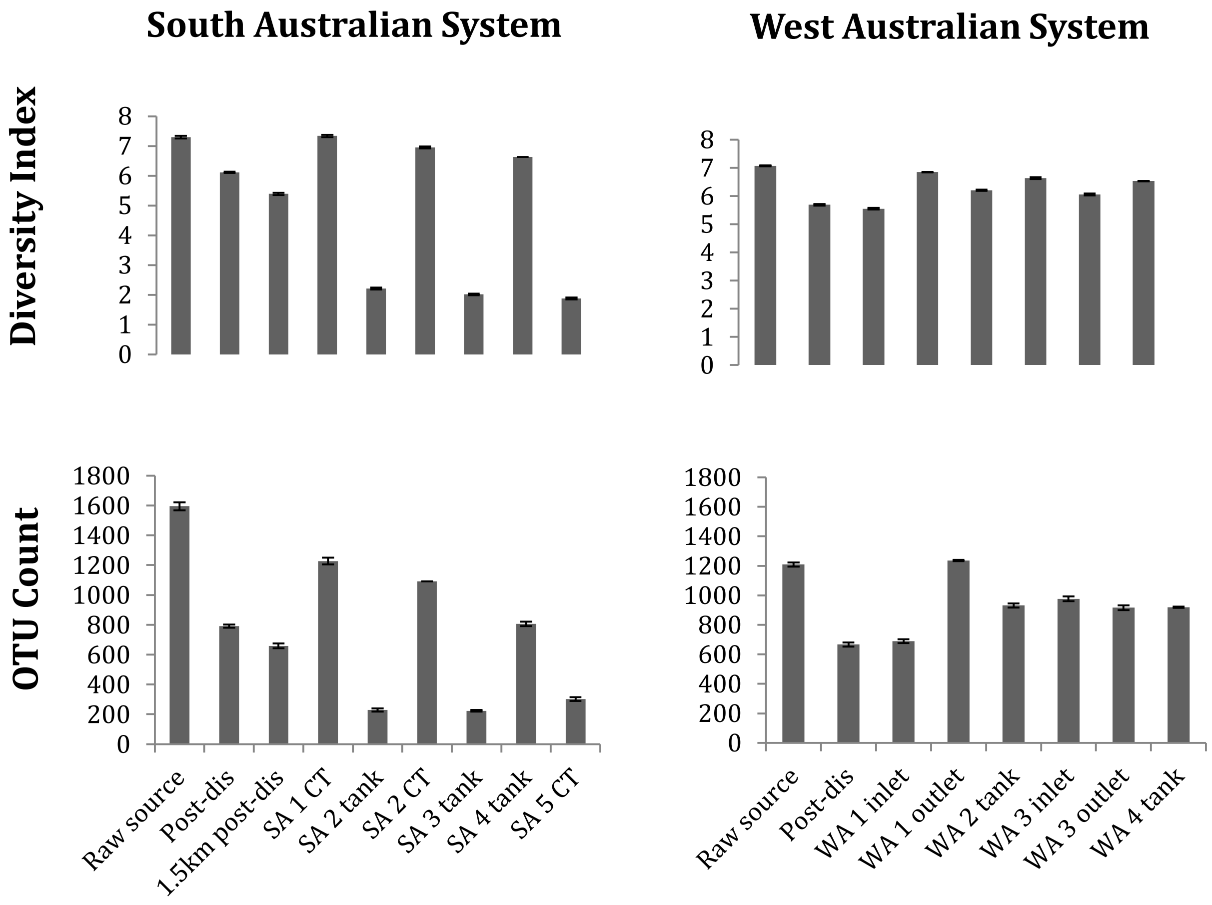
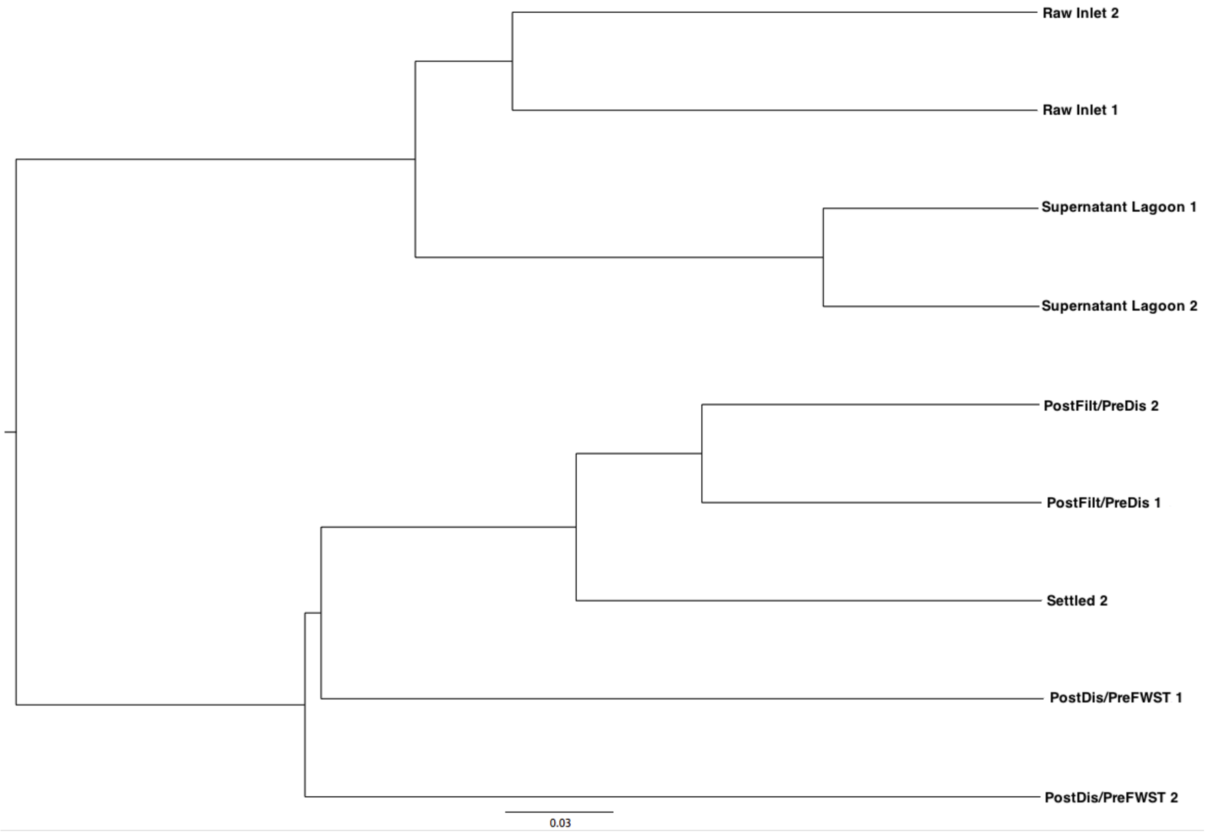
Supplementary Materials for: Using amplicon sequencing to characterize and monitor bacterial diversity in drinking water distribution systems.



SM-1. Shannon Diversity index of a SA and WA DWDS samples, and the number of OTUs found in SA and WA DWDS samples.



SM-2. Cluster plot of samples taken from SA WTP two-weeks apart (1 & 2). Sample names indicate different treatment stages within the SA WTP. Cluster dendogram of sample similarity is based on jack-knifed (e = 10) UNIFRAC bacterial community assemblage. *one of the settled samples failed to amplify, possibly due to PCR inhibition caused by high amounts of chemicals and humics.

SM-3: Percentage of taxa identified per sample for the WA DWDS. Clustered at 97% and rarefied at 8904 sequences.

Taxon	Source Water	Post-dis	WA-1 Inlet	WA-1 Outlet	WA-2	WA-3 Inlet	WA-3 Outlet	WA-4 CT
Acidobacteria;Acidobacteria_Gp4;Gp4;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Acidobacteria;Acidobacteria_Gp6;Gp6;Other;Other	0.29%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Other	0.00%	0.00%	0.00%	0.15%	0.10%	0.14%	0.12%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%

Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	0.00%	0.09%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Other	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Other	2.74%	0.53%	0.55%	7.81%	14.19%	18.44%	15.89%	7.89%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.64%
Actinobacteria;Actinobacteria;Actinomycetales;Other;Other	0.63%	0.42%	0.58%	3.62%	1.30%	0.99%	1.28%	1.64%
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Other	0.00%	0.00%	0.10%	0.08%	0.01%	0.00%	0.01%	0.01%
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	0.00%	0.00%	0.42%	0.00%	0.02%	0.00%	0.00%	0.01%
Actinobacteria;Actinobacteria;Other;Other;Other	2.18%	0.16%	0.60%	2.86%	1.22%	2.42%	2.26%	1.07%
Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Fluviicola	0.03%	0.00%	0.00%	0.08%	0.06%	0.24%	0.10%	0.01%
Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Other	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.01%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Capnocytophaga	0.00%	0.00%	0.00%	0.03%	0.00%	0.04%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Elizabethkingia	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0.03%	0.00%	0.87%	0.00%	0.00%	0.00%	0.01%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Other	0.02%	0.00%	0.02%	0.03%	0.02%	0.02%	0.02%	0.03%
Bacteroidetes;Flavobacteria;Flavobacteriales;Other;Other	0.21%	0.00%	0.01%	0.00%	0.00%	0.05%	0.03%	0.00%
Bacteroidetes;Other;Other;Other;Other	1.29%	0.13%	0.14%	1.68%	0.52%	3.26%	1.78%	0.31%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Ferruginibacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Other	0.39%	0.00%	0.00%	0.00%	0.04%	0.28%	0.23%	0.06%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Sediminibacterium	0.64%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cyclobacteriaceae;Algoriphagus	0.03%	0.00%	0.00%	0.03%	0.25%	0.77%	0.33%	0.09%

Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cyclobacteriaceae;Other	0.27%	0.00%	0.00%	0.00%	0.01%	0.02%	0.05%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Cytophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Other;Other	0.37%	0.00%	0.26%	0.40%	0.21%	0.24%	0.27%	0.03%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Other	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Bacillariophyta;Other	0.00%	8.86%	4.94%	1.96%	0.18%	0.16%	0.04%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Chlorophyta;Other	0.00%	0.02%	0.11%	0.00%	0.00%	0.00%	0.02%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Cryptomonadaceae;Other	0.00%	0.00%	0.06%	0.05%	0.04%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Other;Other	0.06%	1.88%	2.26%	0.20%	0.20%	0.03%	0.07%	0.03%
Cyanobacteria;Cyanobacteria;Chloroplast;Streptophyta;Other	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Family I;GpI;Other	0.00%	0.00%	0.09%	0.18%	0.03%	0.05%	0.01%	0.00%
Cyanobacteria;Cyanobacteria;Family II;GpIIa;Other	6.58%	3.22%	1.69%	0.95%	9.46%	7.93%	10.86%	4.42%
Cyanobacteria;Cyanobacteria;Family II;Other;Other	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Family XI;GpXI;Other	0.03%	0.14%	0.73%	0.13%	0.01%	0.01%	0.07%	0.03%
Cyanobacteria;Cyanobacteria;Other;Other;Other	0.22%	2.50%	0.70%	3.44%	0.54%	0.22%	0.55%	1.53%
Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Meiothermus	0.00%	0.00%	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Bacillaceae;Other	0.00%	0.00%	0.00%	0.00%	0.01%	0.03%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Granulicatella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.11%
Firmicutes;Bacilli;Lactobacillales;Other;Other	0.02%	0.00%	0.23%	0.00%	0.00%	0.00%	0.00%	0.01%
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Other	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0.00%	0.00%	0.31%	0.03%	0.03%	0.00%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Other	0.00%	0.00%	0.00%	0.25%	0.01%	0.02%	0.09%	0.00%
Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Finegoldia	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.01%	0.00%
Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Other	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Lachnospirac	0.00%	0.00%	0.00%	0.03%	0.01%	0.01%	0.01%	0.00%

eae;Other								
Firmicutes;Clostridia;Clostridiales;Other;Other	0.00%	0.00%	0.00%	0.75%	0.18%	0.61%	0.32%	0.14%
Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Other	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Acetivibrio	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Other	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Other	0.00%	0.16%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Firmicutes;Clostridia;Other;Other;Other	0.01%	0.00%	0.00%	0.13%	0.03%	0.07%	0.04%	0.16%
Firmicutes;Other;Other;Other;Other	0.00%	0.00%	0.00%	0.00%	0.02%	0.09%	0.06%	0.06%
Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Cetobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Leptotrichia	0.00%	0.00%	0.14%	0.03%	0.00%	0.00%	0.00%	0.00%
Fusobacteria;Fusobacteria;Fusobacteriales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.01%	0.00%
Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	0.13%	0.00%	0.00%	0.08%	0.02%	0.01%	0.00%	0.63%
Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Other;Other;Other;Other;Other	27.30%	51.92%	55.70%	33.39%	17.13%	15.62%	15.95%	16.27%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata	0.01%	0.04%	0.03%	0.03%	0.02%	0.00%	0.00%	0.00%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Other	0.22%	0.92%	0.70%	0.83%	0.26%	0.17%	0.14%	0.94%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces	0.01%	0.06%	0.09%	0.18%	0.02%	0.04%	0.01%	0.06%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Zavarzinella	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_incertae_sedis;Insolitispirillum;Other	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_incertae_sedis;Novispirillum;Other	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0.04%	0.00%	0.04%	0.05%	0.03%	0.02%	0.01%	0.16%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Other	0.24%	0.00%	0.79%	0.18%	0.23%	0.48%	0.10%	0.57%
	0.00%	0.01%	0.01%	0.05%	0.01%	0.03%	0.04%	0.03%

Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium								
Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Hyphomonas	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.01%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Other;Other	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%	0.03%	0.01%
Proteobacteria;Alphaproteobacteria;Other;Other;Other	5.22%	0.06%	0.64%	4.64%	2.48%	4.42%	4.53%	19.08%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bosea	0.00%	0.00%	0.11%	0.00%	0.00%	0.03%	0.01%	1.08%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Other	1.71%	0.00%	0.00%	0.03%	0.13%	0.44%	0.33%	0.33%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;Methylocystis	0.00%	0.01%	0.12%	0.00%	0.01%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;Other	0.00%	0.26%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Other;Other	0.13%	0.07%	0.06%	0.05%	0.02%	0.18%	0.10%	0.21%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Mesorhizobium	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Other	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Other	0.02%	0.00%	0.11%	0.03%	0.00%	0.02%	0.01%	0.03%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Craurococcus	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Other	7.41%	0.00%	0.04%	0.83%	1.06%	0.94%	1.25%	0.88%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Other;Other	0.24%	0.01%	0.02%	0.08%	0.04%	0.18%	0.01%	0.01%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Other	0.00%	0.86%	3.27%	0.18%	0.09%	0.04%	0.00%	0.06%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Rhodocista	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rickettsiales;Other;Other	0.00%	0.00%	0.00%	0.25%	0.02%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR11;Pelagibacter	15.27%	0.01%	0.27%	3.57%	33.37%	24.33%	28.68%	4.14%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Croceicoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%

Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythromicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Other	0.96%	0.00%	0.00%	0.45%	0.32%	0.18%	0.31%	0.14%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Other;Other	0.42%	0.00%	0.06%	1.53%	2.21%	1.46%	1.27%	1.27%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	0.02%	0.00%	0.00%	0.05%	0.00%	0.01%	0.05%	6.46%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Other	5.15%	0.00%	0.35%	1.23%	0.73%	0.68%	0.57%	0.54%
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Achromobacter	0.00%	0.24%	0.11%	0.00%	0.00%	0.03%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Other	0.00%	6.46%	5.45%	0.38%	0.05%	0.27%	0.06%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Other	0.05%	0.03%	0.05%	0.00%	0.03%	0.00%	0.01%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia	0.00%	6.20%	2.94%	0.33%	0.00%	0.00%	0.02%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Methylibium	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Other	0.11%	0.00%	0.00%	0.03%	0.02%	0.05%	0.01%	0.06%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Paucibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0.00%	0.02%	0.04%	0.03%	0.00%	0.00%	0.02%	0.03%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Other	0.02%	0.01%	0.06%	0.10%	0.03%	0.22%	0.09%	0.66%
Proteobacteria;Betaproteobacteria;Burkholderiales;Other;Other	2.10%	0.25%	0.50%	5.47%	3.77%	6.61%	5.00%	1.40%
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.06%	0.01%
Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;Thiobacillus	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;Methylophilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;Other	0.01%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.01%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Chromobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Neisseria	0.00%	0.19%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Other	0.00%	0.01%	0.00%	0.43%	0.13%	0.23%	0.11%	0.30%
Proteobacteria;Betaproteobacteria;Other;Other;Other	0.53%	0.05%	0.12%	0.58%	0.60%	0.33%	0.31%	0.47%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azonexus	0.00%	0.10%	0.00%	0.30%	0.12%	0.60%	0.15%	0.16%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira	0.00%	0.00%	0.00%	0.13%	0.03%	0.11%	0.03%	0.03%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Denitratisoma	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.03%	0.00%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Other	0.00%	0.03%	0.03%	0.68%	0.06%	0.09%	0.04%	0.09%
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Peredibacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0.04%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Kofleria	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Nannocystaceae;Nannocystis	0.01%	0.00%	0.00%	0.10%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Other;Other	0.07%	0.25%	0.00%	0.03%	0.00%	0.01%	0.03%	0.04%
Proteobacteria;Deltaproteobacteria;Myxococcales;Phaselicystidaceae;Phaselicystis	0.01%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Other;Other;Other	0.03%	0.01%	0.11%	0.05%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.06%	0.01%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.03%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfuricurvum	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.03%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%

Proteobacteria;Epsilonproteobacteria;Campylobacterales;Other;Other	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	0.00%	0.00%	0.28%	0.05%	0.00%	0.03%	0.07%	0.11%
Proteobacteria;Gammaproteobacteria;Alteromonadales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Buttiauxella	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	0.08%	8.48%	5.57%	0.20%	0.09%	0.44%	0.26%	1.01%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Morganella	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Other	0.38%	0.12%	0.19%	0.18%	0.14%	0.13%	0.18%	0.04%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Plesiomonas	0.00%	0.01%	0.00%	0.03%	0.01%	0.02%	0.01%	0.14%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	1.32%	0.00%	0.00%	0.00%	0.03%	0.09%	0.00%	0.04%
Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Aquicella	0.04%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella	0.02%	0.02%	0.00%	0.00%	0.00%	0.02%	0.03%	0.06%
Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Other	0.34%	0.36%	0.01%	0.03%	0.00%	0.01%	0.03%	0.07%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Other	0.03%	0.00%	0.15%	0.00%	0.01%	0.02%	0.01%	0.00%
Proteobacteria;Gammaproteobacteria;Other;Other;Other	6.46%	2.31%	2.12%	3.46%	2.10%	1.74%	1.24%	0.63%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Other;Other	0.00%	0.00%	0.01%	5.47%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Other	0.03%	0.00%	0.00%	0.05%	0.02%	0.01%	0.09%	0.09%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.03%	0.10%
Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichales_incertae_sedis;Caedibacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Other	1.69%	0.02%	0.07%	0.00%	0.02%	0.02%	0.01%	0.00%
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Rhodanobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%

Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Other;Other;Other;Other	5.87%	2.47%	4.59%	8.94%	5.56%	2.91%	3.97%	22.93%
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Leptospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Turneriella	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Other;Other;Other;Other	0.03%	0.00%	0.00%	0.03%	0.00%	0.08%	0.02%	0.00%
Verrucomicrobia;Spartobacteria;Other;Other;Other	0.00%	0.00%	0.10%	0.00%	0.00%	0.02%	0.00%	0.00%
Verrucomicrobia;Spartobacteria;Spartobacteria_genera_incertae_sedis;Other;Other	0.00%	0.02%	0.00%	0.13%	0.00%	0.02%	0.01%	0.01%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Other	0.01%	0.00%	0.02%	0.00%	0.00%	0.04%	0.00%	0.01%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Prosthecobacter	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Roseibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
WS3;WS3_genera_incertae_sedis;Other;Other;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Table SM-4: Percentage of OTUs identified per sample for the SA System. Clustered at 97% and rarefied at 8904 sequences.

Taxon	**Source Water**	**Post-dis**	**Post-dis 1.5km**	**SA-1 CT**	**SA-2**	**SA-2 CT**	**SA-3**	**SA-4**	**SA-5 CT**
Acidobacteria;Acidobacteria_Gp1;Gp1;Other;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp10;Gp10;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp11;Gp11;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp13;Gp13;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp15;Gp15;Other;Other	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp16;Gp16;Other;Other	0.10%	0.00%	0.00%	0.00%	0.00%	0.09%	0.00%	0.08%	0.00%
Acidobacteria;Acidobacteria_Gp17;Gp17;Other;Other	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Acidobacteria;Acidobacteria_Gp18;Gp18;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp22;Gp22;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp3;Gp3;Other;Other	0.06%	0.00%	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp4;Gp4;	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Other;Other									
Acidobacteria;Acidobacteria_Gp5;Gp5;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Acidobacteria_Gp6;Gp6;Other;Other	0.27%	0.00%	0.00%	0.20%	0.00%	0.01%	0.00%	0.11%	0.00%
Acidobacteria;Acidobacteria_Gp7;Gp7;Other;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Holophagae;Other;Other;Other	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Acidobacteria;Other;Other;Other;Other	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Acidimicrobiales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces	0.00%	0.03%	0.21%	0.08%	0.04%	0.02%	0.00%	0.00%	0.01%
Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	0.00%	0.00%	0.19%	0.12%	0.04%	0.18%	0.01%	1.27%	0.08%
Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Turicella	0.00%	0.30%	0.08%	0.20%	0.01%	0.00%	0.03%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Dietziaceae;Dietzia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.75%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;Ornithinimicrobium	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Other	0.62%	0.16%	0.48%	0.16%	0.00%	0.17%	0.02%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Nesterenkonia	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0.00%	0.00%	0.18%	0.27%	0.00%	0.09%	0.00%	1.63%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Mycobacteriaceae;Mycobacterium	0.02%	0.02%	0.00%	0.20%	0.00%	0.00%	0.00%	0.00%	0.01%
Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;Other	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0.00%	0.00%	0.00%	0.13%	0.01%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.17%	0.00%
Actinobacteria;Actinobacteria;Actinomycetales;Other;Other	0.70%	1.19%	2.27%	3.85%	0.19%	1.08%	0.59%	4.23%	0.28%
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Other	0.00%	1.60%	0.77%	0.41%	0.06%	0.18%	0.05%	5.82%	0.07%
Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	0.06%	23.10%	28.45%	18.11%	3.04%	8.15%	0.73%	6.24%	1.24%
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Eggerthella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%
Actinobacteria;Actinobacteria;Nitriliruptorales;Nitriliruptoraceae;Nitriliruptor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Other;Other;Other	5.96%	0.40%	0.08%	1.11%	0.01%	0.54%	0.01%	0.86%	0.05%
Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;Rubrobacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Actinobacteria;Actinobacteria;Solirubrobacterales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.00%	0.17%	0.07%	0.01%	0.00%	0.00%	0.01%	0.10%	0.06%
Bacteroidetes;Bacteroidia;Bacteroidales;Other;Other	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.20%	0.04%
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Dysgonomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%

Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Tannerella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%
Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Capnocytophaga	0.00%	0.00%	0.05%	0.24%	0.00%	0.00%	0.00%	0.00%	0.02%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Gelidibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Other	0.13%	0.00%	0.01%	0.04%	0.01%	0.01%	0.00%	0.34%	0.03%
Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Planobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Bacteroidetes;Flavobacteria;Flavobacteriales;Other;Other	0.01%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Other;Other;Other;Other	1.07%	0.02%	0.01%	0.53%	0.00%	0.18%	0.00%	0.51%	0.02%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Ferruginibacter	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Flavisolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Lacibacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Other	0.62%	0.07%	0.00%	0.22%	0.00%	4.72%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Sediminibacterium	0.10%	0.89%	0.00%	0.00%	0.02%	0.00%	0.04%	0.00%	0.19%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Terrimonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.15%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cyclobacteriaceae;Algoriphagus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Emticicia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Flexibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Leadbetterella	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Other	0.09%	0.01%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Runella	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Spirosoma	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Other;Other	0.13%	0.03%	0.00%	0.33%	0.01%	0.29%	0.00%	0.00%	0.11%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Saprospiraceae;Haliscomenobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedob	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%

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Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Chloroflexi;Dehalococcoidetes;Dehalogenimonas;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.96%	0.00%
Chloroflexi;Other;Other;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Bacillariophyta;Other	0.75%	0.02%	0.00%	0.02%	0.00%	0.06%	0.00%	0.00%	0.01%
Cyanobacteria;Cyanobacteria;Chloroplast;Chlorophyta;Other	0.05%	0.03%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Cryptomonadaceae;Other	0.01%	0.44%	0.00%	0.05%	0.00%	0.06%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Other;Other	0.13%	0.06%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Chloroplast;Streptophyta;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.38%	0.00%	0.01%
Cyanobacteria;Cyanobacteria;Family I;GpI;Other	0.00%	0.13%	0.89%	0.16%	0.00%	0.00%	0.00%	0.93%	0.06%
Cyanobacteria;Cyanobacteria;Family II;GpIIa;Other	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.21%	0.00%
Cyanobacteria;Cyanobacteria;Family XI;GpXI;Other	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%
Cyanobacteria;Cyanobacteria;Family XIII;GpXIII;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Cyanobacteria;Cyanobacteria;Other;Other;Other	5.72%	0.17%	0.06%	0.05%	0.00%	0.24%	0.01%	0.04%	0.13%
Deinococcus-Thermus;Deinococci;Deinococcales;Deinococcaceae;Deinococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Deinococcus-Thermus;Deinococci;Other;Other;Other	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Bacillaceae;Anoxybacillus	0.00%	0.00%	0.00%	0.19%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.00%	0.00%	0.00%	0.32%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Bacillaceae;Oceanobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Bacillaceae;Other	0.00%	0.30%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Other;Other	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%
Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Cohnella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Gemella	0.00%	0.26%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	0.00%	0.20%	0.43%	0.37%	0.13%	0.28%	0.03%	0.28%	0.09%
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Alkalibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Alloiococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Granulicatella	0.00%	0.00%	1.08%	0.71%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Other	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	0.00%	0.01%	0.56%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Other;Other	0.00%	1.22%	0.26%	0.02%	0.00%	0.00%	0.00%	2.58%	0.09%
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	0.00%	0.00%	0.01%	0.42%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Other	0.00%	0.00%	0.14%	0.02%	0.00%	0.01%	0.01%	0.05%	0.00%
Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0.00%	2.01%	10.41%	1.68%	0.08%	0.61%	0.05%	6.64%	0.08%
Firmicutes;Bacilli;Other;Other;Other	0.00%	0.05%	0.05%	0.01%	0.00%	0.01%	0.00%	0.04%	0.00%
Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Anaerococcus	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Finegoldia	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Peptoniphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.52%	0.00%
Firmicutes;Clostridia;Clostridiales;Other;Other	0.01%	0.20%	0.00%	0.00%	0.00%	0.00%	0.00%	0.77%	0.01%
Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Phascolarctobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	0.00%	0.03%	0.39%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Firmicutes;Clostridia;Other;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Firmicutes;Other;Other;Other;Other	0.00%	0.29%	2.79%	0.27%	0.12%	0.05%	0.12%	1.65%	0.49%
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Leptotrichia	0.00%	0.00%	0.00%	0.71%	0.00%	0.00%	0.00%	0.00%	0.05%
Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Other	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	1.31%	0.04%	0.00%	1.21%	0.03%	2.84%	0.02%	0.00%	0.00%
Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Other;Other;Other;Other;Other	28.35%	2.52%	3.08%	5.98%	0.15%	7.10%	0.38%	18.62%	0.52%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Schlesneria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Asticcacaulis	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0.00%	1.02%	0.00%	0.00%	0.01%	1.88%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Other	0.25%	0.07%	0.00%	0.47%	0.61%	1.07%	0.03%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0.06%	0.00%	0.00%	0.00%	0.00%	0.15%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Caulobacterales;Other;Other	0.00%	0.00%	0.00%	0.01%	0.03%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Other;Other;Other	2.19%	1.10%	0.13%	1.24%	0.04%	2.02%	0.03%	0.24%	0.10%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Chelatococcus	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Other	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bosea	0.01%	0.25%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Other	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Devosia	0.00%	0.05%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Hyphomicrobium	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Other	0.14%	0.01%	0.00%	0.21%	0.00%	0.06%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Methylobacterium	0.01%	0.18%	0.01%	0.51%	0.05%	0.01%	0.00%	0.00%	0.00%

Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;Methylocystis	0.02%	0.44%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylocystaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Other;Other	0.48%	23.34%	0.57%	3.16%	0.45%	1.23%	0.02%	0.13%	0.12%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhodobiaceae;Parvibaculum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Other	0.09%	0.00%	0.02%	0.05%	0.03%	0.80%	0.01%	0.12%	0.01%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus	0.00%	0.00%	0.20%	0.10%	0.54%	0.07%	0.01%	0.18%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rubellimicrobium	0.00%	0.00%	0.15%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Other	0.48%	0.04%	2.54%	0.53%	0.00%	0.00%	0.17%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Other;Other	0.13%	0.00%	0.03%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Other	0.02%	0.00%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Rickettsiales;SAR11;Pelagibacter	12.64%	2.04%	0.01%	12.74%	0.02%	6.66%	0.03%	0.00%	0.11%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Other;Other	0.06%	7.52%	0.40%	0.07%	0.01%	2.35%	0.10%	0.09%	0.17%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	0.23%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Other	0.05%	0.83%	0.61%	0.15%	0.09%	16.97%	0.16%	0.00%	0.18%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.06%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.43%	0.00%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingosinicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Zymomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.12%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Achromobacter	0.01%	2.72%	7.71%	2.24%	0.10%	0.56%	0.02%	1.14%	0.16%
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Azohydromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Other	0.05%	0.09%	0.09%	0.13%	0.01%	0.08%	0.00%	0.02%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus	0.00%	0.98%	0.00%	0.00%	0.00%	0.00%	0.00%	0.48%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Other	0.13%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Polynucle	0.65%	0.65%	0.22%	3.69%	0.01%	2.85%	0.00%	0.00%	0.00%

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Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	0.05%	0.03%	0.00%	0.01%	0.08%	0.00%	0.00%	0.00%	0.02%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Methylibium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Other	0.33%	0.26%	0.45%	0.11%	0.00%	0.03%	0.00%	0.00%	0.01%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Paucibacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Rubrivivax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.70%	0.04%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Brachymonas	0.58%	0.25%	0.00%	1.52%	0.00%	0.55%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia	0.01%	5.18%	1.91%	0.67%	0.16%	1.50%	0.07%	6.29%	0.37%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga	0.04%	0.00%	0.00%	0.02%	0.00%	0.05%	0.01%	0.00%	87.07%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Other	4.17%	8.36%	14.04%	22.89%	0.03%	16.05%	95.42%	19.58%	6.14%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas	0.01%	1.86%	3.07%	0.69%	0.00%	0.05%	0.01%	1.48%	0.03%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.06%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pseudorhodoferax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax	0.02%	0.00%	0.00%	0.00%	0.01%	0.06%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Roseateles	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Schlegelella	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Other;Other	2.98%	0.57%	0.40%	2.13%	0.01%	3.19%	0.27%	0.15%	0.05%
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Other	0.09%	0.04%	0.00%	0.05%	0.34%	0.37%	0.03%	0.13%	0.00%
Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;Thi	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.84%	0.00%

obacillus									
Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;Other	0.38%	0.01%	0.00%	0.02%	0.00%	0.05%	0.00%	0.00%	0.01%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Chitinibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Deefgea	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Kingella	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Neisseria	0.00%	0.00%	0.00%	0.08%	0.01%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Simonsiella	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vogesella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Other;Other;Other	1.01%	0.77%	0.53%	0.66%	0.00%	7.90%	0.03%	2.20%	0.11%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azonexus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechloromonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Other	0.41%	0.27%	0.70%	0.11%	0.00%	0.36%	0.00%	0.05%	0.03%
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Bacteriovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Peredibacter	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Other	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiaceae;Desulfomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.14%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Other;Other	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Anaeromyxobacter	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Kofleria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Myxococcales;Other;Other	0.02%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Other;Other;Other	0.21%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	2.41%	0.00%
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Deltaproteobacteria;Syntrophorhabdaceae;Syntrophorhabdus;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Campylobacter	0.00%	0.00%	0.00%	0.27%	0.00%	0.00%	0.00%	0.10%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Other	1.72%	0.09%	0.01%	0.04%	0.00%	0.34%	0.00%	0.00%	0.06%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfuricurvum	0.44%	0.00%	0.00%	0.32%	0.00%	0.07%	0.00%	0.00%	0.14%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurovum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Other;Other	15.09%	0.03%	0.30%	0.54%	0.00%	0.03%	0.00%	0.93%	0.00%
Proteobacteria;Epsilonproteobacteria;Other;Other;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	0.00%	0.00%	0.32%	0.00%	0.00%	0.00%	0.01%	0.93%	0.03%
Proteobacteria;Gammaproteobacteria;Aeromonadales;Other;Other	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Alteromonas	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Cardiobacteriales;Cardiobacteriaceae;Cardiobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;Thiovirga	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Buttiauxella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	0.00%	0.36%	0.20%	0.08%	0.01%	0.02%	0.05%	0.99%	0.18%
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Other	0.00%	0.04%	0.02%	0.01%	0.01%	0.00%	0.00%	0.17%	0.03%
Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Aquicella	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosoma	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Other	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Other;Other;Other	3.87%	0.31%	4.62%	1.14%	75.99%	1.32%	0.05%	0.29%	0.14%
Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Haemophilus	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%

Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0.00%	0.02%	0.12%	0.00%	0.77%	0.00%	0.00%	0.01%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Other	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Perlucidibaca	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Other;Other	0.00%	0.00%	0.99%	0.10%	0.31%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Other	0.00%	0.01%	0.09%	0.00%	4.59%	0.01%	0.00%	0.03%	0.00%
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0.00%	0.00%	0.11%	0.00%	10.72%	0.00%	0.00%	0.02%	0.00%
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae;Steroidobacter	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Other	0.03%	1.29%	4.57%	1.72%	0.01%	0.09%	0.02%	0.53%	0.10%
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.00%	0.79%	0.02%	0.01%	0.04%	0.18%	0.02%	0.09%	0.09%
Proteobacteria;Other;Other;Other;Other	2.25%	1.78%	1.65%	2.66%	0.83%	3.15%	0.06%	3.87%	0.36%
Spirochaetes;Spirochaetes;Spirochaetales;Leptospiraceae;Turneriella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
TM7;TM7_genera_incertae_sedis;Other;Other;Other	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Subdivision3;Subdivision3_genera_incertae_sedis;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
WS3;WS3_genera_incertae_sedis;Other;Other;Other	1.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

SM-5. BLASTN 2.2.31 results for reads extracted from fasta file.

WA 1 inlet

Enterobacteria reads extracted (*pathogenic hits: *Shigella sonnei, Shigella dystentry, Escherichia fergunsonii, E coli*, …)

	Max Score	Total Score	Query Cover	E value	Identity
Escherichia fergusonii strain ATCC 35469 16S ribosomal RNA gene, complete sequence	305	305	96%	3e-83	98%
Shigella sonnei Ss046 strain Ss046 16S ribosomal RNA, complete sequence	305	305	96%	3e-83	98%
Shigella dysenteriae Sd197 strain Sd197 16S ribosomal RNA, complete sequence	305	305	96%	3e-83	98%
Escherichia coli O157:H7 str. Sakai strain Sakai 16S ribosomal RNA, complete sequence	305	305	96%	3e-83	98%
Shigella flexneri 2a str. 301 strain 301 16S ribosomal RNA, complete sequence	305	305	96%	3e-83	98%
Escherichia fergusonii strain NBRC 102419 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Escherichia coli strain NBRC 102203 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Shigella sonnei strain CECT 4887 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Pectobacterium carotovorum strain ATCC 15713 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Brenneria alni strain pvfi20 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Escherichia coli str. K-12 substr. MG1655 strain K-12 16S ribosomal RNA, complete sequence	305	305	96%	3e-83	98%

	Max Score	Total Score	Query Cover	E value	Identity
Escherichia coli strain JCM 1649 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Escherichia fergusonii strain ATCC 35469 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Escherichia albertii strain Albert 19982 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Shigella flexneri strain ATCC 29903 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Shigella dysenteriae strain ATCC 13313 16S ribosomal RNA gene, partial sequence	305	305	96%	3e-83	98%
Escherichia vulneris strain ATCC 33821 16S ribosomal RNA gene, complete sequence	303	303	95%	1e-82	98%
Escherichia coli strain U 5/41 16S ribosomal RNA gene, partial sequence	302	302	96%	4e-82	97%
Shigella boydii strain P288 16S ribosomal RNA gene, partial sequence	300	300	96%	1e-81	97%
Shigella boydii Sb227 strain Sb227 16S ribosomal RNA, complete sequence	300	300	96%	1e-81	97%
Erwinia pyrifoliae Ep1/96 strain Ep1/96 16S ribosomal RNA, complete sequence	283	283	96%	1e-76	96%
Xenorhabdus ishibashii strain GDh7 16S ribosomal RNA gene, partial sequence	283	283	96%	1e-76	96%
Citrobacter amalonaticus strain CECT 863 16S ribosomal RNA gene, partial sequence	283	283	96%	1e-76	96%
Citrobacter amalonaticus strain LMG 7873 16S ribosomal RNA gene, partial sequence	283	283	96%	1e-76	96%
Erwinia pyrifoliae strain DSM 12163 16S ribosomal RNA gene, partial sequence	283	283	96%	1e-76	96%

WA source water

Enterobacteria reads extracted (*pathogenic hits: *Shigella sonnei, Shigella dystentry, Escherichia fergunsonii, E coli*, …)

	Max Score	Total Score	Query Cover	E value	Identity
Escherichia fergusonii strain ATCC 35469 16S ribosomal RNA gene, complete sequence	294	294	98%	7e-80	97%
Shigella sonnei Ss046 strain Ss046 16S ribosomal RNA, complete sequence	294	294	98%	7e-80	97%
Shigella dysenteriae Sd197 strain Sd197 16S ribosomal RNA, complete sequence	294	294	98%	7e-80	97%
Escherichia coli O157:H7 str. Sakai strain Sakai 16S ribosomal RNA, complete sequence	294	294	98%	7e-80	97%
Shigella flexneri 2a str. 301 strain 301 16S ribosomal RNA, complete sequence	294	294	98%	7e-80	97%
Escherichia fergusonii strain NBRC 102419 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Escherichia coli strain NBRC 102203 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Shigella sonnei strain CECT 4887 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Brenneria alni strain pvfi20 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Escherichia coli str. K-12 substr. MG1655 strain K-12 16S ribosomal RNA, complete sequence	294	294	98%	7e-80	97%
Escherichia coli strain JCM 1649 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Escherichia fergusonii strain ATCC 35469 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Escherichia albertii strain Albert 19982 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%

	Max Score	Total Score	Query Cover	E value	Identity
Shigella flexneri strain ATCC 29903 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Shigella dysenteriae strain ATCC 13313 16S ribosomal RNA gene, partial sequence	294	294	98%	7e-80	97%
Escherichia vulneris strain ATCC 33821 16S ribosomal RNA gene, complete sequence	294	294	98%	7e-80	97%
Escherichia coli strain U 5/41 16S ribosomal RNA gene, partial sequence	291	291	98%	8e-79	97%
Shigella boydii strain P288 16S ribosomal RNA gene, partial sequence	289	289	98%	3e-78	97%
Pectobacterium carotovorum strain ATCC 15713 16S ribosomal RNA gene, partial sequence	289	289	98%	3e-78	97%
Shigella boydii Sb227 strain Sb227 16S ribosomal RNA, complete sequence	289	289	98%	3e-78	97%
Erwinia chrysanthemi strain DSM 4610 16S ribosomal RNA gene, partial sequence	267	267	98%	1e-71	94%

SA-2 tank

Gammaproteobacteria reads extracted

	Max Score	Total Score	Query Cover	E value	Identity
Pseudomonas guineae strain M8 16S ribosomal RNA gene, partial sequence	287	287	96%	1e-77	96%
Pseudomonas peli strain R-20805 16S ribosomal RNA gene, partial sequence	287	287	96%	1e-77	96%
Serpens flexibilis strain ATCC 29606 16S ribosomal RNA gene, partial sequence	281	281	96%	6e-76	96%
Pseudomonas tuomuerensis strain 78-123 16S ribosomal RNA gene, partial sequence	281	281	96%	6e-76	96%
Pseudomonas cuatrocienegasensis strain 1N 16S ribosomal RNA gene, partial sequence	272	272	93%	4e-73	95%
Pseudomonas oleovorans strain ATCC 8062 16S ribosomal RNA gene, partial sequence	267	267	96%	2e-71	94%
Pseudomonas pohangensis strain H3-R18 16S ribosomal RNA gene, partial sequence	267	267	93%	2e-71	95%
Pseudomonas pseudoalcaligenes strain NBRC 14167 16S ribosomal RNA gene, partial sequence	265	265	96%	6e-71	94%
Pseudomonas anguilliseptica strain S 1 16S ribosomal RNA gene, partial sequence	265	265	96%	6e-71	94%
Pseudomonas indoloxydans strain IPL-1 16S ribosomal RNA gene, partial sequence	265	265	96%	6e-71	94%
Pseudomonas pseudoalcaligenes strain JCM 5968 16S ribosomal RNA gene, complete sequence	265	265	96%	6e-71	94%
Pseudomonas pseudoalcaligenes strain Stanier 63 16S ribosomal RNA gene, partial sequence	265	265	96%	6e-71	94%
Pseudomonas helmanticensis strain OHA11 16S ribosomal RNA gene, partial sequence	261	261	93%	8e-70	94%

	Max Score	Total Score	Query Cover	E value	Identity
Pseudomonas taeanensis strain MS-3 16S ribosomal RNA gene, partial sequence	261	261	93%	8e-70	94%
Pseudomonas sabulinigri strain J64 16S ribosomal RNA gene, partial sequence	261	261	93%	8e-70	94%
Pseudomonas chengduensis strain MBR 16S ribosomal RNA gene, partial sequence	259	259	96%	3e-69	93%
Pseudomonas alcaliphila strain NBRC 102411 16S ribosomal RNA gene, partial sequence	259	259	96%	3e-69	93%

SA source water

Mycobacterium reads extracted

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium smegmatis strain DSM 43756 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium smegmatis str. MC2 155 strain MC2 155 16S ribosomal RNA, complete sequence	268	268	100%	4e-72	99%
Mycobacterium bacteremicum strain ATCC 25791 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium neoaurum strain ATCC 25795 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium wolinskyi strain ATCC 700010 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium smegmatis strain ATCC 19420 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium hackensackense strain 147-0552 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium fluoranthenivorans strain FA4 16S ribosomal RNA gene, complete sequence	268	268	100%	4e-72	99%
Mycobacterium diernhoferi strain ATCC 19340 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium neoaurum strain ATCC 25795 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium cosmeticum strain LTA-388 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium frederiksbergense strain DSM 44346 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium smegmatis strain ATCC 19420 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium peregrinum strain ATCC 14467 16S ribosomal RNA gene, partial sequence	268	268	100%	4e-72	99%
Mycobacterium goodii strain M069 16S ribosomal RNA gene, partial sequence	265	265	100%	5e-71	99%
Mycobacterium smegmatis strain DSM 43756 16S ribosomal RNA gene, partial sequence	265	265	100%	5e-71	99%
Mycobacterium canariasense strain 502329 16S ribosomal RNA gene, partial sequence	263	263	100%	2e-70	99%
Mycobacterium mageritense strain CIP 104973 16S ribosomal RNA gene, partial sequence	263	263	100%	2e-70	99%
Mycobacterium mageritense strain 938 16S ribosomal RNA gene, complete sequence	263	263	100%	2e-70	99%
Mycobacterium fortuitum subsp. acetamidolyticum strain NCH E11620 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium setense strain CIP109395 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium fortuitum subsp. fortuitum strain CIP 104534 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium porcinum strain E10241-1 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium septicum strain DSM 44393 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium peregrinum strain CIP 105382 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium neworleansense strain ATCC 49404 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium houstonense strain ATCC 49403 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium peregrinum strain ATCC 14467 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium septicum strain W4964 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium senegalense strain ATCC 35796 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium porcinum strain ATCC 33776 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium conceptionense strain D16 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium houstonense strain Ho1as 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium fortuitum subsp. fortuitum strain DSM 46621 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium neworleansense strain W6705 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium boenickei strain W5998 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium peregrinum strain ATCC 14467 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%
Mycobacterium farcinogenes strain ATCC 35753 16S ribosomal RNA gene, partial sequence	291	291	95%	8e-79	100%

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Mycobacterium reads extracted

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium fortuitum subsp. acetamidolyticum strain NCH E11620 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium setense strain CIP109395 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium fortuitum subsp. fortuitum strain CIP 104534 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium porcinum strain E10241-1 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium septicum strain DSM 44393 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium peregrinum strain CIP 105382 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium neworleansense strain ATCC 49404 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium houstonense strain ATCC 49403 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium peregrinum strain ATCC 14467 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium septicum strain W4964 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium senegalense strain ATCC 35796 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium porcinum strain ATCC 33776 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium conceptionense strain D16 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium houstonense strain Ho1as 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium fortuitum subsp. fortuitum strain DSM 46621 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium neworleansense strain W6705 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium boenickei strain W5998 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium peregrinum strain ATCC 14467 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium farcinogenes strain ATCC 35753 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium alvei strain CR-21 16S ribosomal RNA gene, partial sequence	287	287	98%	1e-77	99%
Mycobacterium fortuitum subsp. fortuitum strain ATCC 6841 16S ribosomal RNA gene, partial sequence	283	283	95%	1e-76	99%

SA 1 CT

Mycobacterium reads extracted

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium gordonae strain ATCC 14470 16S ribosomal RNA gene, partial sequence	318	318	99%	4e-87	99%
Mycobacterium gordonae strain DSM 44160 16S ribosomal RNA gene, partial sequence	318	318	99%	4e-87	99%
Mycobacterium gordonae strain ATCC 14470 16S ribosomal RNA gene, complete sequence	315	315	99%	5e-86	99%
Mycobacterium shinjukuense strain GTC 2738 16S ribosomal RNA gene, partial sequence	313	313	99%	2e-85	99%
Mycobacterium paragordonae strain 49061 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium szulgai strain ATCC 35799 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium avium 104 strain 104 16S ribosomal RNA, complete sequence	302	302	99%	4e-82	98%
Mycobacterium intracellulare MOTT-02 strain MOTT-02 16S ribosomal RNA, complete sequence	302	302	99%	4e-82	98%
Mycobacterium timonense strain 5351974 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium colombiense strain 10B 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium intracellulare strain ATCC 13950 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium conspicuum strain 3895/92 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium malmoense strain ATCC 29571 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium nebraskense strain ATCC BAA-837 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%

	Max Score	Total Score	Query Cover	E value	Identity
Mycobacterium intracellulare strain ATCC 13950 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium colombiense strain CIP 108962 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium arosiense strain ATCC BAA-1401 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium avium strain ATCC 25291 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%
Mycobacterium bouchedurhonense strain 4355387 16S ribosomal RNA gene, partial sequence	302	302	99%	4e-82	98%