s__	100	denovo5378
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Microvirgula;s__aerodenitrificans	100	denovo5791
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo6261
k__Bacteria;p__Bacteroidetes;o__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__	100	denovo6569
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__morganii	100	denovo6835
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Anaeromusa;s__	100	denovo6979
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo6999
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter	100	denovo7795
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo7855
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__marcescens	100	denovo7864
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__	100	denovo7933
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo8066
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__s__	100	denovo8391
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__coli	100	denovo8968
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__	100	denovo9059
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo9178
Unassigned	100	denovo9379
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo9646
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo9658
k__Bacteria;p__Bacteroidetes;o__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__	100	denovo9841
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo9861
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo9909
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo10049
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__s__	100	denovo10227
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__s__	100	denovo10437
k__Bacteria;p__Cyanobacteria;o__Chloroplast;o__Chlorophyta;f__Trebouxiophyceae;g__s__	100	denovo10896
Unassigned	100	denovo10956
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus;s__	100	denovo11500
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__	100	denovo11624
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Anaeromusa;s__	100	denovo11699
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Providencia;s__	100	denovo11767
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__vadinHB04;s__	100	denovo11970
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo12226
k__Bacteria;p__Firmicutes;o__Clostridia;o__Clostridiales;f__Veillonellaceae;g__s__	100	denovo12370

Fig. VIII.A.4. OTU table heat map showing taxonomy assignment for each OTU. The OTU heat map displays raw OTU counts per sample, where the counts are colored based on the contribution of each OTU to the total OTU count present in that sample (blue: contributes low percentage of OTUs to sample; red: contributes high percentage of OTUs). Cutoff of 120 was taken for the snapshot.

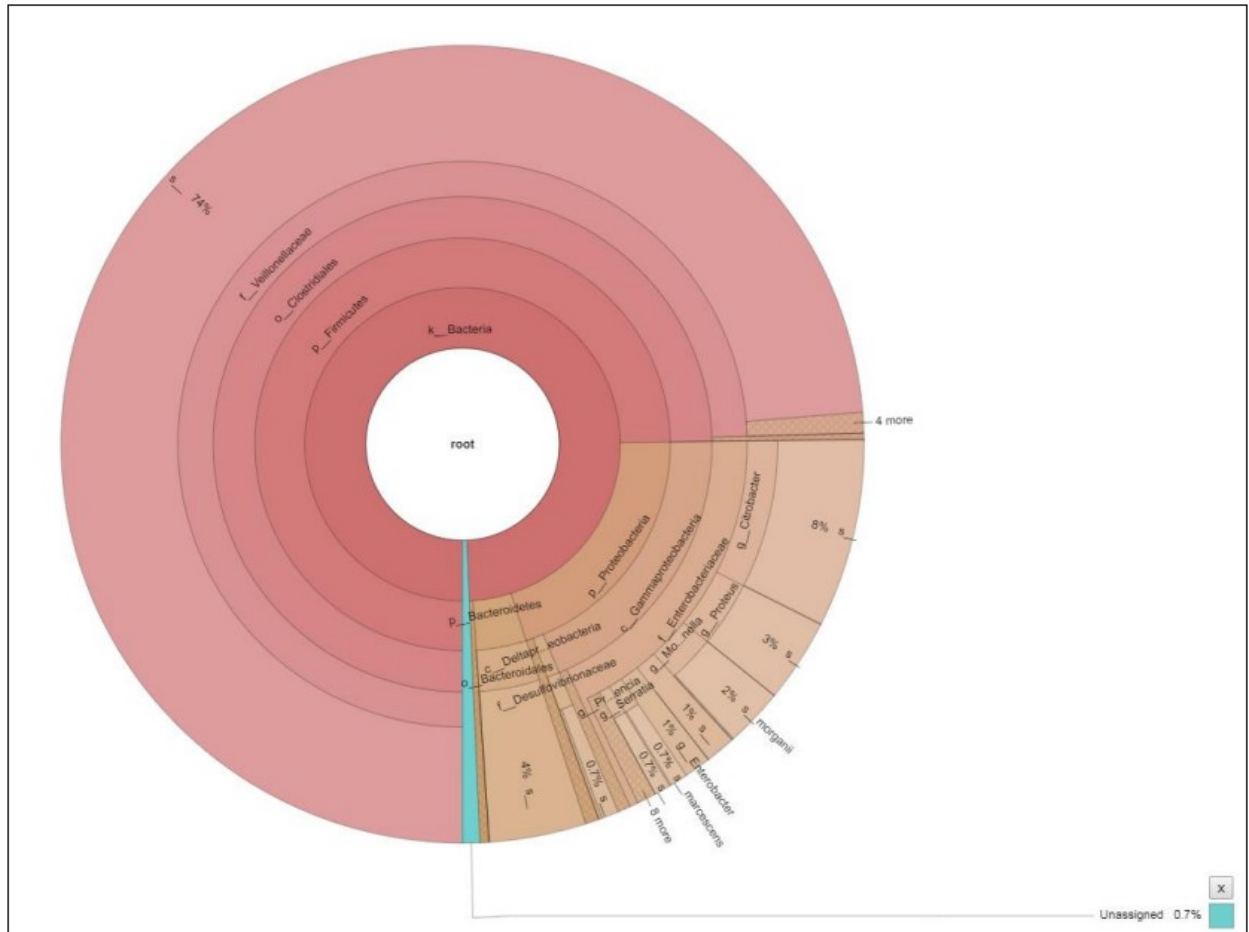


Fig. VIII.A.5. Krona graph showing the relative abundance of *Barilius bendelisis* sample at root level.