

Diversity and Dynamics of the Microbial Population Associated with Drinking Water Distribution Networks and their Impact on Drinking Water Quality

(SUPPLEMENTARY MATERIAL TO WRC REPORT 2469/1/18)

by

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INDIVIDUAL FIGURES FROM THE REPORT

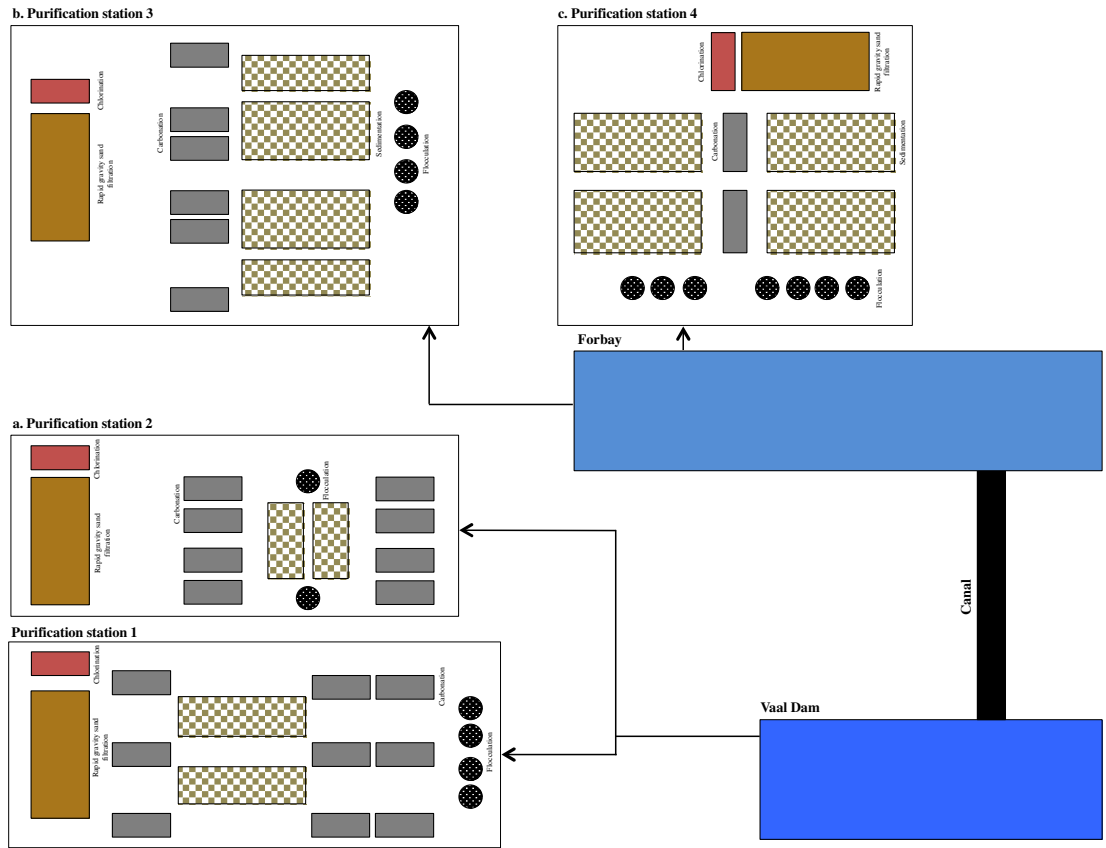


Figure 3.1 Schematic representation of the first drinking water treatment plant. Sampling was conducted over four months on a monthly basis at designated rapid sand filters harbored within the filter galleries of purification station 1, 3 and 4.

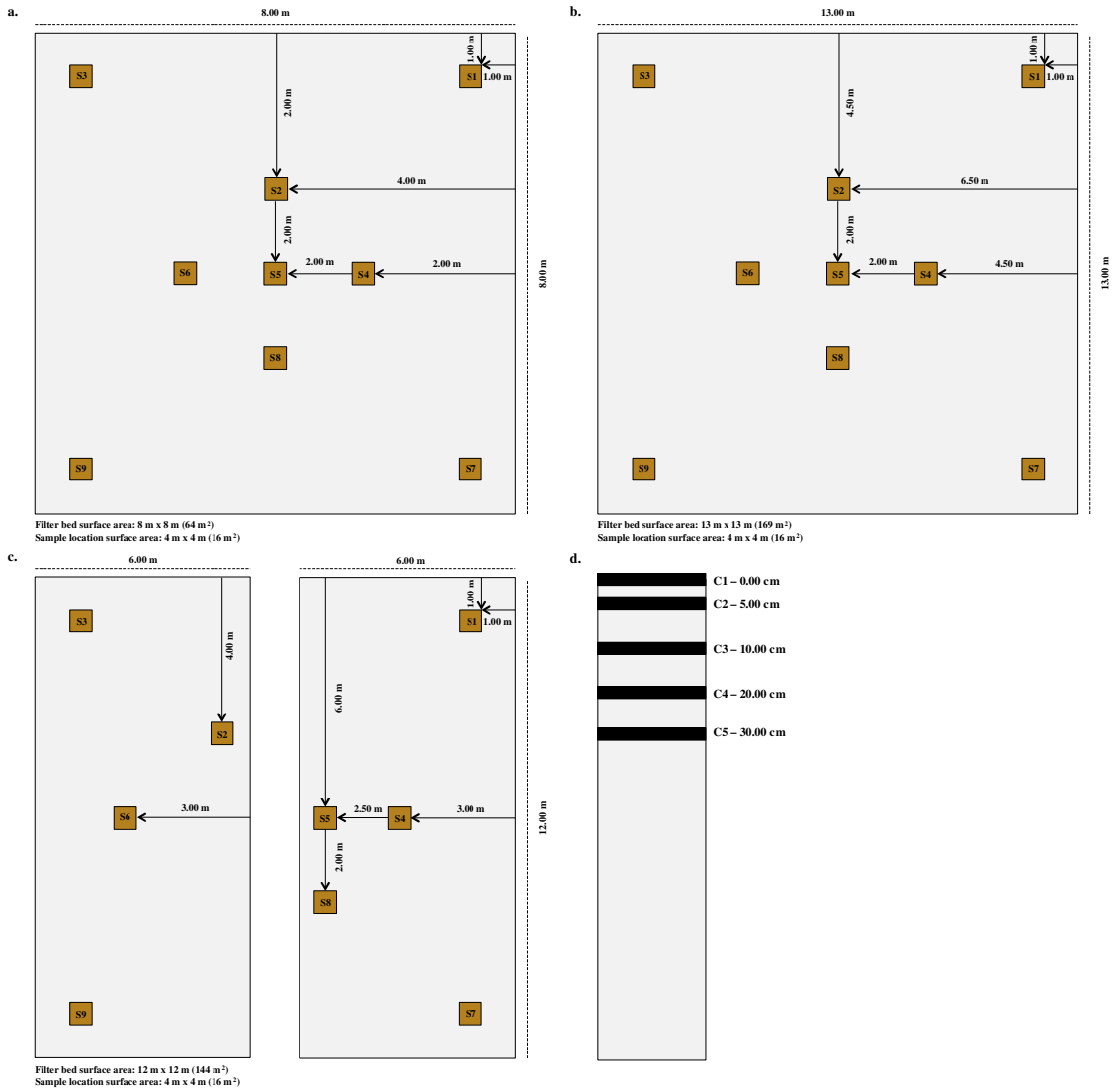


Figure 3.2 Schematic representation and specifications of the surface area of (a) RS filter 46 of PS1, (b) RS filter 93 of PS3, and (c) RS filter 66 of PS4; that were sampled monthly over 4 months along the surface and depth of the RS filter bed. The nine surface locations, designated S1 to S9 are indicated with red squares; and (d) the five core locations, designated C1 to C5 with associated depths are indicated with broad black lines.

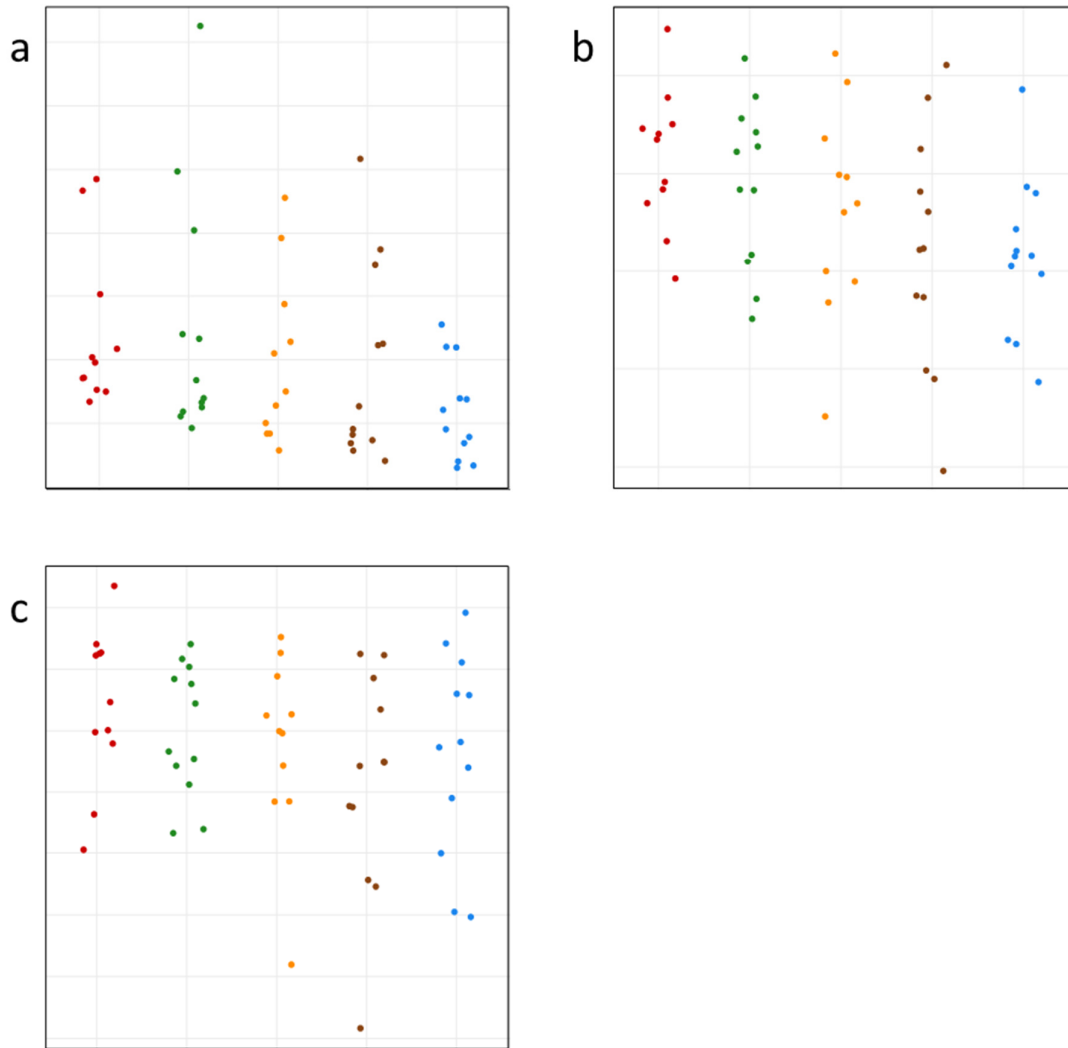


Figure 3.3 Alpha diversity indexes (a) observed species (S_{obs}), (b) Shannon index (H') and (c) Pielou's evenness index (J) for samples affiliated to spatial groupings: core location 1 (C1, red, $n_{samples} = 11$), core location 2 (C2, green, $n_{samples} = 12$), core location 3 (C3, orange, $n_{samples} = 11$), core location 4 (C4, brown, $n_{samples} = 12$) and core location 5 (C5, blue, $n_{samples} = 12$). See Table A5 for means, standard deviations and ANOVA tables.

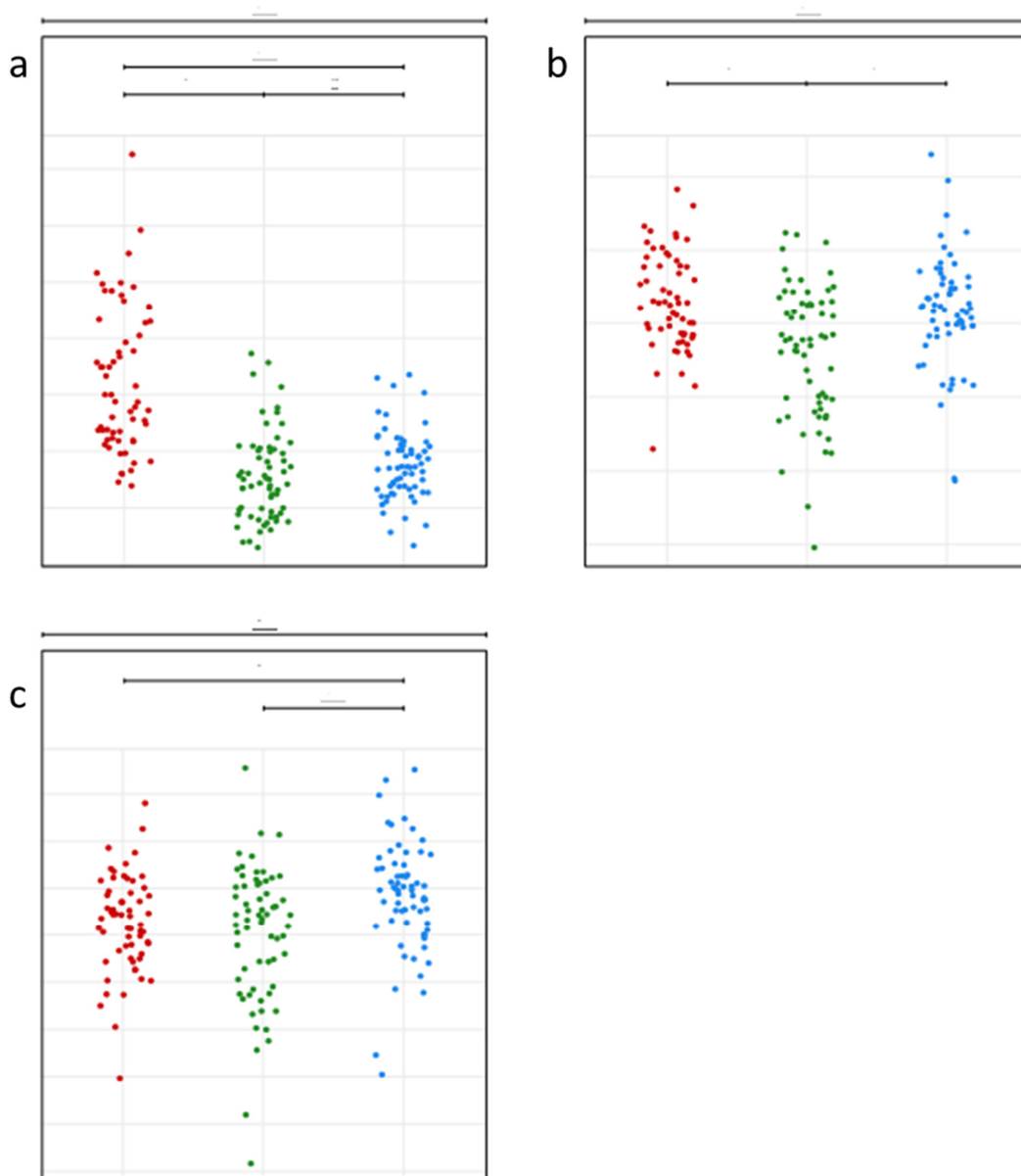


Figure 3.4 Alpha diversity indexes (a) observed species (S_{obs}), (b) Shannon index (H') and (c) Pielou's evenness index (J) for samples affiliated to spatial groupings: purification station 1 (PS1, red, $n_{samples} = 60$), purification station 3 (C2, green, $n_{samples} = 64$) and purification station 4 (C3, blue, $n_{samples} = 64$). All significant values are indicated with bars at the top of the figures (p values: * = $0.01 < p \leq 0.05$, ** = $0.001 < p \leq 0.01$, *** = $0.0001 < p \leq 0.001$, **** = $p \leq 0.001$). See Table A7 for means, standard deviations, ANOVA tables and post-hoc Tukey HSD tests.

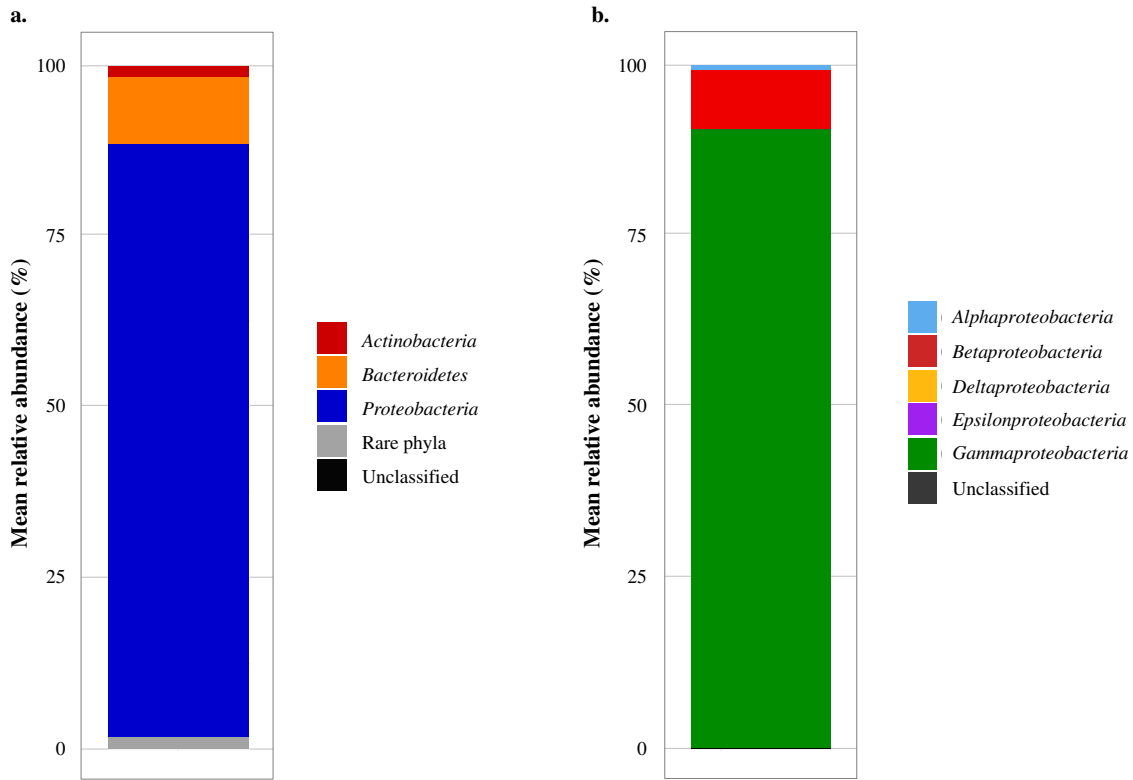


Figure 3.5 (a) Stacked bar charts displaying the mean relative abundance of the (a) three dominant microbial phyla recovered from the rapid sand filters. (b) Stacked bar charts displaying the mean relative abundance of the *Proteobacteria* subphyla recovered from the study sites.

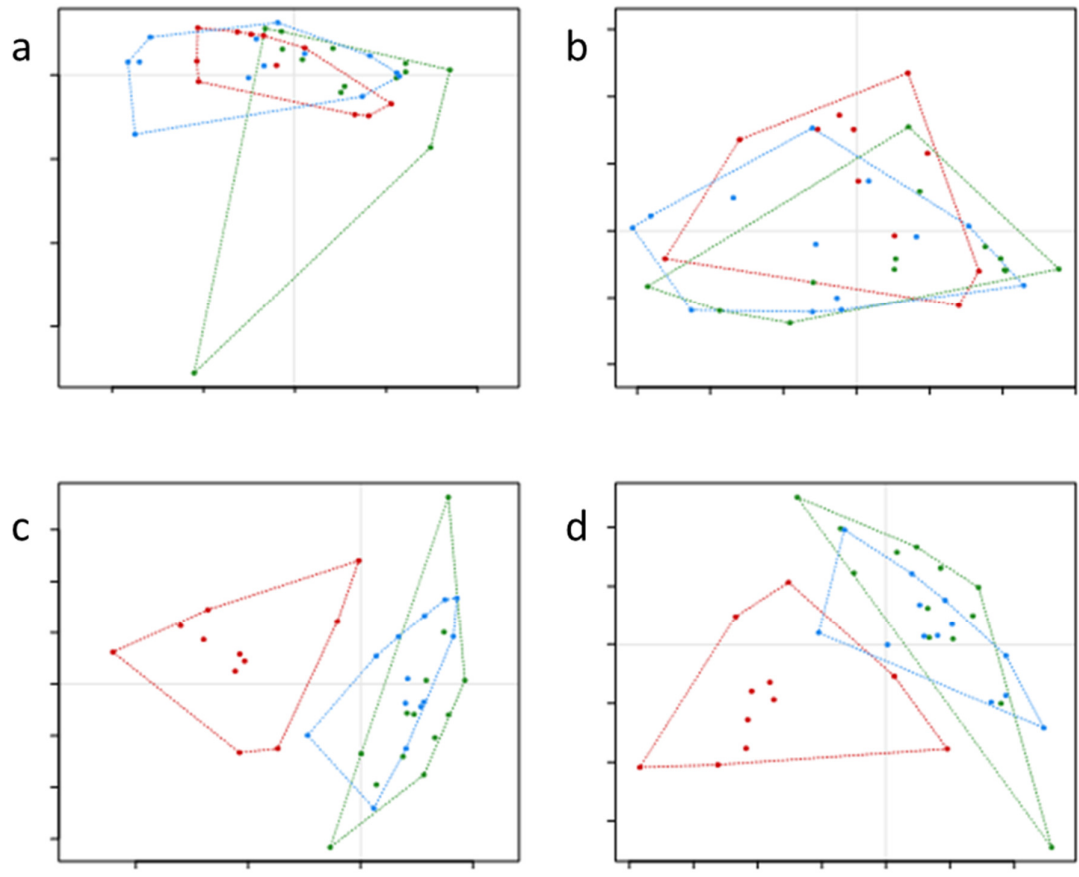


Figure 3.6 Principal coordinate ordination of the RS filter data showing the distribution of purification station 1 (red), purification station 3 (green) and purification station 4 (blue) samples in the first two axis of a multidimensional space using (a) Bray-Curtis, (b) weighted UniFrac, (c) Jaccard and (d) unweighted UniFrac distances. The percentages on the axis represents the variance explained by each of the coordinates.

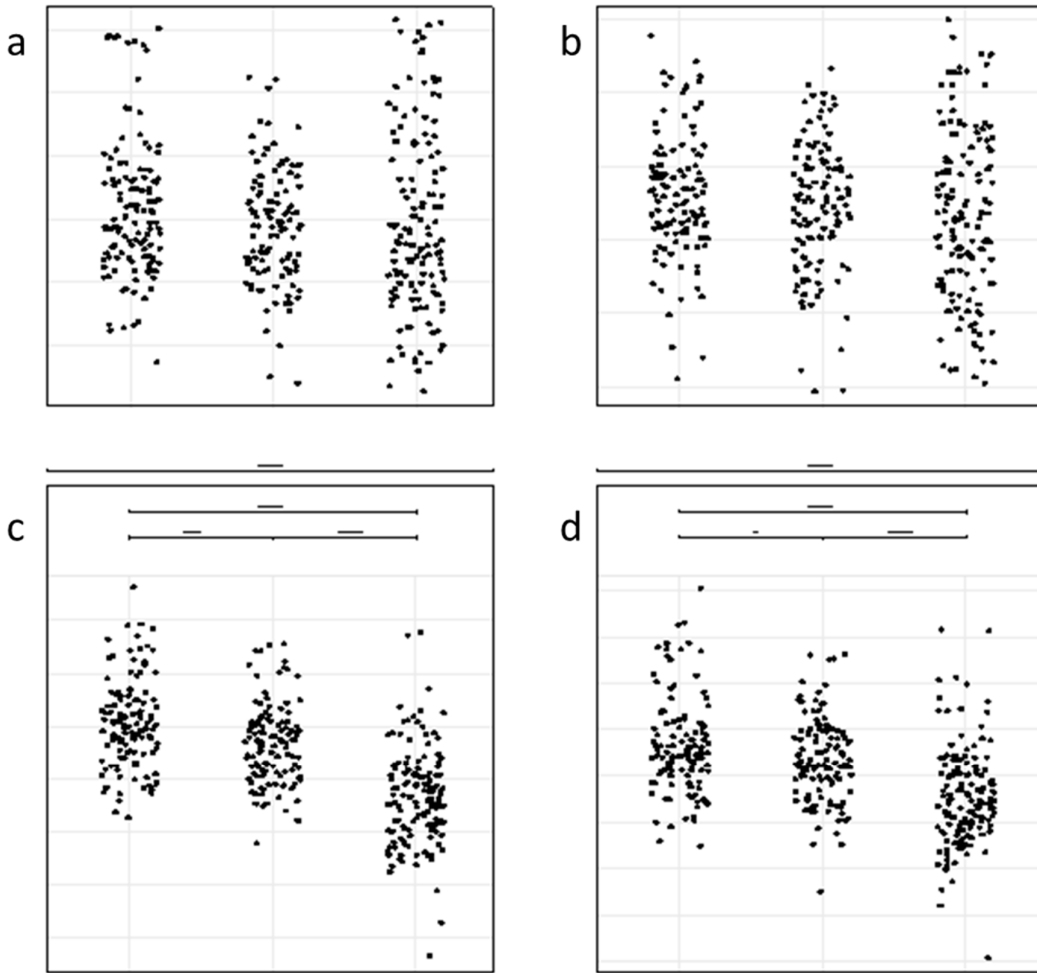


Figure 3.7 Pairwise (a) Bray-Curtis, (b) weighted UniFrac, (c) Jaccard and (d) unweighted UniFrac distances between samples of spatial groupings: (i) PS1 vs. PS3 ($n_{\text{samples}} = 120$), (ii) PS1 vs. PS4 ($n_{\text{samples}} = 120$) and (iii) PS3 vs. PS4 ($n_{\text{samples}} = 144$). All significant values are indicated with bars at the top of the figures (p values: * = $0.01 < p \leq 0.05$, ** = $0.001 < p \leq 0.01$, *** = $0.0001 < p \leq 0.001$, **** = $p \leq 0.001$). See Table B3.15 for means, standard deviations, ANOVA tables and post hoc Tukey HSD tests.

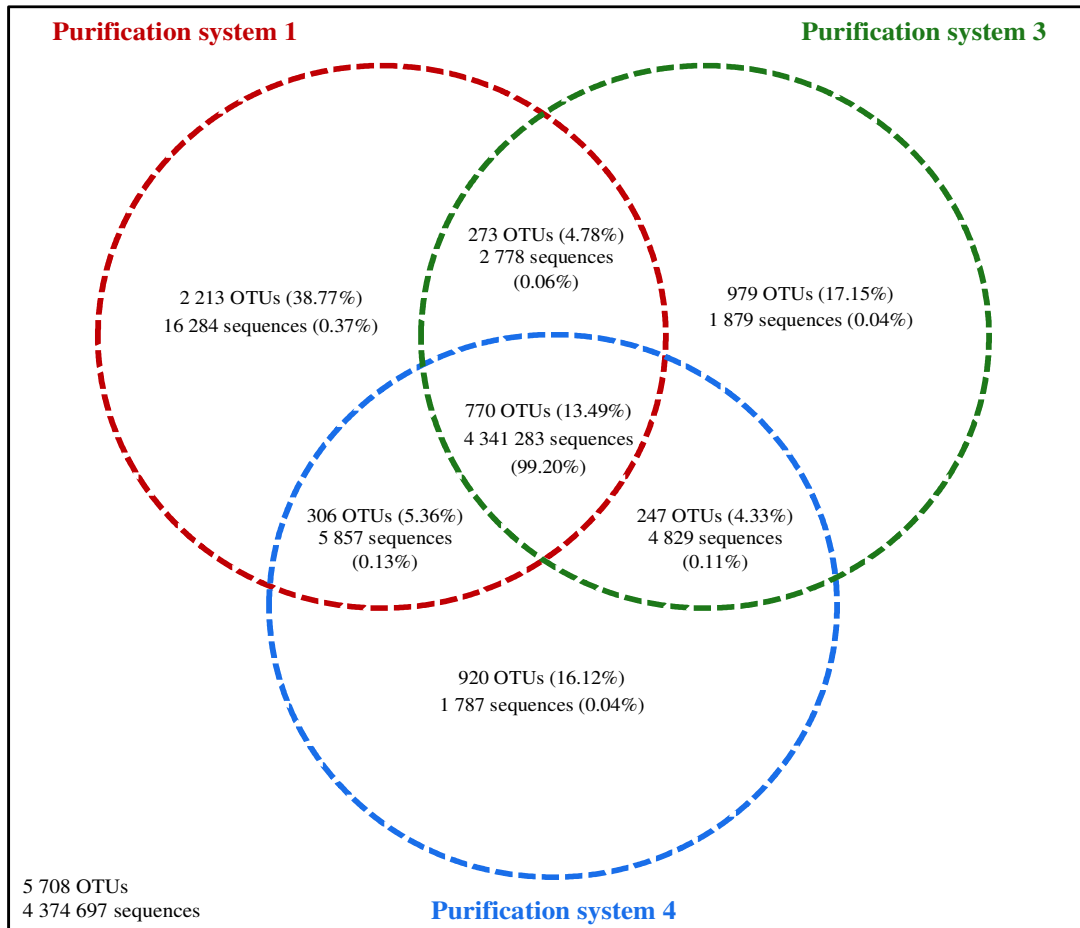
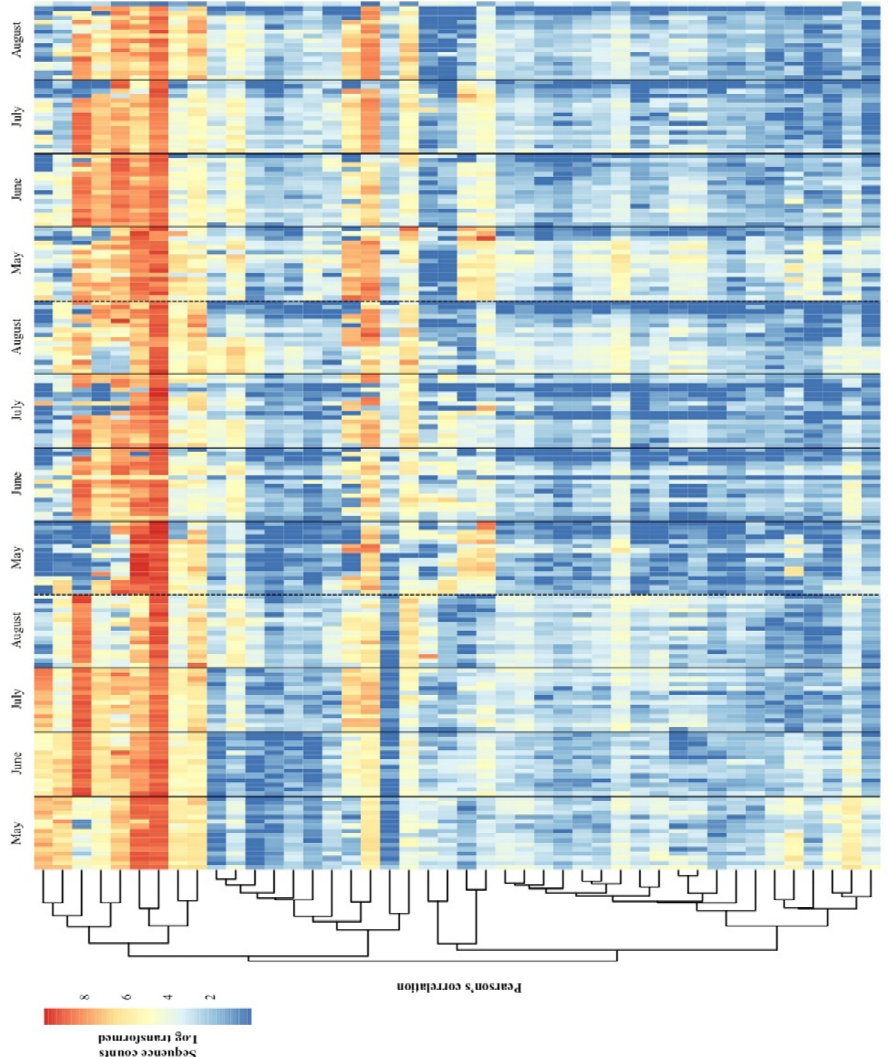


Figure 3.8 Venn diagrams displaying the shared and unshared OTUs in terms of counts and sequence abundances detected amongst purification station 1 (red), purification station 3 (green) and purification station 4 (blue).

Month



OTU#	Phyla	Class
OTU12	Proteobacteria	Gammaproteobacteria
OTU11	Proteobacteria	Gammaproteobacteria
OTU3	Proteobacteria	Gammaproteobacteria
OTU7	Proteobacteria	Gammaproteobacteria
OTU4	Bacteroidetes	Flavobacteriia
OTU2	Proteobacteria	Gammaproteobacteria
OTU1	Proteobacteria	Gammaproteobacteria
OTU13	Proteobacteria	Gammaproteobacteria
OTU6	Proteobacteria	Betaproteobacteria
OTU24	Bacteroidetes	Spingobacteriia
OTU10	Proteobacteria	Betaproteobacteria
OTU36	Proteobacteria	Gammaproteobacteria
OTU5	Proteobacteria	Alphaproteobacteria
OTU8	Proteobacteria	Betaproteobacteria
OTU54	Bacteroidetes	Flavobacteriia
OTU8	Proteobacteria	Betaproteobacteria
OTU5	Proteobacteria	Gammaproteobacteria
OTU17	Cyanobacteria	Synechococophycoidae
OTU9	Proteobacteria	Gammaproteobacteria
OTU31	Proteobacteria	Gammaproteobacteria
OTU19	Proteobacteria	Betaproteobacteria
OTU21	Bacteroidetes	Flavobacteriia
OTU14	Proteobacteria	Betaproteobacteria
OTU47	Bacteroidetes	Flavobacteriia
OTU43	Bacteroidetes	Synproprinae
OTU77	Proteobacteria	Betaproteobacteria
OTU99	Acidobacteria	Chloracidobacteria
OTU62	Proteobacteria	Alphaproteobacteria
OTU35	Proteobacteria	Alphaproteobacteria
OTU25	Proteobacteria	Gammaproteobacteria
OTU65	Acidobacteria	Acidobacteria
OTU49	Planctomycetes	Planctomycetia
OTU39	Proteobacteria	Alphaproteobacteria
OTU38	Proteobacteria	Gammaproteobacteria
OTU94	Planctomycetes	Planctomycetia
OTU83	Acidobacteria	Acidobacteria
OTU34	Acidobacteria	Acidobacteria
OTU88	Proteobacteria	Alphaproteobacteria
OTU37	Acidobacteria	Acidobacteria
OTU40	Proteobacteria	Gammaproteobacteria
OTU26	Acidobacteria	Acidobacteria
OTU18	Proteobacteria	Betaproteobacteria
OTU59	Acidobacteria	MB-42-108

Order	Family	Genus
Alteromonadales	Chromatiales	Rivibacteria
Enterobacteriales	Enterobacteriaceae	unclassified
Pseudomonadales	Moraxellaceae	Acinetobacter
Pseudomonadales	Pseudomonadaceae	Pseudomonas
Flavobacteriales	Flavobacteriaceae	Flavobacterium
Pseudomonadales	Moraxellaceae	Acinetobacter
Actinomadales	Actinomadales	Actinonema
Pseudomonadales	Pseudomonadaceae	Pseudomonas
Burkholderiales	Oxalobacteraceae	Jamilaobacterium
Spingobacteriales	Spingobacteriaceae	Spingobacterium
Neisseriales	Neisseriaceae	Dreyfia
Pseudomonadales	Pseudomonadaceae	Pseudomonas
Spingomonadales	Spingomonadaceae	Norspingobium
Burkholderiales	Oxalobacteraceae	Polynucleobacter
Rhodocyclales	Rhodocyclaceae	Dactylomonas
Flavobacteriales	Weeksellaceae	Chrysochloridium
Burkholderiales	Comamonadaceae	Comamonas
Alteromonadales	Shewanellaceae	Shewanella
Synechococales	Synechococcaceae	Synechococcus
Moraxellales	Moraxellaceae	Acinetobacter
Pseudomonadales	Pseudomonadaceae	Pseudomonas
Neisseriales	Neisseriaceae	Neisseria
Flavobacteriales	Flavobacteriaceae	Flavobacterium
Burkholderiales	Comamonadaceae	unclassified
Flavobacteriales	Weeksellaceae	Chrysochloridium
Saprospirales	Chitinophagaceae	Solanibacterium
Hydrogenophiales	Hydrogenophiliaceae	Thiohalobium
RB41	Ethn6075	unclassified
Rhizobiales	unclassified	unclassified
Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
Alteromonadales	Chromatiales	Rivibacteria
Actinomycetales	ACK-M1	unclassified
Planctomycetales	Planctomycetaceae	Planctomyces
Rhodobacteriales	Rhodobacteraceae	Rhodobacter
Pseudomonadales	Moraxellaceae	Psychrobacter
Gemmatiales	Leptothraceaceae	unclassified
Actinomycetales	unclassified	unclassified
Actinomycetales	ACK-M1	unclassified
Spingomonadales	Spingomonadaceae	Spingomonas
Actinomycetales	unclassified	unclassified
Xanthomonadales	Xanthomonadaceae	Senartrichomonas
Actinomycetales	ACK-M1	unclassified
Burkholderiales	Comamonadaceae	Hydrogenophaga
6319-714	unclassified	unclassified

Taxonomy

Purification system

Purification system 4

Purification system 3

Purification system 1

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Figure 3.9 Heatmap constructed using the absolute sequence abundances (log transformed) of 55 OTUs that were selected based on their relative abundance within a sample (i.e. relative abundance threshold $\geq 1\%$) and by the percentage of samples in which they were detected (i.e. detection frequency threshold $\geq 75\%$). The heatmap boxes were colored from red-to-blue to represent higher-to-lower abundances, and OTUs not represented by a sequence were assigned 10^{-6} (displayed as dark blue).

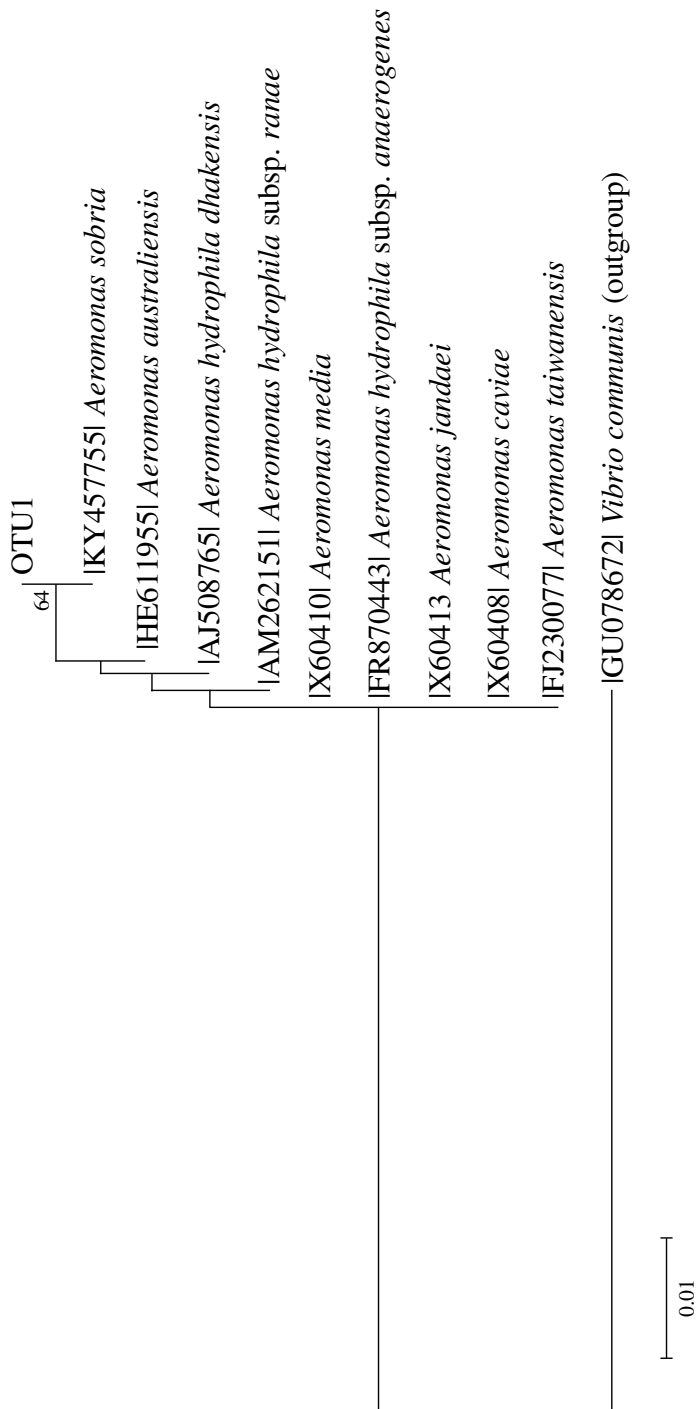


Figure 3.10 Neighbour joining phylogenetic tree showing the relationship between OTU1 and *Aeromonas* type sequences obtained from the NCBI GenBank® sequence database. The tree was rooted with *Vivrio communis* as the outgroup and bootstrap analysis of 1 000 replicates. Bootstrap values are indicated as percentages and values below 50 were excluded.

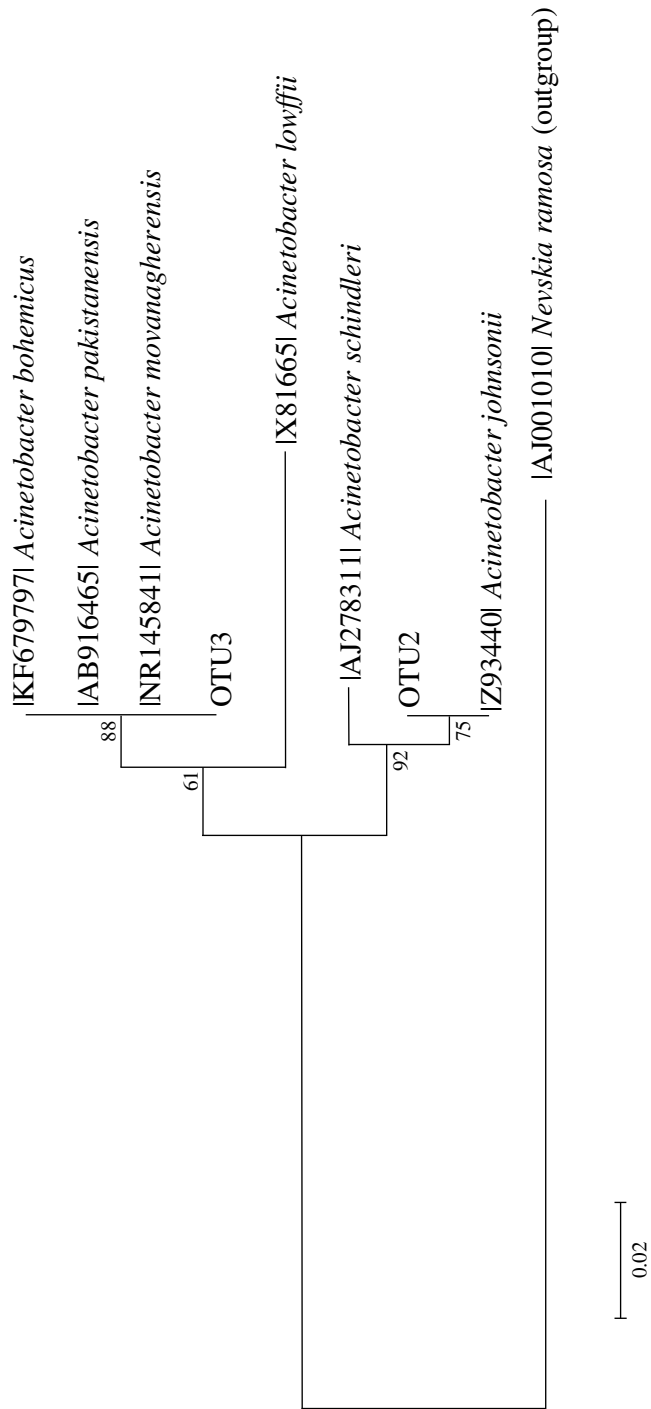


Figure 3.11 Neighbour joining phylogenetic tree showing the relationship between OTU2 and OTU3, and *Acinetobacter* type sequences obtained from the NCBI GenBank® sequence database. The tree was rooted with *Nevskia ramosa* as the outgroup and bootstrap analysis of 1 000 replicates. Bootstrap values are indicated as percentages and values below 50 were excluded.

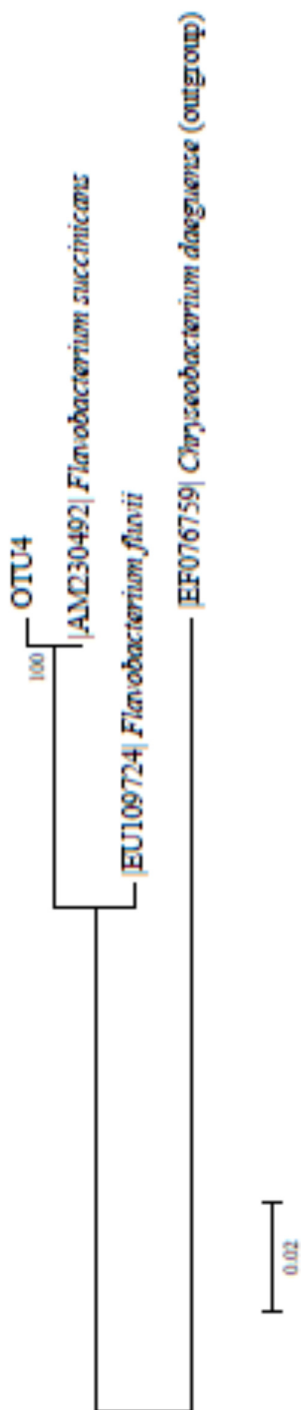


Figure 3.12 Neighbour joining phylogenetic tree showing the relationship between OTU4 and *Flavobacterium* type sequences obtained from the NCBI GenBank® sequence database. The tree was rooted with *Chryseobacterium daeguense* as the outgroup and bootstrap analysis of 1 000 replicates. Bootstrap values are indicated as percentages and values below 50 were excluded.

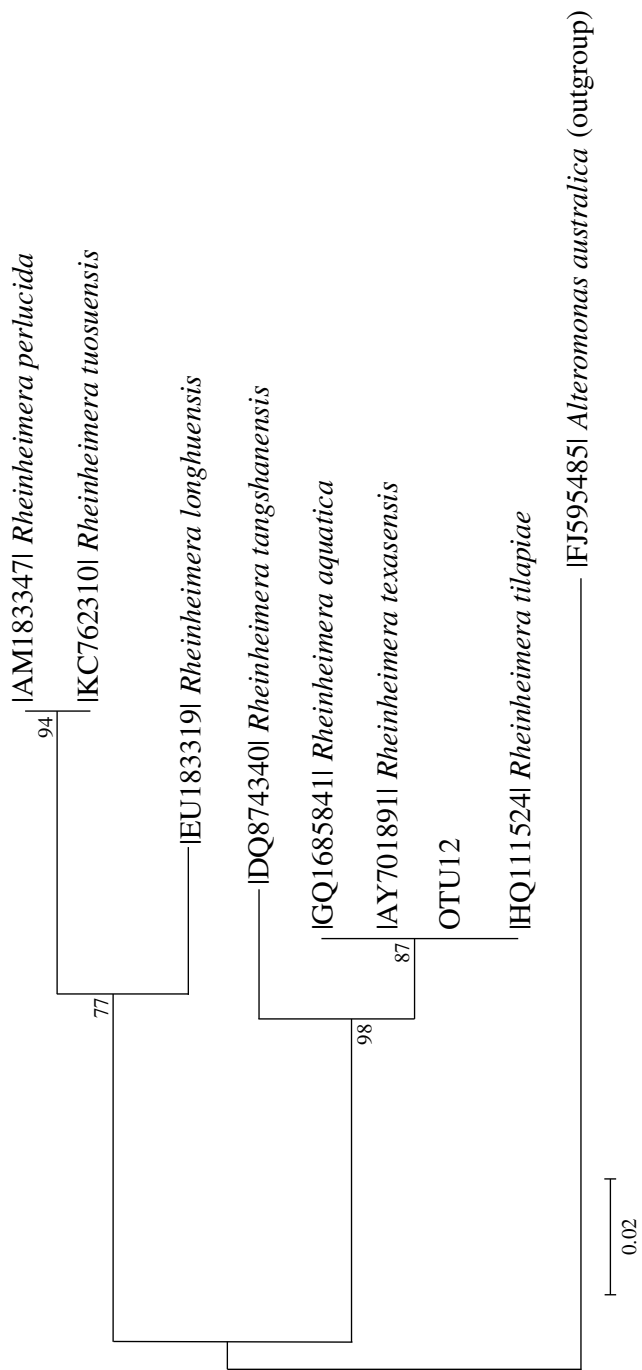


Figure 3.13 Neighbor joining phylogenetic tree showing the relationship between OTU12 and *Rheinheimera* type sequences obtained from the NCBI GenBank® sequence database. The tree was rooted with *Alteromonas australica* as the outgroup and bootstrap analysis of 1 000 replicates. Bootstrap values are indicated as percentages and values below 50 were excluded.

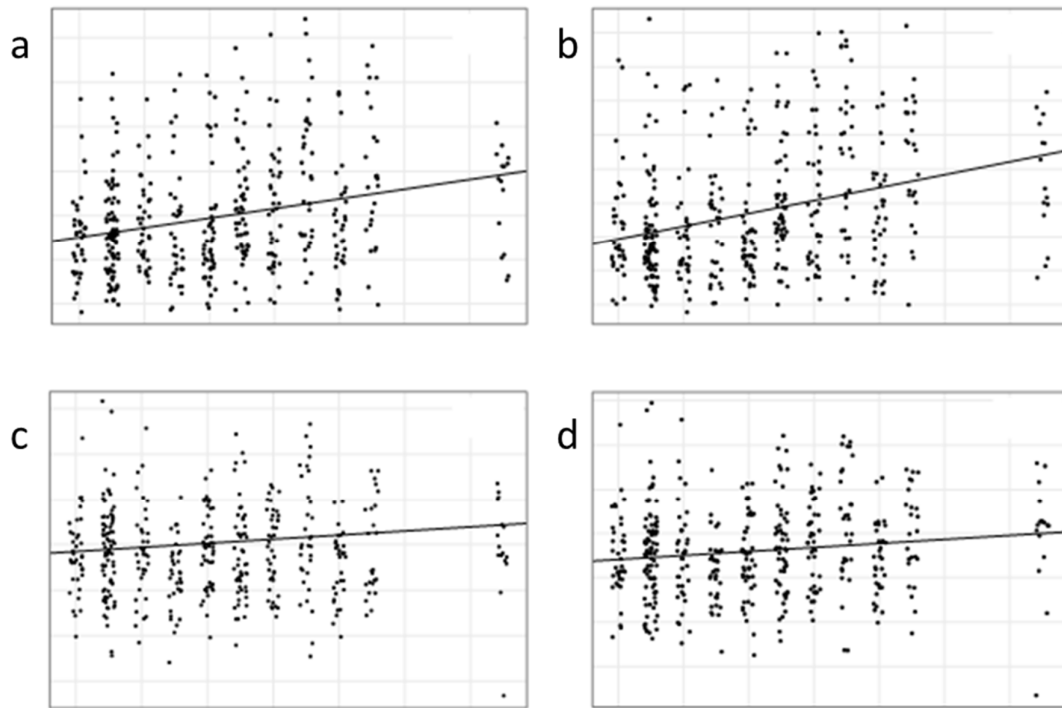


Figure 3.14 Correlations between (a) Bray-Curtis, (b) weighted UniFrac, (c) Jaccard and (d) unweighted UniFrac distances of microbial communities sampled at any two surface locations situated across the surface of the rapid sand filter bed. See Table 3.3 for means and standard deviations.

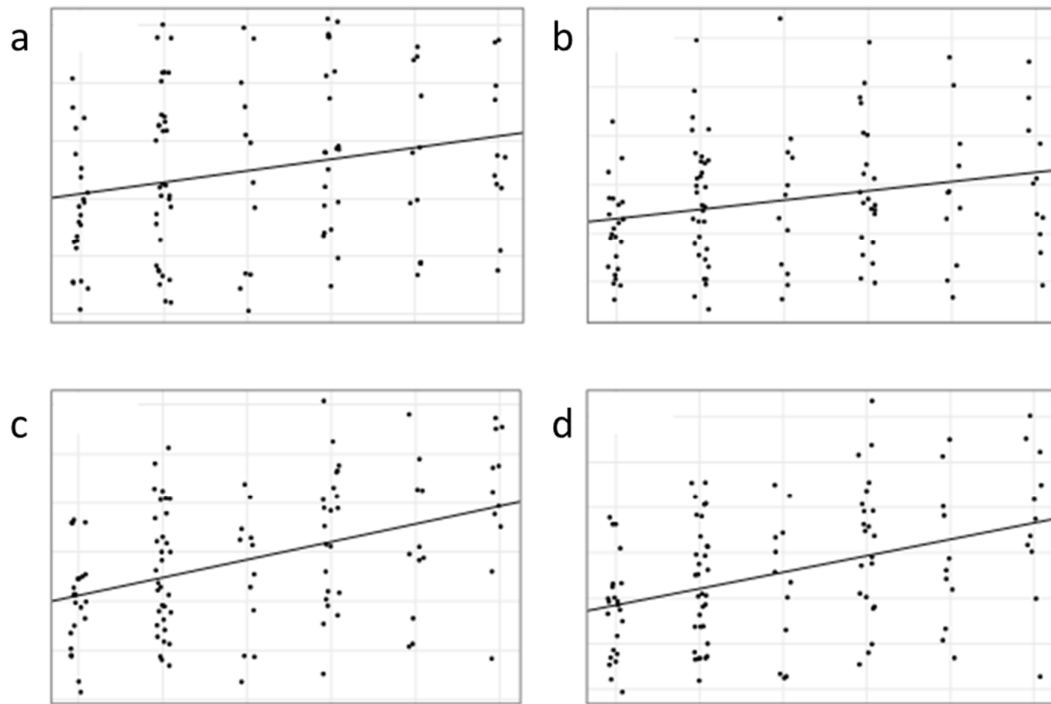


Figure 3.15 Correlations between (a) Bray-Curtis, (b) weighted UniFrac, (c) Jaccard and (d) unweighted UniFrac distances of microbial communities sampled at any two core locations situated along the depth of the rapid sand filter bed. See Table 3.4 for means and standard deviations.

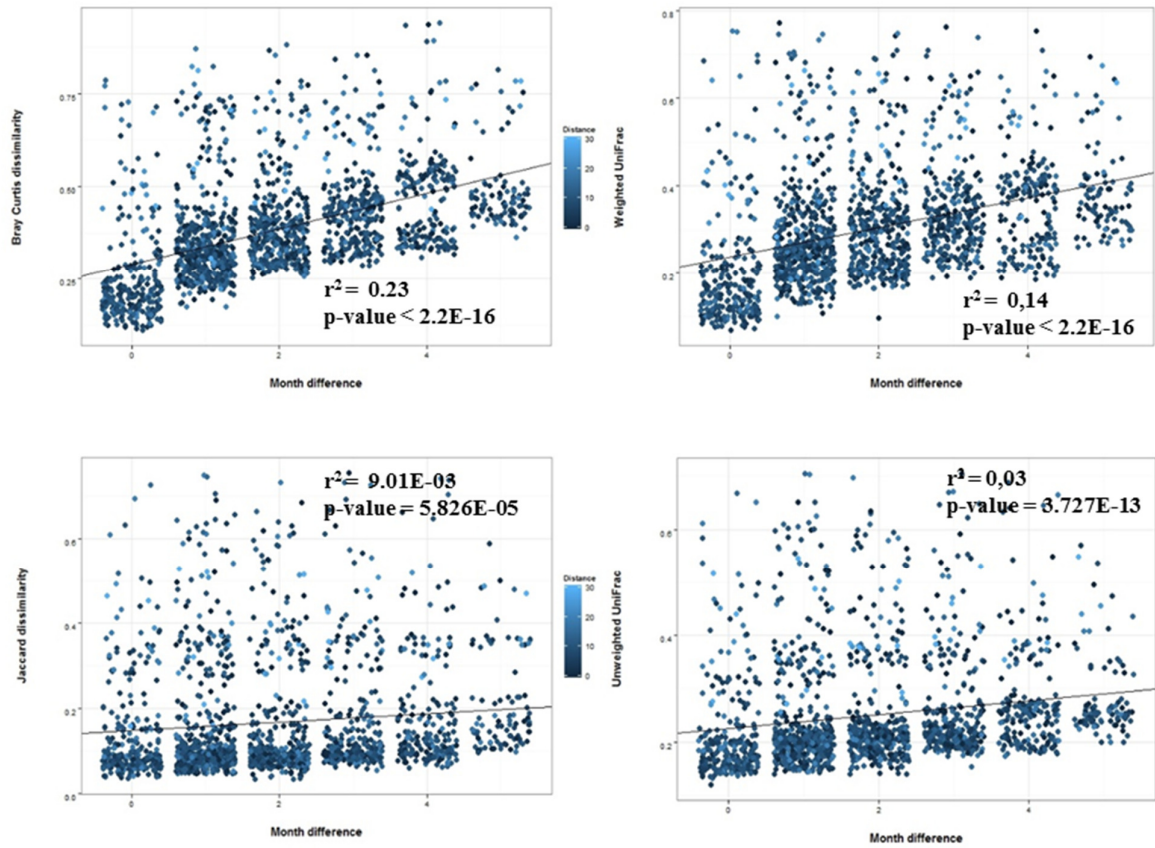
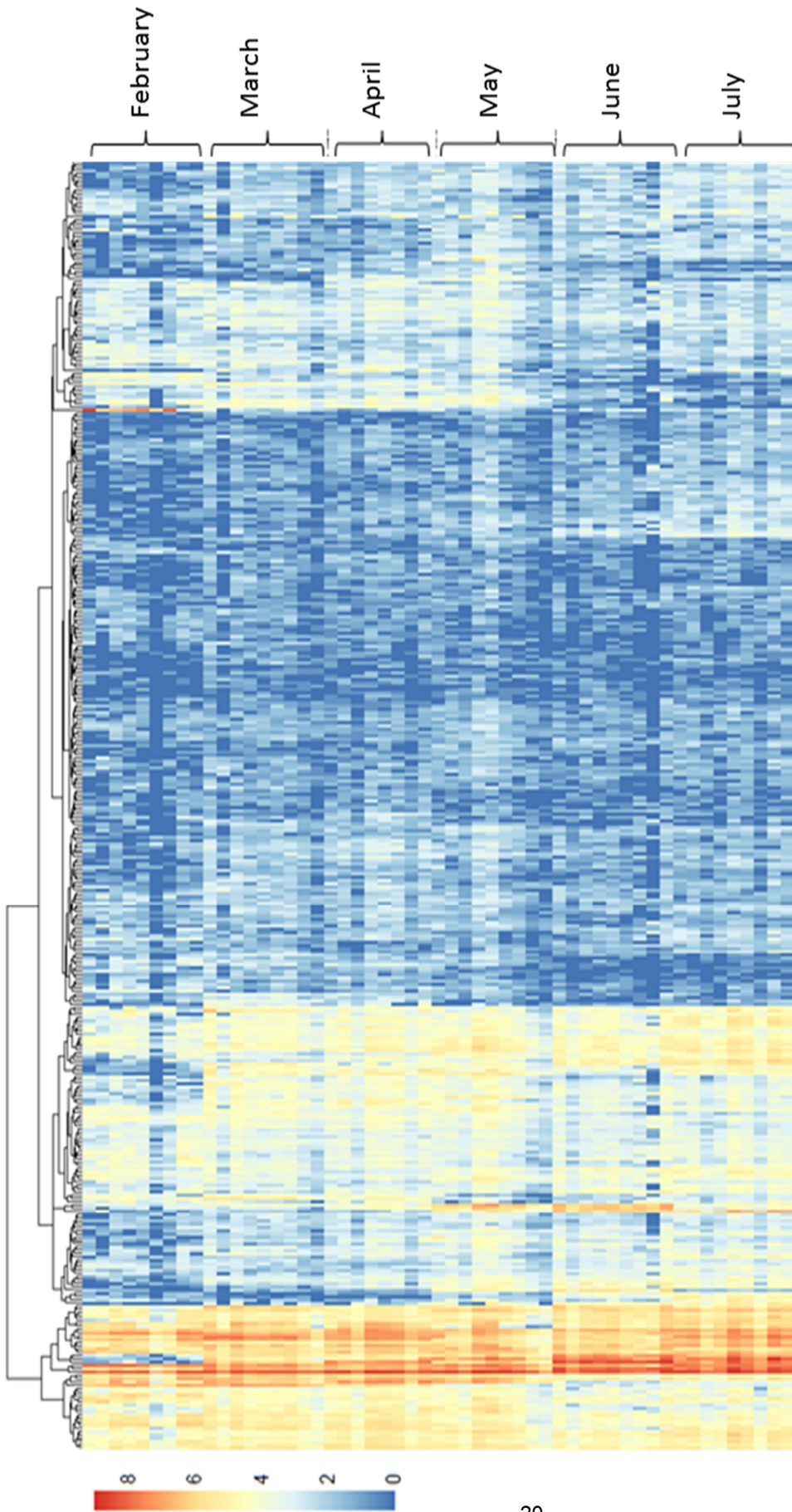


Figure 3.16 Temporal decay relationship illustrating how temporal trends can influence the RS filter community structure (A) Bray-Curtis dissimilarity and (B) Weighted UniFrac and community membership (C) Jaccard dissimilarity and (D) Unweighted UniFrac as a based on month difference.



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Figure 3.17 Heatmap constructed using the absolute sequence abundances (log transformed) of 251 OTUs that were selected based on their relative abundance within a sample (i.e. relative abundance threshold $\geq 1\%$) and by the percentage of samples in which they were detected (i.e. detection frequency threshold $\geq 75\%$). The heatmap boxes were colored from red-to-blue to represent higher-to-lower abundances, and OTUs not represented by a sequence were assigned 10^{-6} (displayed as dark blue).

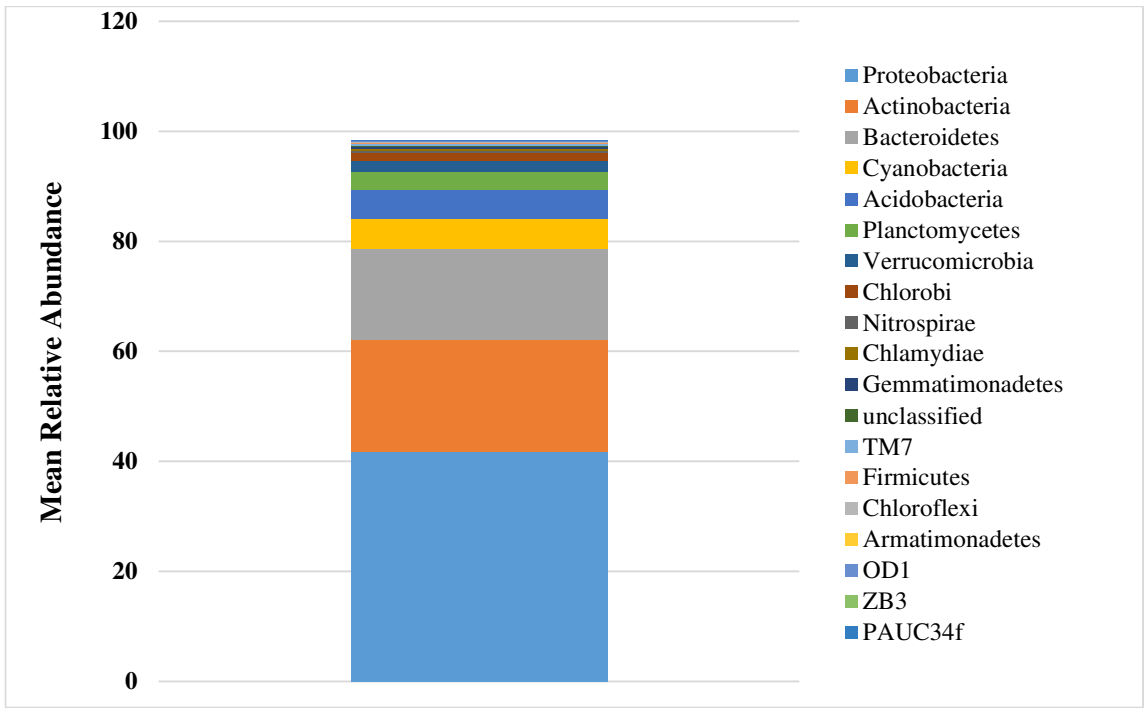


Figure 3.18 Stacked bar charts presenting the mean relative abundance of the bacterial phyla identified and classified in RS filter sand samples.

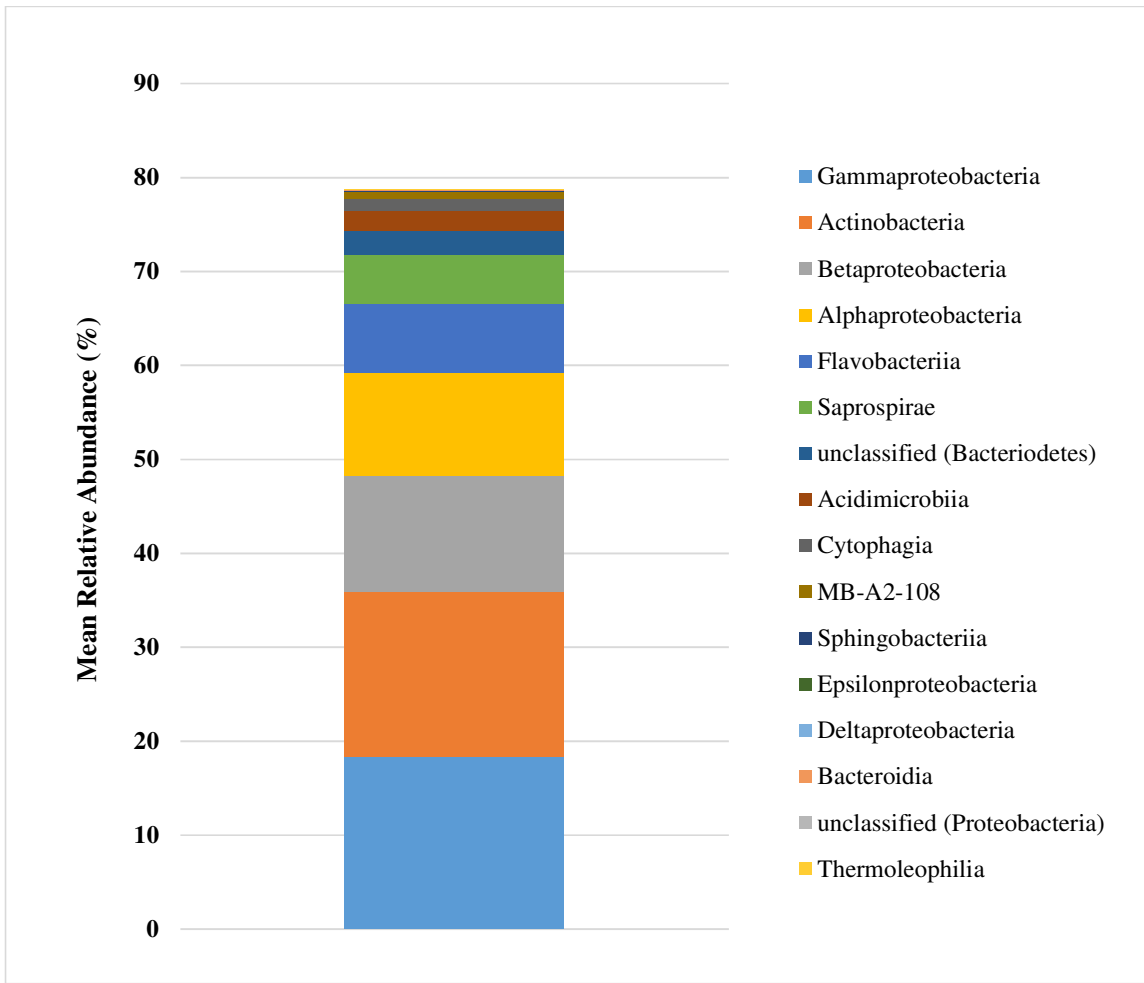


Figure 3.19 Stacked bar charts presenting the mean relative abundance of the bacterial classes identified and classified in RS filter samples, which are associated with the three most dominant phyla.

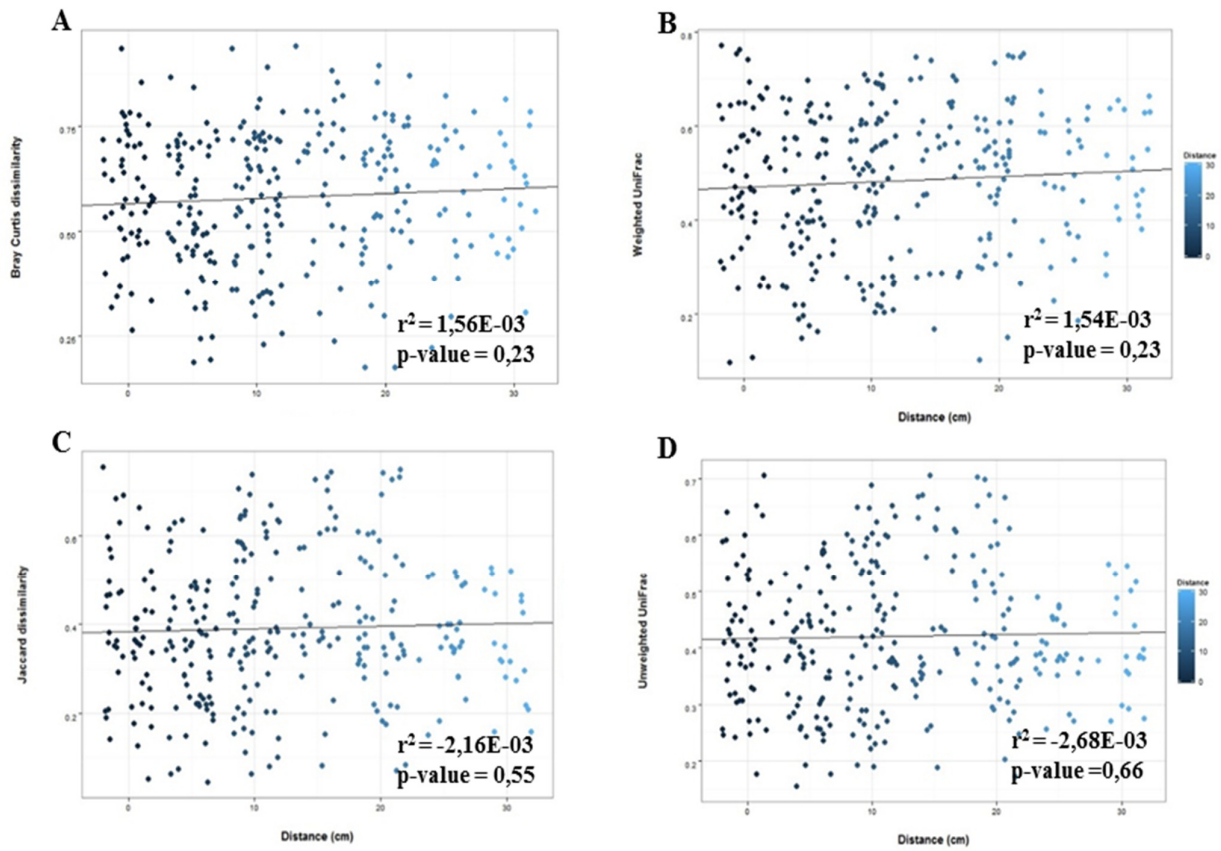


Figure 3.17 Distance-decay relationship along the depth of the filter bed based on microbial community structure, (A) Bray-Curtis pairwise distance metric and (B) Weighted UniFrac metrics, and the microbial community membership (C) Jaccard pairwise distance metric and (D) Unweighted UniFrac.

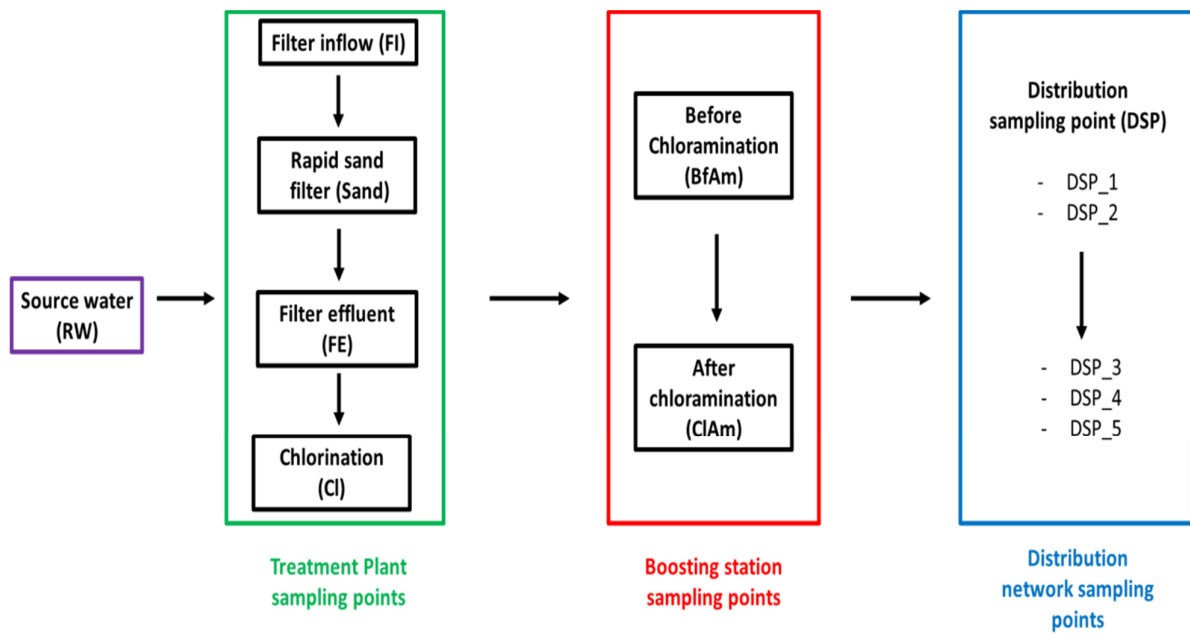


Figure 4.1. A schematic layout of the treatment works and DWDS points sampled during this study.

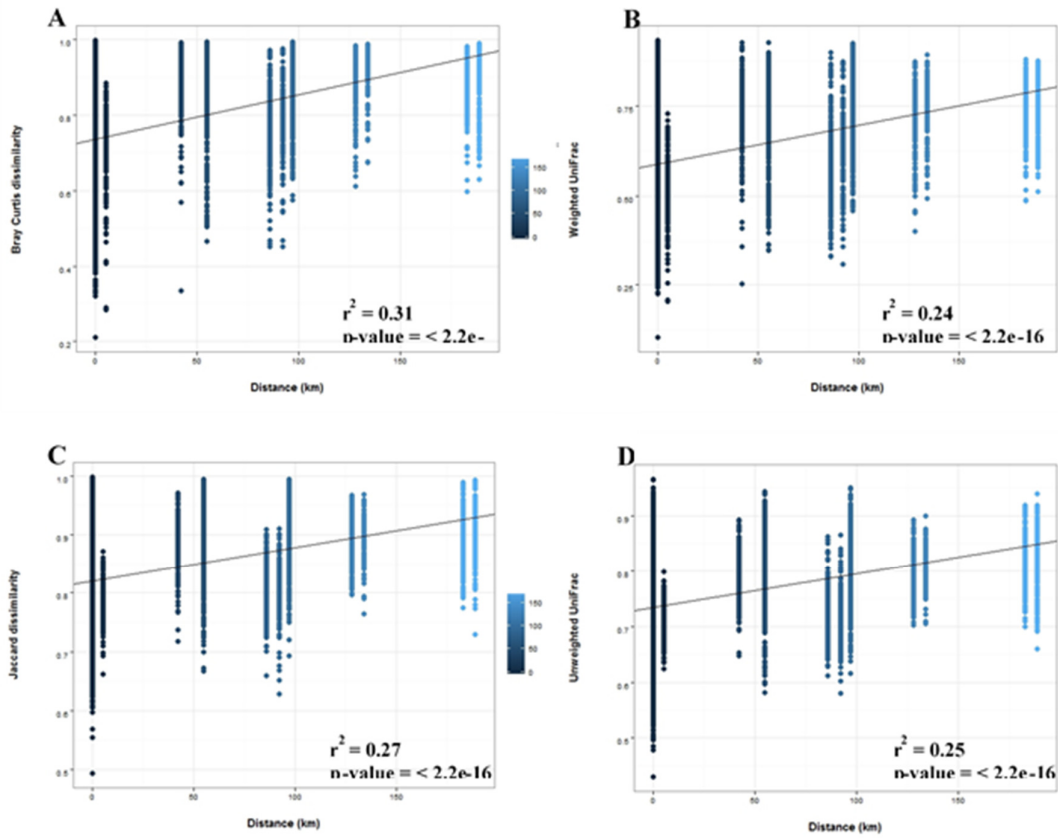
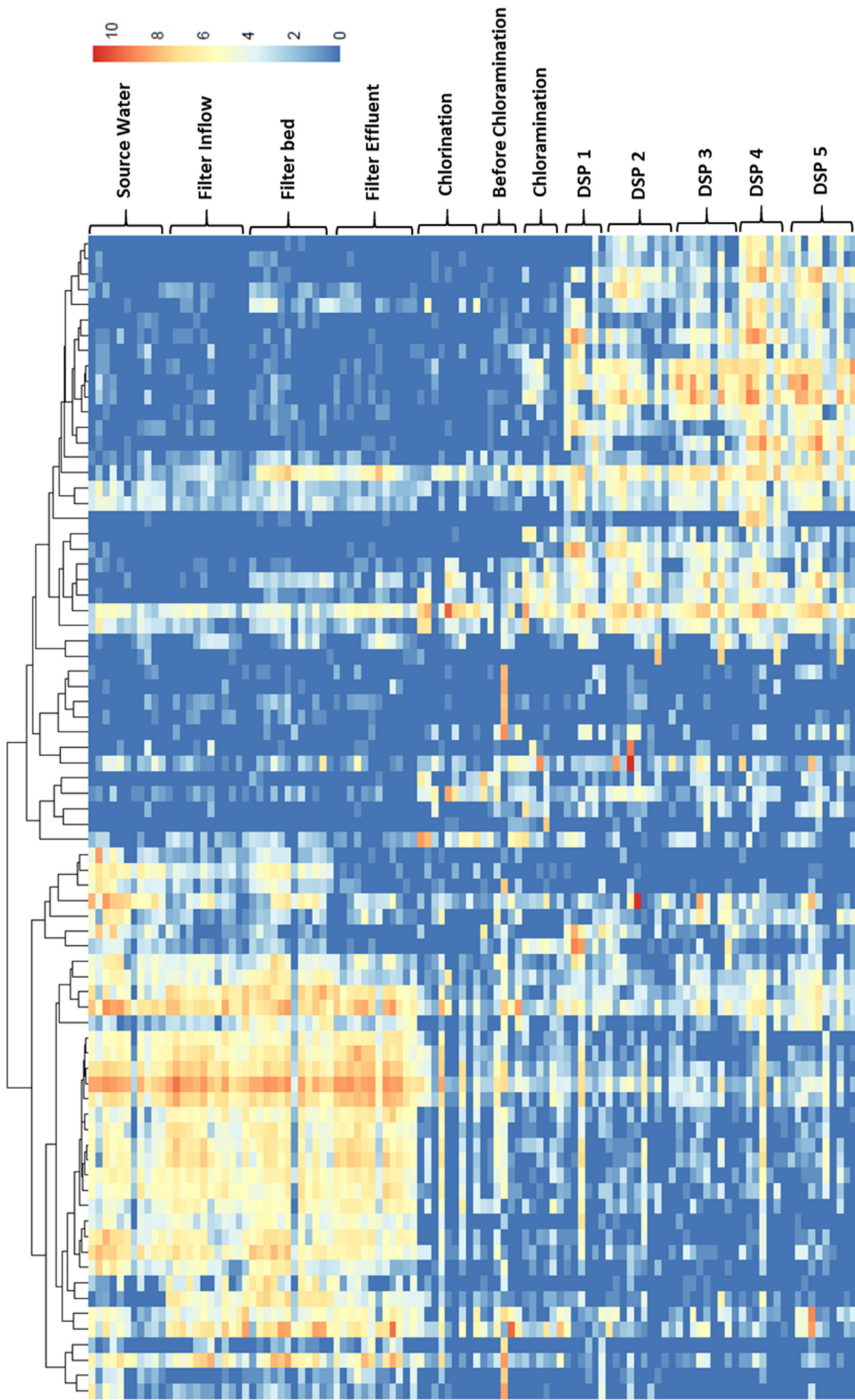


Figure 4.2 Distance-decay relationship showing that as the distance between DWDS sampling point increase is there an increase in dissimilarity in the microbial community structure, (A) Bray-Curtis pairwise distance metric and (B) Weighted UniFrac metrics, and the microbial community membership (C) Jaccard pairwise distance metric and (D) Unweighted UniFrac.



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Figure 4.3 Heatmap constructed using the absolute sequence abundances (log transformed) of 75 OTUs that were selected based on their relative abundance within a sample (i.e. relative abundance threshold $\geq 1\%$) and by the percentage of samples in which they were detected (i.e. detection frequency threshold $\geq 75\%$). The heatmap boxes were colored from red-to-blue to represent higher-to-lower abundances, and OTUs not represented by a sequence were assigned 10^{-6} (displayed as dark blue).

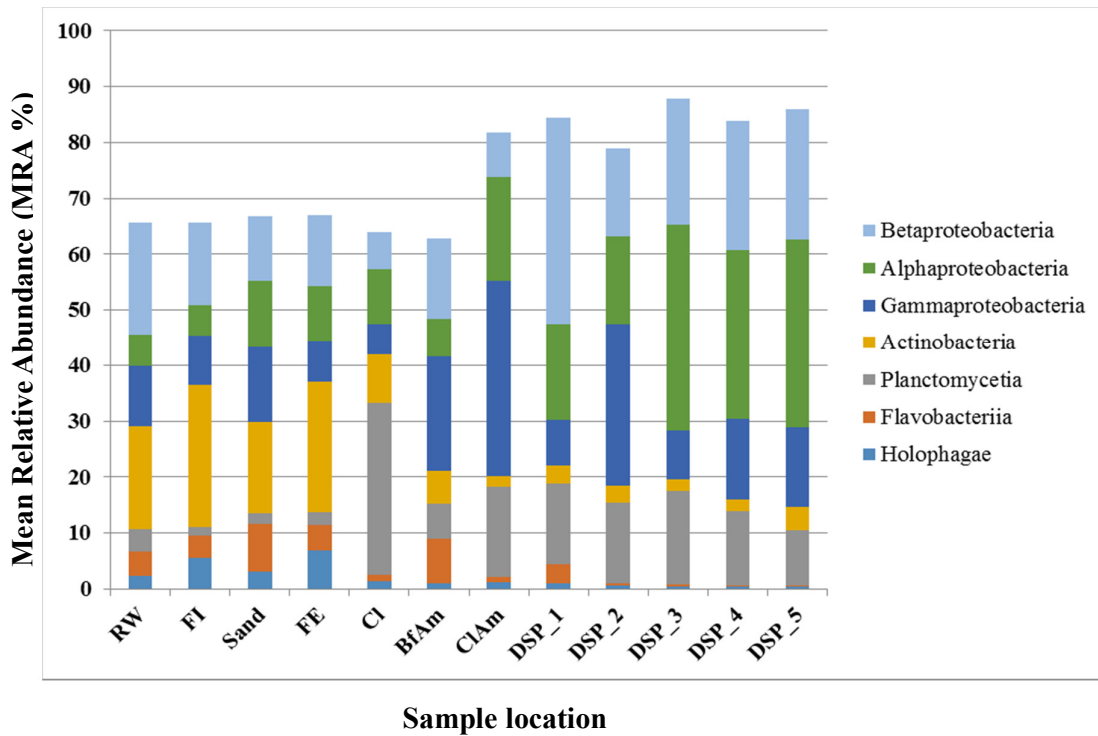


Figure 4.4 Mean relative abundance of the seven most abundant bacterial classes present at all sampling sites within the treatment plant (Source water (RW), filter influent (FI), Rapid Sand Filter media (Sand) and filter effluent (FE)) as well as the distribution system ((Chlorination (Cl), before chloramination (BfAm), chloramination (ClAm), distribution system points (DSP)) over a 12 month period.

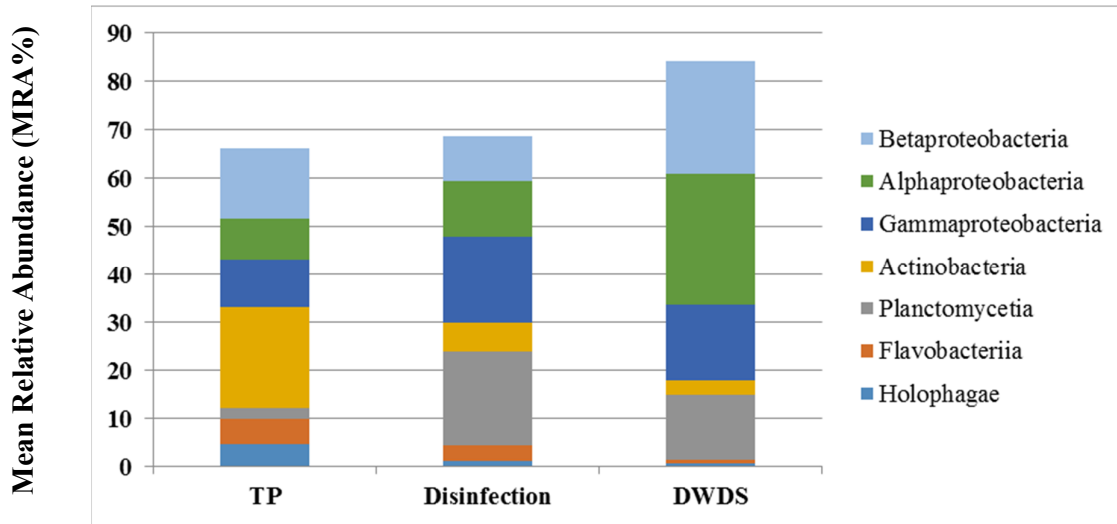


Figure 4.5 Mean relative abundance of the five most abundant bacterial classes in the different stages of treatment (Treatment plant (TP), Disinfection stage, Distribution system (DWDS) over a 12-month period.

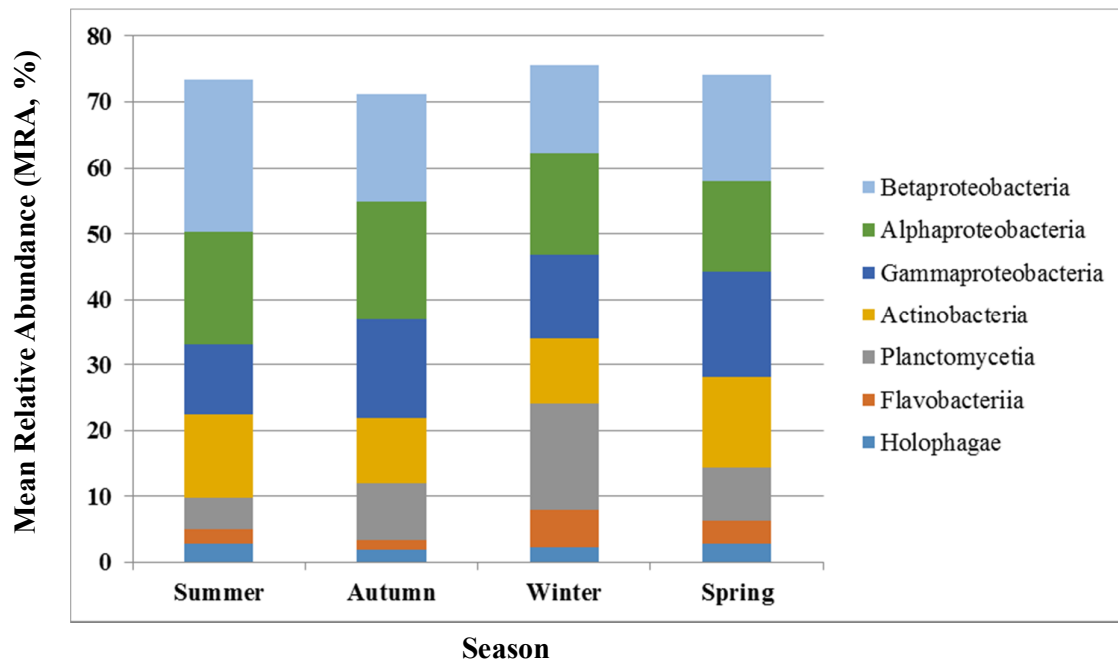


Figure 4.6 Mean relative abundance of the five dominant bacterial classes in DWDS samples showing slight changes due to the temporal groupings.

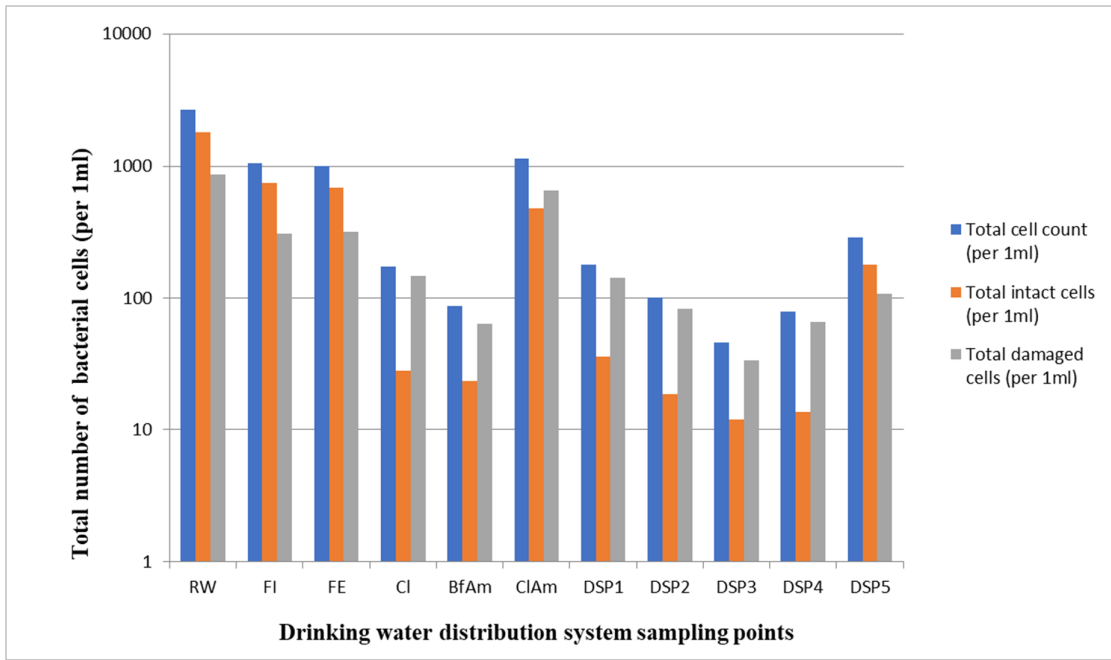


Figure 4.7 The average number of total microbial cell count and intact microbial cell count across all DWDS sampling points.

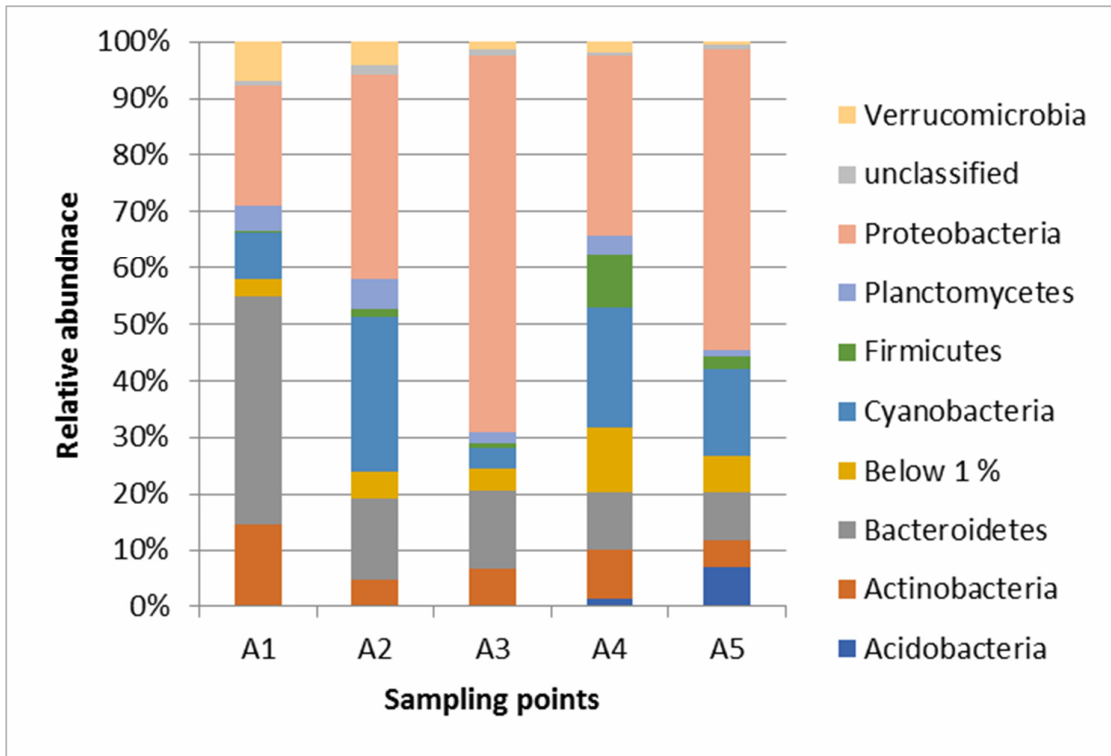


Figure 5.4 Mean relative abundances of the dominant phyla across all five sampling points over a period of 12 months.

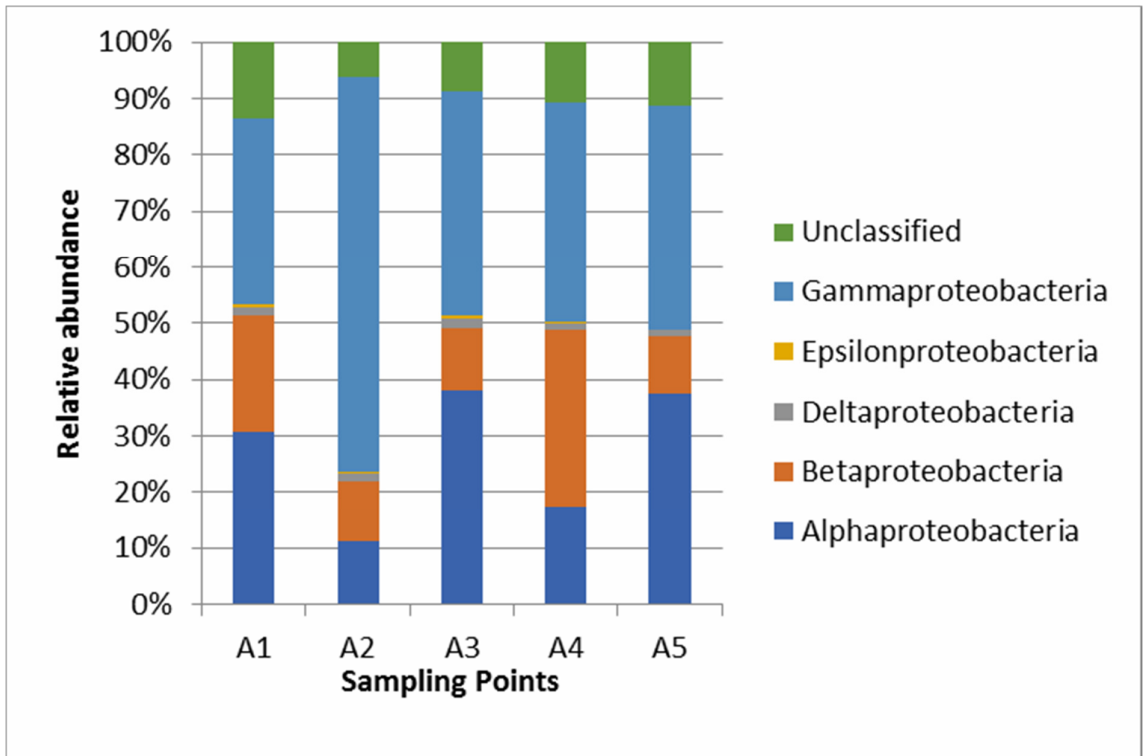


Figure 5.5 Mean relative abundances of the proteobacterial across all five sampling points over a period of 12 months.

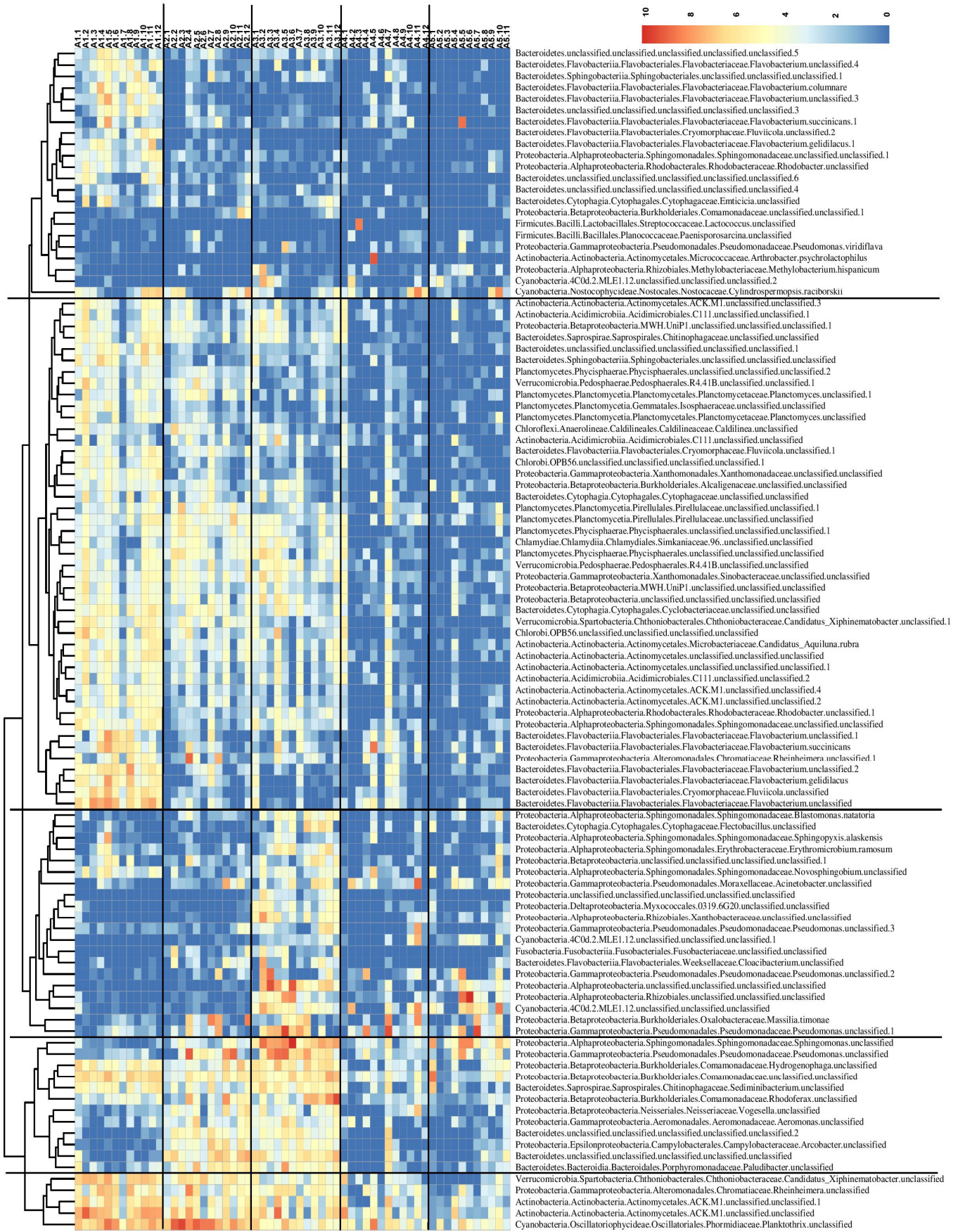


Figure 5.6 Heatmap showing the distribution of the most dominant OTUs in the system using an alternative

treatment approach.

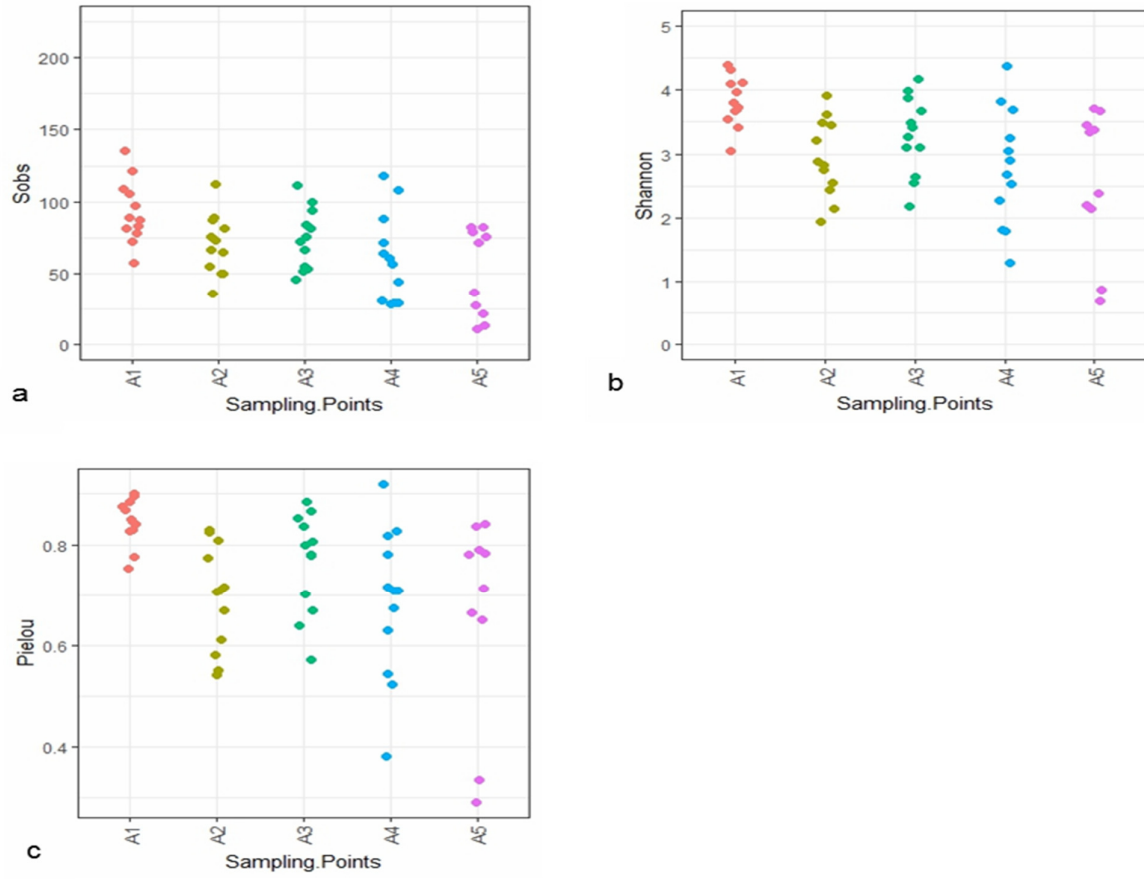


Figure 5.7 Observed species (S_{obs}), Shannon diversity (H') and Pielou's evenness (J) values as determined for samples collected at all five sampling points over a 12-month period.

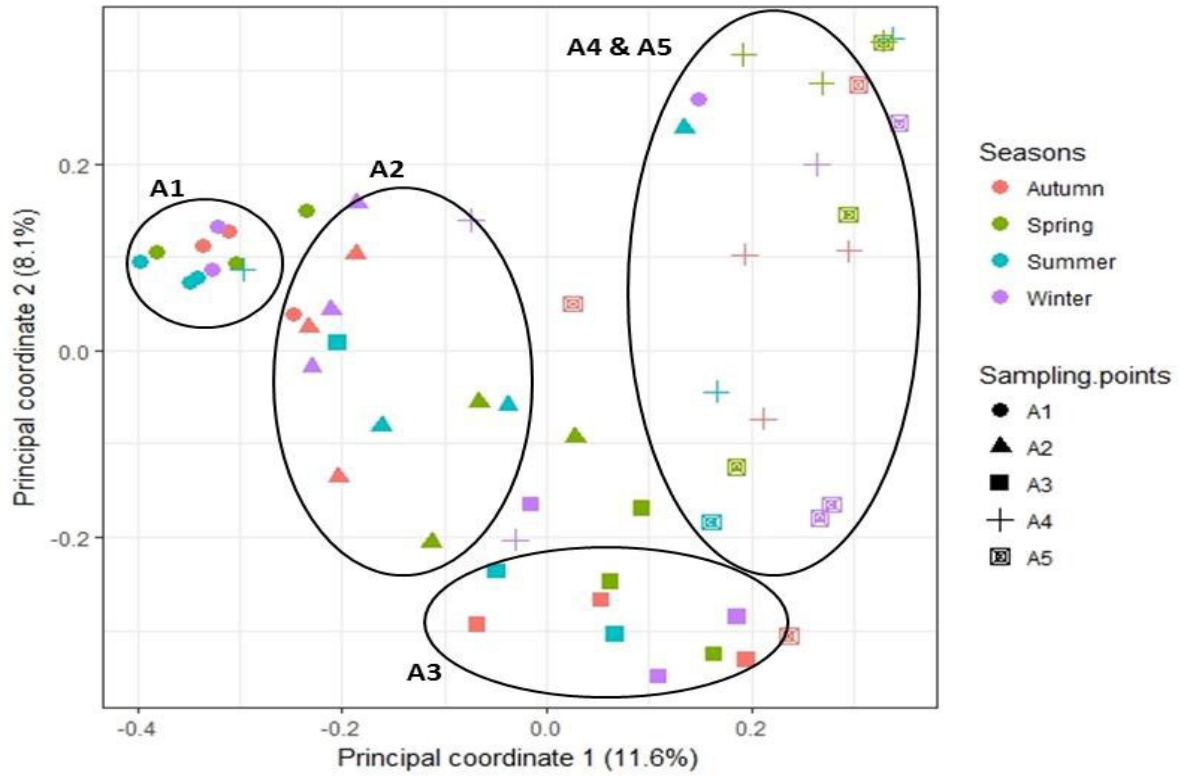


Figure 5.8 PCoA plot showing the community relation of all five sampling points over 12 months with corresponding seasonal changes.

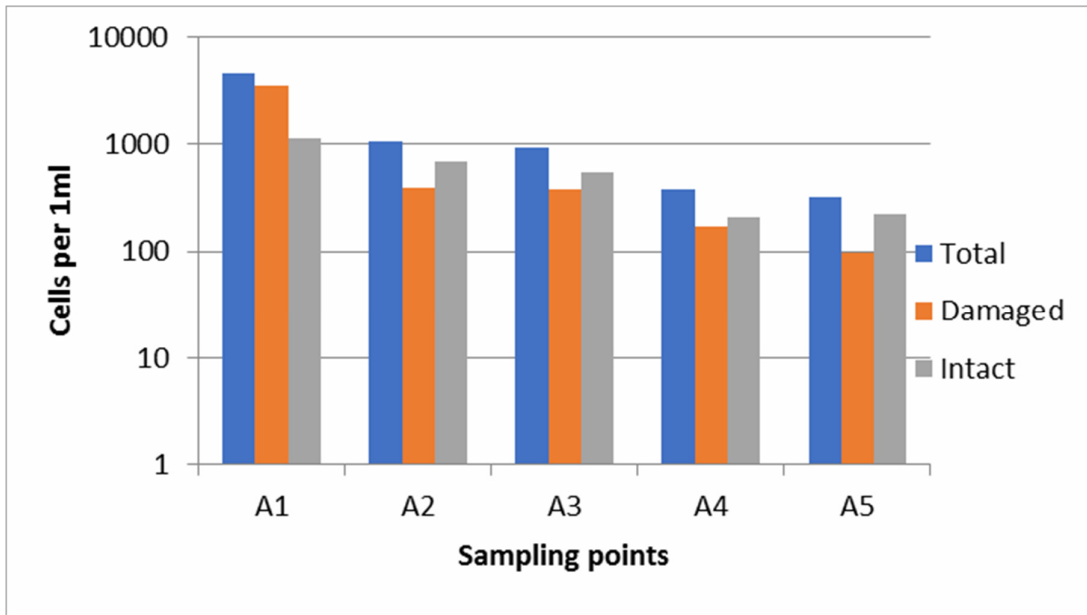


Figure 5.9 Flow cytometry results averaged over a five-month period for all five sampling points, representing total cell count, dead cell count and alive cell count in 1 ml of water.

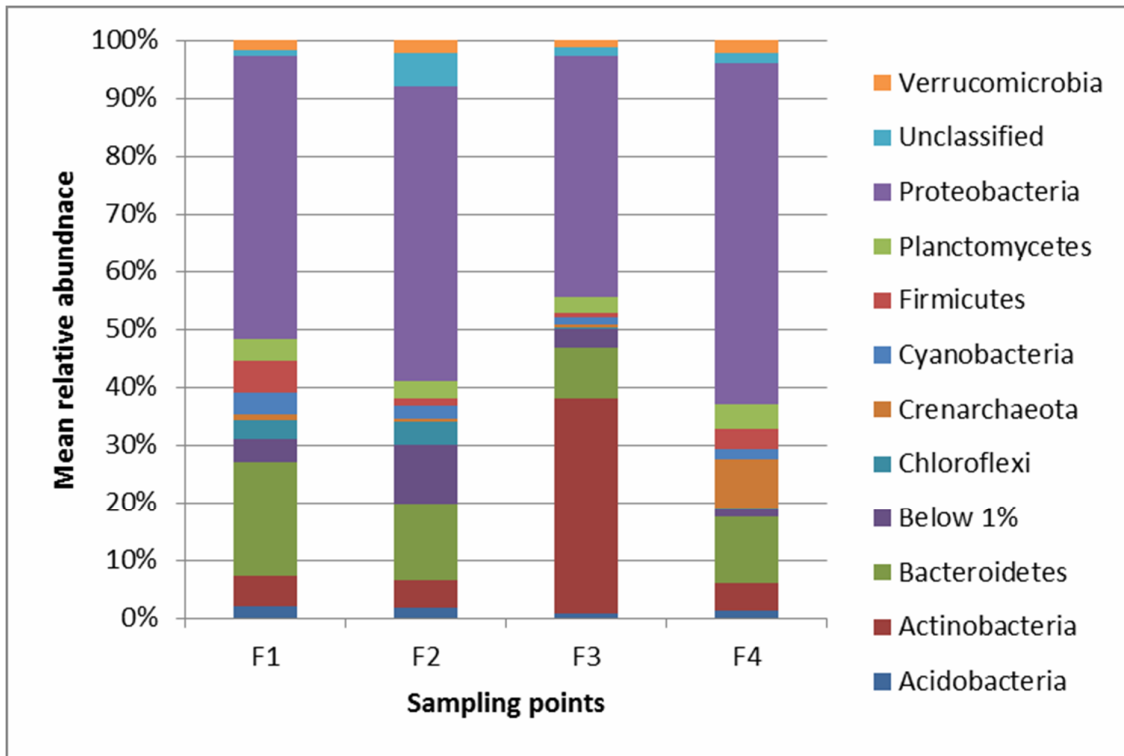


Figure 5.10 Mean relative abundances of the dominant phyla across all four sampling points over a period of 11 months

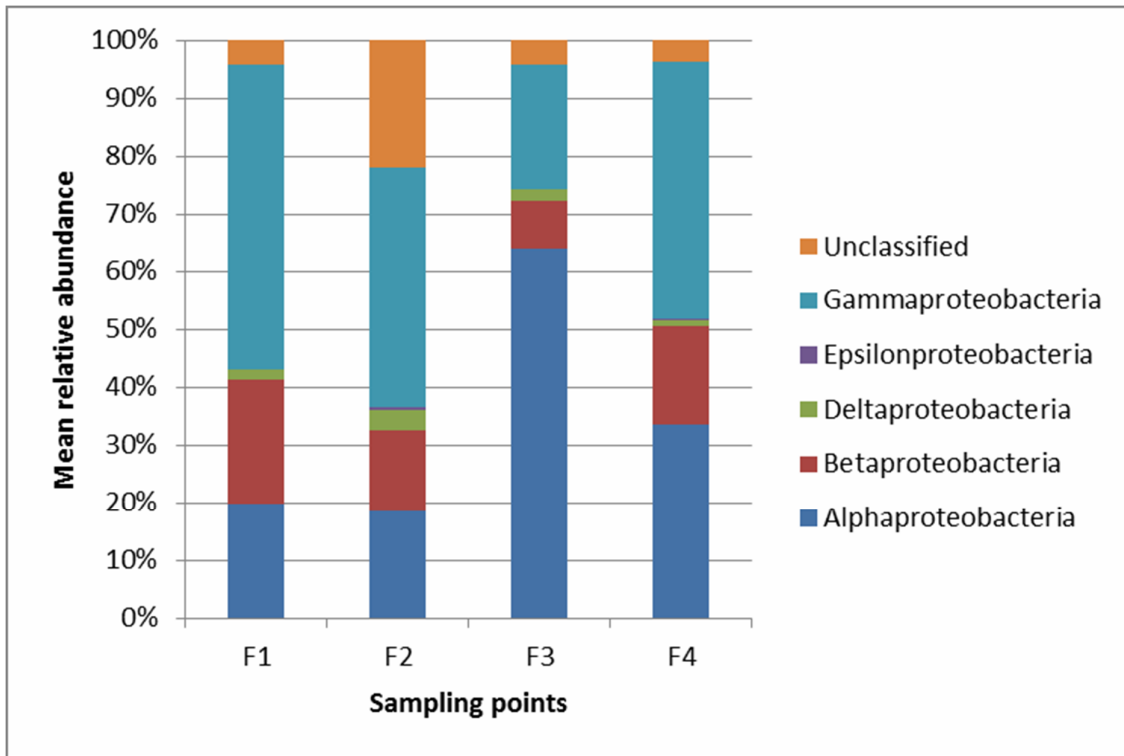


Figure 5.11 Mean relative abundances of the proteobacterial classes across all four sampling points over a period of 11 months



PREVIOUS PAGE: Figure 5.12 Heatmap showing the distribution of the most dominant OTUs in a groundwater

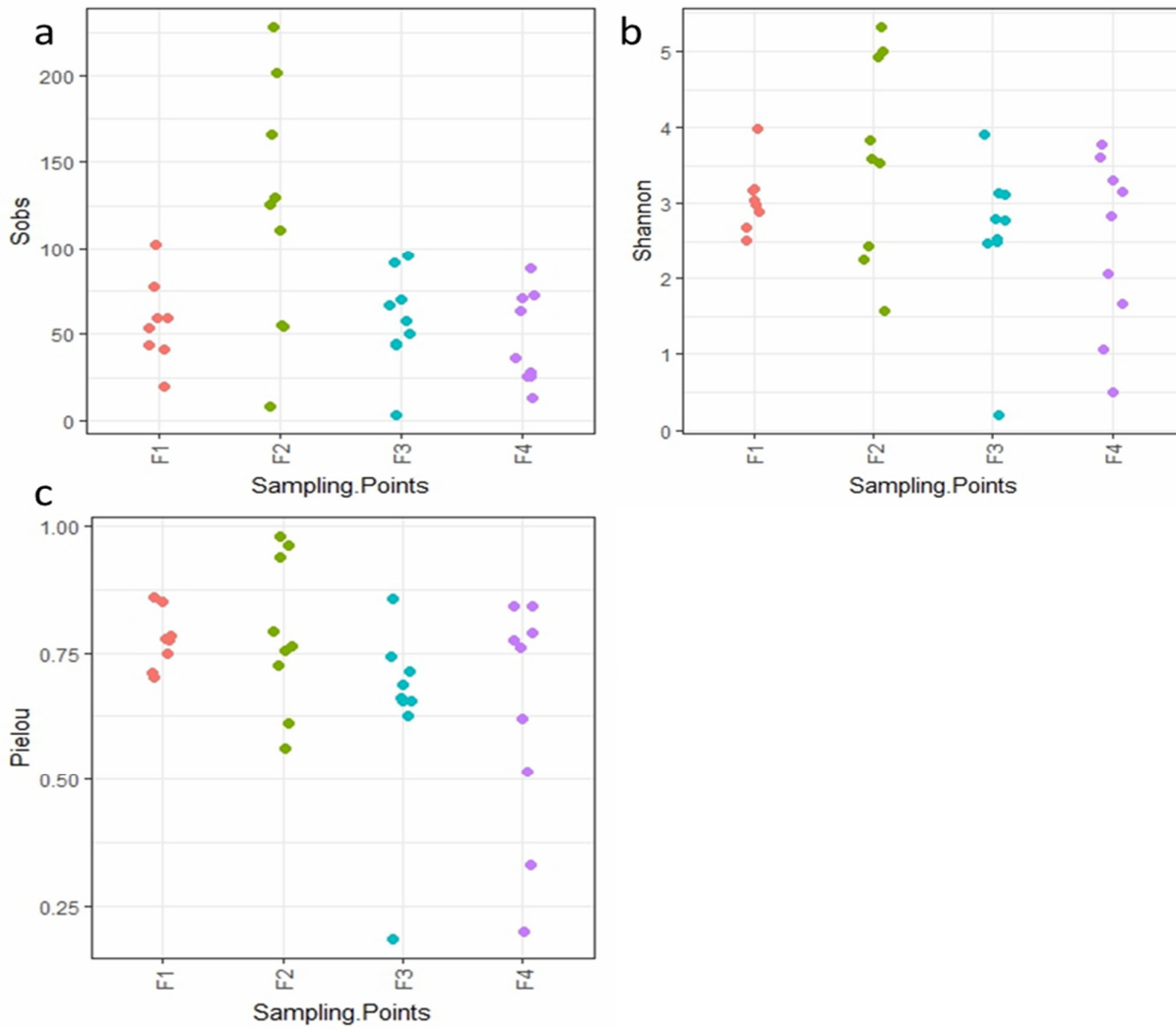


Figure 5.13 Observed species (S_{obs}), Shannon diversity index (H') and Pielou's evenness (J) values for all communities sampled across all four sampling points over a 11 month period.

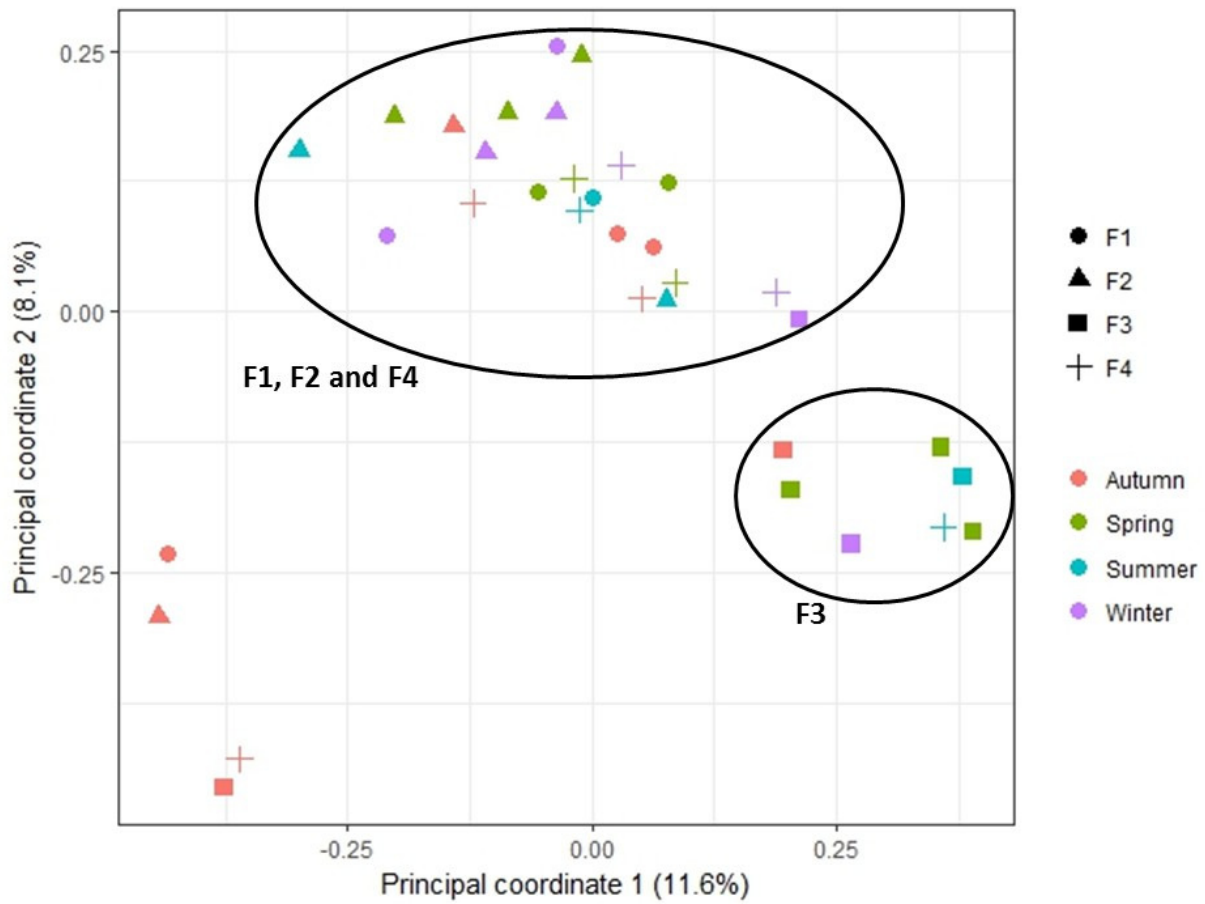


Figure 5.14 PCoA plot showing the community relation of all for sampling points over 11 months with corresponding seasonal changes.

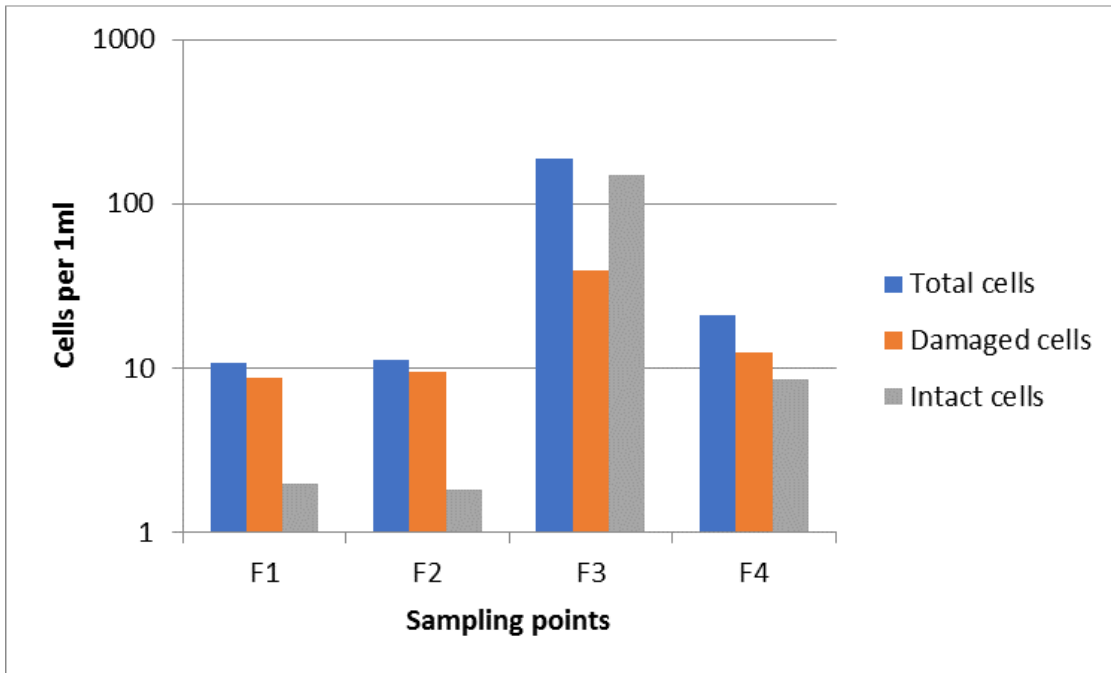


Figure 5.15 Flow cytometry results averaged over a five-month period for all four sampling points, representing total cell count, dead cell count and alive cell count in 1 ml of water.

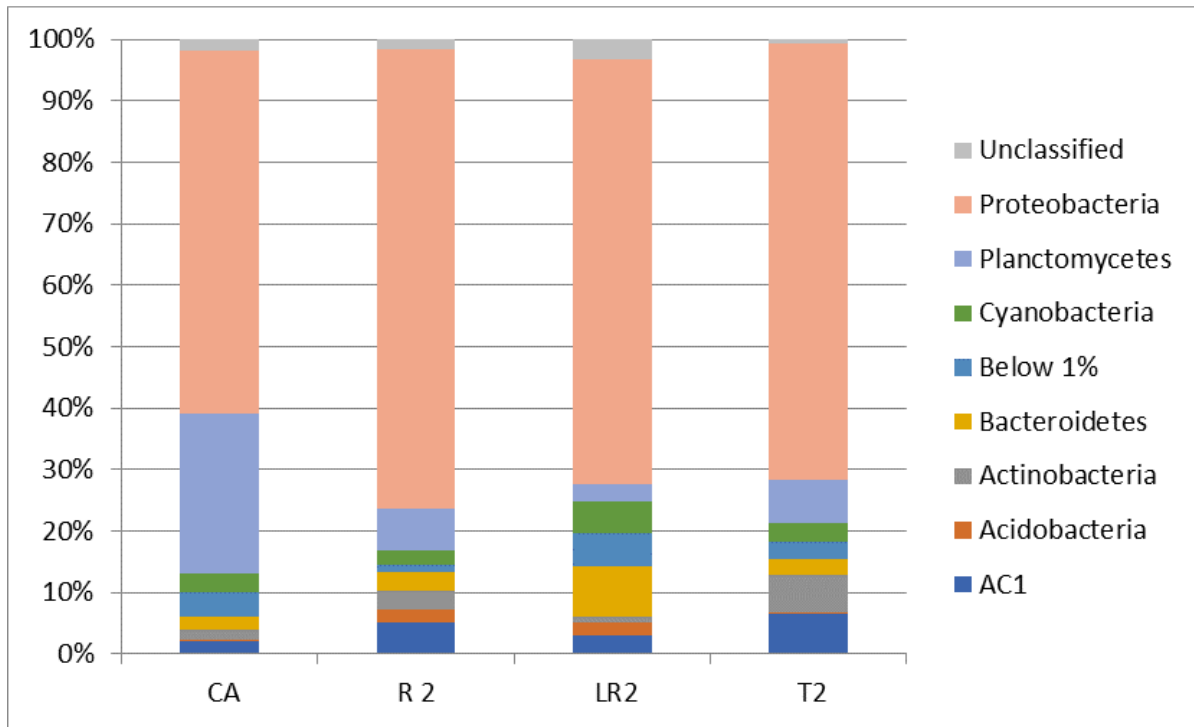


Figure 5.16 Mean relative abundances of the dominant phyla across all sampling points over a period 6 of months.

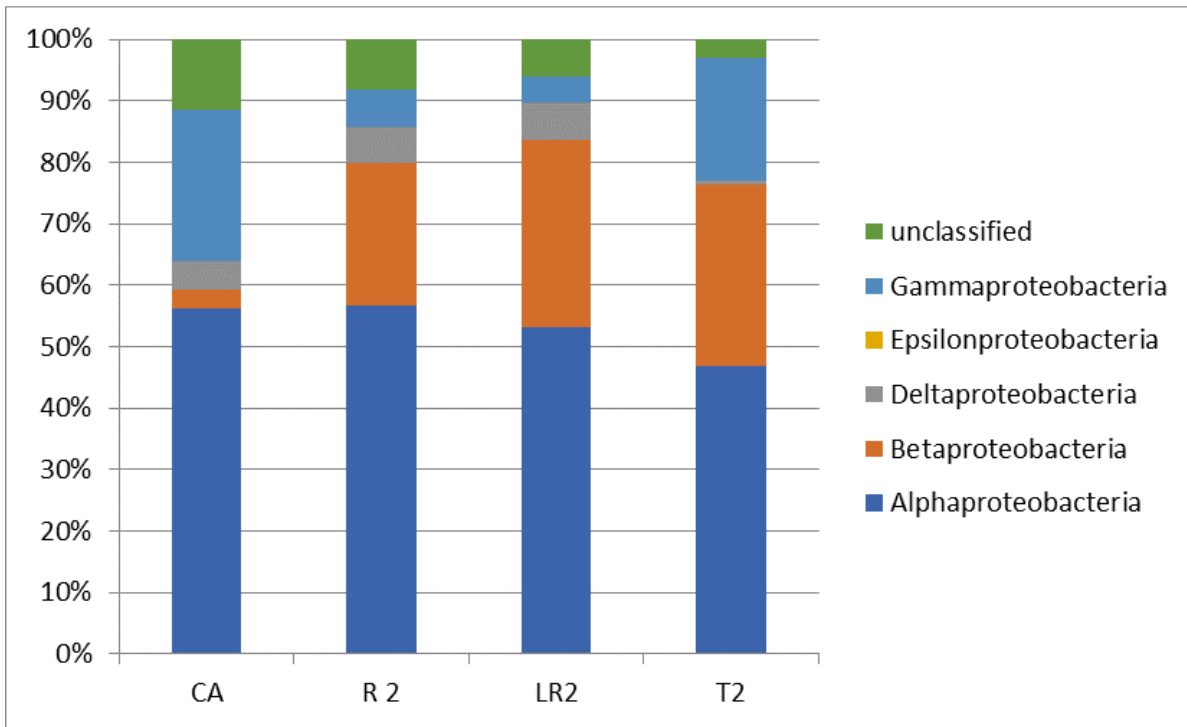


Figure 5.17 Mean relative abundances of the proteobacterial classes across all sampling points over a period of 6 months.

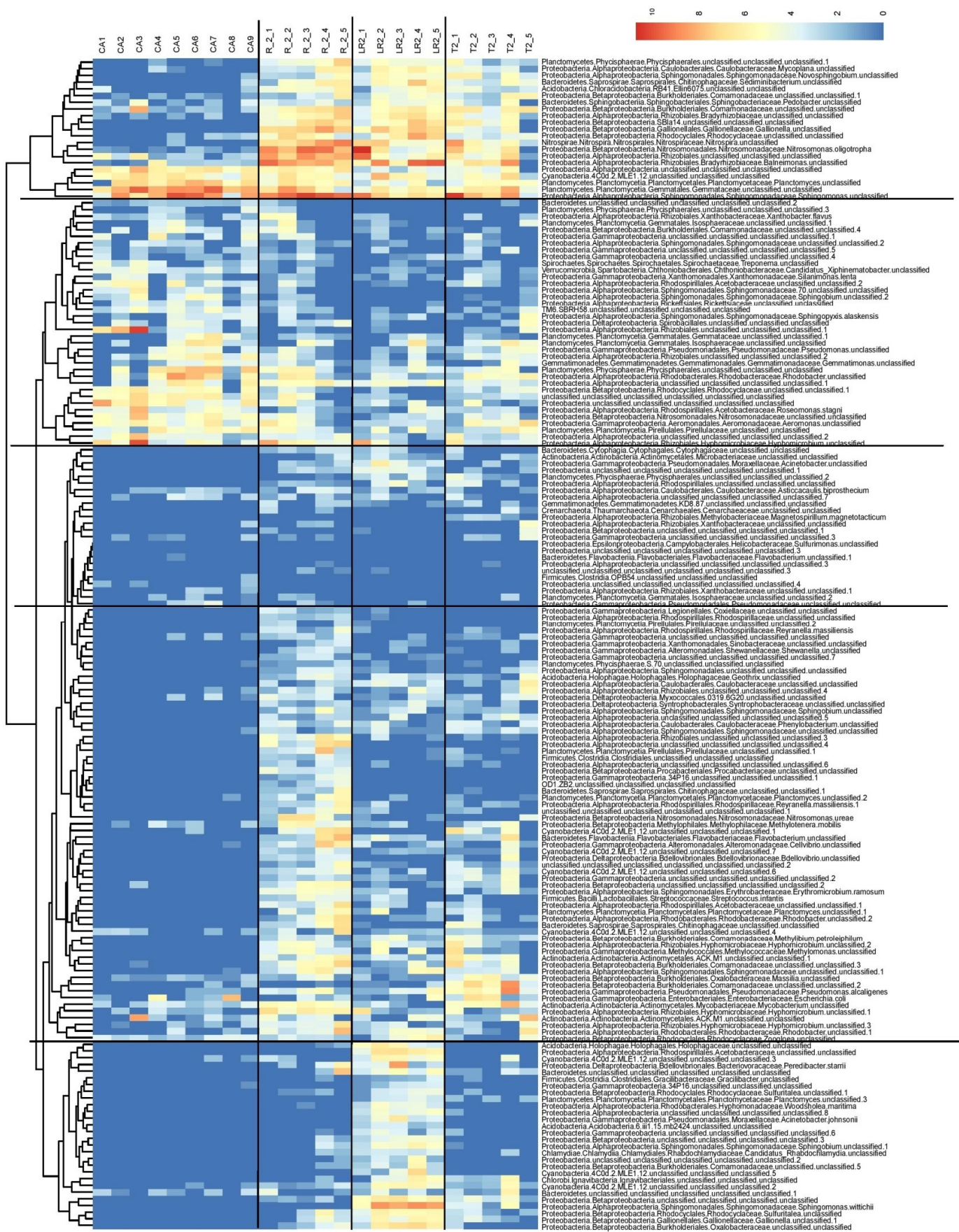


Figure 5.18 Heatmap showing the distribution of the most dominant OTUs in the system.

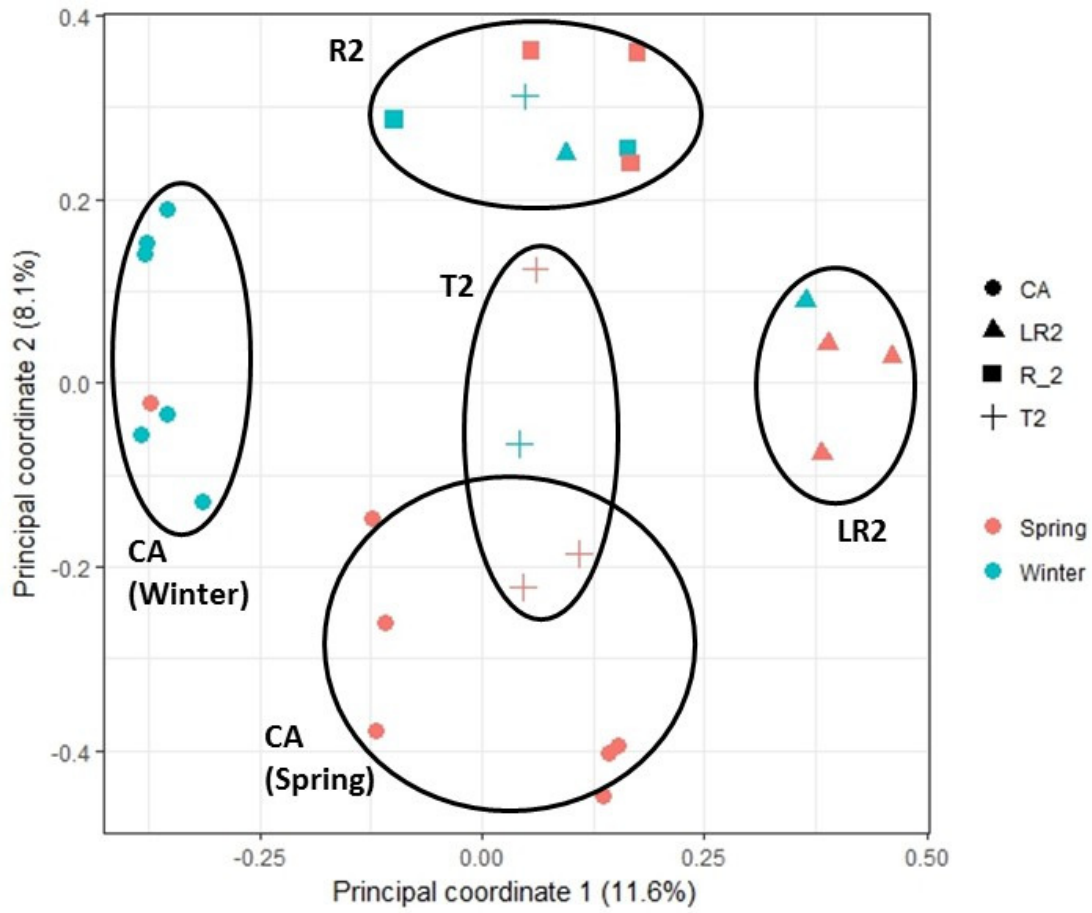


Figure 5.19 PCoA plot showing the community relation of all five sampling points over 6 months with corresponding seasonal changes.

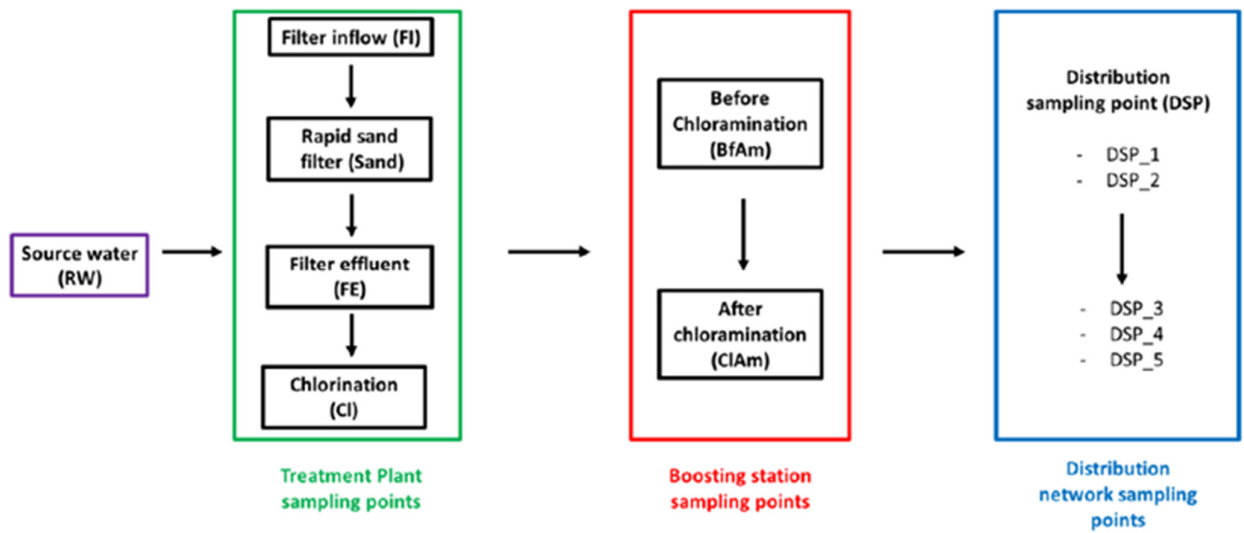


Figure 6.1 A schematic layout of the treatment works and DWDS points sampled during this study.

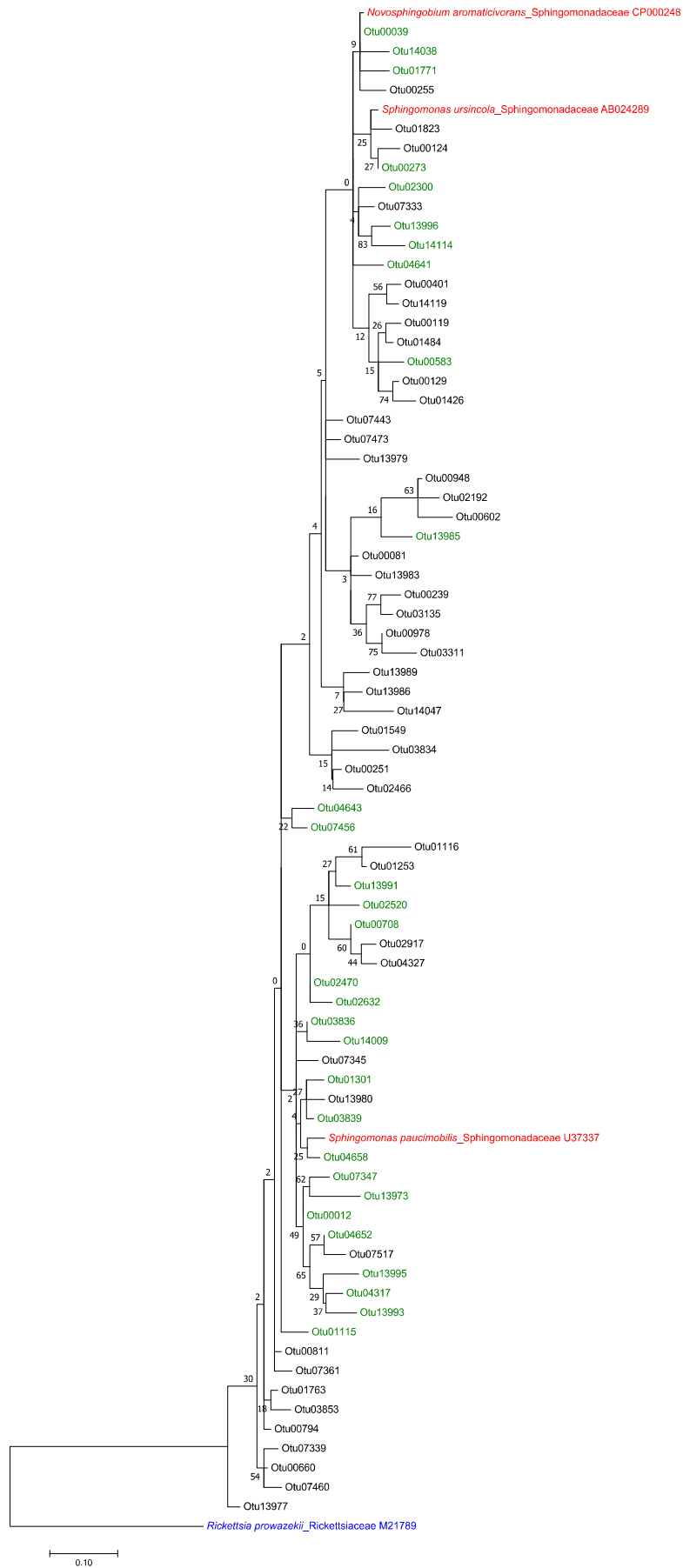


Figure 6.2 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Spingomonadaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

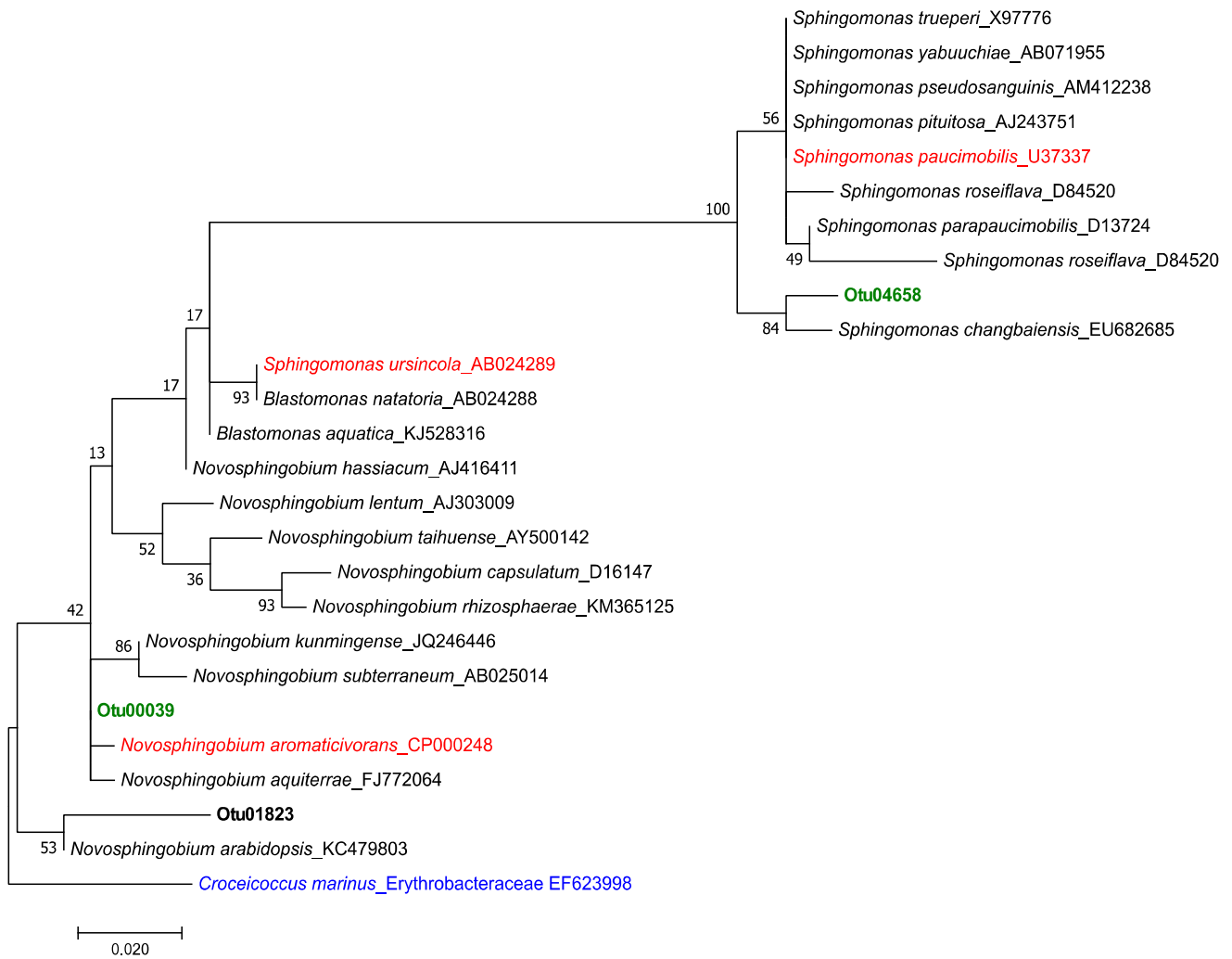


Figure 6.2 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family *Sphingomonadaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

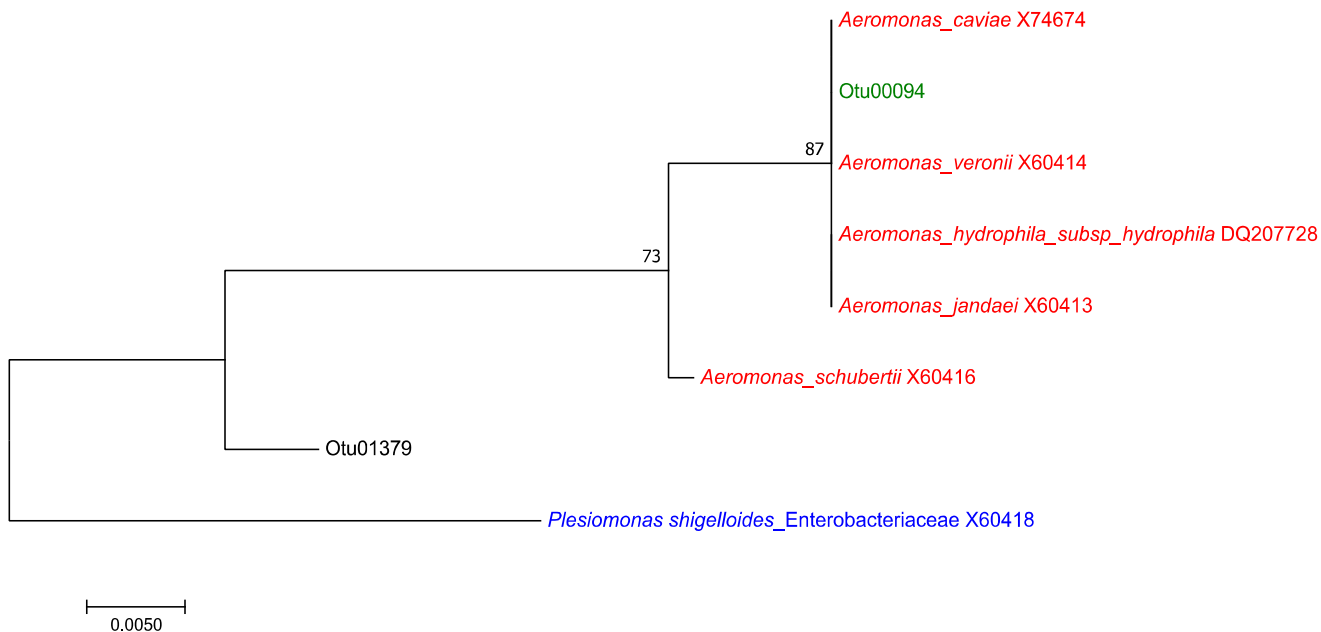


Figure 6.3 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Aeromonadaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

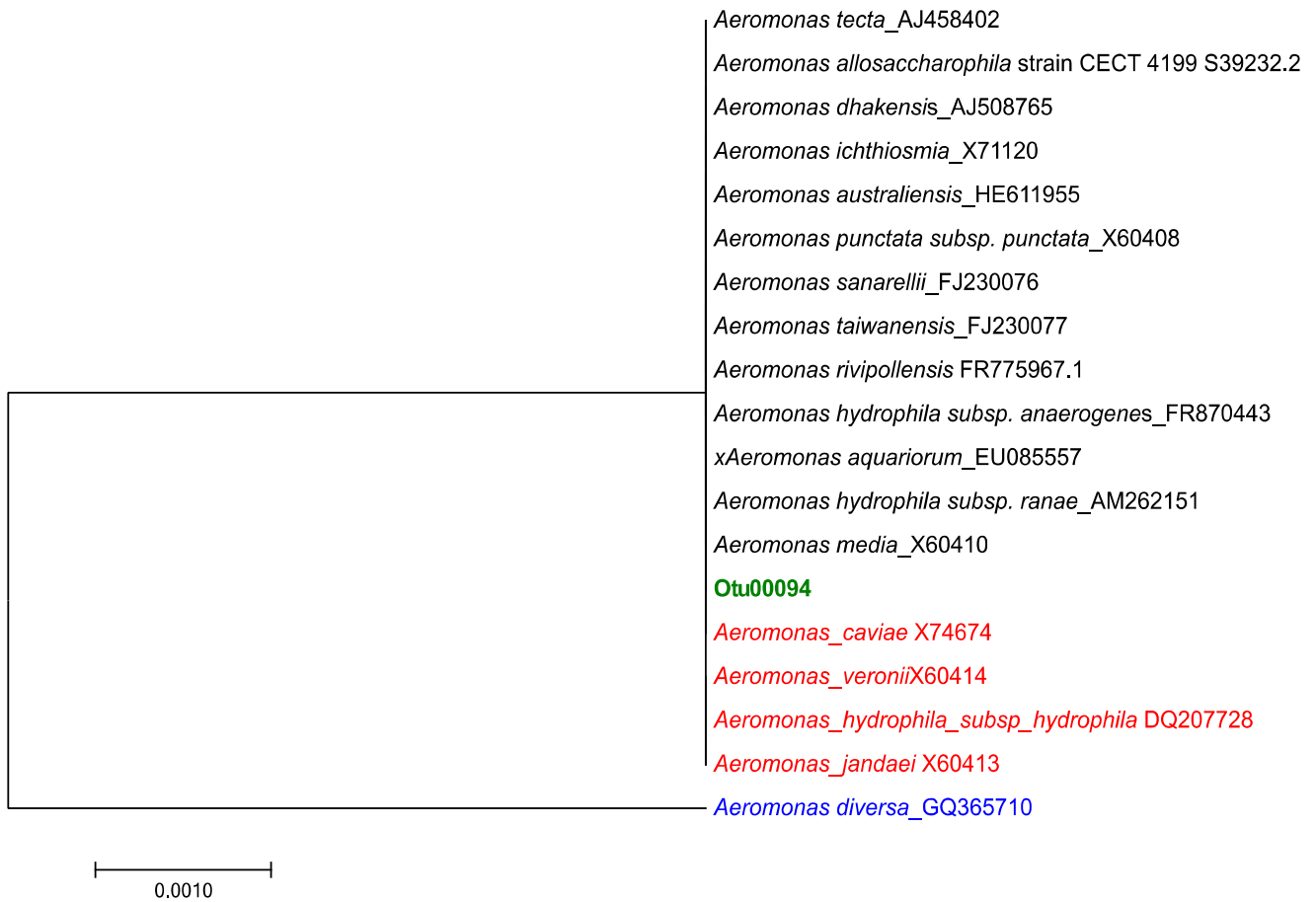


Figure 6.3 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Aeromonadaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

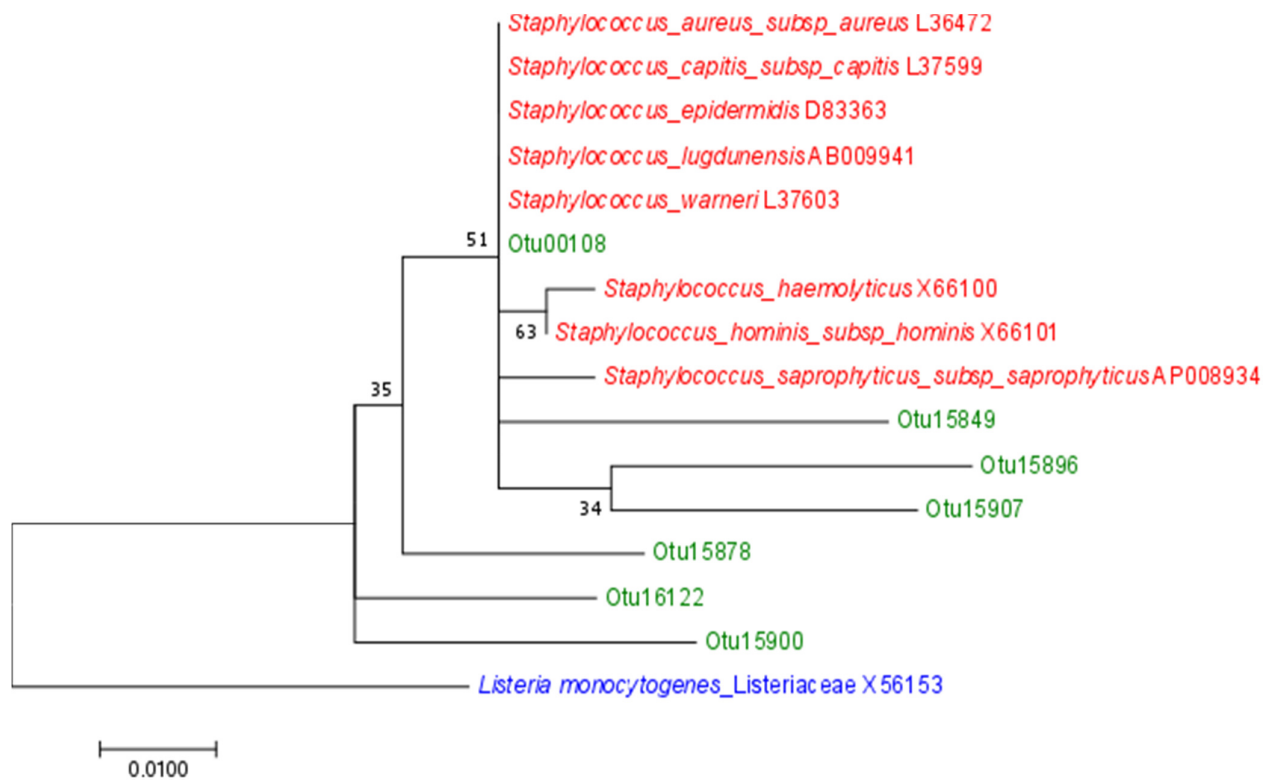


Figure 6.4 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Staphylococcaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

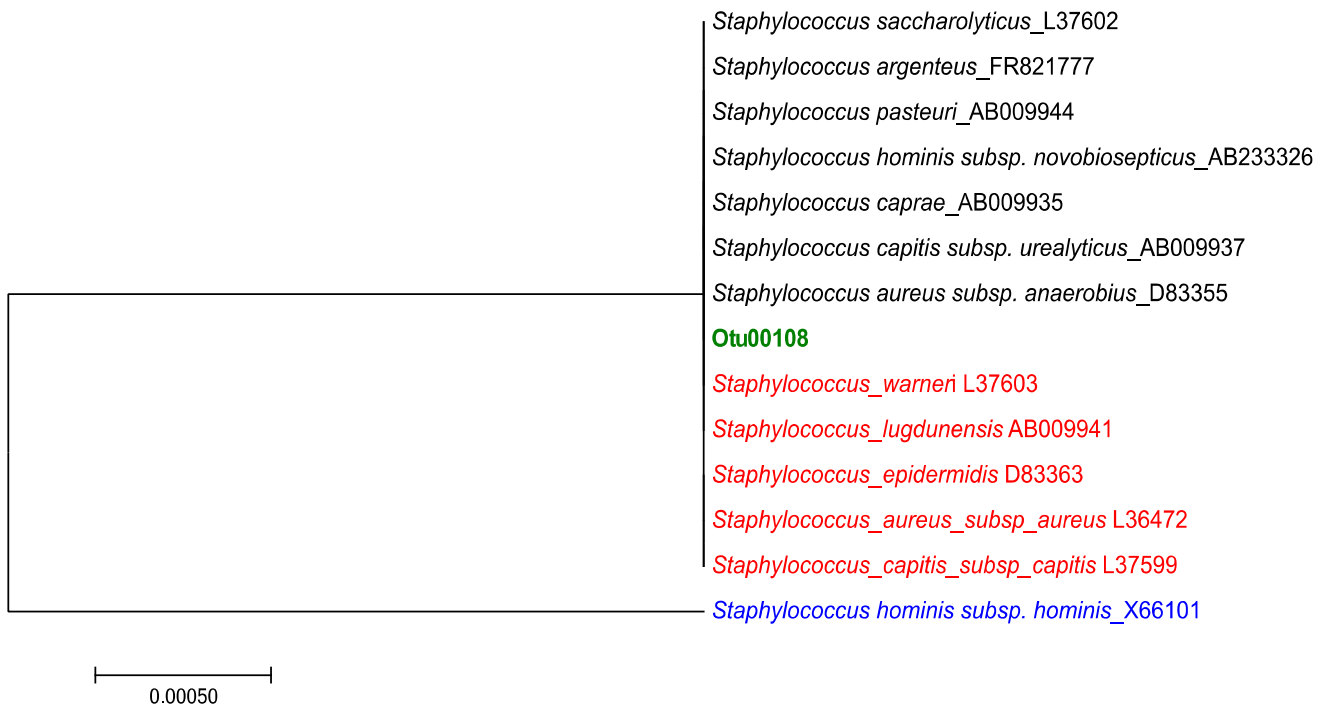


Figure 6.4 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Staphylococcaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

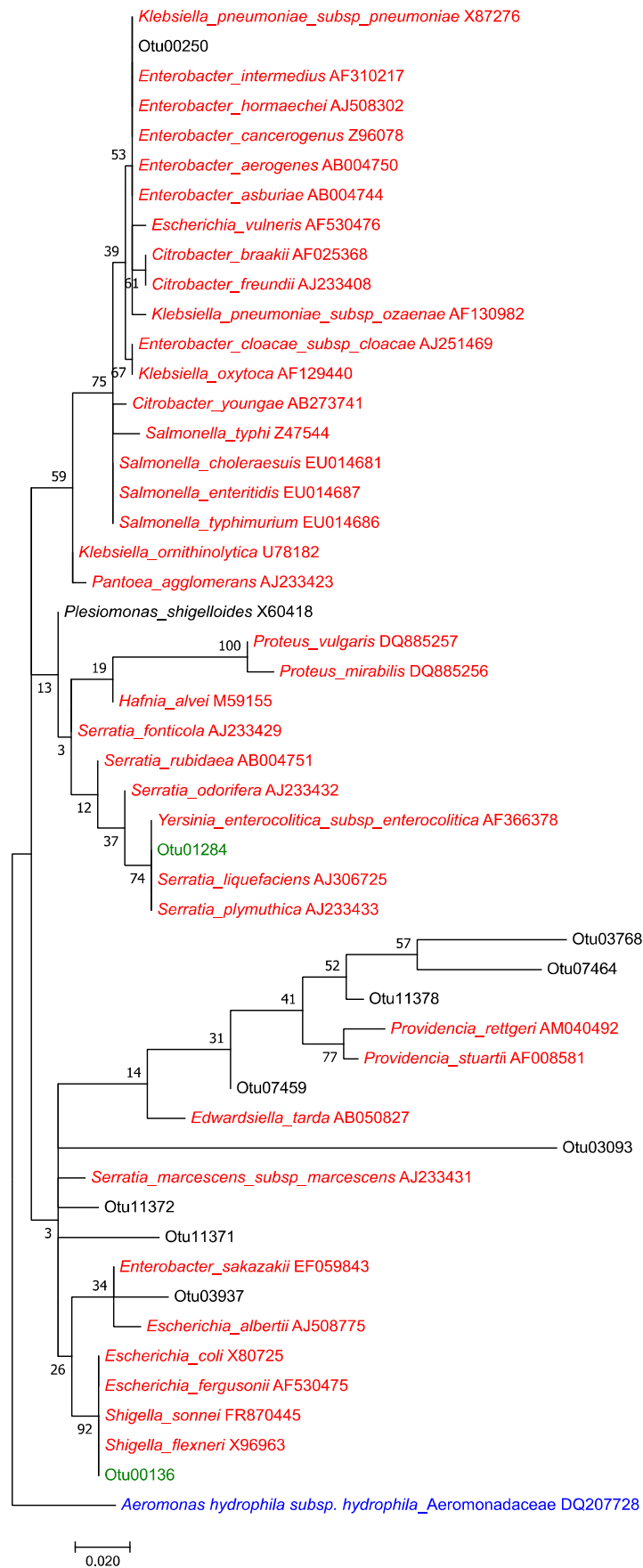


Figure 6.5 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Enterobacteriaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

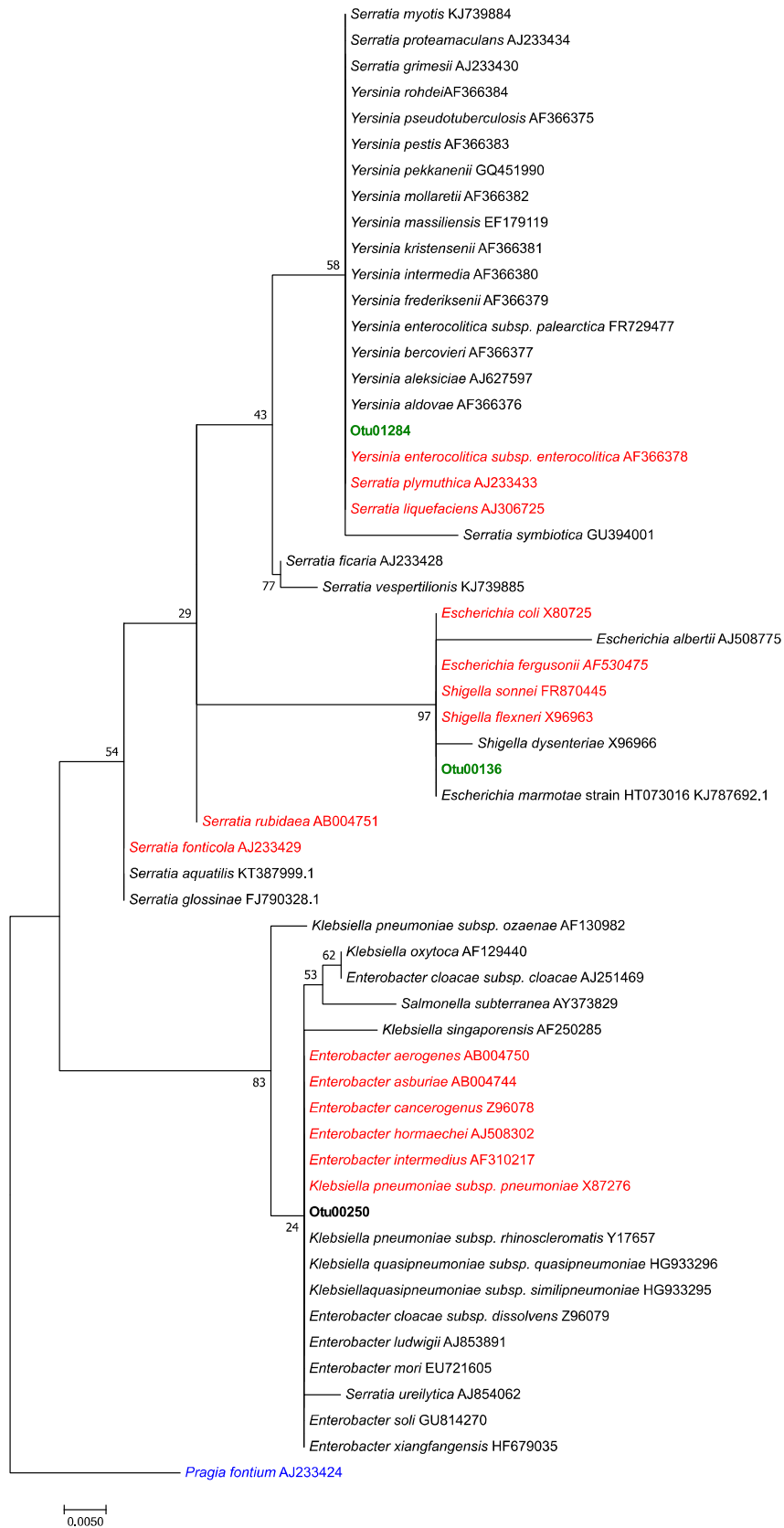


Figure 6.5 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Enterobacteriaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

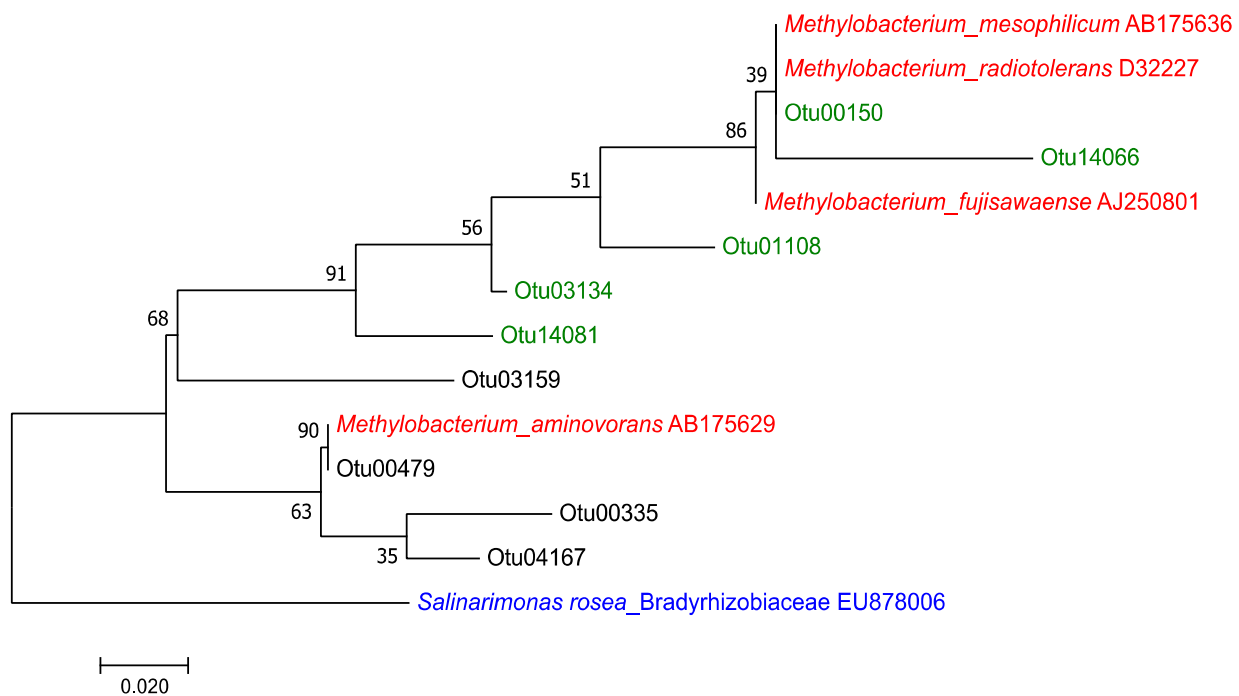


Figure 6.6 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Methylobacteriaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

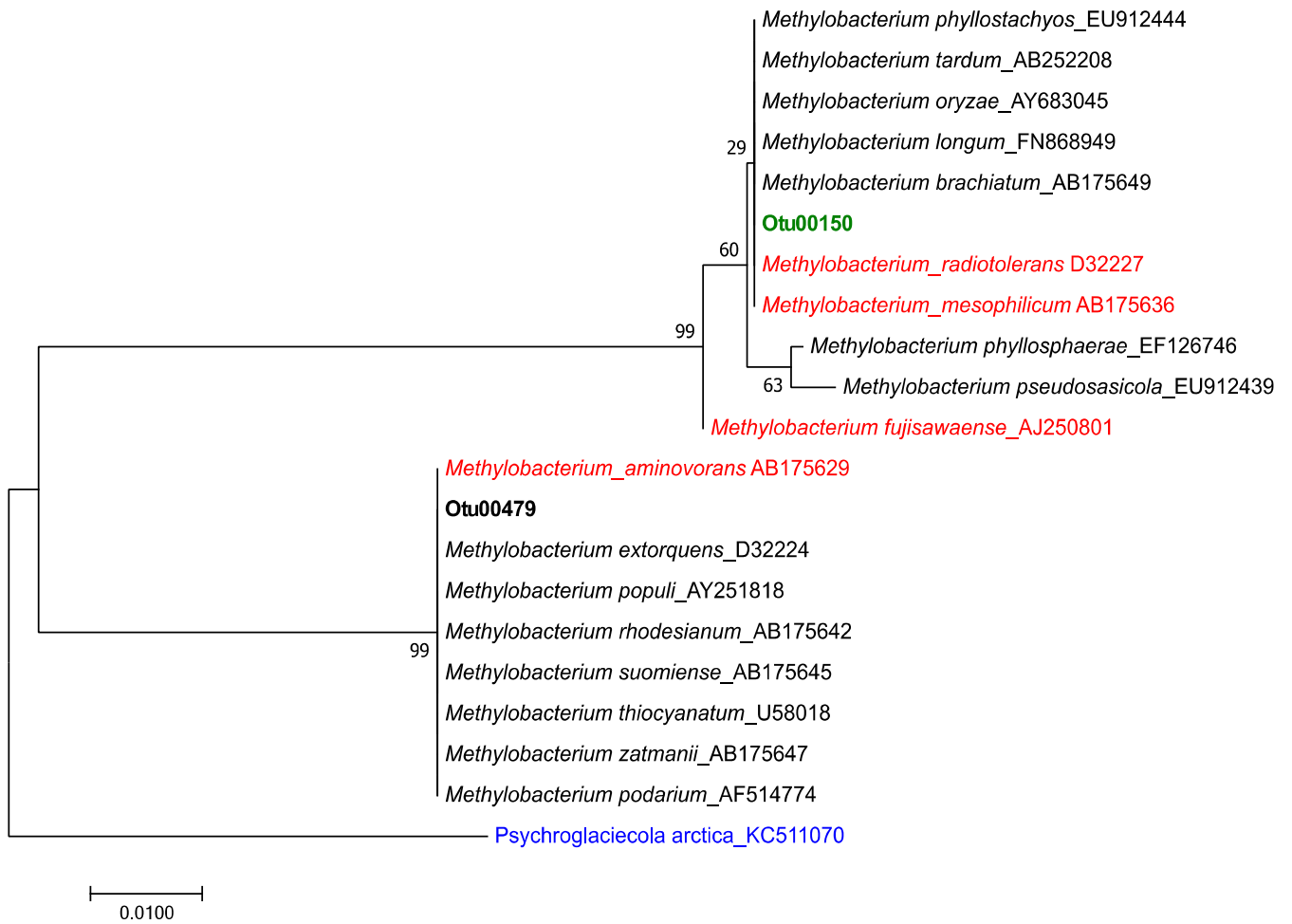


Figure 6.6 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Methylobacteriaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

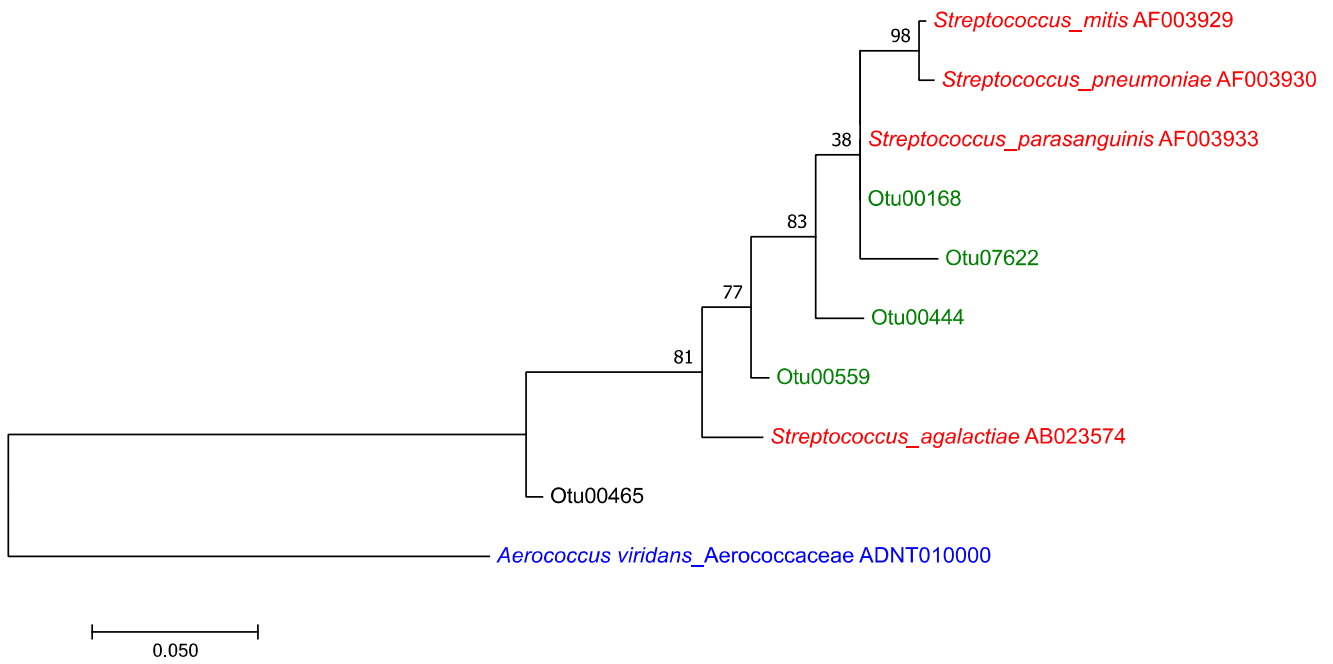


Figure 6.7 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Streptococcaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.



Figure 6.7 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Streptococcaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

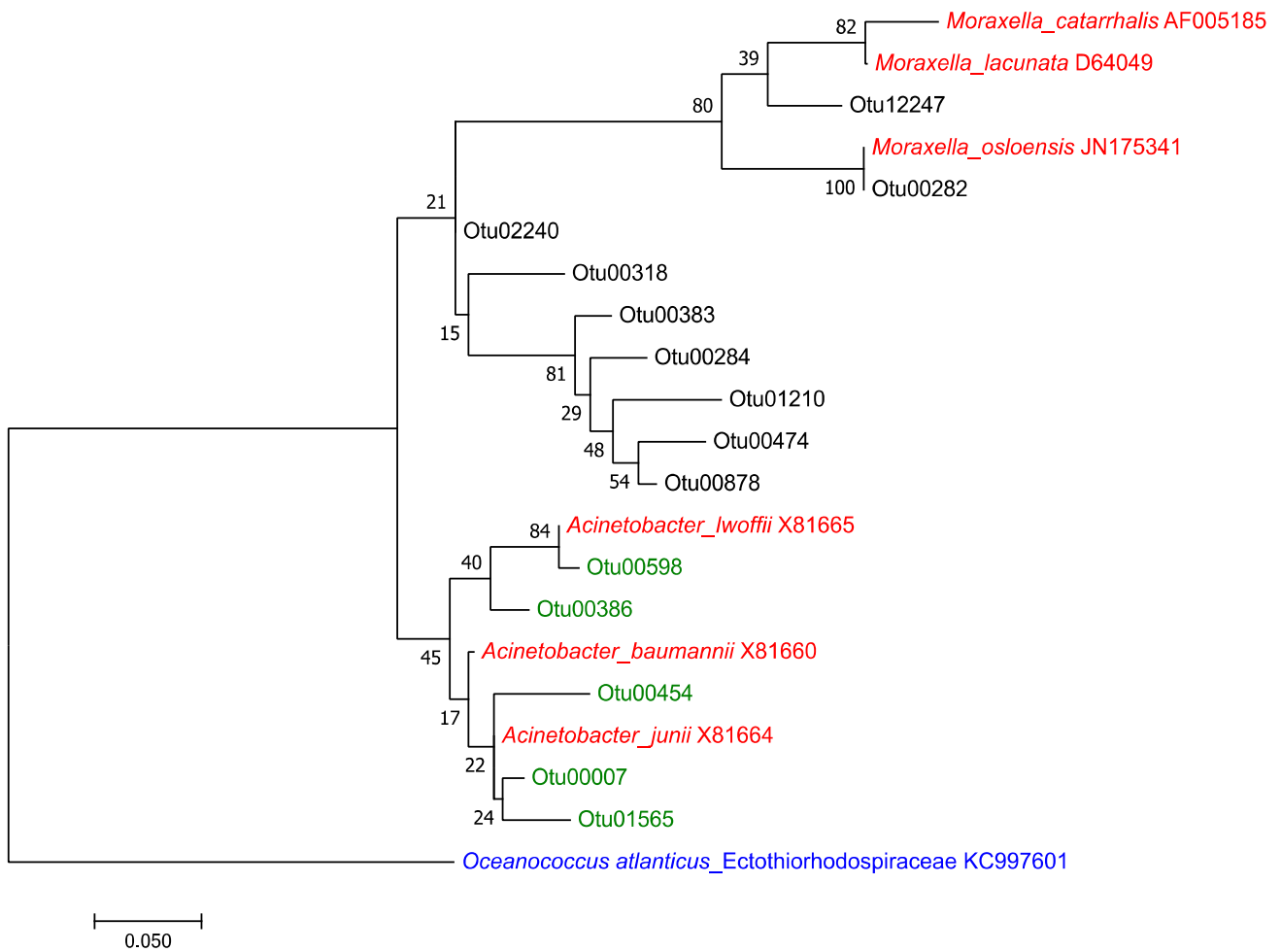


Figure 6.8 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Moraxellaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

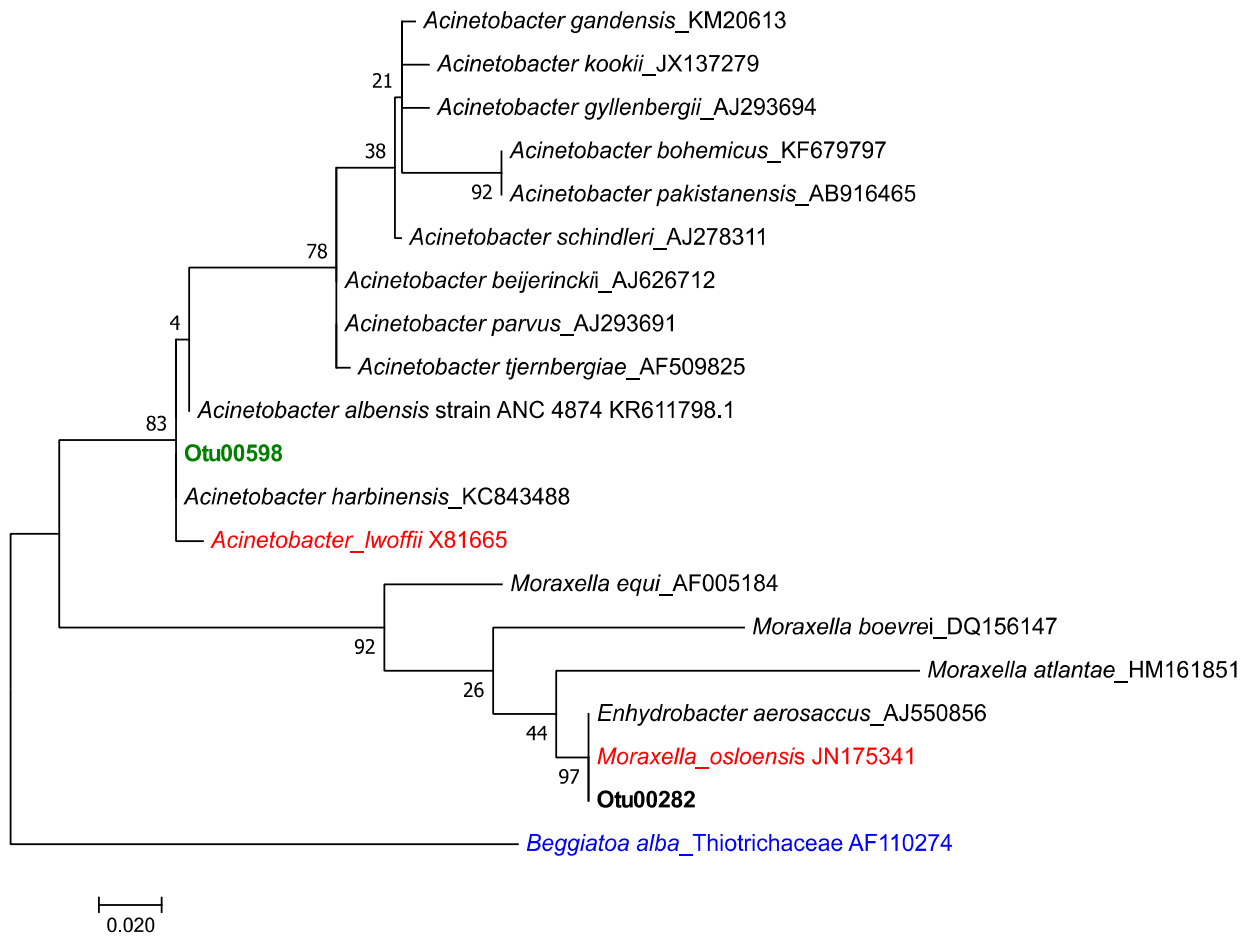


Figure 6.8 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Moraxellaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

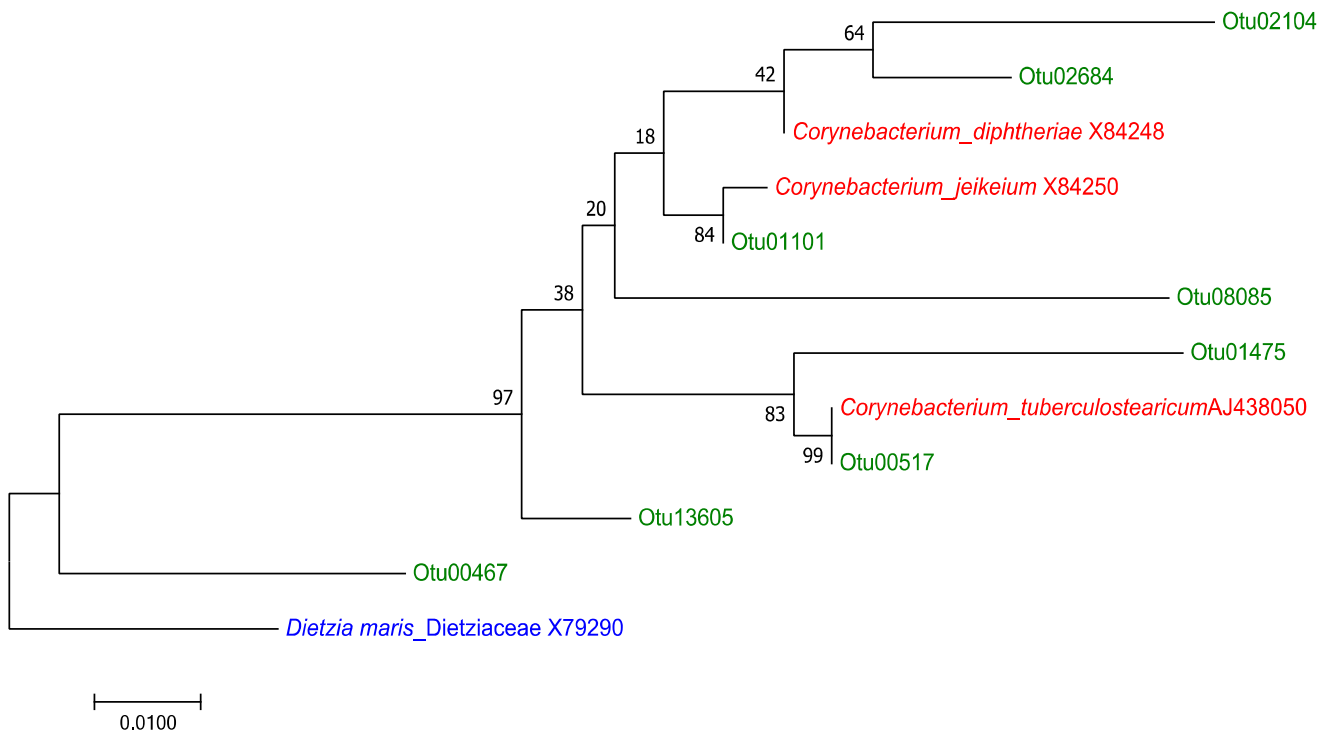


Figure 6.9 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Corynebacteriaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

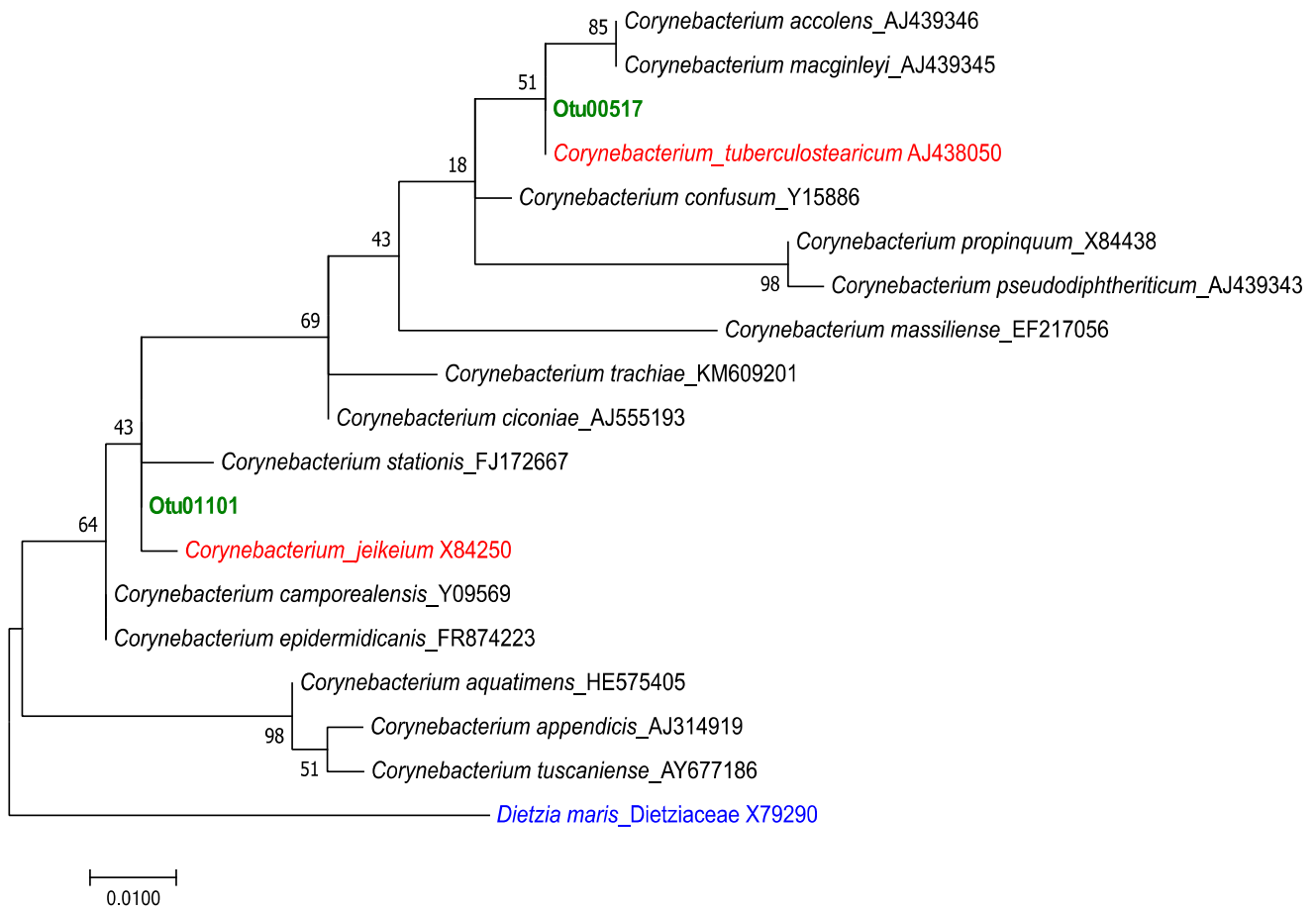


Figure 6.9 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Corynebacteriaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

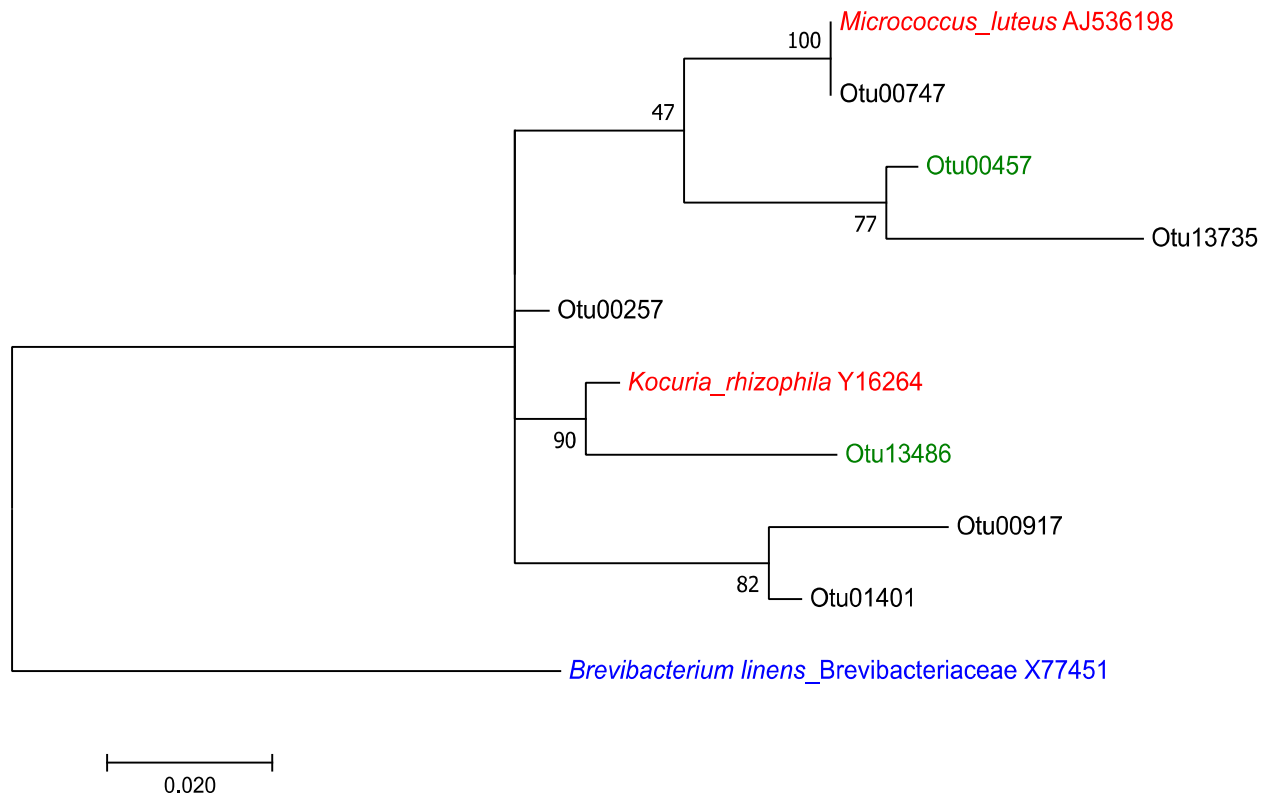


Figure 6.10 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Micrococcaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

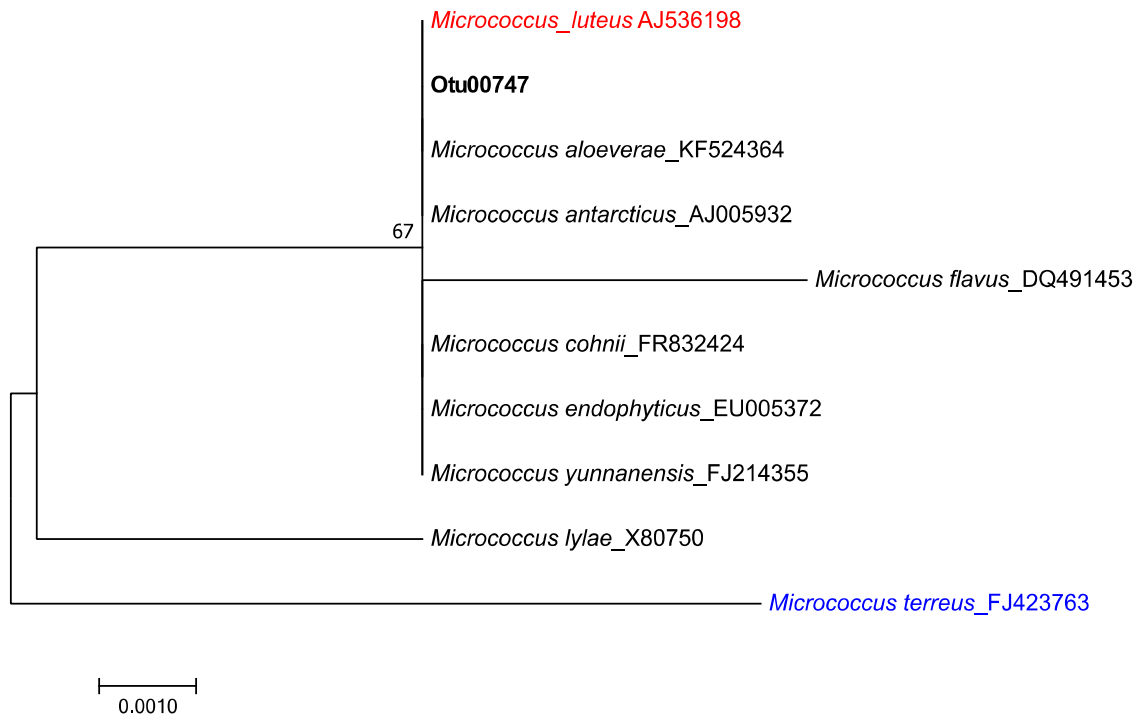


Figure 6.10 (B) Maximum likelihood tree representing the potentially OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Micrococcaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

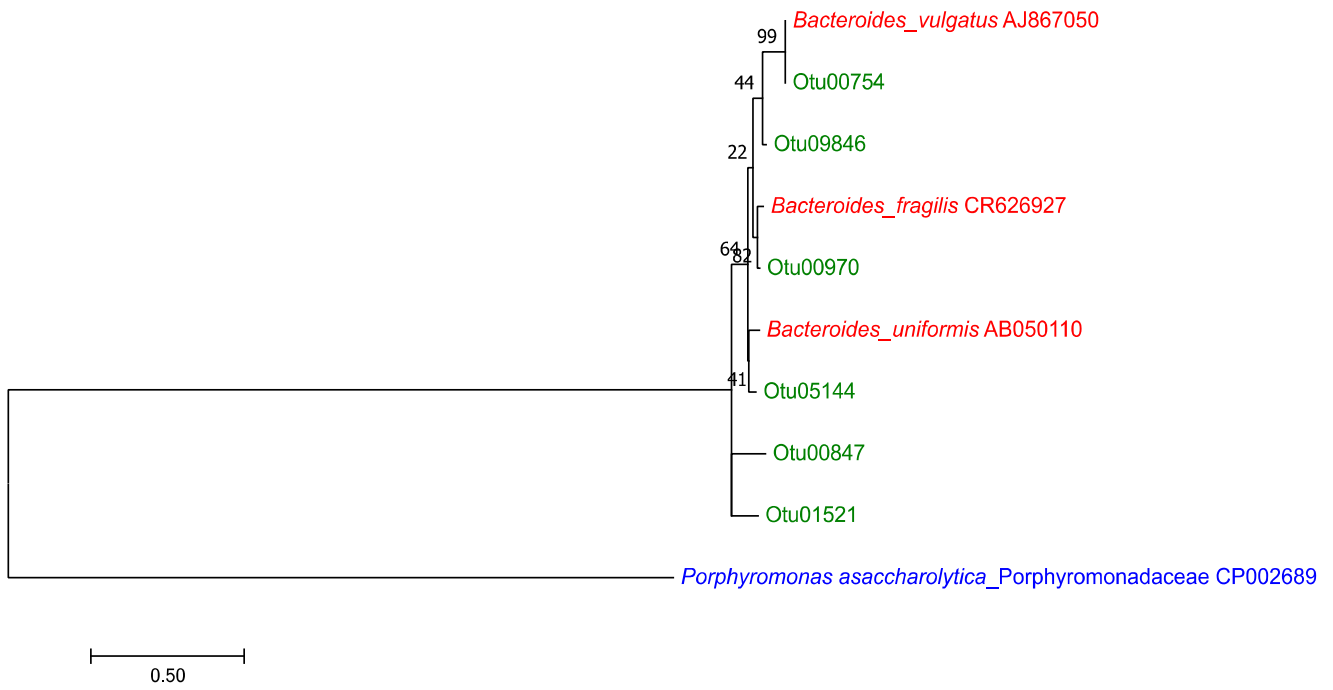


Figure 6.11 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Bacteroidaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

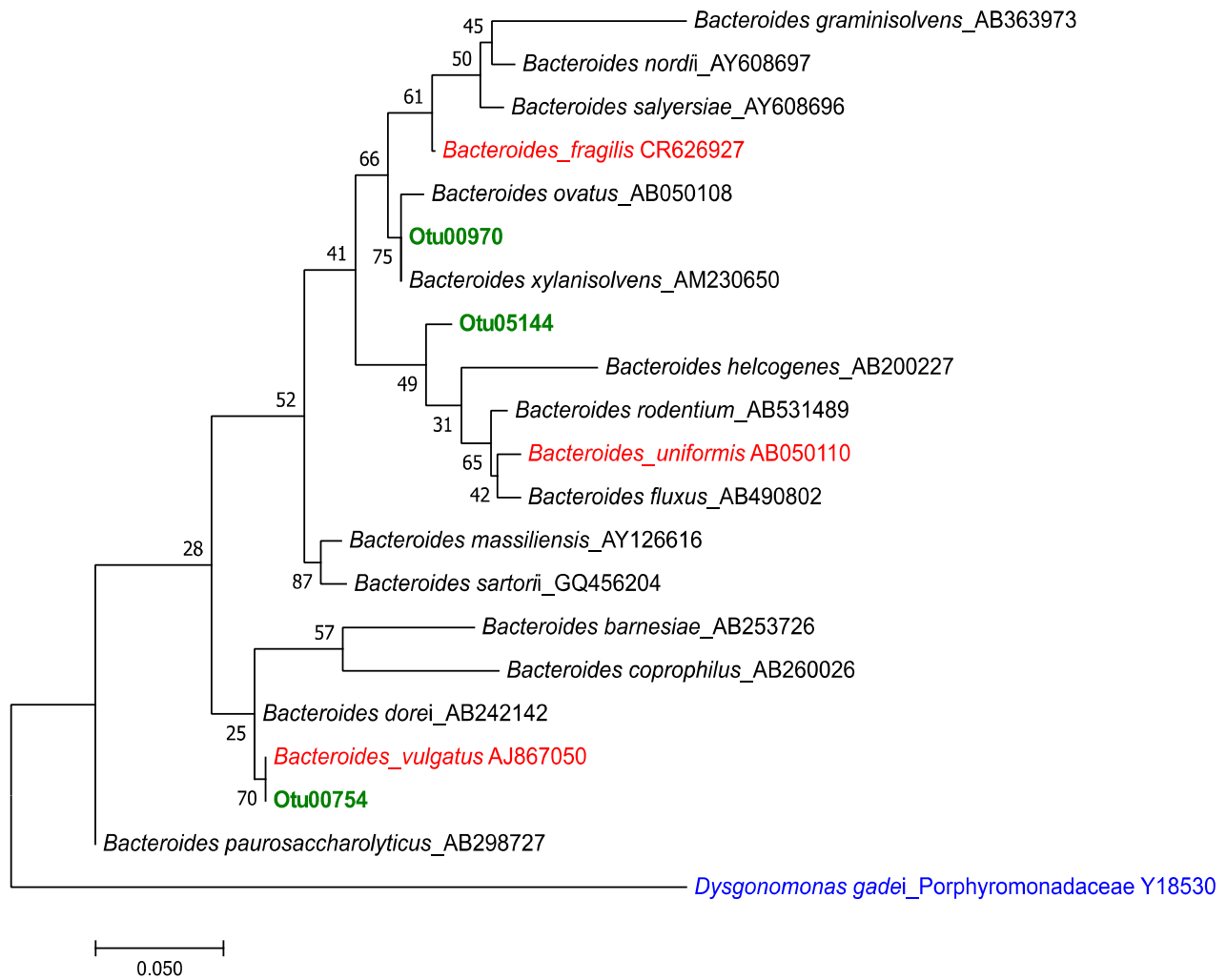


Figure 6.11 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Bacteroidaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

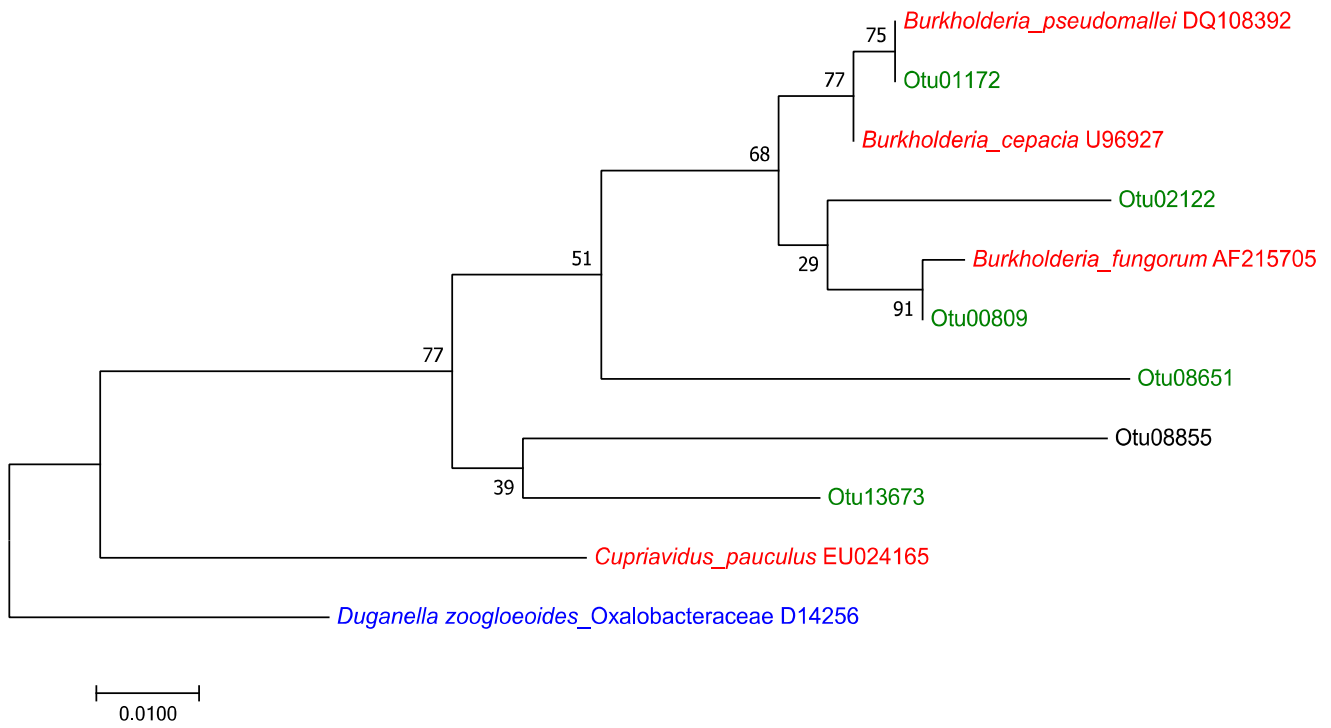


Figure 6.12 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Burkholderiaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

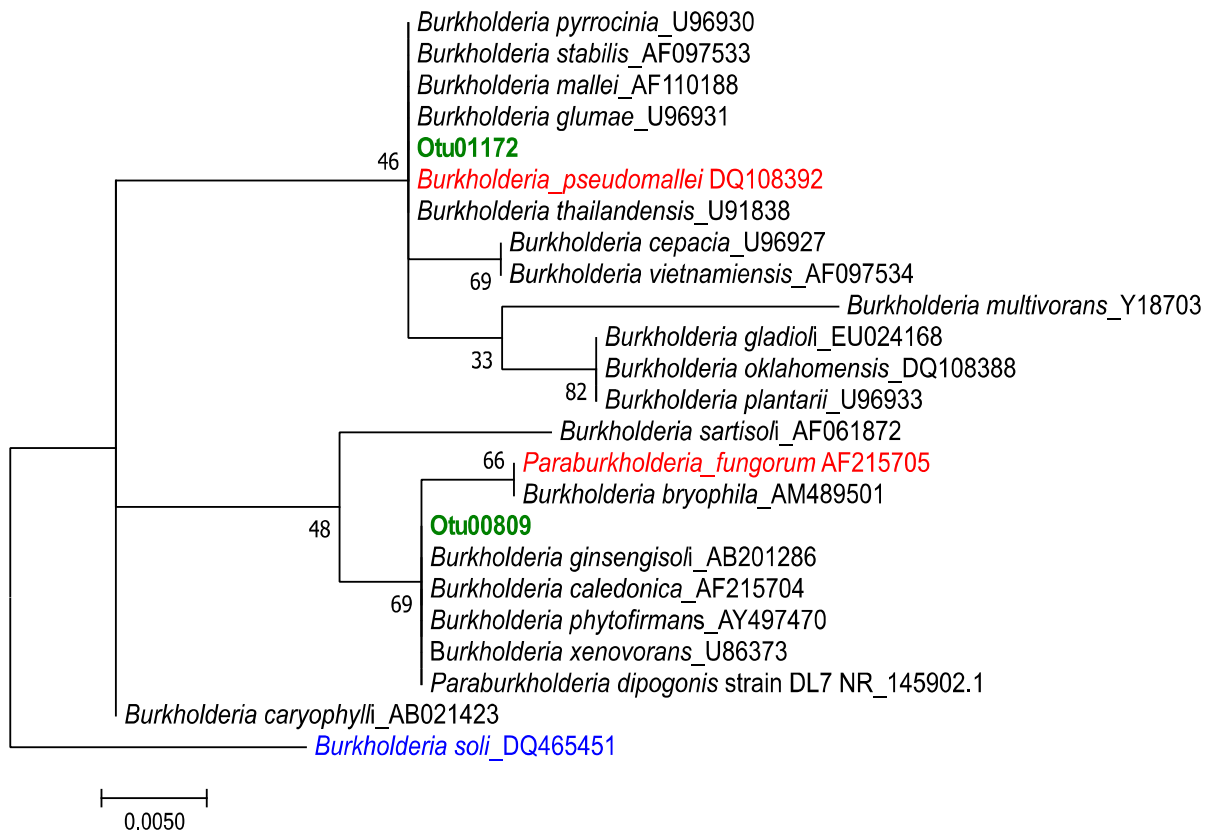


Figure 6.12 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Burkholderiaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

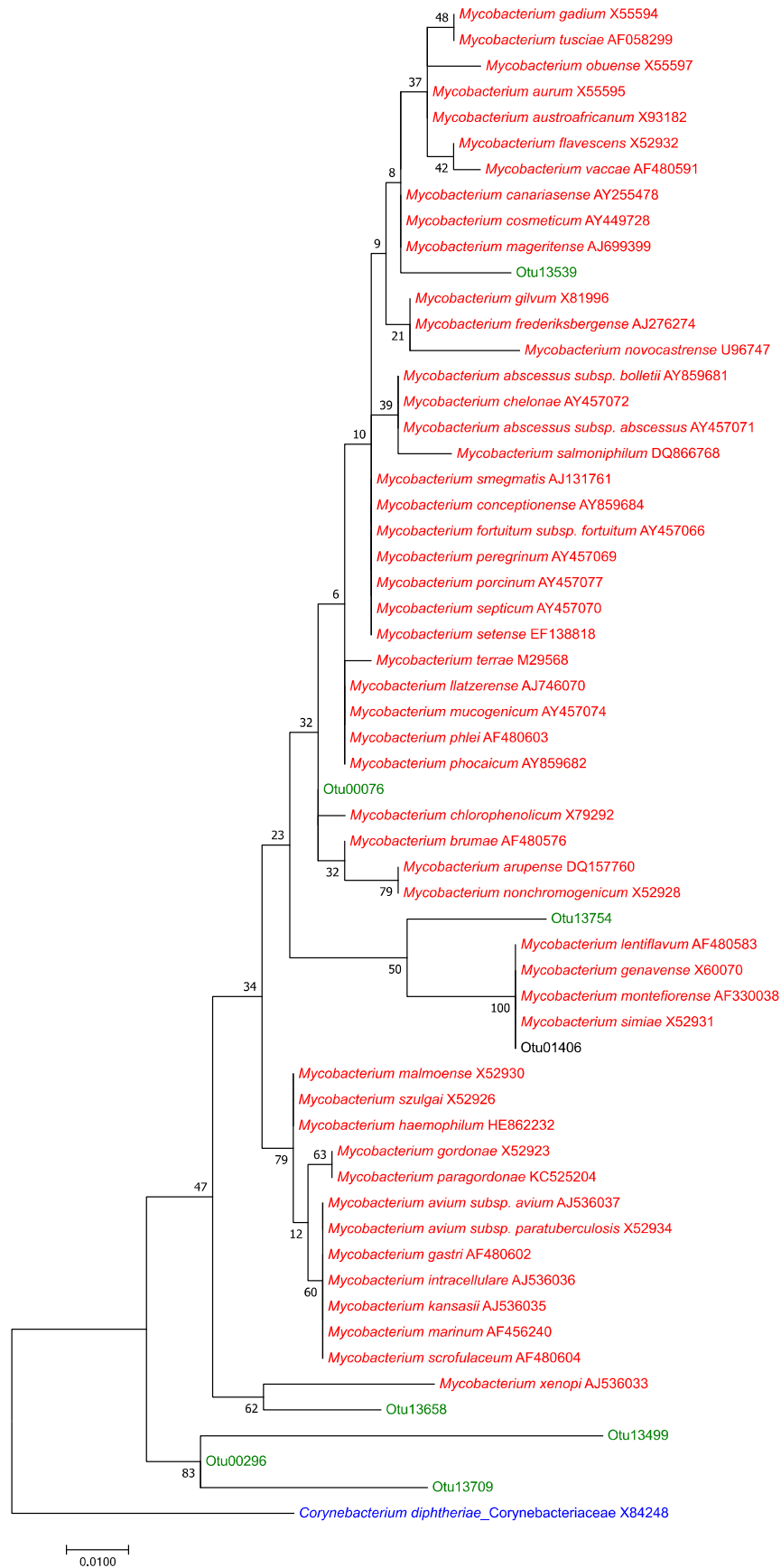


Figure 6.13 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Mycobacteriaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

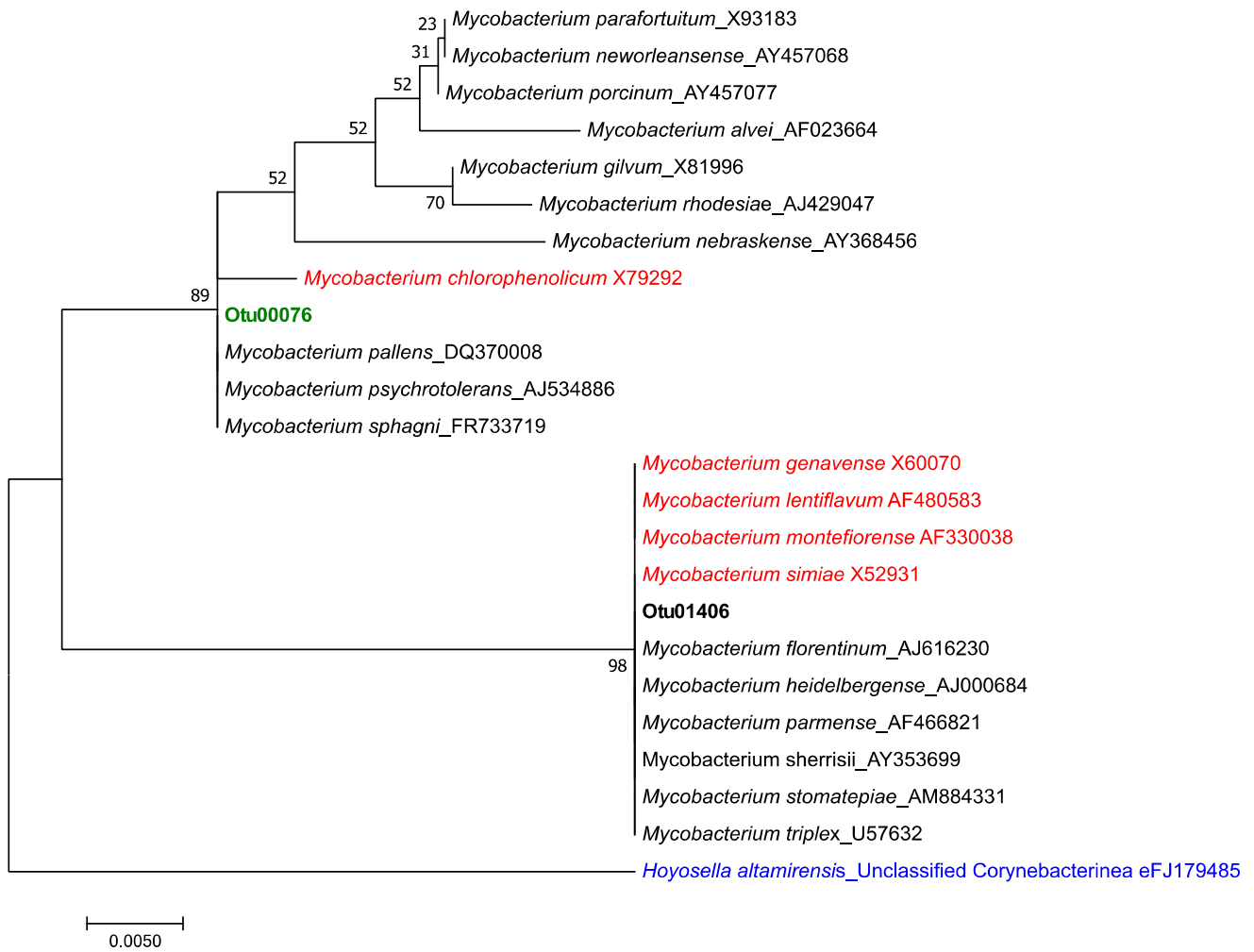


Figure 6.13 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Mycobacteriaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

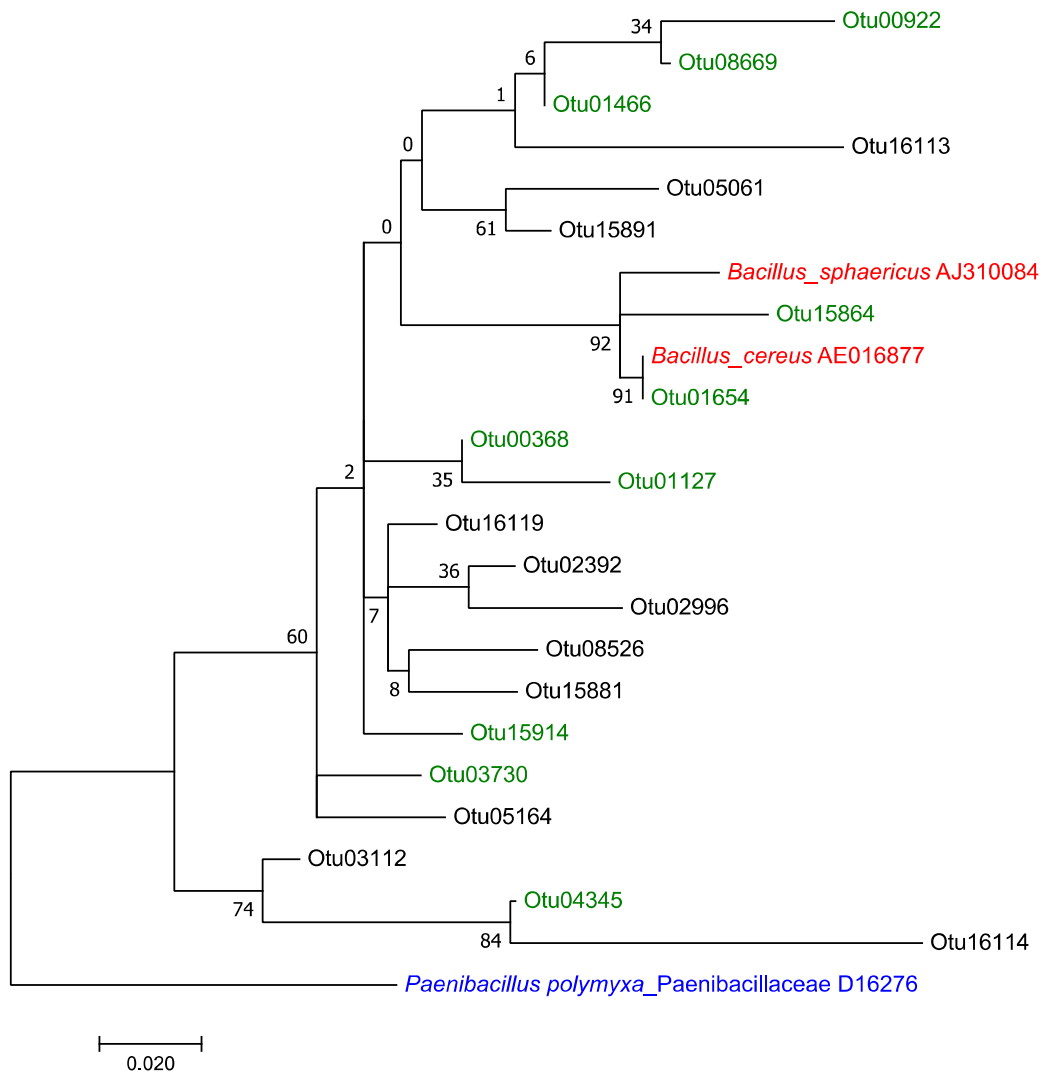


Figure 6.14 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Bacillaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

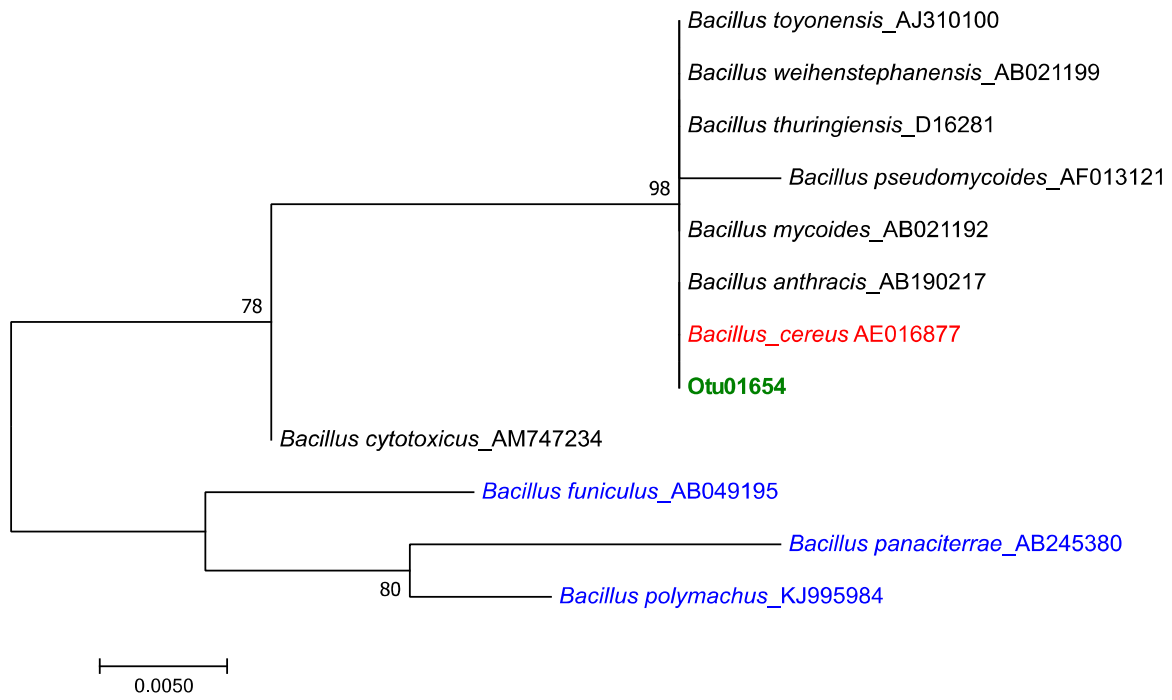


Figure 6.14 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Bacillaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

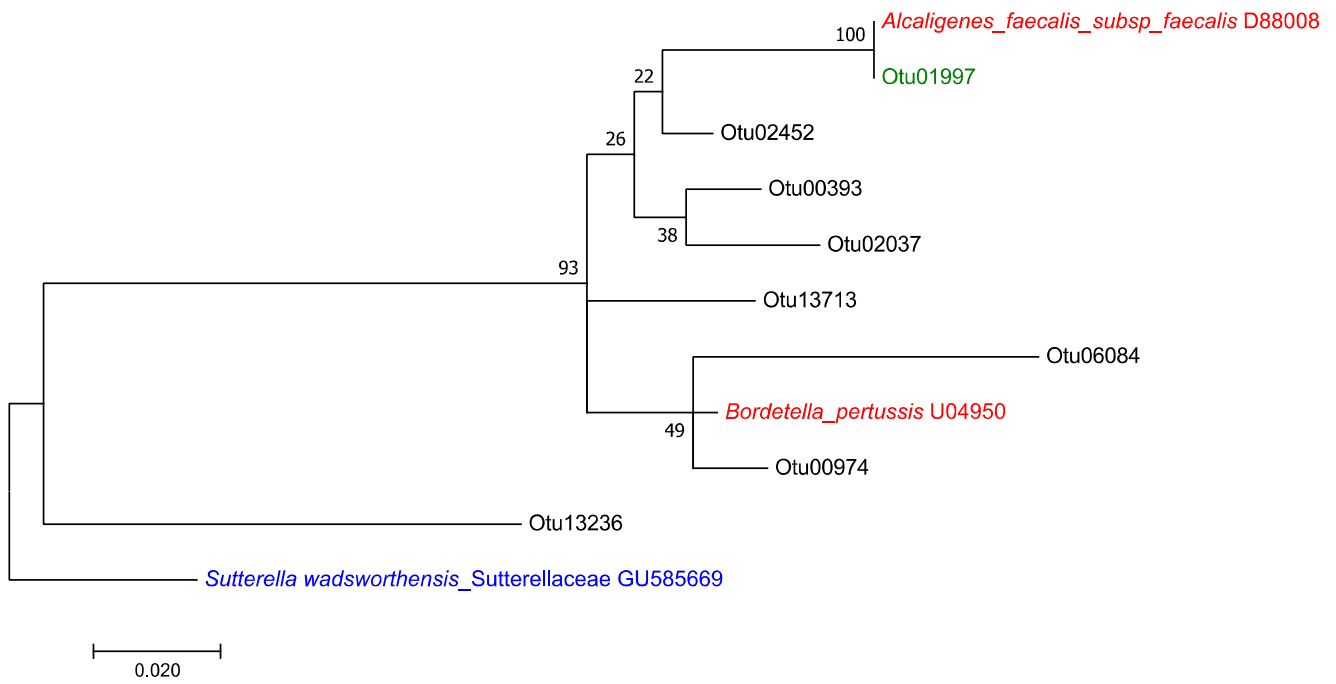


Figure 6.15 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Alcaligenaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

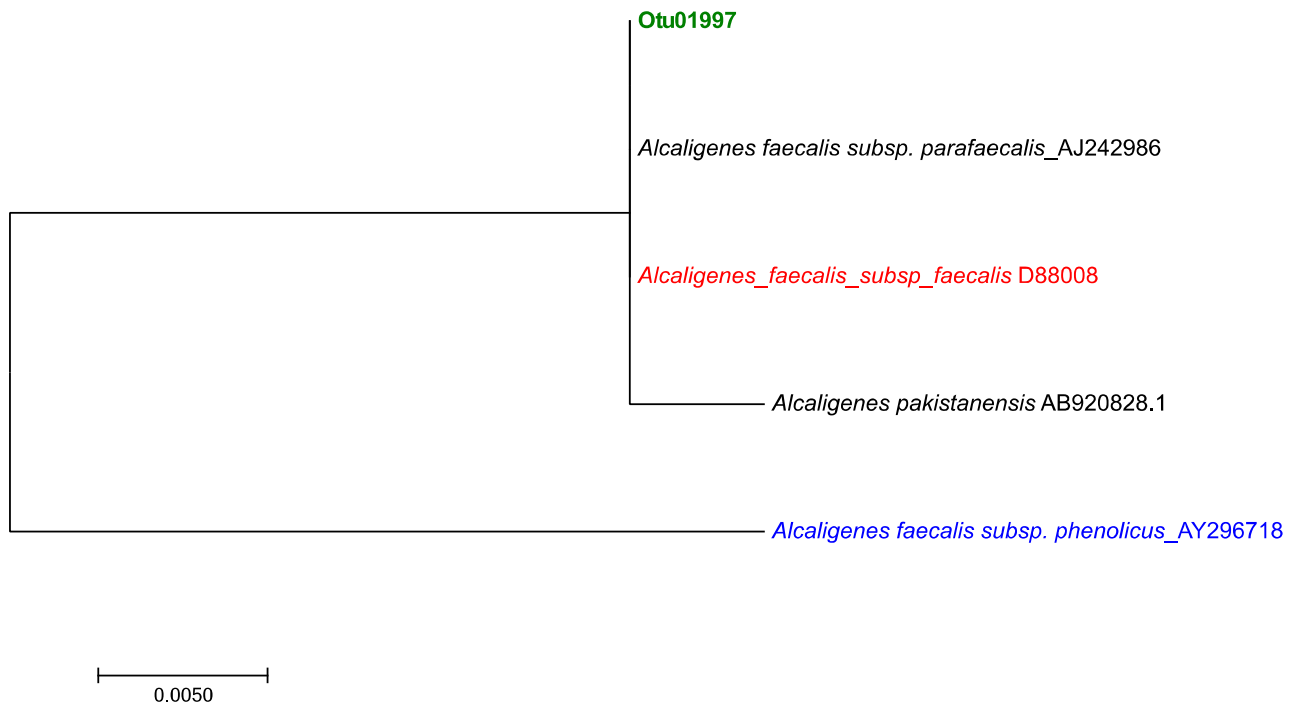
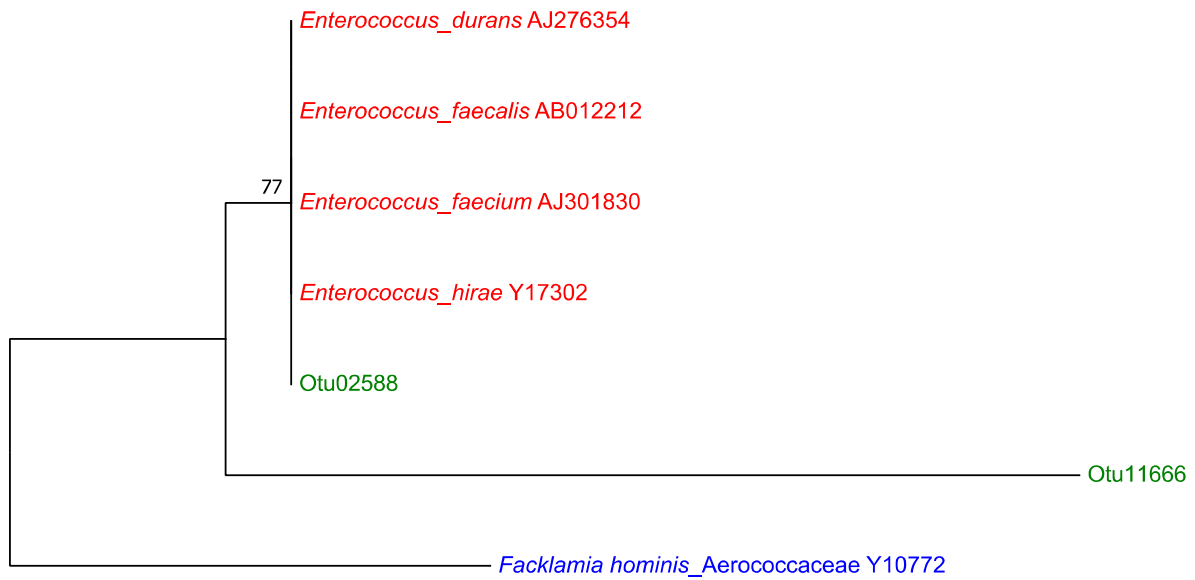


Figure 6.15 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Alcaligenaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.



0.0050

Figure 6.16 (A) Maximum likelihood tree representing potentially pathogenic OTUs within the family *Enterococcaceae*. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

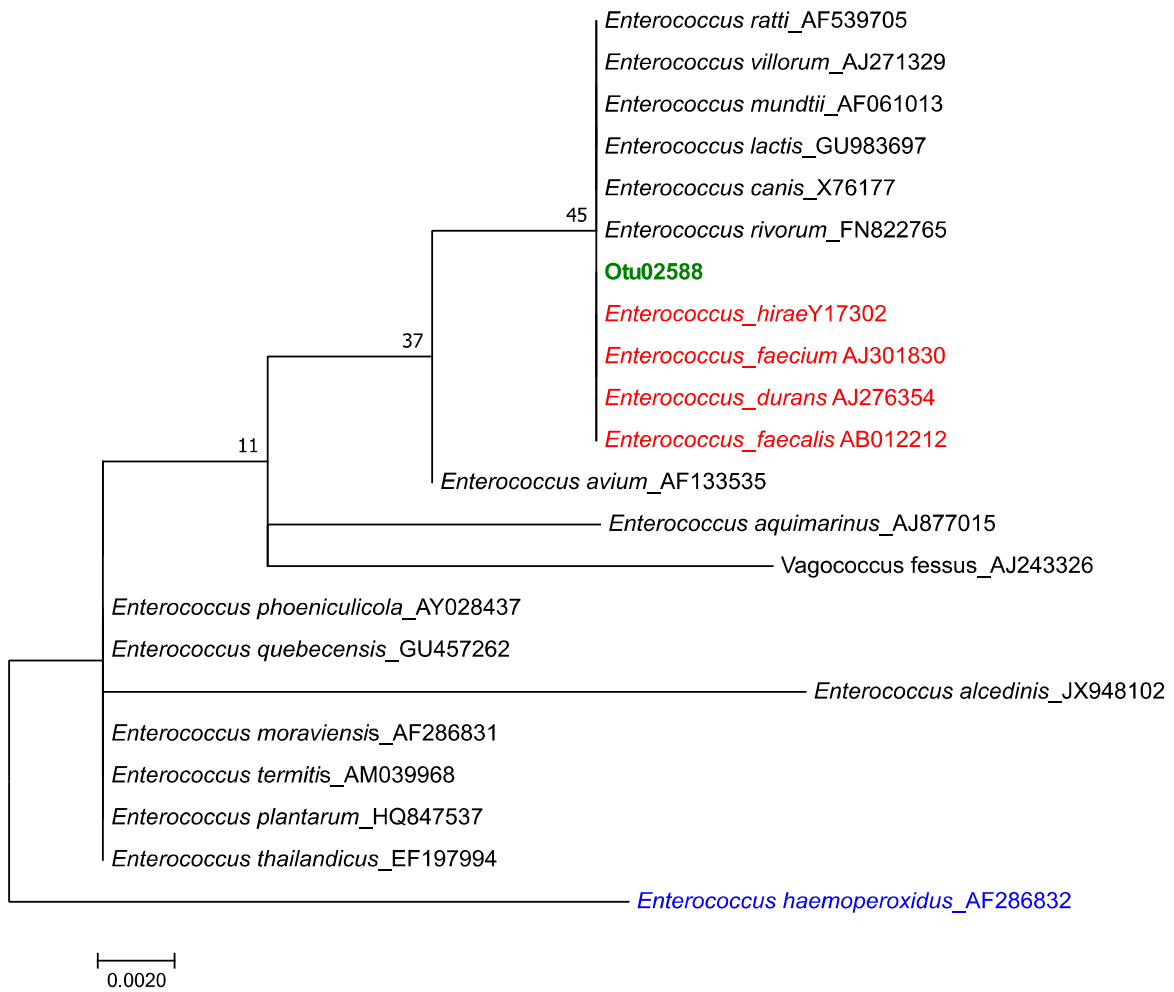


Figure 6.16 (B) Maximum likelihood tree representing the potentially pathogenic OTU compared to both the potential pathogenic species as well as other non-pathogenic related species of the family Enterococcaceae. Values indicated are representative of 100 bootstrap replicates. The pathogenic bacterial strains are shown in red, OTUs classified up to the genus level (within the family) are shown in green and the outgroup is shown in blue.

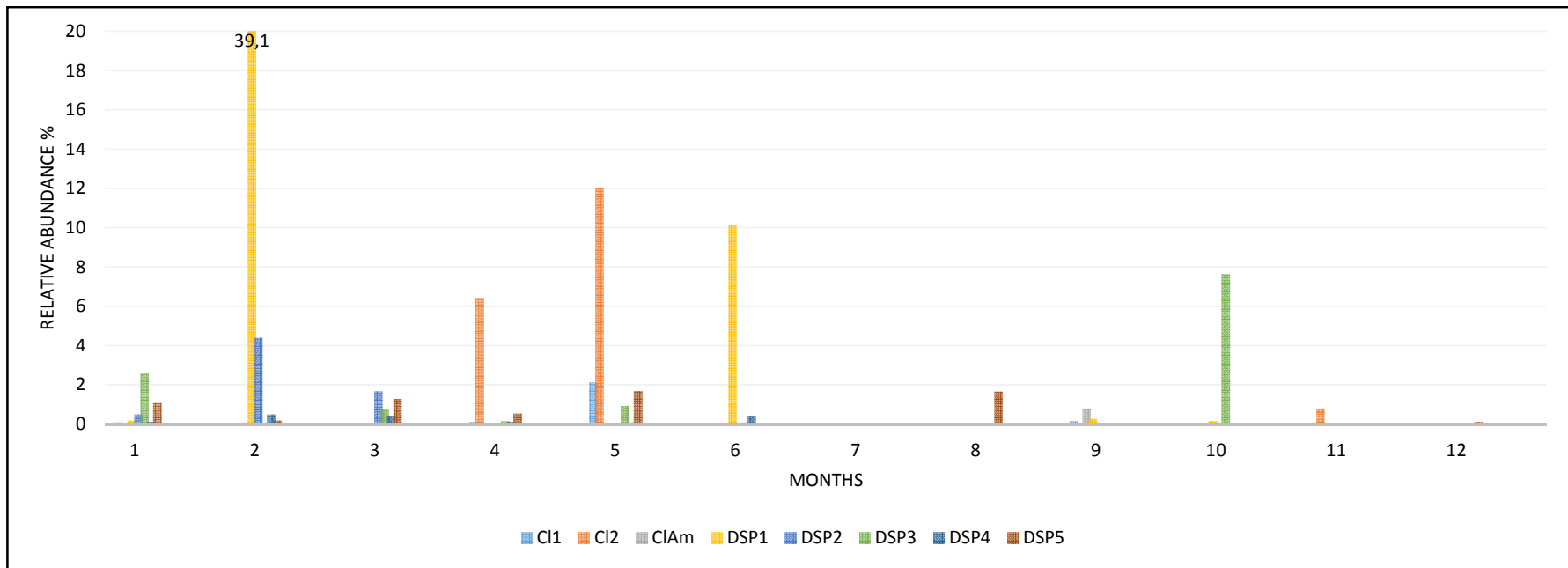


Figure 6.17 Relative abundance graph representing OTU00039 potentially *Novosphingobium aromaticivorans* across different months and sampling points.

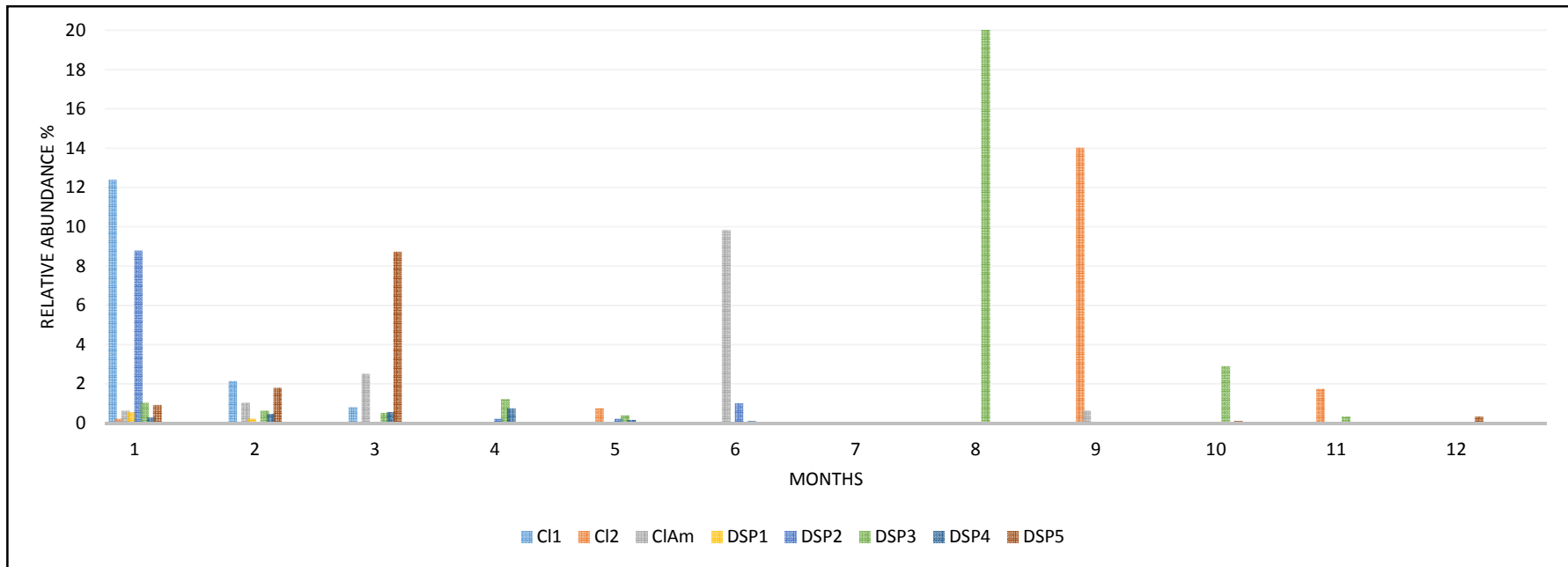


Figure 6.18 Relative abundance graph representing OTU00094 potentially *Aeromonas caviae*/ *Aeromonas veronii*/ *Aeromonas hydrophila subsp. hydrophila*/ *Aeromonas jandaei* across different months and sampling points.

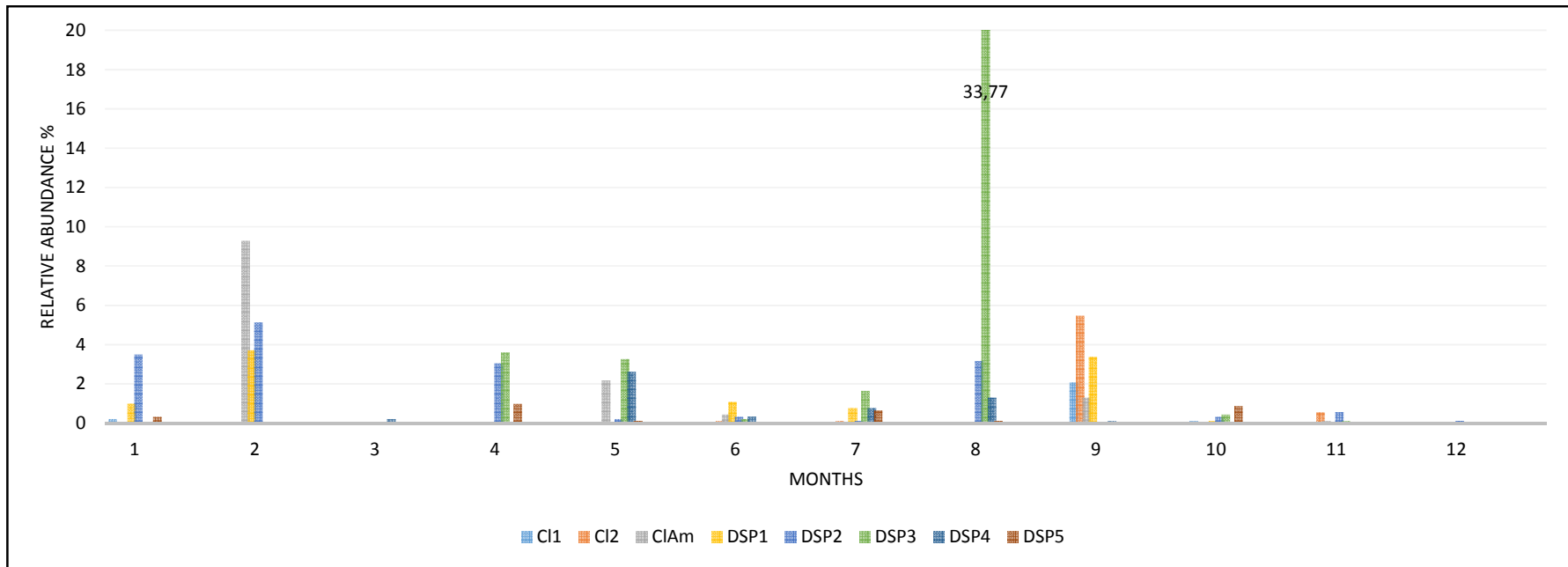


Figure 6.19 Relative abundance graph representing OTU00108 potentially *Staphylococcus warneri*/ *Staphylococcus lugdunensis*/ *Staphylococcus epidermidis*/ *Staphylococcus capitis subsp. capitis*/ *Staphylococcus aureus subsp. aureus* across different months and sampling points.

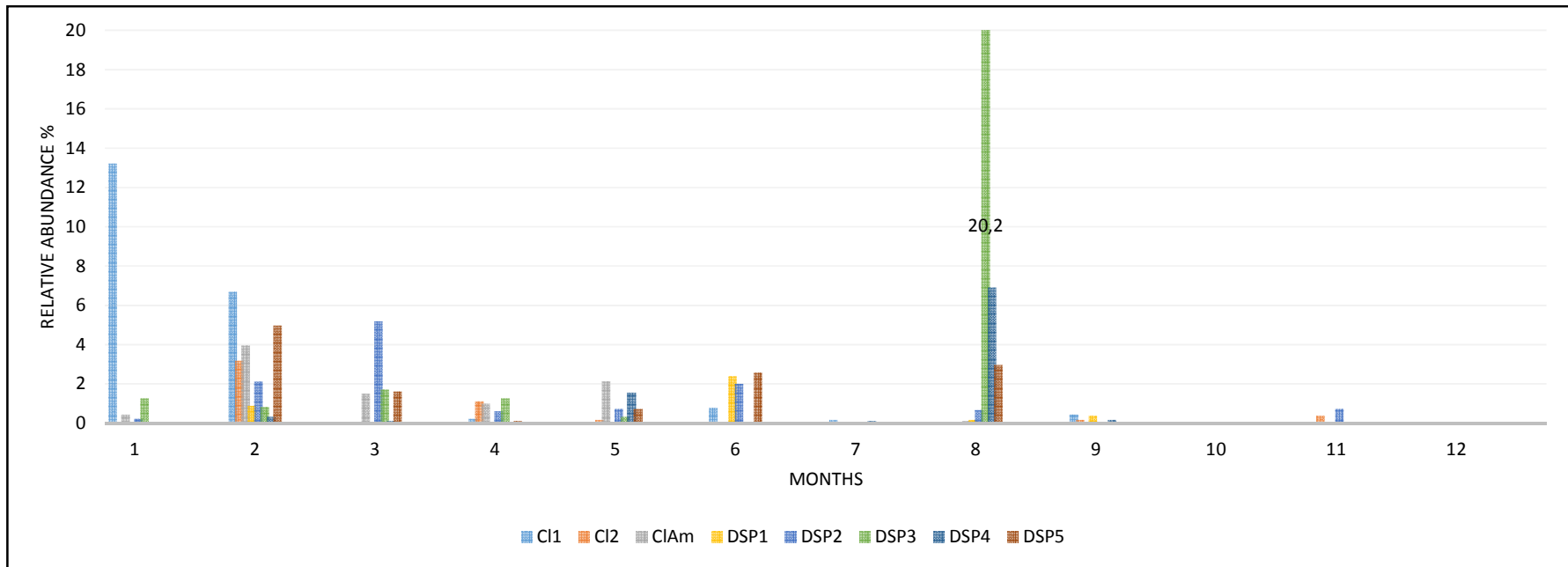


Figure 6.20 Relative abundance graph representing OTU00136 potentially *Escherichia coli*/ *Escherichia fergusonii*/ *Shigella sonnei*/ *Shigella flexneri* across different months and sampling points.

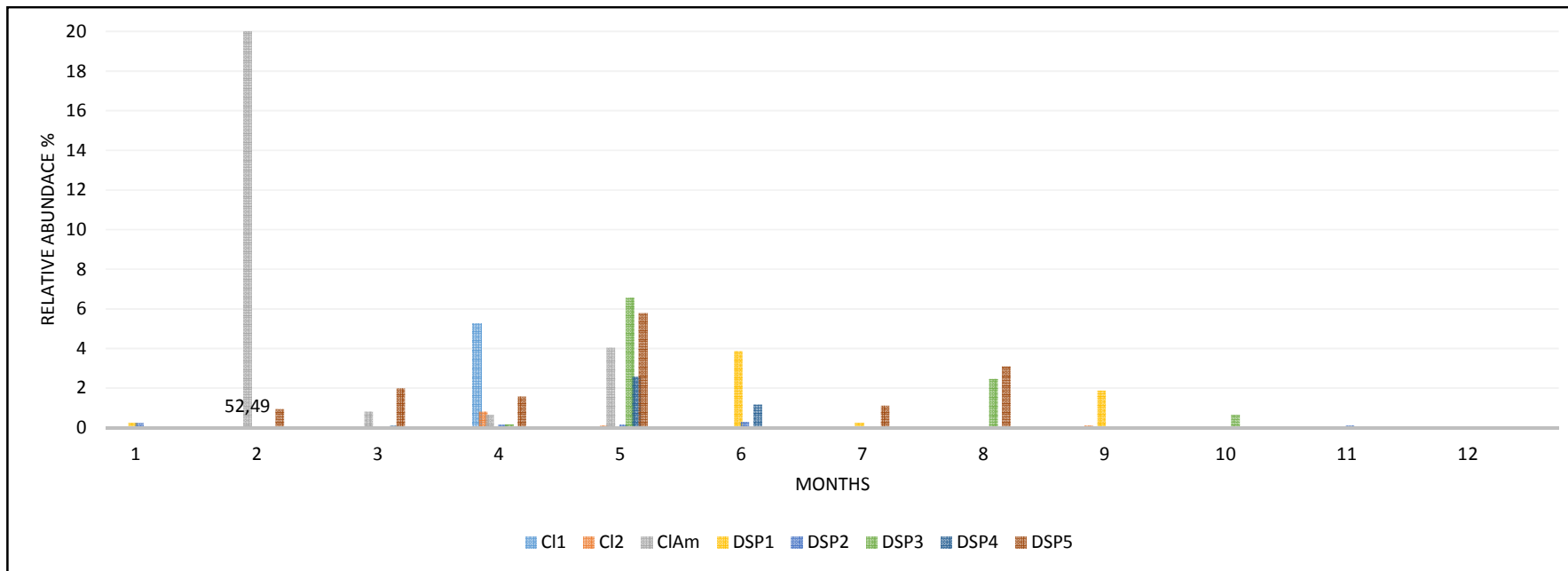


Figure 6.21 Relative abundance graph representing OTU00150 potentially *Methylobacterium radiotolerans*/ *Methylobacterium mesophilicum* across different months and sampling points.

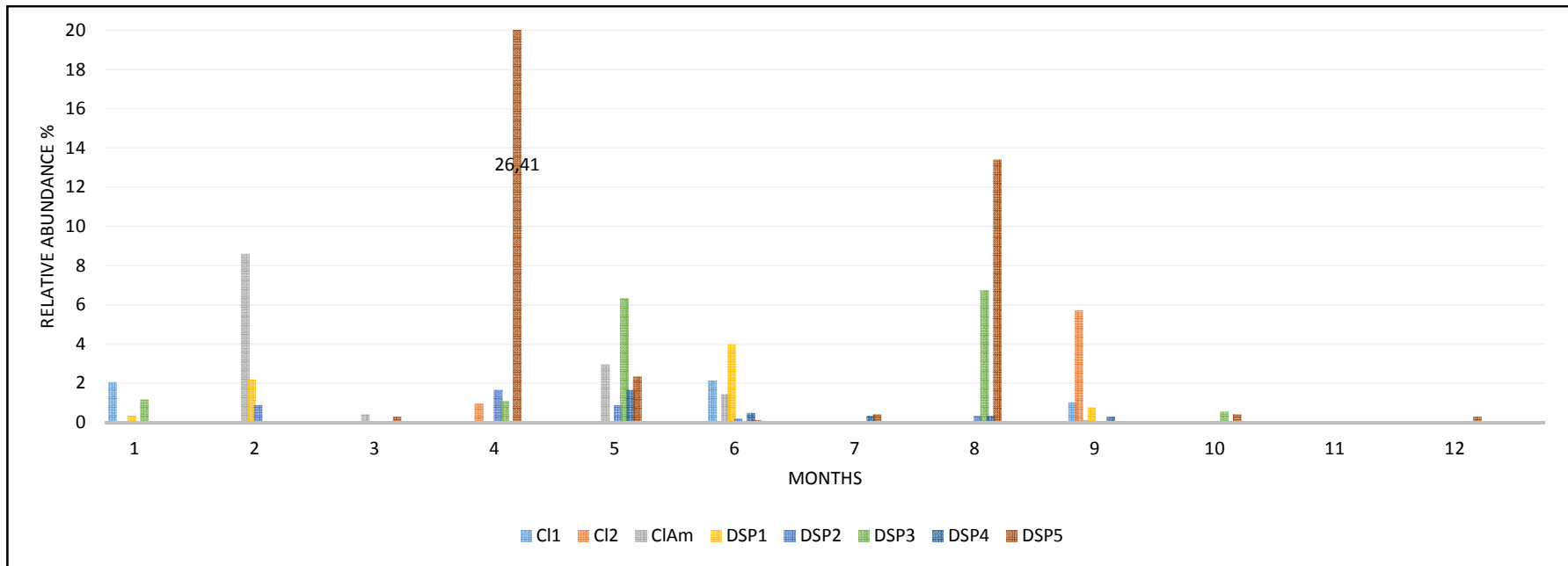


Figure 6.22 Relative abundance graph representing OTU00168 potentially *Streptococcus parasanguinis* across different months and sampling points.

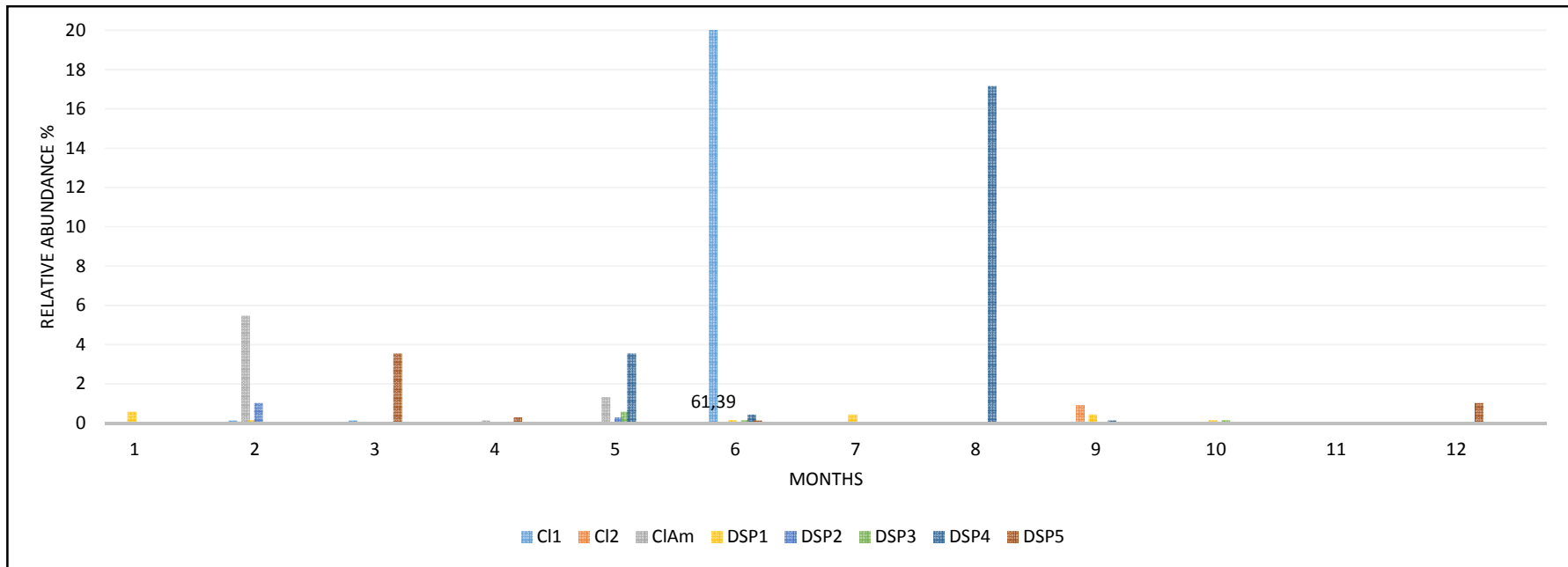


Figure 6.23 Relative abundance graph representing OTU00250 potentially *Klebsiella pneumoniae subsp. pneumoniae*/ *Enterobacter aerogenes*/ *Enterobacter asburiae*/ *Enterobacter cancerogenus*/ *Enterobacter hormaechei*/ *Enterobacter intermedius* across different months and sampling points.

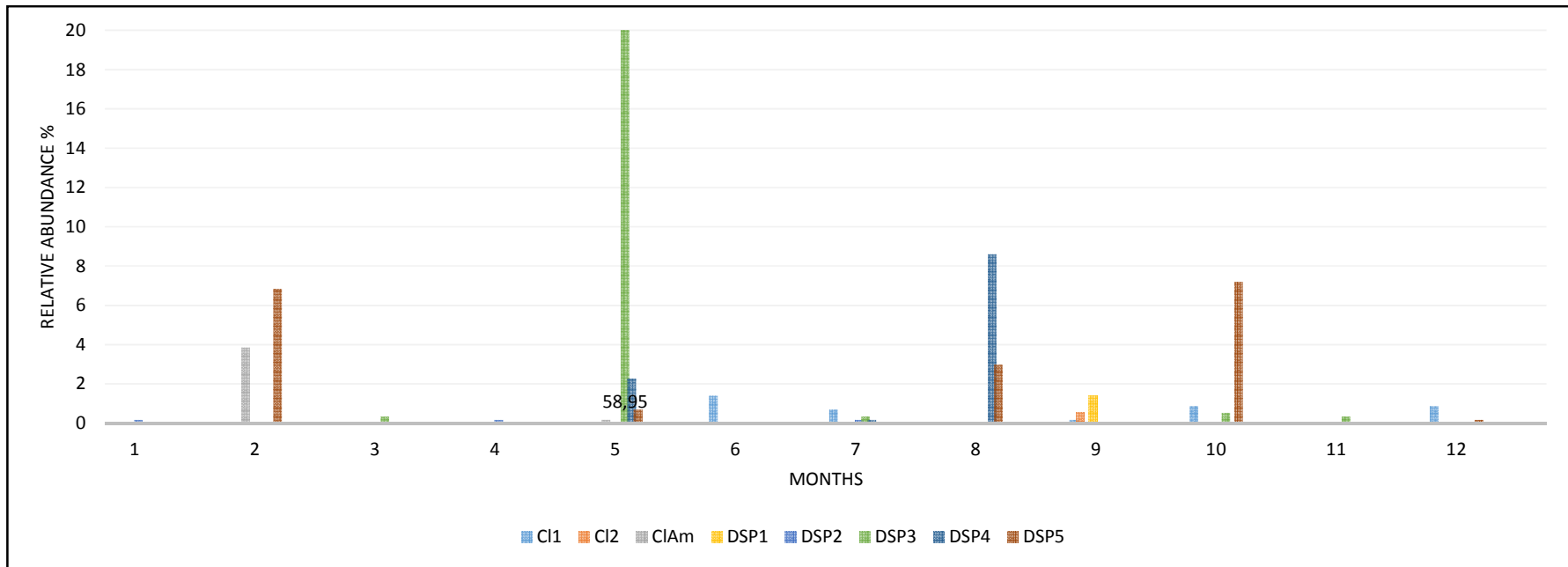


Figure 6.24 Relative abundance graph representing OTU00282 potentially *Moraxella osloensis* across different months and sampling points.

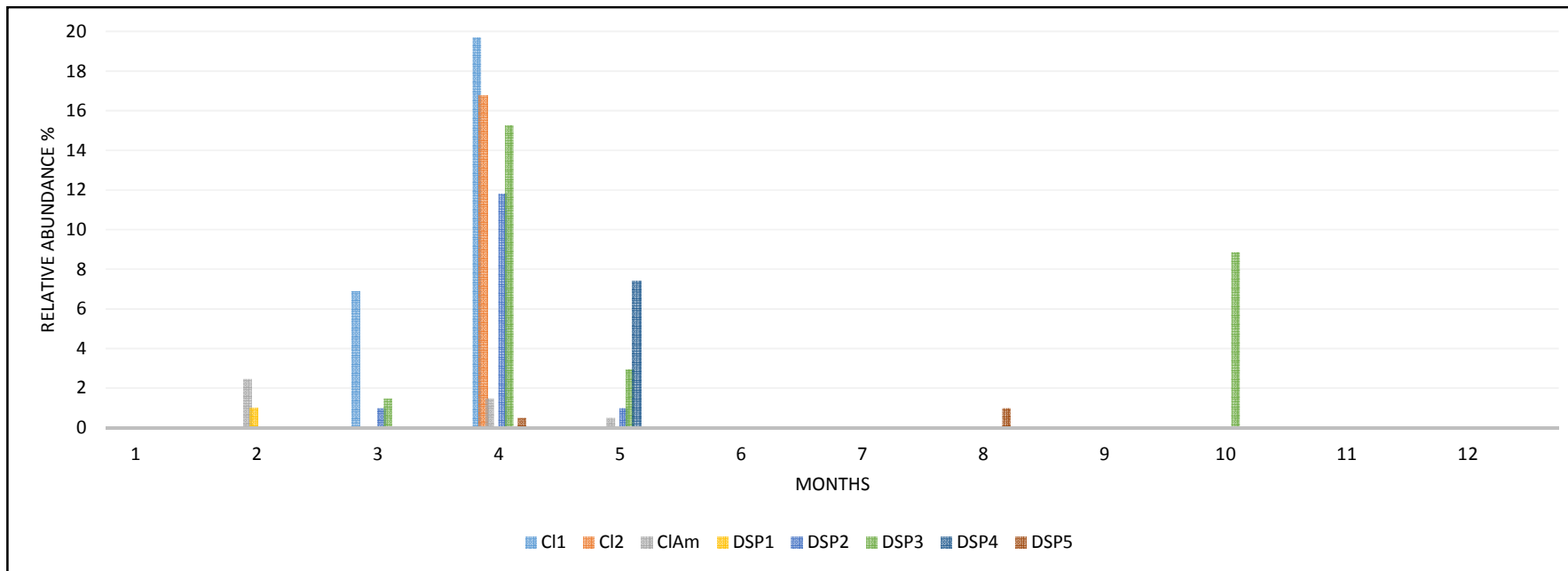


Figure 6.25 Relative abundance graph representing OTU00479 potentially *Methylobacterium aminovorans* across different months and sampling points.

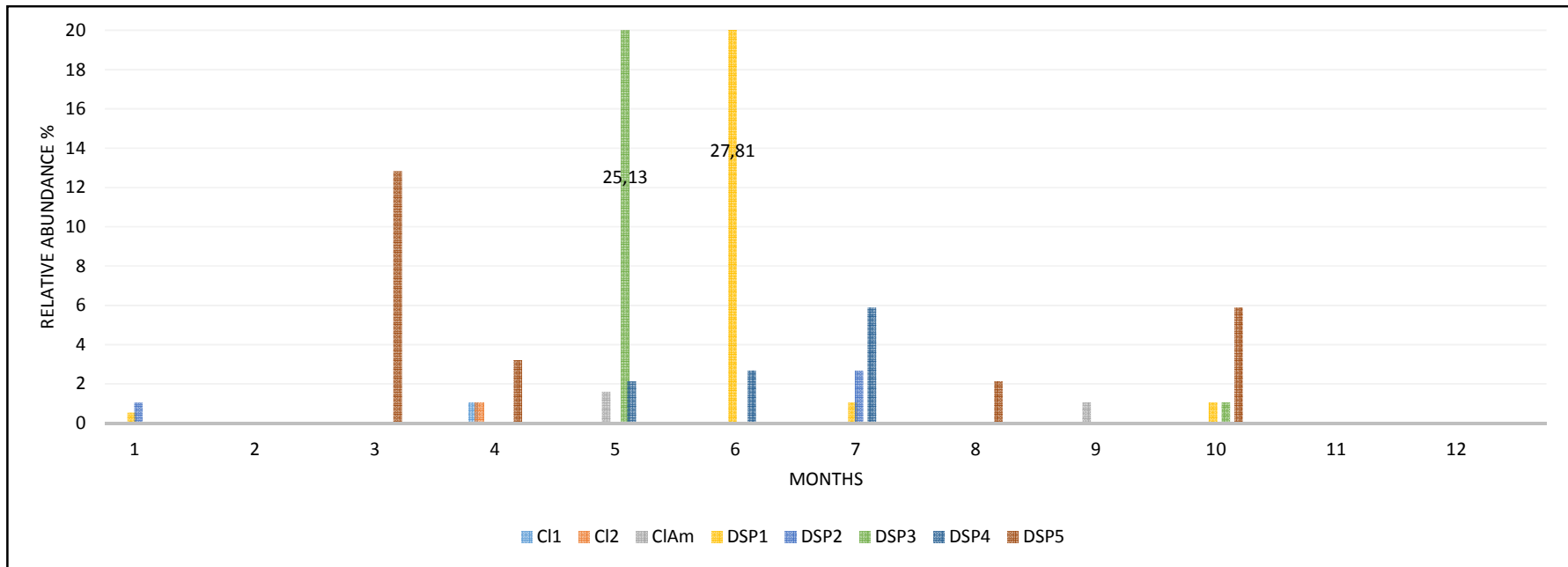


Figure 6.26 Relative abundance graph representing OTU00517 potentially *Corynebacterium tuberculostearicum* across different months and sampling points.

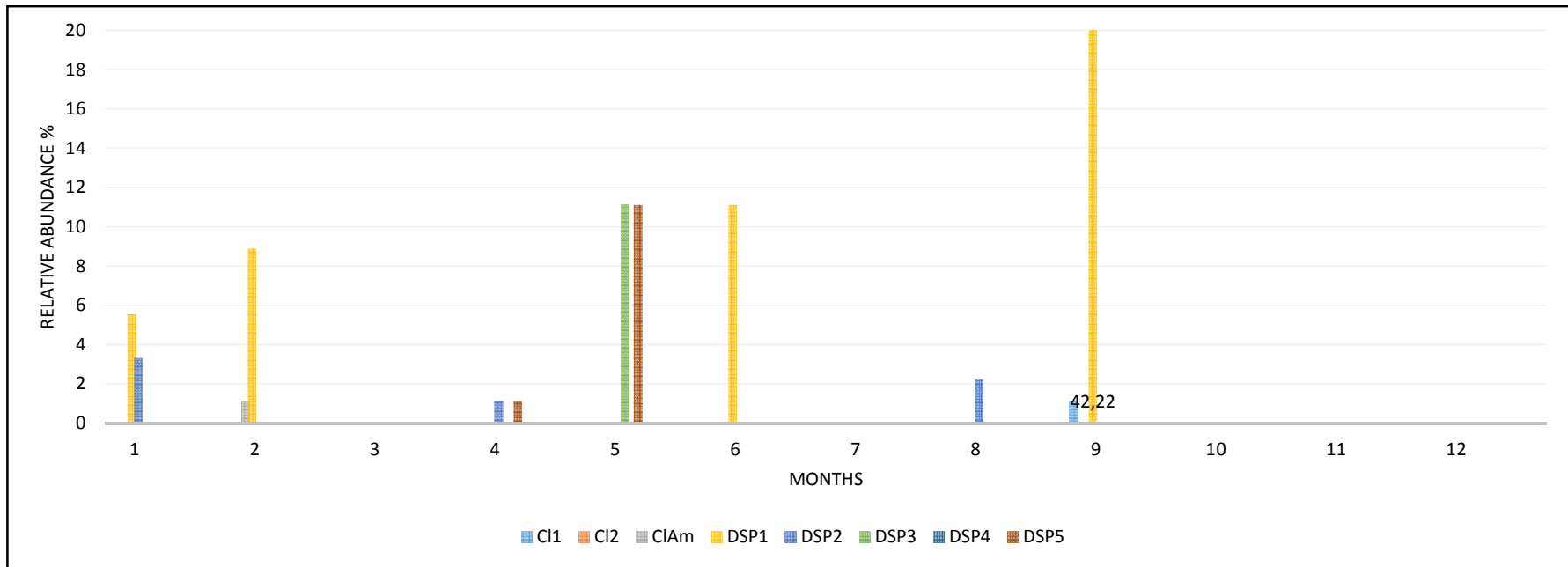


Figure 6.27 Relative abundance graph representing OTU00747 potentially *Micrococcus luteus* across different months and sampling points.

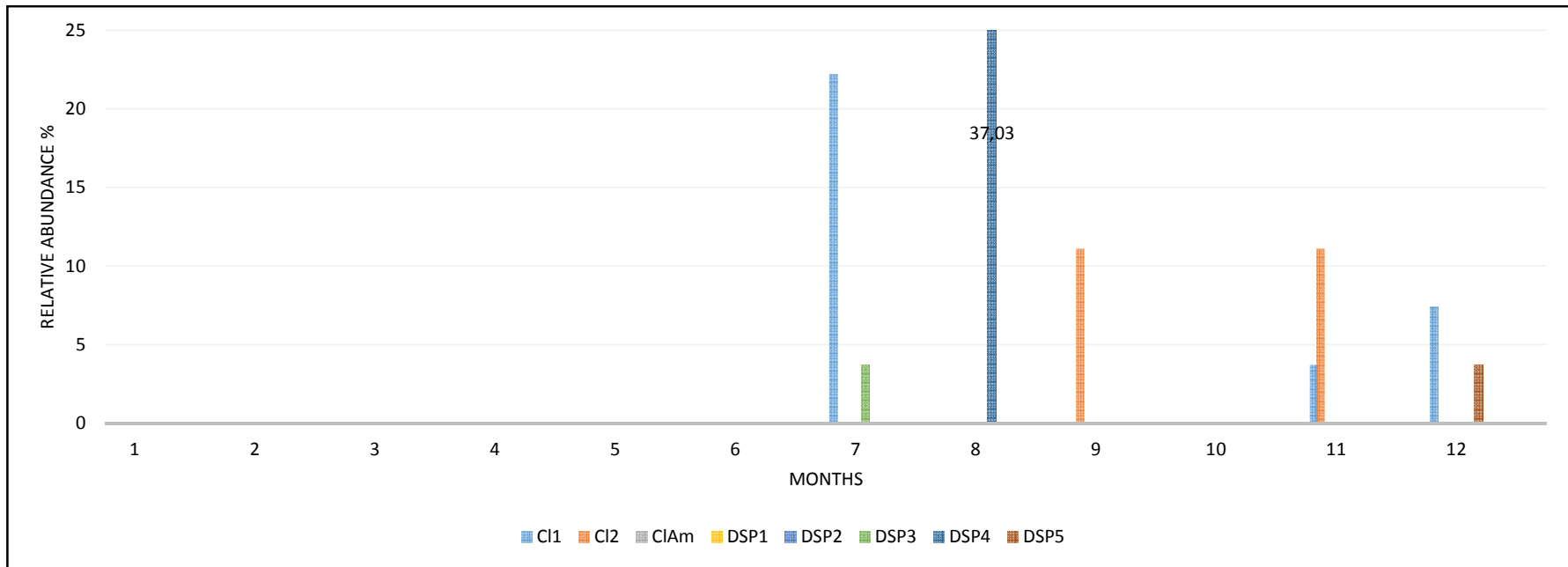


Figure 6.28 Relative abundance graph representing OTU01172 potentially *Burkholderia pseudomallei* across different months and sampling points.

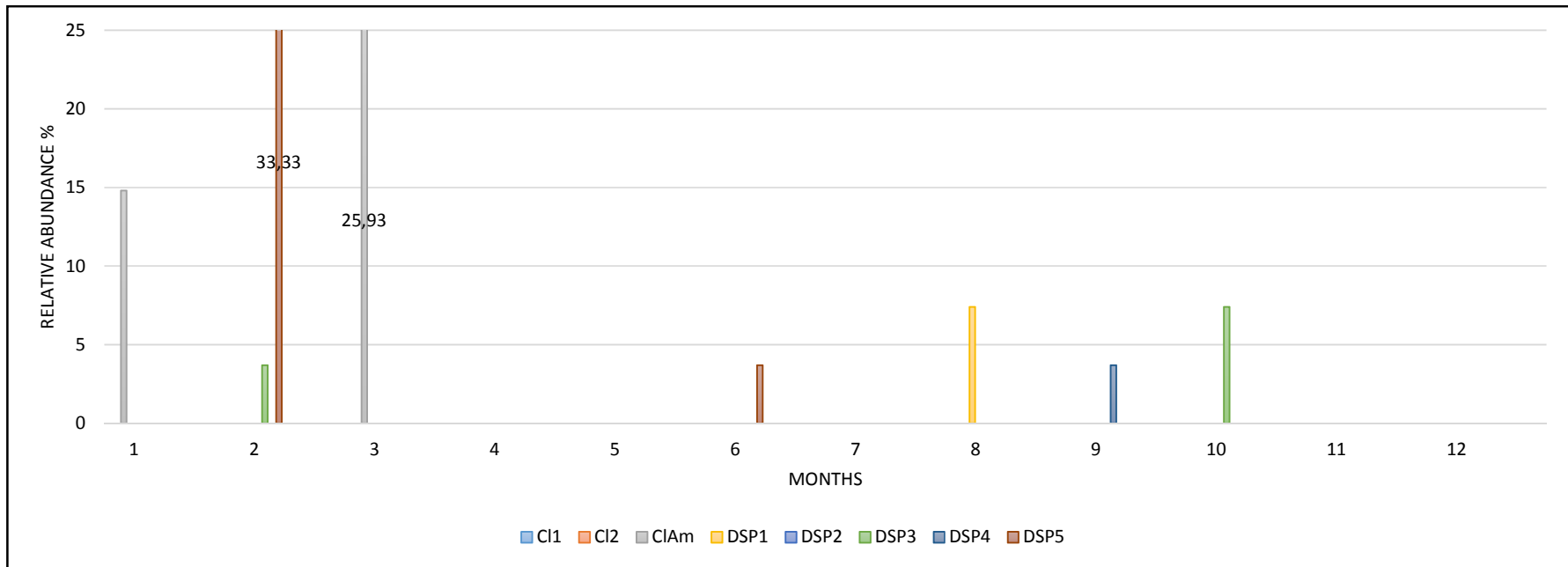


Figure 6.29 Relative abundance graph representing OTU01284 potentially *Yersinia enterocolitica subsp. enterocolitica*/ *Serratia liquefaciens*/ *Serratia plymuthica* across different months and sampling points.

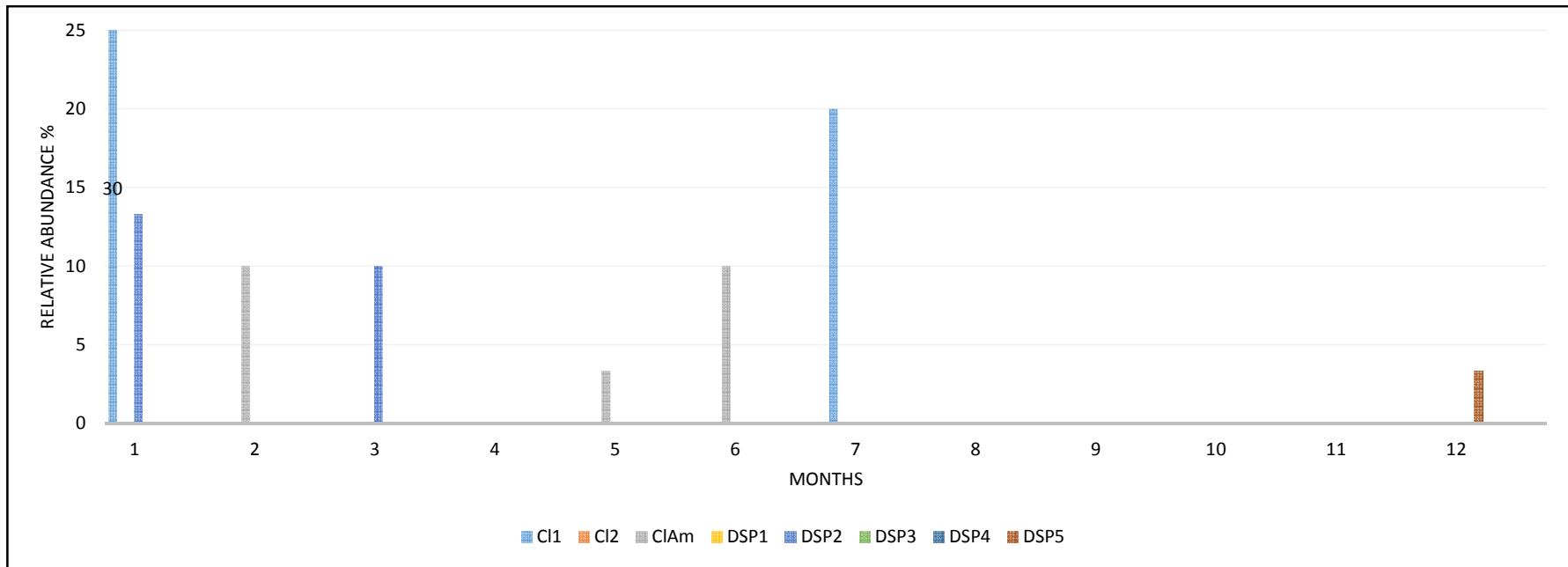


Figure 6.30 Relative abundance graph representing OTU01406 potentially *Mycobacterium lentiflavum*/ *Mycobacterium genavense*/ *Mycobacterium montefiorensis*/ *Mycobacterium simiae* across different months and points sampled.

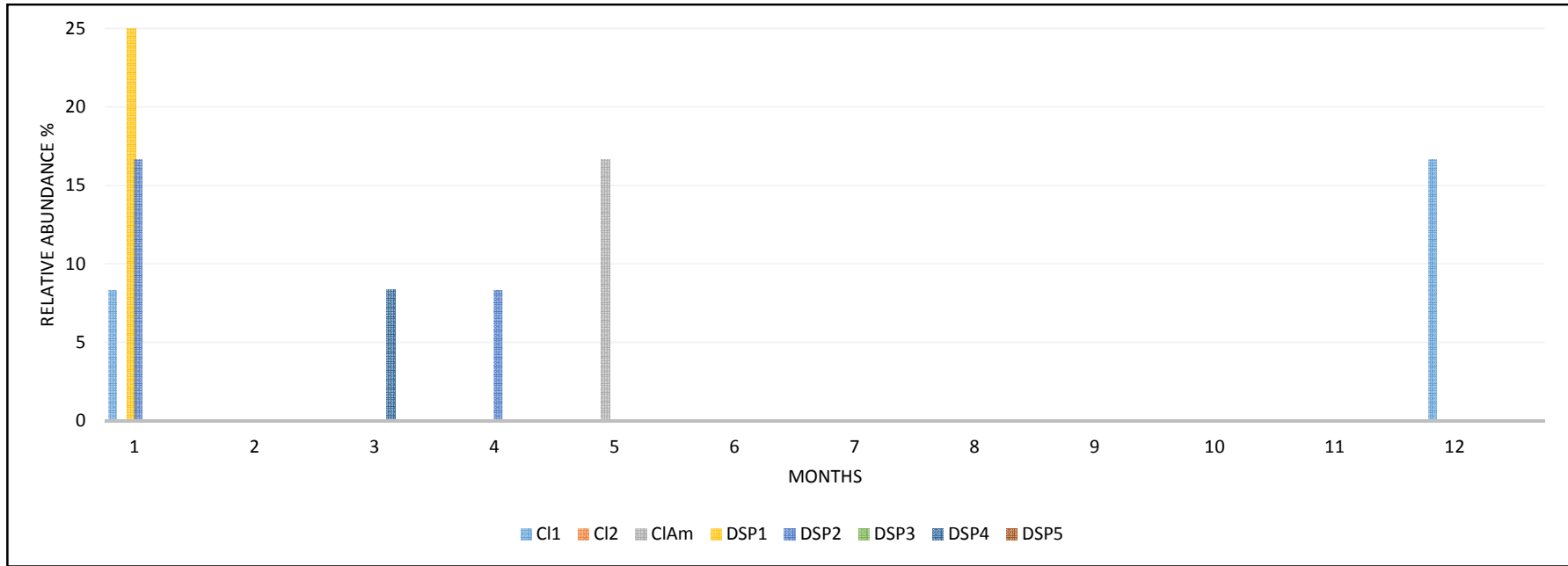


Figure 6.31 Relative abundance graph representing OTU01654 potentially *Bacillus cereus* across different months and sampling points.

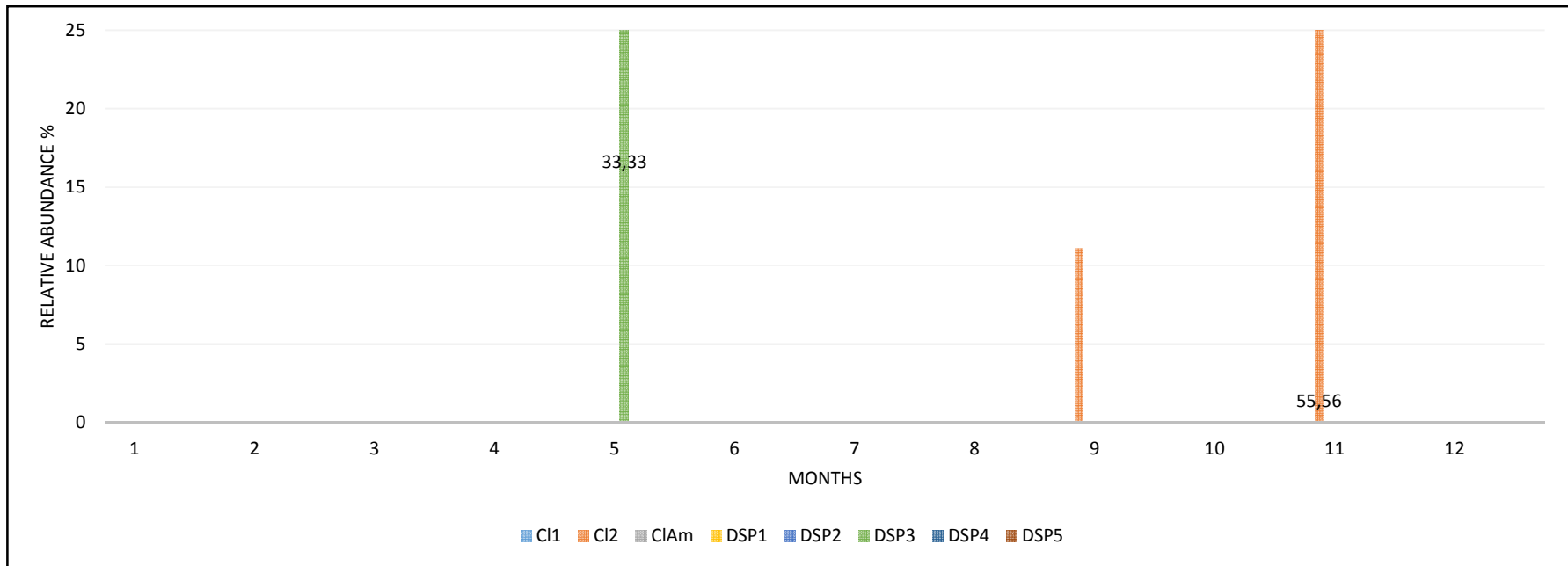


Figure 6.32 Relative abundance graph representing OTU01997 potentially *Alcaligenes faecalis subsp. faecalis* across different months and sampling points.

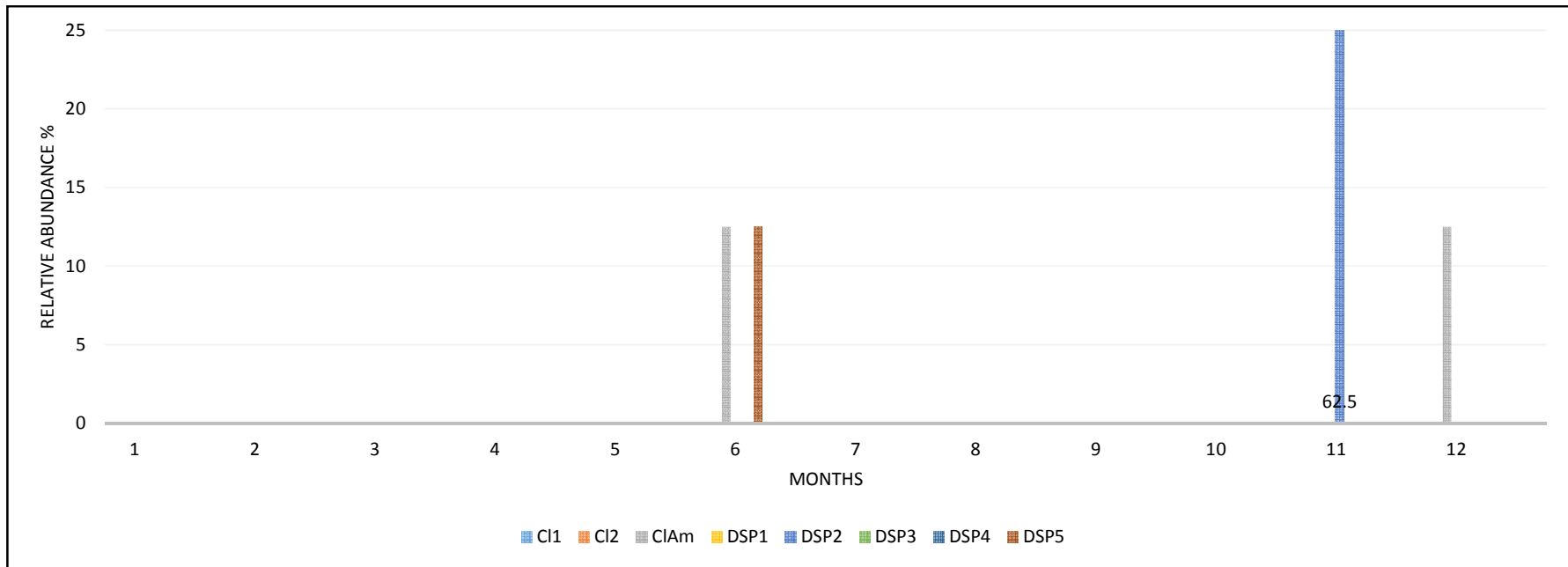


Figure 6.33 Relative abundance graph representing OTU02588 potentially *Enterococcus durans*/ *Enterococcus faecalis*/ *Enterococcus faecium*/ *Enterococcus hirae* across different months and sampling points.

APPENDIX A: SUPPLEMENTARY DATA FOR CHAPTER 3

Table A1 Sample database

Number	PS	RS filter	Location ^a	Month ^b	Study name ^c
1	PS1	RS filter 46	Surface 1	May	PS1_RS F46_S1_MAY_FB1
2	PS1	RS filter 46	Surface 2	May	PS1_RS F46_S2_MAY_FB2
3	PS1	RS filter 46	Surface 3	May	PS1_RS F46_S3_MAY_FB3
4	PS1	RS filter 46	Surface 4	May	PS1_RS F46_S4_MAY_FB4
5	PS1	RS filter 46	Surface 5	May	PS1_RS F46_S5_MAY_FB5
6	PS1	RS filter 46	Surface 6	May	PS1_RS F46_S6_MAY_FB6
7	PS1	RS filter 46	Surface 7	May	PS1_RS F46_S7_MAY_FB7
8	PS1	RS filter 46	Surface 8	May	PS1_RS F46_S8_MAY_FB8
9	PS1	RS filter 46	Surface 9	May	PS1_RS F46_S9_MAY_FB9
10	PS1	RS filter 49	Surface 5	May	PS1_RS F49_S5_MAY_FB10
11	PS1	RS filter 50	Surface 5	May	PS1_RS F50_S5_MAY_FB11
12	PS1	RS filter 46	Core 1	May	PS1_RS F46_C1_MAY_FB12
13	PS1	RS filter 46	Core 2	May	PS1_RS F46_C2_MAY_FB13
14	PS1	RS filter 46	Core 3	May	PS1_RS F46_C3_MAY_FB14
15	PS1	RS filter 46	Core 4	May	PS1_RS F46_C4_MAY_FB15
16	PS1	RS filter 46	Core 5	May	PS1_RS F46_C5_MAY_FB16
17	PS3	RS filter 93	Surface 1	May	PS3_RS F93_S1_MAY_FB17
18	PS3	RS filter 93	Surface 2	May	PS3_RS F93_S2_MAY_FB18
19	PS3	RS filter 93	Surface 3	May	PS3_RS F93_S3_MAY_FB19
20	PS3	RS filter 93	Surface 4	May	PS3_RS F93_S4_MAY_FB20
21	PS3	RS filter 93	Surface 5	May	PS3_RS F93_S5_MAY_FB21
22	PS3	RS filter 93	Surface 6	May	PS3_RS F93_S6_MAY_FB22
23	PS3	RS filter 93	Surface 7	May	PS3_RS F93_S7_MAY_FB23
24	PS3	RS filter 93	Surface 8	May	PS3_RS F93_S8_MAY_FB24
25	PS3	RS filter 93	Surface 9	May	PS3_RS F93_S9_MAY_FB25
26	PS3	RS filter 94	Surface 5	May	PS3_RS F93_S5_MAY_FB26
27	PS3	RS filter 95	Surface 5	May	PS3_RS F93_S5_MAY_FB27
28	PS3	RS filter 93	Core 1	May	PS3_RS F93_C1_MAY_FB28
29	PS3	RS filter 93	Core 2	May	PS3_RS F93_C2_MAY_FB29
30	PS3	RS filter 93	Core 3	May	PS3_RS F93_C3_MAY_FB30
31	PS3	RS filter 93	Core 4	May	PS3_RS F93_C4_MAY_FB31
32	PS3	RS filter 93	Core 5	May	PS3_RS F93_C5_MAY_FB32
33	PS4	RS filter 66	Surface 1	May	PS4_RS F66_S1_MAY_FB33
34	PS4	RS filter 66	Surface 2	May	PS4_RS F66_S2_MAY_FB34
35	PS4	RS filter 66	Surface 3	May	PS4_RS F66_S3_MAY_FB35
36	PS4	RS filter 66	Surface 4	May	PS4_RS F66_S4_MAY_FB36
37	PS4	RS filter 66	Surface 5	May	PS4_RS F66_S5_MAY_FB37
38	PS4	RS filter 66	Surface 6	May	PS4_RS F66_S6_MAY_FB38
39	PS4	RS filter 66	Surface 7	May	PS4_RS F66_S7_MAY_FB39
40	PS4	RS filter 66	Surface 8	May	PS4_RS F66_S8_MAY_FB40
41	PS4	RS filter 66	Surface 9	May	PS4_RS F66_S9_MAY_FB41
42	PS4	RS filter 54	Surface 5	May	PS4_RS F66_S5_MAY_FB42
43	PS4	RS filter 51	Surface 5	May	PS4_RS F66_S5_MAY_FB43
44	PS4	RS filter 66	Core 1	May	PS4_RS F66_C1_MAY_FB44
45	PS4	RS filter 66	Core 2	May	PS4_RS F66_C2_MAY_FB45
46	PS4	RS filter 66	Core 3	May	PS4_RS F66_C3_MAY_FB46
47	PS4	RS filter 66	Core 4	May	PS4_RS F66_C4_MAY_FB47
48	PS4	RS filter 66	Core 5	May	PS4_RS F66_C5_MAY_FB48
49	PS1	RS filter 46	Surface 1	June	PS1_RS F46_S1_JUN_FB49

50	PS1	RS filter 46	Surface 2	June	PS1_RS F46_S2_JUN_FB50
51	PS1	RS filter 46	Surface 3	June	PS1_RS F46_S3_JUN_FB51
52	PS1	RS filter 46	Surface 4	June	PS1_RS F46_S4_JUN_FB52
53	PS1	RS filter 46	Surface 5	June	PS1_RS F46_S5_JUN_FB53
54	PS1	RS filter 46	Surface 6	June	PS1_RS F46_S6_JUN_FB54
55	PS1	RS filter 46	Surface 7	June	PS1_RS F46_S7_JUN_FB55
56	PS1	RS filter 46	Surface 8	June	PS1_RS F46_S8_JUN_FB56
57	PS1	RS filter 46	Surface 9	June	PS1_RS F46_S9_JUN_FB57
58	PS1	RS filter 49	Surface 5	June	PS1_RS F49_S5_JUN_FB58
59	PS1	RS filter 50	Surface 5	June	PS1_RS F50_S5_JUN_FB59
60	PS1	RS filter 46	Core 1	June	PS1_RS F46_C1_JUN_FB60
61	PS1	RS filter 46	Core 2	June	PS1_RS F46_C2_JUN_FB61
62	PS1	RS filter 46	Core 3	June	PS1_RS F46_C3_JUN_FB62
63	PS1	RS filter 46	Core 4	June	PS1_RS F46_C4_JUN_FB63
64	PS1	RS filter 46	Core 5	June	PS1_RS F46_C5_JUN_FB64
65	PS3	RS filter 93	Surface 1	June	PS3_RS F93_S1_JUN_FB65
66	PS3	RS filter 93	Surface 2	June	PS3_RS F93_S2_JUN_FB66
67	PS3	RS filter 93	Surface 3	June	PS3_RS F93_S3_JUN_FB67
68	PS3	RS filter 93	Surface 4	June	PS3_RS F93_S4_JUN_FB68
69	PS3	RS filter 93	Surface 5	June	PS3_RS F93_S5_JUN_FB69
70	PS3	RS filter 93	Surface 6	June	PS3_RS F93_S6_JUN_FB70
71	PS3	RS filter 93	Surface 7	June	PS3_RS F93_S7_JUN_FB71
72	PS3	RS filter 93	Surface 8	June	PS3_RS F93_S8_JUN_FB72
73	PS3	RS filter 93	Surface 9	June	PS3_RS F93_S9_JUN_FB73
74	PS3	RS filter 94	Surface 5	June	PS3_RS F94_S5_JUN_FB74
75	PS3	RS filter 95	Surface 5	June	PS3_RS F95_S5_JUN_FB75
76	PS3	RS filter 93	Core 1	June	PS3_RS F93_C1_JUN_FB76
77	PS3	RS filter 93	Core 2	June	PS3_RS F93_C2_JUN_FB77
78	PS3	RS filter 93	Core 3	June	PS3_RS F93_C3_JUN_FB78
79	PS3	RS filter 93	Core 4	June	PS3_RS F93_C4_JUN_FB79
80	PS3	RS filter 93	Core 5	June	PS3_RS F93_C5_JUN_FB80
81	PS4	RS filter 66	Surface 1	June	PS4_RS F66_S1_JUN_FB81
82	PS4	RS filter 66	Surface 2	June	PS4_RS F66_S2_JUN_FB82
83	PS4	RS filter 66	Surface 3	June	PS4_RS F66_S3_JUN_FB83
84	PS4	RS filter 66	Surface 4	June	PS4_RS F66_S4_JUN_FB84
85	PS4	RS filter 66	Surface 5	June	PS4_RS F66_S5_JUN_FB85
86	PS4	RS filter 66	Surface 6	June	PS4_RS F66_S6_JUN_FB86
87	PS4	RS filter 66	Surface 7	June	PS4_RS F66_S7_JUN_FB87
88	PS4	RS filter 66	Surface 8	June	PS4_RS F66_S8_JUN_FB88
89	PS4	RS filter 66	Surface 9	June	PS4_RS F66_S9_JUN_FB89
90	PS4	RS filter 54	Surface 5	June	PS4_RS F54_S5_JUN_FB90
91	PS4	RS filter 51	Surface 5	June	PS4_RS F51_S5_JUN_FB91
92	PS4	RS filter 66	Core 1	June	PS4_RS F66_C1_JUN_FB92
93	PS4	RS filter 66	Core 2	June	PS4_RS F66_C2_JUN_FB93
94	PS4	RS filter 66	Core 3	June	PS4_RS F66_C3_JUN_FB94
95	PS4	RS filter 66	Core 4	June	PS4_RS F66_C4_JUN_FB95
96	PS4	RS filter 66	Core 5	June	PS4_RS F66_C5_JUN_FB96
97	PS1	RS filter 46	Surface 1	July	PS1_RS F46_S1_JUL_FB97
98	PS1	RS filter 46	Surface 2	July	PS1_RS F46_S2_JUL_FB98
99	PS1	RS filter 46	Surface 3	July	PS1_RS F46_S3_JUL_FB99
100	PS1	RS filter 46	Surface 4	July	PS1_RS F46_S4_JUL_FB100
101	PS1	RS filter 46	Surface 5	July	PS1_RS F46_S5_JUL_FB101
102	PS1	RS filter 46	Surface 6	July	PS1_RS F46_S6_JUL_FB102
103	PS1	RS filter 46	Surface 7	July	PS1_RS F46_S7_JUL_FB103
104	PS1	RS filter 46	Surface 8	July	PS1_RS F46_S8_JUL_FB104
105	PS1	RS filter 46	Surface 9	July	PS1_RS F46_S9_JUL_FB105
106	PS1	RS filter 49	Surface 5	July	PS1_RS F49_S5_JUL_FB106

107	PS1	RS filter 50	Surface 5	July	PS1_RS F50_S5_JUL_FB107
108	PS1	RS filter 46	Core 1	July	PS1_RS F46_C1_JUL_FB108
109	PS1	RS filter 46	Core 2	July	PS1_RS F46_C2_JUL_FB109
110	PS1	RS filter 46	Core 3	July	PS1_RS F46_C3_JUL_FB110
111	PS1	RS filter 46	Core 4	July	PS1_RS F46_C4_JUL_FB111
112	PS1	RS filter 46	Core 5	July	PS1_RS F46_C5_JUL_FB112
113	PS3	RS filter 93	Surface 1	July	PS3_RS F93_S1_JUL_FB113
114	PS3	RS filter 93	Surface 2	July	PS3_RS F93_S2_JUL_FB114
115	PS3	RS filter 93	Surface 3	July	PS3_RS F93_S3_JUL_FB115
116	PS3	RS filter 93	Surface 4	July	PS3_RS F93_S4_JUL_FB116
117	PS3	RS filter 93	Surface 5	July	PS3_RS F93_S5_JUL_FB117
118	PS3	RS filter 93	Surface 6	July	PS3_RS F93_S6_JUL_FB118
119	PS3	RS filter 93	Surface 7	July	PS3_RS F93_S7_JUL_FB119
120	PS3	RS filter 93	Surface 8	July	PS3_RS F93_S8_JUL_FB120
121	PS3	RS filter 93	Surface 9	July	PS3_RS F93_S9_JUL_FB121
122	PS3	RS filter 93	Core 1	July	PS3_RS F93_C1_JUL_FB122
123	PS3	RS filter 93	Core 2	July	PS3_RS F93_C2_JUL_FB123
124	PS3	RS filter 93	Core 3	July	PS3_RS F93_C3_JUL_FB124
125	PS3	RS filter 93	Core 4	July	PS3_RS F93_C4_JUL_FB125
126	PS3	RS filter 93	Core 5	July	PS3_RS F93_C5_JUL_FB126
127	PS3	RS filter 94	Surface 5	July	PS3_RS F94_S5_JUL_FB127
128	PS3	RS filter 95	Surface 5	July	PS3_RS F95_S5_JUL_FB128
129	PS4	RS filter 66	Surface 1	July	PS4_RS F66_S1_JUL_FB129
130	PS4	RS filter 66	Surface 2	July	PS4_RS F66_S2_JUL_FB130
131	PS4	RS filter 66	Surface 3	July	PS4_RS F66_S3_JUL_FB131
132	PS4	RS filter 66	Surface 4	July	PS4_RS F66_S4_JUL_FB132
133	PS4	RS filter 66	Surface 5	July	PS4_RS F66_S5_JUL_FB133
134	PS4	RS filter 66	Surface 6	July	PS4_RS F66_S6_JUL_FB134
135	PS4	RS filter 66	Surface 7	July	PS4_RS F66_S7_JUL_FB135
136	PS4	RS filter 66	Surface 8	July	PS4_RS F66_S8_JUL_FB136
137	PS4	RS filter 66	Surface 9	July	PS4_RS F66_S9_JUL_FB137
138	PS4	RS filter 54	Surface 5	July	PS4_RS F54_S5_JUL_FB138
139	PS4	RS filter 51	Surface 5	July	PS4_RS F51_S5_JUL_FB139
140	PS4	RS filter 66	Core 1	July	PS4_RS F66_C1_JUL_FB140
141	PS4	RS filter 66	Core 2	July	PS4_RS F66_C2_JUL_FB141
142	PS4	RS filter 66	Core 3	July	PS4_RS F66_C3_JUL_FB142
143	PS4	RS filter 66	Core 4	July	PS4_RS F66_C4_JUL_FB143
144	PS4	RS filter 66	Core 5	July	PS4_RS F66_C5_JUL_FB144
145	PS1	RS filter 46	Surface 1	August	PS1_RS F46_S1_AUG_FB145
146	PS1	RS filter 46	Surface 2	August	PS1_RS F46_S2_AUG_FB146
147	PS1	RS filter 46	Surface 3	August	PS1_RS F46_S3_AUG_FB147
148	PS1	RS filter 46	Surface 4	August	PS1_RS F46_S4_AUG_FB148
149	PS1	RS filter 46	Surface 5	August	PS1_RS F46_S5_AUG_FB149
150	PS1	RS filter 46	Surface 6	August	PS1_RS F46_S6_AUG_FB150
151	PS1	RS filter 46	Surface 7	August	PS1_RS F46_S7_AUG_FB151
152	PS1	RS filter 46	Surface 8	August	PS1_RS F46_S8_AUG_FB152
153	PS1	RS filter 46	Surface 9	August	PS1_RS F46_S9_AUG_FB153
154	PS1	RS filter 49	Surface 5	August	PS1_RS F49_S5_AUG_FB154
155	PS1	RS filter 50	Surface 5	August	PS1_RS F50_S5_AUG_FB155
156	PS1	RS filter 46	Core 1	August	PS1_RS F46_C1_AUG_FB156
157	PS1	RS filter 46	Core 2	August	PS1_RS F46_C2_AUG_FB157
158	PS1	RS filter 46	Core 3	August	PS1_RS F46_C3_AUG_FB158
159	PS1	RS filter 46	Core 4	August	PS1_RS F46_C4_AUG_FB159
160	PS1	RS filter 46	Core 5	August	PS1_RS F46_C5_AUG_FB160
161	PS3	RS filter 93	Surface 1	August	PS3_RS F93_S1_AUG_FB161
162	PS3	RS filter 93	Surface 2	August	PS3_RS F93_S2_AUG_FB162
163	PS3	RS filter 93	Surface 3	August	PS3_RS F93_S3_AUG_FB163

164	PS3	RS filter 93	Surface 4	August	PS3_RS F93_S4_AUG_FB164
165	PS3	RS filter 93	Surface 5	August	PS3_RS F93_S5_AUG_FB165
166	PS3	RS filter 93	Surface 6	August	PS3_RS F93_S6_AUG_FB166
167	PS3	RS filter 93	Surface 7	August	PS3_RS F93_S7_AUG_FB167
168	PS3	RS filter 93	Surface 8	August	PS3_RS F93_S8_AUG_FB168
169	PS3	RS filter 93	Surface 9	August	PS3_RS F93_S9_AUG_FB169
170	PS3	RS filter 94	Surface 5	August	PS3_RS F94_S5_AUG_FB170
171	PS3	RS filter 95	Surface 5	August	PS3_RS F95_S5_AUG_FB171
172	PS3	RS filter 93	Core 1	August	PS3_RS F93_C1_AUG_FB172
173	PS3	RS filter 93	Core 2	August	PS3_RS F93_C2_AUG_FB173
174	PS3	RS filter 93	Core 3	August	PS3_RS F93_C3_AUG_FB174
175	PS3	RS filter 93	Core 4	August	PS3_RS F93_C4_AUG_FB175
176	PS3	RS filter 93	Core 5	August	PS3_RS F93_C5_AUG_FB176
177	PS4	RS filter 66	Surface 1	August	PS4_RS F66_S1_AUG_FB177
178	PS4	RS filter 66	Surface 2	August	PS4_RS F66_S2_AUG_FB178
179	PS4	RS filter 66	Surface 3	August	PS4_RS F66_S3_AUG_FB179
180	PS4	RS filter 66	Surface 4	August	PS4_RS F66_S4_AUG_FB180
181	PS4	RS filter 66	Surface 5	August	PS4_RS F66_S5_AUG_FB181
182	PS4	RS filter 66	Surface 6	August	PS4_RS F66_S6_AUG_FB182
183	PS4	RS filter 66	Surface 7	August	PS4_RS F66_S7_AUG_FB183
184	PS4	RS filter 66	Surface 8	August	PS4_RS F66_S8_AUG_FB184
185	PS4	RS filter 66	Surface 9	August	PS4_RS F66_S9_AUG_FB185
186	PS4	RS filter 54	Surface 5	August	PS4_RS F54_S5_AUG_FB186
187	PS4	RS filter 51	Surface 5	August	PS4_RS F51_S5_AUG_FB187
188	PS4	RS filter 66	Core 1	August	PS4_RS F66_C1_AUG_FB188
189	PS4	RS filter 66	Core 2	August	PS4_RS F66_C2_AUG_FB189
190	PS4	RS filter 66	Core 3	August	PS4_RS F66_C3_AUG_FB190
191	PS4	RS filter 66	Core 4	August	PS4_RS F66_C4_AUG_FB191
192	PS4	RS filter 66	Core 5	August	PS4_RS F66_C5_AUG_FB192

^a Location: Site of sample collection

^b Month: Month of sample collection.

^c Study name: Abbreviated name of individual samples used within the text, tables and figures. Samples were abbreviated using the purification station, rapid sand filter, sampling location and month in which sampling was conducted: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; **RS**, rapid sand; **RSF**, rapid sand filter; **C1**, core location 1; **C2**, core location 2; **C3**, core location 3; **C4**, core location 4; **C5**, core location 5; **S1**, surface location 1; **S2**, surface location 2; **S3**, surface location 3; **S4**, surface location 4; **S5**, surface location 5; **S6**, surface location 6; **S7**, surface location 7; **S8**, surface location 8; **S9**, surface location 9; **JUN**, June; **JUL**, July; **AUG**, August; **FB**, filter bed media.

Table A2 Sequence database

Number	Study name ^a	Raw reads ^b	Processed reads ^c	Goods coverage ^d
1	PS1_RSF46_S1_MAY_FB1	36 828	29 783	0.994
2	PS1_RSF46_S2_MAY_FB2	23 910	19 406	0.993
3	PS1_RSF46_S3_MAY_FB3	44 923	36 639	0.996
4	PS1_RSF46_S4_MAY_FB4	35 660	28 825	0.995
5	PS1_RSF46_S5_MAY_FB5	25 080	19 743	0.992
6	PS1_RSF46_S6_MAY_FB6	34 085	27 452	0.995
7	PS1_RSF46_S7_MAY_FB7	32 666	26 313	0.997
8	PS1_RSF46_S8_MAY_FB8	35 412	28 526	0.995
9	PS1_RSF46_S9_MAY_FB9	28 107	23 182	0.997
10	PS1_RSF49_S5_MAY_FB10	25 056	19 324	0.995
11	PS1_RSF50_S5_MAY_FB11	27 938	21 120	0.995
12	PS1_RSF46_C1_MAY_FB12	29 487	24 280	0.999
13	PS1_RSF46_C2_MAY_FB13	32 444	26 063	0.995
14	PS1_RSF46_C3_MAY_FB14	29 353	23 649	0.994
15	PS1_RSF46_C4_MAY_FB15	36 339	29 543	0.996
16	PS1_RSF46_C5_MAY_FB16	39 159	31154	0.995
17	PS3_RSF93_S1_MAY_FB17	39 954	31 615	0.999
18	PS3_RSF93_S2_MAY_FB18	36 935	28 328	0.998
19	PS3_RSF93_S3_MAY_FB19	39 825	32 477	0.999
20	PS3_RSF93_S4_MAY_FB20	36 778	29 730	0.999
21	PS3_RSF93_S5_MAY_FB21	43 702	34 615	0.999
22	PS3_RSF93_S6_MAY_FB22	46 698	37 443	0.999
23	PS3_RSF93_S7_MAY_FB23	39 851	32 627	0.998
24	PS3_RSF93_S8_MAY_FB24	36 833	30 281	0.999
25	PS3_RSF93_S9_MAY_FB25	36 746	30 893	0.999
26	PS3_RSF93_S5_MAY_FB26	36 068	27 315	0.998
27	PS3_RSF93_S5_MAY_FB27	27 230	20 286	0.998
28	PS3_RSF93_C1_MAY_FB28	48 085	37 713	0.999
29	PS3_RSF93_C2_MAY_FB29	40 193	31 140	0.999
30	PS3_RSF93_C3_MAY_FB30	43 110	33 705	0.999
31	PS3_RSF93_C4_MAY_FB31	43 629	34 287	0.999
32	PS3_RSF93_C5_MAY_FB32	36 914	28 880	0.999
33	PS4_RSF66_S1_MAY_FB33	34 498	27 058	0.999
34	PS4_RSF66_S2_MAY_FB34	36 544	28 859	0.999
35	PS4_RSF66_S3_MAY_FB35	36 215	28 947	0.999
36	PS4_RSF66_S4_MAY_FB36	35 409	28 283	0.998
37	PS4_RSF66_S5_MAY_FB37	44 339	35 428	0.999
38	PS4_RSF66_S6_MAY_FB38	11 307	9 169	0.997
39	PS4_RSF66_S7_MAY_FB39	32 368	24 381	0.998
40	PS4_RSF66_S8_MAY_FB40	34 292	26 379	0.998
41	PS4_RSF66_S9_MAY_FB41	32 750	25 081	0.996
42	PS4_RSF66_S5_MAY_FB42	33 622	26 258	0.996
43	PS4_RSF66_S5_MAY_FB43	31 702	24 665	0.999
44	PS4_RSF66_C1_MAY_FB44	38 872	29 625	0.997
45	PS4_RSF66_C2_MAY_FB45	32 512	25 785	0.997
46	PS4_RSF66_C3_MAY_FB46	39 814	32 808	0.998
47	PS4_RSF66_C4_MAY_FB47	27 837	23 178	0.998
48	PS4_RSF66_C5_MAY_FB48	38 084	30 267	0.999
49	PS1_RSF46_S1_JUN_FB49	50 495	41 614	0.998
50	PS1_RSF46_S2_JUN_FB50	33 749	27 847	0.997
51	PS1_RSF46_S3_JUN_FB51	27 648	22 338	0.998
52	PS1_RSF46_S4_JUN_FB52	20 861	17 328	0.996
53	PS1_RSF46_S5_JUN_FB53	32 674	26 361	0.998
54	PS1_RSF46_S6_JUN_FB54	37 800	30 649	0.996
55	PS1_RSF46_S7_JUN_FB55	38 700	31 022	0.998

56	PS1_RSF46_S8_JUN_FB56	43 226	34 003	0.997
57	PS1_RSF46_S9_JUN_FB57	23 983	19 575	0.997
58	PS1_RSF49_S5_JUN_FB58	32 792	26 365	0.997
59	PS1_RSF46_C1_JUN_FB60	24 422	19 445	0.996
60	PS1_RSF46_C2_JUN_FB61	23 414	19 042	0.996
61	PS1_RSF46_C4_JUN_FB63	25 251	20 615	0.996
62	PS1_RSF46_C5_JUN_FB64	18 777	15 261	0.995
63	PS3_RSF93_S1_JUN_FB65	6 178	5 008	0.993
64	PS3_RSF93_S2_JUN_FB66	19 389	15 320	0.997
65	PS3_RSF93_S3_JUN_FB67	25 610	20 143	0.997
66	PS3_RSF93_S4_JUN_FB68	31 588	25 195	0.998
67	PS3_RSF93_S5_JUN_FB69	37 008	29 186	0.997
68	PS3_RSF93_S6_JUN_FB70	28 483	22 988	0.998
69	PS3_RSF93_S7_JUN_FB71	21 590	17 556	0.997
70	PS3_RSF93_S8_JUN_FB72	39 725	32 261	0.999
71	PS3_RSF93_S9_JUN_FB73	36 995	29 596	0.997
72	PS3_RSF94_S5_JUN_FB74	2 540	2 050	0.992
73	PS3_RSF95_S5_JUN_FB75	37 534	29 306	0.997
74	PS3_RSF93_C1_JUN_FB76	36 375	28 489	0.998
75	PS3_RSF93_C2_JUN_FB77	28 722	22 672	0.998
76	PS3_RSF93_C3_JUN_FB78	27 550	22 675	0.999
77	PS3_RSF93_C4_JUN_FB79	21 125	16 390	0.999
78	PS3_RSF93_C5_JUN_FB80	23 053	18 138	0.997
79	PS4_RSF66_S1_JUN_FB81	28 064	22 879	0.997
80	PS4_RSF66_S2_JUN_FB82	42 146	34 288	0.998
81	PS4_RSF66_S3_JUN_FB83	26 079	20 659	0.996
82	PS4_RSF66_S4_JUN_FB84	25 462	20 572	0.996
83	PS4_RSF66_S5_JUN_FB85	31 244	24 754	0.998
84	PS4_RSF66_S6_JUN_FB86	27 292	21 653	0.997
85	PS4_RSF66_S7_JUN_FB87	31 787	25 194	0.998
86	PS4_RSF66_S8_JUN_FB88	29 805	23 938	0.998
87	PS4_RSF66_S9_JUN_FB89	32 601	25 837	0.998
88	PS4_RSF54_S5_JUN_FB90	25 589	21 280	0.997
89	PS4_RSF51_S5_JUN_FB91	18 922	15 759	0.998
90	PS4_RSF66_C1_JUN_FB92	26 272	21 585	0.998
91	PS4_RSF66_C2_JUN_FB93	27 283	22 212	0.998
92	PS4_RSF66_C3_JUN_FB94	35 015	28 864	0.999
93	PS4_RSF66_C4_JUN_FB95	31 074	25 502	0.997
94	PS4_RSF66_C5_JUN_FB96	20 614	16 595	0.998
95	PS1_RSF46_S1_JUL_FB97	19 574	16 179	0.995
96	PS1_RSF46_S2_JUL_FB98	35 114	28 581	0.996
97	PS1_RSF46_S3_JUL_FB99	33 885	28 077	0.997
98	PS1_RSF46_S4_JUL_FB100	27 351	22 585	0.997
99	PS1_RSF46_S5_JUL_FB101	29 555	24 206	0.998
100	PS1_RSF46_S6_JUL_FB102	25 457	20 933	0.997
101	PS1_RSF46_S7_JUL_FB103	30 492	25 219	0.998
102	PS1_RSF46_S8_JUL_FB104	30 545	24 967	0.998
103	PS1_RSF46_S9_JUL_FB105	18 070	14 217	0.996
104	PS1_RSF49_S5_JUL_FB106	32 260	27 017	0.999
105	PS1_RSF46_C1_JUL_FB108	27 622	22 096	0.996
106	PS1_RSF46_C2_JUL_FB109	35 387	28 754	0.995
107	PS1_RSF46_C3_JUL_FB110	33 342	26 838	0.997
108	PS1_RSF46_C4_JUL_FB111	34 613	27 746	0.996
109	PS3_RSF93_S1_JUL_FB113	40 275	31 470	0.998
110	PS3_RSF93_S2_JUL_FB114	24 553	19 462	0.997
111	PS3_RSF93_S3_JUL_FB115	31 628	25 128	0.998
112	PS3_RSF93_S4_JUL_FB116	27 016	21 563	0.997

113	PS3_RSF93_S5_JUL_FB117	27 269	21 126	0.997
114	PS3_RSF93_S6_JUL_FB118	35 207	28 162	0.997
115	PS3_RSF93_S7_JUL_FB119	13 617	11 170	0.998
116	PS3_RSF93_S8_JUL_FB120	23 309	18 277	0.999
117	PS3_RSF93_S9_JUL_FB121	32 899	25 512	0.998
118	PS3_RSF93_C1_JUL_FB122	29 752	22 677	0.997
119	PS3_RSF93_C2_JUL_FB123	28 394	20 878	0.998
120	PS3_RSF93_C3_JUL_FB124	32 833	25 093	0.999
121	PS3_RSF93_C4_JUL_FB125	26 366	20 062	0.999
122	PS3_RSF93_C5_JUL_FB126	22 669	18 383	0.999
123	PS3_RSF94_S5_JUL_FB127	31 232	24 943	0.998
124	PS3_RSF95_S5_JUL_FB128	25 200	20 249	0.998
125	PS4_RSF66_S1_JUL_FB129	29 569	23 863	0.996
126	PS4_RSF66_S2_JUL_FB130	19 614	16 225	0.998
127	PS4_RSF66_S3_JUL_FB131	18 501	15 230	0.997
128	PS4_RSF66_S4_JUL_FB132	27 948	22 314	0.998
129	PS4_RSF66_S5_JUL_FB133	18 593	15 271	0.997
130	PS4_RSF66_S6_JUL_FB134	25 963	20 989	0.997
131	PS4_RSF66_S7_JUL_FB135	21 183	17 584	0.999
132	PS4_RSF66_S8_JUL_FB136	26 647	21 829	0.998
133	PS4_RSF66_S9_JUL_FB137	26 356	21 405	0.997
134	PS4_RSF54_S5_JUL_FB138	19 798	16 096	0.997
135	PS4_RSF51_S5_JUL_FB139	27 615	21 977	0.998
136	PS4_RSF66_C1_JUL_FB140	26 251	21 427	0.998
137	PS4_RSF66_C2_JUL_FB141	22 497	17 820	0.998
138	PS4_RSF66_C3_JUL_FB142	24 956	19 403	0.999
139	PS4_RSF66_C4_JUL_FB143	20 808	16 995	0.999
140	PS4_RSF66_C5_JUL_FB144	18 602	15 022	0.998
141	PS1_RSF46_S1_AUG_FB145	17 261	14 775	0.990
142	PS1_RSF46_S2_AUG_FB146	16 818	14 417	0.991
143	PS1_RSF46_S3_AUG_FB147	33 396	28 780	0.995
144	PS1_RSF46_S4_AUG_FB148	24 303	20 575	0.994
145	PS1_RSF46_S5_AUG_FB149	15 382	13 022	0.993
146	PS1_RSF46_S6_AUG_FB150	33 756	29 319	0.995
147	PS1_RSF46_S7_AUG_FB151	24 302	20 749	0.993
148	PS1_RSF46_S8_AUG_FB152	25 654	22 379	0.993
149	PS1_RSF46_S9_AUG_FB153	23 990	20 856	0.995
150	PS1_RSF49_S5_AUG_FB154	16 769	14 267	0.994
151	PS1_RSF50_S5_AUG_FB155	25 262	21 299	0.994
152	PS1_RSF46_C1_AUG_FB156	24 713	21 142	0.995
153	PS1_RSF46_C2_AUG_FB157	19 340	16 600	0.989
154	PS1_RSF46_C3_AUG_FB158	17 667	14 602	0.989
155	PS1_RSF46_C4_AUG_FB159	35 427	30 314	0.991
156	PS1_RSF46_C5_AUG_FB160	28 783	24 739	0.992
157	PS3_RSF93_S1_AUG_FB161	27 300	22 967	0.995
158	PS3_RSF93_S2_AUG_FB162	18 131	15 486	0.995
159	PS3_RSF93_S3_AUG_FB163	31 500	27 025	0.995
160	PS3_RSF93_S4_AUG_FB164	17 992	14 987	0.994
161	PS3_RSF93_S5_AUG_FB165	20 161	17 028	0.993
162	PS3_RSF93_S6_AUG_FB166	21 085	17 982	0.994
163	PS3_RSF93_S7_AUG_FB167	16 560	13 951	0.995
164	PS3_RSF93_S8_AUG_FB168	21 229	17 694	0.996
165	PS3_RSF93_S9_AUG_FB169	32 534	27 307	0.998
166	PS3_RSF94_S5_AUG_FB170	26 250	21 888	0.997
167	PS3_RSF95_S5_AUG_FB171	27 125	23 292	0.997
168	PS3_RSF93_C1_AUG_FB172	37 207	32 931	0.998
169	PS3_RSF93_C2_AUG_FB173	31 875	27 168	0.998

170	PS3_RSF93_C3_AUG_FB174	26 513	22 611	0.999
171	PS3_RSF93_C4_AUG_FB175	25 294	22 467	0.999
172	PS3_RSF93_C5_AUG_FB176	17 626	15 848	0.999
173	PS4_RSF66_S1_AUG_FB177	18 827	16 108	0.995
174	PS4_RSF66_S2_AUG_FB178	21 653	17 851	0.997
175	PS4_RSF66_S3_AUG_FB179	15 409	12 914	0.995
176	PS4_RSF66_S4_AUG_FB180	17 394	14 570	0.996
177	PS4_RSF66_S5_AUG_FB181	32 923	27 997	0.998
178	PS4_RSF66_S6_AUG_FB182	29 530	24 281	0.997
179	PS4_RSF66_S7_AUG_FB183	24 662	20 776	0.996
180	PS4_RSF66_S8_AUG_FB184	26 747	22 175	0.997
181	PS4_RSF66_S9_AUG_FB185	32 244	26 777	0.997
182	PS4_RSF54_S5_AUG_FB186	10 963	9 774	0.995
183	PS4_RSF51_S5_AUG_FB187	29 168	24 191	0.995
184	PS4_RSF66_C1_AUG_FB188	24 715	20 589	0.996
185	PS4_RSF66_C2_AUG_FB189	22 881	19 939	0.997
186	PS4_RSF66_C3_AUG_FB190	22 766	19 181	0.996
187	PS4_RSF66_C4_AUG_FB191	20 106	17 574	0.999
188	PS4_RSF66_C5_AUG_FB192	15 702	13 996	0.999

^a Study name: Abbreviated name of individual samples used within the text, tables and figures. Samples were abbreviated using the purification station, rapid sand filter, sampling location and month in which sampling was conducted: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; **RS**, rapid sand; **RSF**, rapid sand filter; **C1**, core location 1; **C2**, core location 2; **C3**, core location 3; **C4**, core location 4; **C5**, core location 5; **S1**, surface location 1; **S2**, surface location 2; **S3**, surface location 3; **S4**, surface location 4; **S5**, surface location 5; **S6**, surface location 6; **S7**, surface location 7; **S8**, surface location 8; **S9**, surface location 9; **JUN**, June; **JUL**, July; **AUG**, August; **FB**, filter bed media.

^b Raw sequence reads: unprocessed Illumina MiSeq sequence reads.

^c Processed sequence reads: processed Illumina MiSeq reads.

^d Goods coverage: Calculated Goods coverage estimate after subsampling the sequence dataset of each sample to 2 050 sequence per sample.

Table A3 Alpha diversity indexes

Number	Study name ^a	Observed species	Shannon index	Pielou's evenness index
1	PS1_RS46_S1_MAY_FB1	592	2.91	0.44
2	PS1_RS46_S2_MAY_FB2	433	2.57	0.41
3	PS1_RS46_S3_MAY_FB3	551	2.63	0.41
4	PS1_RS46_S4_MAY_FB4	477	2.51	0.40
5	PS1_RS46_S5_MAY_FB5	499	2.80	0.44
6	PS1_RS46_S6_MAY_FB6	492	2.66	0.42
7	PS1_RS46_S7_MAY_FB7	257	2.23	0.39
8	PS1_RS46_S8_MAY_FB8	485	2.52	0.40
9	PS1_RS46_S9_MAY_FB9	243	1.98	0.35
10	PS1_RS49_S5_MAY_FB10	300	2.11	0.36
11	PS1_RS50_S5_MAY_FB11	288	2.27	0.39
12	PS1_RS46_C1_MAY_FB12	139	1.90	0.38
13	PS1_RS46_C2_MAY_FB13	349	2.39	0.39
14	PS1_RS46_C3_MAY_FB14	456	2.61	0.41
15	PS1_RS46_C4_MAY_FB15	497	2.59	0.41
16	PS1_RS46_C5_MAY_FB16	485	2.39	0.37
17	PS3_RS93_S1_MAY_FB17	144	1.78	0.35
18	PS3_RS93_S2_MAY_FB18	183	2.18	0.41
19	PS3_RS93_S3_MAY_FB19	97	1.88	0.40
20	PS3_RS93_S4_MAY_FB20	100	1.37	0.29
21	PS3_RS93_S5_MAY_FB21	124	1.42	0.29
22	PS3_RS93_S6_MAY_FB22	89	1.40	0.30
23	PS3_RS93_S7_MAY_FB23	151	1.25	0.24
24	PS3_RS93_S8_MAY_FB24	77	1.22	0.27
25	PS3_RS93_S9_MAY_FB25	76	1.12	0.25
26	PS3_RS93_S5_MAY_FB26	209	2.05	0.38
27	PS3_RS93_S5_MAY_FB27	157	1.81	0.35
28	PS3_RS93_C1_MAY_FB28	134	1.46	0.28
29	PS3_RS93_C2_MAY_FB29	93	1.26	0.27
30	PS3_RS93_C3_MAY_FB30	84	1.34	0.29
31	PS3_RS93_C4_MAY_FB31	91	1.37	0.29
32	PS3_RS93_C5_MAY_FB32	79	1.13	0.25
33	PS4_RS66_S1_MAY_FB33	192	2.47	0.46
34	PS4_RS66_S2_MAY_FB34	145	2.00	0.39
35	PS4_RS66_S3_MAY_FB35	133	2.23	0.44
36	PS4_RS66_S4_MAY_FB36	191	2.35	0.43
37	PS4_RS66_S5_MAY_FB37	138	2.38	0.47
38	PS4_RS66_S6_MAY_FB38	120	2.52	0.52
39	PS4_RS66_S7_MAY_FB39	209	2.02	0.37
40	PS4_RS66_S8_MAY_FB40	222	2.62	0.47
41	PS4_RS66_S9_MAY_FB41	316	2.97	0.50
42	PS4_RS66_S5_MAY_FB42	330	3.15	0.53
43	PS4_RS66_S5_MAY_FB43	106	1.71	0.35
44	PS4_RS66_C1_MAY_FB44	303	2.74	0.47
45	PS4_RS66_C2_MAY_FB45	240	2.28	0.40
46	PS4_RS66_C3_MAY_FB46	210	1.98	0.36
47	PS4_RS66_C4_MAY_FB47	127	1.62	0.32
48	PS4_RS66_C5_MAY_FB48	121	1.58	0.32
49	PS1_RS46_S1_JUN_FB49	358	1.81	0.30
50	PS1_RS46_S2_JUN_FB50	238	2.03	0.36
51	PS1_RS46_S3_JUN_FB51	197	1.78	0.33
52	PS1_RS46_S4_JUN_FB52	212	2.07	0.37
53	PS1_RS46_S5_JUN_FB53	235	2.00	0.36
54	PS1_RS46_S6_JUN_FB54	349	2.29	0.37

55	PS1_RSF46_S7_JUN_FB55	270	2.16	0.38
56	PS1_RSF46_S8_JUN_FB56	427	2.30	0.37
57	PS1_RSF46_S9_JUN_FB57	166	2.00	0.38
58	PS1_RSF49_S5_JUN_FB58	260	2.14	0.37
59	PS1_RSF46_C1_JUN_FB60	219	1.93	0.34
60	PS1_RSF46_C2_JUN_FB61	223	1.81	0.32
61	PS1_RSF46_C4_JUN_FB63	233	1.92	0.33
62	PS1_RSF46_C5_JUN_FB64	217	1.92	0.34
63	PS3_RSF93_S1_JUN_FB65	99	2.14	0.44
64	PS3_RSF93_S2_JUN_FB66	135	1.92	0.38
65	PS3_RSF93_S3_JUN_FB67	163	1.81	0.34
66	PS3_RSF93_S4_JUN_FB68	164	1.89	0.36
67	PS3_RSF93_S5_JUN_FB69	270	2.08	0.36
68	PS3_RSF93_S6_JUN_FB70	135	1.90	0.37
69	PS3_RSF93_S7_JUN_FB71	161	1.69	0.32
70	PS3_RSF93_S8_JUN_FB72	151	1.90	0.37
71	PS3_RSF93_S9_JUN_FB73	249	2.30	0.40
72	PS3_RSF94_S5_JUN_FB74	61	2.22	0.53
73	PS3_RSF95_S5_JUN_FB75	269	2.35	0.40
74	PS3_RSF93_C1_JUN_FB76	196	2.23	0.41
75	PS3_RSF93_C2_JUN_FB77	140	1.92	0.37
76	PS3_RSF93_C3_JUN_FB78	84	1.50	0.32
77	PS3_RSF93_C4_JUN_FB79	69	0.99	0.23
78	PS3_RSF93_C5_JUN_FB80	138	1.53	0.30
79	PS4_RSF66_S1_JUN_FB81	170	1.91	0.36
80	PS4_RSF66_S2_JUN_FB82	251	2.07	0.36
81	PS4_RSF66_S3_JUN_FB83	212	2.14	0.38
82	PS4_RSF66_S4_JUN_FB84	265	2.38	0.41
83	PS4_RSF66_S5_JUN_FB85	178	2.09	0.39
84	PS4_RSF66_S6_JUN_FB86	202	2.09	0.38
85	PS4_RSF66_S7_JUN_FB87	164	2.04	0.38
86	PS4_RSF66_S8_JUN_FB88	160	1.97	0.38
87	PS4_RSF66_S9_JUN_FB89	187	2.17	0.40
88	PS4_RSF54_S5_JUN_FB90	202	2.10	0.39
89	PS4_RSF51_S5_JUN_FB91	124	1.99	0.41
90	PS4_RSF66_C1_JUN_FB92	171	2.18	0.41
91	PS4_RSF66_C2_JUN_FB93	133	1.55	0.31
92	PS4_RSF66_C3_JUN_FB94	150	1.85	0.36
93	PS4_RSF66_C4_JUN_FB95	225	1.61	0.29
94	PS4_RSF66_C5_JUN_FB96	91	1.58	0.34
95	PS1_RSF46_S1_JUL_FB97	238	2.06	0.36
96	PS1_RSF46_S2_JUL_FB98	357	2.34	0.39
97	PS1_RSF46_S3_JUL_FB99	248	1.93	0.34
98	PS1_RSF46_S4_JUL_FB100	196	1.86	0.34
99	PS1_RSF46_S5_JUL_FB101	160	1.97	0.37
100	PS1_RSF46_S6_JUL_FB102	179	2.14	0.40
101	PS1_RSF46_S7_JUL_FB103	207	1.92	0.35
102	PS1_RSF46_S8_JUL_FB104	182	2.03	0.37
103	PS1_RSF46_S9_JUL_FB105	161	2.45	0.46
104	PS1_RSF49_S5_JUL_FB106	146	2.48	0.49
105	PS1_RSF46_C1_JUL_FB108	255	2.43	0.42
106	PS1_RSF46_C2_JUL_FB109	375	2.55	0.41
107	PS1_RSF46_C3_JUL_FB110	287	2.47	0.43
108	PS1_RSF46_C4_JUL_FB111	405	2.39	0.39
109	PS3_RSF93_S1_JUL_FB113	207	2.04	0.37
110	PS3_RSF93_S2_JUL_FB114	210	2.15	0.39
111	PS3_RSF93_S3_JUL_FB115	201	2.13	0.39

112	PS3_RSF93_S4_JUL_FB116	206	2.13	0.38
113	PS3_RSF93_S5_JUL_FB117	216	2.30	0.41
114	PS3_RSF93_S6_JUL_FB118	249	2.22	0.39
115	PS3_RSF93_S7_JUL_FB119	66	1.85	0.42
116	PS3_RSF93_S8_JUL_FB120	85	1.49	0.32
117	PS3_RSF93_S9_JUL_FB121	173	1.51	0.28
118	PS3_RSF93_C1_JUL_FB122	204	2.25	0.41
119	PS3_RSF93_C2_JUL_FB123	125	1.36	0.27
120	PS3_RSF93_C3_JUL_FB124	101	0.76	0.16
121	PS3_RSF93_C4_JUL_FB125	74	0.48	0.11
122	PS3_RSF93_C5_JUL_FB126	40	1.49	0.38
123	PS3_RSF94_S5_JUL_FB127	172	2.22	0.42
124	PS3_RSF95_S5_JUL_FB128	132	2.07	0.41
125	PS4_RSF66_S1_JUL_FB129	335	2.60	0.44
126	PS4_RSF66_S2_JUL_FB130	143	1.98	0.39
127	PS4_RSF66_S3_JUL_FB131	138	2.13	0.41
128	PS4_RSF66_S4_JUL_FB132	203	2.20	0.40
129	PS4_RSF66_S5_JUL_FB133	126	2.00	0.40
130	PS4_RSF66_S6_JUL_FB134	200	2.12	0.38
131	PS4_RSF66_S7_JUL_FB135	111	1.93	0.40
132	PS4_RSF66_S8_JUL_FB136	120	2.01	0.41
133	PS4_RSF66_S9_JUL_FB137	190	2.08	0.38
134	PS4_RSF54_S5_JUL_FB138	173	2.42	0.45
135	PS4_RSF51_S5_JUL_FB139	161	2.32	0.44
136	PS4_RSF66_C1_JUL_FB140	150	2.20	0.42
137	PS4_RSF66_C2_JUL_FB141	111	1.59	0.33
138	PS4_RSF66_C3_JUL_FB142	128	1.45	0.29
139	PS4_RSF66_C4_JUL_FB143	57	0.95	0.22
140	PS4_RSF66_C5_JUL_FB144	69	0.93	0.20
141	PS1_RSF46_S1_AUG_FB145	367	1.96	0.31
142	PS1_RSF46_S2_AUG_FB146	315	2.14	0.35
143	PS1_RSF46_S3_AUG_FB147	349	2.00	0.33
144	PS1_RSF46_S4_AUG_FB148	278	1.86	0.31
145	PS1_RSF46_S5_AUG_FB149	220	1.57	0.27
146	PS1_RSF46_S6_AUG_FB150	377	1.88	0.30
147	PS1_RSF46_S7_AUG_FB151	333	1.87	0.30
148	PS1_RSF46_S8_AUG_FB152	430	1.81	0.29
149	PS1_RSF46_S9_AUG_FB153	238	1.66	0.29
150	PS1_RSF49_S5_AUG_FB154	272	2.40	0.41
151	PS1_RSF50_S5_AUG_FB155	300	2.15	0.35
152	PS1_RSF46_C1_AUG_FB156	220	1.15	0.20
153	PS1_RSF46_C2_AUG_FB157	517	2.13	0.32
154	PS1_RSF46_C3_AUG_FB158	393	2.18	0.35
155	PS1_RSF46_C4_AUG_FB159	726	2.21	0.32
156	PS1_RSF46_C5_AUG_FB160	467	1.66	0.25
157	PS3_RSF93_S1_AUG_FB161	337	2.15	0.35
158	PS3_RSF93_S2_AUG_FB162	224	2.04	0.36
159	PS3_RSF93_S3_AUG_FB163	373	2.37	0.38
160	PS3_RSF93_S4_AUG_FB164	277	1.92	0.33
161	PS3_RSF93_S5_AUG_FB165	357	2.61	0.42
162	PS3_RSF93_S6_AUG_FB166	314	2.62	0.43
163	PS3_RSF93_S7_AUG_FB167	182	2.51	0.46
164	PS3_RSF93_S8_AUG_FB168	189	2.55	0.46
165	PS3_RSF93_S9_AUG_FB169	157	1.89	0.36
166	PS3_RSF94_S5_AUG_FB170	200	2.07	0.37
167	PS3_RSF95_S5_AUG_FB171	142	1.68	0.31
168	PS3_RSF93_C1_AUG_FB172	153	1.85	0.35

169	PS3_RS F93_C2_AUG_FB173	119	2.14	0.42
170	PS3_RS F93_C3_AUG_FB174	58	1.80	0.39
171	PS3_RS F93_C4_AUG_FB175	41	1.37	0.37
172	PS3_RS F93_C5_AUG_FB176	30	1.61	0.41
173	PS4_RS F66_S1_AUG_FB177	218	2.41	0.43
174	PS4_RS F66_S2_AUG_FB178	153	2.21	0.42
175	PS4_RS F66_S3_AUG_FB179	173	2.25	0.41
176	PS4_RS F66_S4_AUG_FB180	139	2.12	0.40
177	PS4_RS F66_S5_AUG_FB181	173	2.05	0.38
178	PS4_RS F66_S6_AUG_FB182	196	2.36	0.42
179	PS4_RS F66_S7_AUG_FB183	224	2.27	0.39
180	PS4_RS F66_S8_AUG_FB184	197	2.25	0.40
181	PS4_RS F66_S9_AUG_FB185	217	2.24	0.40
182	PS4_RS F54_S5_AUG_FB186	139	2.31	0.44
183	PS4_RS F51_S5_AUG_FB187	270	2.02	0.34
184	PS4_RS F66_C1_AUG_FB188	172	1.96	0.35
185	PS4_RS F66_C2_AUG_FB189	168	2.11	0.39
186	PS4_RS F66_C3_AUG_FB190	228	1.99	0.35
187	PS4_RS F66_C4_AUG_FB191	82	1.91	0.41
188	PS4_RS F66_C5_AUG_FB192	34	1.72	0.45

^a Study name: Abbreviated name of individual samples used within the text, tables and figures. Samples were abbreviated using the purification station, rapid sand filter, sampling location and month in which sampling was conducted: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; **RS**, rapid sand; **RSF**, rapid sand filter; **C1**, core location 1; **C2**, core location 2; **C3**, core location 3; **C4**, core location 4; **C5**, core location 5; **S1**, surface location 1; **S2**, surface location 2; **S3**, surface location 3; **S4**, surface location 4; **S5**, surface location 5; **S6**, surface location 6; **S7**, surface location 7; **S8**, surface location 8; **S9**, surface location 9; **JUN**, June; **JUL**, July; **AUG**, August; **FB**, filter bed media.

Table A4 Descriptive statistics and ANOVA table determined using the alpha diversity indexes of spatial groupings across the surface of the rapid sand filter

Table A4a Descriptive statistics

Alpha diversity index		S_{obs}		H'		J	
Study site	$n_{samples}$	M	SD	M	SD	M	SD
S1	12	271	134	2.19	0.34	0.38	0.05
S2	12	232	94	2.14	0.18	0.38	0.02
S3	12	236	129	2.11	0.25	0.38	0.04
S4	12	226	96	2.05	0.31	0.37	0.04
S5	12	225	109	2.11	0.39	0.38	0.06
S6	12	242	119	2.18	0.35	0.39	0.06
S7	12	195	72	1.98	0.32	0.37	0.06
S8	12	227	140	2.06	0.43	0.37	0.06
S9	12	198	61	2.03	0.47	0.37	0.07

Abbreviations: **S1**, surface location 1; **S2**, surface location 2; **S3**, surface location 3; **S4**, surface location 4; **S5**, surface location 5; **S6**, surface location 6; **S7**, surface location 7; **S8**, surface location 8; **S9**, surface location 9; S_{obs} , observed species; H' , Shannon index; J , Pielou's evenness index; $n_{samples}$, number of samples; M , mean; SD , standard deviation.

Table A4b One-way ANOVA summary for observed species

	df	SS	MS	F_{ST}	p
Between groups	8	50 539	6 317.40	0.53	8.32E-01
Within groups	99	1 181 720	11 936.60		
Total	107	1 232 259			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A4c One-way ANOVA summary for Shannon index

	df	SS	MS	F_{ST}	p
Between groups	8	0.47	0.06	0.49	8.62E-01
Within groups	99	11.99	0.12		
Total	107	12.46			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A4d One-way ANOVA summary for Pielou's evenness index

	df	SS	MS	F_{ST}	p
Between groups	8	0.01	0.001	0.30	9.66E-01
Within groups	99	0.28	0.003		
Total	107	0.29			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A1 Descriptive statistics and ANOVA table determined using the alpha diversity indexes of spatial groupings along the depth of the rapid sand filter

Table A5a Descriptive statistics

Alpha diversity index		S_{obs}		H'		J	
Study site	$n_{samples}$	M	SD	M	SD	M	SD
C1	11	249	125	2.08	0.35	0.37	0.06
C2	12	241	196	1.94	0.42	0.35	0.05
C3	11	198	133	1.81	0.53	0.34	0.07
C4	12	186	154	1.60	0.61	0.31	0.09
C5	12	120	77	1.58	0.40	0.33	0.08

Abbreviations: **C1**, core location 1; **C2**, core location 2; **C3**, core location 3; **C4**, core location 4; **C5**, core location 5; S_{obs} , observed species; H' , Shannon index; J , Pielou's evenness index; $n_{samples}$, number of samples; M , mean; SD , standard deviation.

Table A5b One-way ANOVA summary for observed species

	df	SS	MS	F_{ST}	p
Between groups	4	127 408	31 852	1.56	1.98E-01
Within groups	53	1 080 270	20 382		
Total	57	1 207 678			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A5c One-way ANOVA summary for Shannon index

	df	SS	MS	F_{ST}	p
Between groups	4	2.15	0.54	2.38	6.31E-02
Within groups	53	11.97	0.23		
Total	57	14.12			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A5d One-way ANOVA summary for Pielou's evenness index

	df	SS	MS	F_{ST}	p
Between groups	4	0.03	0.006	1.15	3.45E-01
Within groups	53	0.29	0.005		
Total	57	0.32			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A2 Descriptive statistics and ANOVA table determined using the alpha diversity indexes of spatial groupings across parallel RS filters within a filter gallery

Table B3.6a Descriptive statistics for purification station 1

Alpha diversity index		S_{obs}		H'		J	
Rapid sand filter	n	M	SD	M	SD	M	SD
RS filter 46	4	279	151	2.09	0.52	0.36	0.07
RS filter 49	4	245	68	2.28	0.19	0.41	0.06
RS filter 50	2	294	8	2.21	0.08	0.37	0.02

Abbreviations: **RS filter**, rapid sand filter; S_{obs} , observed species; H' , Shannon index; J , Pielou's evenness index; n , number of samples; M , mean; SD , standard deviation.

Table A6b Descriptive statistics for purification station 3

Alpha diversity index		S_{obs}		H'		J	
Rapid sand filter	n	M	SD	M	SD	M	SD
RS filter 93	4	242	98	2.10	0.50	0.37	0.06
RS filter 94	4	161	68	2.14	0.09	0.42	0.07
RS filter 95	4	175	64	1.98	0.30	0.37	0.05

Abbreviations: **RS filter**, rapid sand filter; S_{obs} , observed species; H' , Shannon index; J , Pielou's evenness index; n , number of samples; M , mean; SD , standard deviation.

Table A6c Descriptive statistics for purification station 4

Alpha diversity index		S_{obs}		H'		J	
Rapid sand filter	n	M	SD	M	SD	M	SD
RS filter 66	4	154	26	2.13	0.17	0.41	0.04
RS filter 51	4	211	83	2.50	0.46	0.45	0.06
RS filter 54	4	165	73	2.01	0.25	0.38	0.05

Abbreviations: **RS filter**, rapid sand filter; S_{obs} , observed species; H' , Shannon index; J , Pielou's evenness index; n , number of samples; M , mean; SD , standard deviation.

Table A6d One-way ANOVA summary for observed species for purification station 1

	df	SS	MS	F_{ST}	p
Between groups	2	4 002	2 001	0.17	8.46E-01
Within groups	7	81 828	11 690		
Total	9	85 830			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A6e One-way ANOVA summary for observed species for purification station 3

	df	SS	MS	F_{ST}	p
Between groups	2	15 023	7 512	1.24	3.35E-01
Within groups	9	54 652	6 072		
Total	11	69 675			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A6f One-way ANOVA summary for observed species for purification station 4

	df	SS	MS	F_{ST}	p
Between groups	2	7 337	3 669	0.85	4.61E-01
Within groups	9	39 049	4 339		
Total	11	46 386			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A6g One-way ANOVA summary for Shannon index for purification station 1

	df	SS	MS	F_{ST}	p
Between groups	2	0.08	0.04	0.30	7.52E-01
Within groups	7	0.91	0.13		
Total	9	0.99			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A6h One-way ANOVA summary for Shannon index for purification station 3

	df	SS	MS	F_{ST}	p
Between groups	2	0.06	0.03	0.24	7.88E-01
Within groups	9	1.05	0.12		
Total	11	1.11			

Abbreviations: df , degrees of freedom; SS , sum of squares; MS , mean square; F_{ST} , F-statistic; p , p-value.

Table A6i One-way ANOVA summary for Shannon index for purification station 4

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.51	0.26	2.58	1.31E-01
Within groups	9	0.89	0.10		
Total	11	1.40			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A6j One-way ANOVA summary for Pielou's evenness index for purification station 1

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.01	0.002	0.69	5.32E-01
Within groups	7	0.03	0.004		
Total	9	0.04			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A6k One-way ANOVA summary for Pielou's evenness index for purification station 3

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.01	0.004	1.05	3.90E-01
Within groups	7	0.03	0.004		
Total	9	0.04			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A6l One-way ANOVA summary for Pielou's evenness index for purification station 4

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.01	0.005	1.85	2.13E-01
Within groups	7	0.02	0.003		
Total	9	0.03			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A3 Descriptive statistics and ANOVA table and post-hoc Tukey honest significant difference test determined using the alpha diversity indexes of spatial groupings across filter galleries

Table A7a Descriptive statistics

Alpha diversity index		S _{obs}		H'		J	
Purification station	<i>n</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
PS1	60	322	127	2.15	0.33	0.36	0.05
PS3	64	156	78	1.81	0.45	0.35	0.07
PS4	64	175	62	2.09	0.38	0.39	0.06

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index; ***n***, number of samples; ***M***, mean; ***SD***, standard deviation.

Table A7b One-way ANOVA summary for observed species

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F</i> _{ST}	<i>p</i>
Between groups	2	1 018 321	509 161	59.71	2.20E-16
Within groups	185	1 577 531	8 527		
Total	187	2 595 852			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F*_{ST}**, F-statistic; ***p***, p-value.

Table A7c One-way ANOVA summary for Shannon index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F</i> _{ST}	<i>p</i>
Between groups	2	4.01	2.002	12.98	5.31E-06
Within groups	185	28.55	0.154		
Total	187	32.56			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F*_{ST}**, F-statistic; ***p***, p-value.

Table A7d One-way ANOVA summary for Pielou's evenness index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F</i> _{ST}	<i>p</i>
Between groups	2	0.06	0.027	7.24	9.43E-04
Within groups	185	0.70	0.003		
Total	187	0.76			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F*_{ST}**, F-statistic; ***p***, p-value.

Table A7e Post-hoc Tukey honest significant difference tests for differences of means

Alpha diversity index	S _{obs}	H'	J
PS3 vs. PS1	1.00E-07	1.17E-05	5.48E-01
PS4 vs. PS1	1.00E-07	6.46E-01	2.77E-02
PS4 vs. PS3	4.86E-01	3.53E-04	8.30E-04

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index.

Table A4a Descriptive statistics and ANOVA table and post-hoc Tukey honest significant difference test determined using the alpha diversity indexes for month groupings at purification station 1

Table B3.8a Descriptive statistics

Alpha diversity index		S _{obs}		H'		J	
Month	<i>n</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
May	16	409	132	2.44	0.29	0.40	0.03
June	14	257	72	2.01	0.17	0.35	0.02
July	14	243	85	2.22	0.25	0.40	0.04
August	16	363	129	1.91	0.31	0.31	0.05

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index; ***n***, number of samples; ***M***, mean; ***SD***, standard deviation.

Table A8b One-way ANOVA summary for observed species

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	294 023	98 008	8.31	1.16E-04
Within groups	56	660 730	11 799		
Total	59	954 753			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A8c One-way ANOVA summary for Shannon index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	2.60	0.87	12.73	1.87E-06
Within groups	56	3.81	0.07		
Total	59	6.41			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A8d One-way ANOVA summary for Pielou's evenness index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.08	0.026	19.02	1.25E-08
Within groups	56	0.08	0.001		
Total	59	0.16			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A8e Post-hoc Tukey honest significant difference tests for differences of means

Alpha diversity index	S _{obs}	H'	J
July vs. August	1.93E-02	1.28E-02	4.00E-07
June vs. August	5.02E-02	7.38E-01	2.13E-02
May vs. August	6.25E-01	2.40E-06	1.00E-07
June vs. July	9.84E-01	1.72E-01	1.46E-02
May vs. July	5.74E-04	9.36E-02	9.98E-01
May vs. June	1.91E-03	1.83E-04	7.21E-03

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index.

Table A5 Descriptive statistics and ANOVA table and post-hoc Tukey honest significant difference test determined using the alpha diversity indexes for month groupings at purification station 3

Table A9a Descriptive statistics

Alpha diversity index		S _{obs}		H'		J	
Month	<i>n</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
May	16	118	41	1.50	0.33	0.31	0.05
June	16	155	65	1.90	0.35	0.37	0.07
July	16	154	65	1.78	0.55	0.34	0.09
August	16	197	110	2.07	0.38	0.39	0.04

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index; **n**, number of samples; **M**, mean; **SD**, standard deviation.

Table A9b One-way ANOVA summary for observed species

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	50 168	16 722	3.02	3.66E-02
Within groups	60	332 252	5 537		
Total	63	382 420			

Abbreviations: **df**, degrees of freedom; **SS**, sum of squares; **MS**, mean square; **F_{ST}**, F-statistic; **p**, p-value.

Table A9c One-way ANOVA summary for Shannon index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	2.78	0.93	5.45	2.22E-03
Within groups	60	10.21	0.17		
Total	63	12.99			

Abbreviations: **df**, degrees of freedom; **SS**, sum of squares; **MS**, mean square; **F_{ST}**, F-statistic; **p**, p-value.

Table A9d One-way ANOVA summary for Pielou's evenness index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.06	0.02	4.26	8.56E-03
Within groups	60	0.27	0.01		
Total	63	0.33			

Abbreviations: **df**, degrees of freedom; **SS**, sum of squares; **MS**, mean square; **F_{ST}**, F-statistic; **p**, p-value.

Table A9e Post-hoc Tukey honest significant difference tests for differences of means

Alpha diversity index	S _{obs}	H'	J
July vs. August	3.62E-01	1.18E-01	3.02E-01
June vs. August	3.92E-01	6.24E-01	8.73E-01
May vs. August	1.97E-02	1.25E-02	6.90E-03
June vs. July	9.99E-01	8.42E-01	7.47E-01
May vs. July	5.28E-01	2.41E-01	3.78E-01
May vs. June	4.95E-01	4.13E-02	5.28E-02

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index.

Table A6 Descriptive statistics and ANOVA table and post-hoc Tukey honest significant difference test determined using the alpha diversity indexes for month groupings at purification station 4

Table A10a Descriptive statistics

Alpha diversity index		S _{obs}		H'		J	
Month	<i>n</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
May	16	194	73	2.29	0.46	0.42	0.07
June	16	180	46	1.98	0.23	0.37	0.04
July	16	151	64	1.93	0.48	0.37	0.07
August	16	174	58	2.14	0.19	0.40	0.03

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index; ***n***, number of samples; ***M***, mean; ***SD***, standard deviation.

Table A10b One-way ANOVA summary for observed species

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	15 469	5156	1.38	2.60E-01
Within groups	60	224 890	3748		
Total	63	240 359			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A10c One-way ANOVA summary for Shannon index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	1.25	0.41	3.17	3.07E-02
Within groups	60	7.90	0.13		
Total	63	9.15			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A10d One-way ANOVA summary for Pielou's evenness index

	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.02	0.01	3.40	2.34E-02
Within groups	60	0.19	0.09		
Total	63	0.21			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A10e Post-hoc Tukey honest significant difference tests for differences of means

Alpha diversity index	S _{obs}	H'	J
July vs. August	7.13E-01	3.88E-01	5.43E-01
June vs. August	9.91E-01	6.34E-01	5.06E-01
May vs. August	7.92E-01	6.34E-01	5.32E-01
June vs. July	5.31E-01	9.78E-01	1.99E-01
May vs. July	2.04E-01	3.49E-02	4.42E-02
May vs. June	9.22E-01	9.10E-02	3.81E-02

Abbreviations: **S_{obs}**, observed species; **H'**, Shannon index; **J**, Pielou's evenness index.

Table A7 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst spatial groupings across the surface of the rapid sand filter

Table A11a Structure-base AMOVA test

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	8	0.33	0.04	0.33	1.00E+00	0.14	0.02	0.34	1.00E+00
Within groups	99	12.22	0.12			5.10	0.05		
Total	107	12.54				5.24			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A11b Membership-base AMOVA test

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	8	1.93	0.24	0.80	1.00E+00	1.60	0.20	0.78	1.00E+00
Within groups	99	30.11	0.30			25.43	0.26		
Total	107	32.04				27.03			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A11c Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
S1-S2	9.98E-01	8.30E-01	1.00E+00	1.00E+00
S1-S3	5.55E-01	9.66E-01	1.00E+00	1.00E+00
S2-S3	9.62E-01	8.07E-01	9.99E-01	9.95E-01
S1-S4	9.69E-01	9.99E-01	1.00E+00	1.00E+00
S2-S4	9.69E-01	8.27E-01	1.00E+00	9.67E-01
S3-S4	9.64E-01	9.74E-01	1.00E+00	9.98E-01
S1-S5	8.06E-01	9.96E-01	1.00E+00	9.99E-01
S2-S5	9.98E-01	9.97E-01	1.00E+00	9.72E-01
S3-S5	9.99E-01	9.98E-01	1.00E+00	1.00E+00
S4-S5	9.98E-01	9.76E-01	1.00E+00	9.64E-01
S1-S6	8.15E-01	9.98E-01	9.97E-01	9.97E-01
S2-S6	9.98E-01	7.98E-01	9.97E-01	9.99E-01
S3-S6	1.00E+00	9.70E-01	9.98E-01	1.00E+00
S4-S6	9.99E-01	9.66E-01	9.98E-01	1.00E+00
S5-S6	1.00E+00	5.34E-01	9.99E-01	1.00E+00
S1-S7	9.67E-01	1.00E+00	1.00E+00	1.00E+00
S2-S7	1.00E+00	9.65E-01	1.00E+00	9.97E-01
S3-S7	9.67E-01	1.00E+00	1.00E+00	9.98E-01
S4-S7	9.73E-01	9.99E-01	1.00E+00	9.98E-01
S5-S7	9.98E-01	9.97E-01	9.98E-01	9.72E-01
S6-S7	9.98E-01	5.70E-01	1.00E+00	1.00E+00
S1-S8	8.03E-01	8.16E-01	9.68E-01	9.64E-01
S2-S8	9.62E-01	8.29E-01	9.96E-01	1.00E+00
S3-S8	9.76E-01	9.99E-01	9.72E-01	9.67E-01
S4-S8	9.98E-01	9.75E-01	9.98E-01	9.99E-01
S5-S8	9.69E-01	9.65E-01	9.61E-01	8.36E-01
S6-S8	9.61E-01	8.39E-01	9.71E-01	9.98E-01
S7-S8	9.68E-01	9.71E-01	9.98E-01	1.00E+00
S1-S9	8.19E-01	8.20E-01	1.00E+00	9.96E-01
S2-S9	8.02E-01	8.27E-01	9.72E-01	9.76E-01
S3-S9	5.31E-01	9.58E-01	9.78E-01	9.70E-01
S4-S9	9.64E-01	9.96E-01	9.75E-01	9.97E-01
S5-S9	9.82E-01	8.14E-01	9.73E-01	8.26E-01
S6-S9	8.37E-01	9.62E-01	9.99E-01	9.68E-01
S7-S9	9.61E-01	8.08E-01	9.68E-01	9.99E-01
S8-S9	8.04E-01	9.97E-01	9.68E-01	9.97E-01

Abbreviations: **S1**, surface location 1; **S2**, surface location 2; **S3**, surface location 3; **S4**, surface location 4; **S5**, surface location 5; **S6**, surface location 6; **S7**, surface location 7; **S8**, surface location 8; **S9**, surface location 9.

Table A8 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst spatial groupings along the depth of the rapid sand filter

Table A12a Structure-base AMOVA test

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	4	0.38	0.10	0.69	8.77E-01	0.23	0.06	0.73	7.64E-01
Within groups	53	7.38	0.14			4.08	0.08		
Total	57	7.76				4.31			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A12b Membership-base AMOVA test

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	4	1.53	0.38	1.13	1.21E-01	1.33	0.33	1.15	1.19E-01
Within groups	53	17.97	0.34			15.29	0.29		
Total	57	19.50				16.62			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A12c Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
C1-C2	9.98E-01	9.79E-01	1.00E+00	8.15E-01
C1-C3	9.88E-01	9.11E-01	1.00E+00	3.50E-01
C2-C3	9.93E-01	9.89E-01	1.00E+00	9.03E-01
C1-C4	8.26E-01	9.71E-01	8.88E-01	2.50E-01
C2-C4	9.61E-01	8.11E-01	8.72E-01	8.29E-01
C3-C4	9.85E-01	6.71E-01	1.00E+00	9.88E-01
C1-C5	8.97E-01	6.84E-01	1.00E+00	7.00E-03
C2-C5	9.03E-01	9.05E-01	1.00E+00	3.79E-01
C3-C5	9.56E-01	4.45E-01	1.00E+00	9.53E-01
C4-C5	9.08E-01	6.52E-01	1.00E+00	1.00E+00

Abbreviations: **C1**, core location 1; **C2**, core location 2; **C3**, core location 3; **C4**, core location 4; **C5**, core location 5.

Table A9 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst spatial groupings across parallel RS filters within a filter gallery

Table A13a Structure-base AMOVA test purification station 1

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.13	0.07	0.61	8.14E-01	0.10	0.05	0.91	5.08E-01
Within groups	7	0.77	0.11			0.37	0.05		
Total	9	0.90				0.47			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A13b Membership-base AMOVA test purification station 1

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.58	0.29	0.98	5.60E-01	0.46	0.23	0.95	6.08E-01
Within groups	7	2.06	0.29			1.70	0.24		
Total	9	2.64				2.16			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A13c Parsimony tests purification station 1

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
RS filter 46 vs. RS filter 49	7.83E-01	7.61E-01	7.71E-01	7.83E-01
RS filter 46 vs. RS filter 50	1.00E+00	1.00E+00	1.00E+00	1.00E+00
RS filter 49 vs. RS filter 50	1.00E+00	1.00E+00	1.00E+00	1.00E+00

Abbreviations: ***RS***, rapid sand.

Table A13d Structure-base AMOVA test purification station 3

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.23	0.12	0.78	8.38E-01	0.89	0.04	0.65	7.37E-01
Within groups	7	1.35	0.15			0.61	0.07		
Total	9	1.58				0.70			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A13e Membership-base AMOVA test purification station 3

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.55	0.27	0.99	5.09E-01	0.47	0.24	1.00	4.43E-01
Within groups	7	2.48	0.28			0.14	0.24		
Total	9	3.03				2.61			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A13f Parsimony tests purification station 3

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
RS filter 93 vs. RS filter 94	7.63E-01	7.87E-01	7.77E-01	7.67E-01
RS filter 93 vs. RS filter 95	7.81E-01	7.58E-01	7.63E-01	7.77E-01
RS filter 94 vs. RS filter 95	7.59E-01	1.00E+01	1.00E+00	1.00E+00

Abbreviations: **RS**, rapid sand.

Table A13g Structure-base AMOVA test purification station 4

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	0.15	0.07	0.58	8.45E-01	0.09	0.05	0.80	5.59E-01
Within groups	7	1.13	0.13			0.51	0.06		
Total	9	1.27				0.60			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A13h Membership-base AMOVA test purification station 4

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	0.51	0.25	1.02	4.45E-01	0.43	0.21	0.98	5.25E-01
Within groups	7	2.27	0.25			1.95	0.22		
Total	9	2.77				2.38			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A13i Parsimony tests purification station 4

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
RS filter 51 vs. RS filter 54	8.00E-01	7.79E-01	1.00E+00	7.73E-01
RS filter 51 vs. RS filter 66	1.00E+00	7.89E-01	1.00E+00	1.00E+00
RS filter 54 vs. RS filter 66	1.00E+00	1.00E+00	1.00E+00	7.78E-01

Abbreviations: **RS**, rapid sand.

Table A10 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst spatial groupings across filter galleries

Table A14a Structure-base AMOVA test purification station 1

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	0.59	0.30	2.44	4.00E-03	0.27	0.14	2.04	2.00E-02
Within groups	31	3.76	0.12			1.77	0.06		
Total	33	4.35				2.04			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A14b Membership-base AMOVA test purification station 1

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	1.12	0.56	2.05	1.00E-03	0.92	0.46	2.00	1.00E-03
Within groups	31	8.44	0.27			7.16	0.23		
Total	33	9.56				8.08			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A14c Post-hoc pair-wise AMOVA tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
PS1 vs. PS3	1.00E-03	1.80E-02	1.00E-03	1.00E-03
PS1 vs. PS4	1.80E-02	2.30E-02	1.00E-03	1.00E-03
PS3 vs. PS4	8.80E-02	1.60E-01	5.90E-02	6.40E-02

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4.

Table A14d Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
PS1 vs. PS3	9.00E-03	9.00E-03	1.00E-03	1.00E-03
PS1 vs. PS4	4.60E-02	4.50E-02	1.00E-03	1.00E-03
PS3 vs. PS4	8.36E-01	5.42E-01	8.10E-02	2.50E-01

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4.

Table A11 Descriptive statistics, ANOVA table and post-hoc Tukey honest significant difference test determined using the beta diversity indexes of spatial groupings across filter galleries

Table A15a Descriptive statistics

Purification station	<i>n</i>	Structure-base diversity matrices				Membership-base diversity matrices			
		Bray-Curtis		Weighted UniFrac		Jaccard		Unweighted UniFrac	
		<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
PS1 vs. PS3	120	0.52	0.14	0.36	0.08	0.80	0.04	0.73	0.05
PS1 vs. PS4	120	0.49	0.11	0.34	0.09	0.78	0.04	0.72	0.05
PS3 vs. PS4	144	0.47	0.18	0.33	0.12	0.73	0.04	0.68	0.05

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4; *n*, number of samples; *M*, mean; *SD*, standard deviation.

Table A15b One-way ANOVA summary for Bray-Curtis and weighted UniFrac

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.08	0.04	1.74	1.17E-01	0.05	0.03	2.61	7.49E-01
Within groups	381	77.66	0.018			3.68	0.01		
Total	383	77.74				3.73			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A15c One-way ANOVA summary for Jaccard and unweighted UniFrac

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	2	0.35	0.17	99.94	2.20E-16	0.22	0.11	43.44	2.20E-16
Within groups	381	0.66	0.00			0.96	0.00		
Total	383	1.01				1.18			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A15d Post-hoc pair-wise ANOVA tests

	Membership-base diversity matrices	
	Jaccard	Unweighted UniFrac
PS1 vs. PS4 and PS1 vs. PS3	8.10E-04	3.44E-02
PS3 vs. PS4 and PS1 vs. PS3	1.00E-07	1.00E-07
PS3 vs. PS4 and PS1 vs. PS4	1.00E-07	1.00E-07

Abbreviations: **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4.

Table A12 Distance-based test of homogeneity of multivariate dispersion amongst spatial groupings across filter galleries

Table A16a Average distance to group centroid

	Structure-base diversity matrices		Membership-base diversity matrices	
	\bar{z}_{BC}	\bar{z}_{WUF}	\bar{z}_J	\bar{z}_{UUF}
PS1	0.29	0.21	0.51	0.46
PS3	0.33	0.23	0.50	0.46
PS4	0.32	0.22	0.48	0.44

Abbreviations: \bar{z} , average structure- or membership-based matrices distance to group centroid; **PS1**, purification station 1; **PS3**, purification station 3; **PS4**, purification station 4.

Table A16b One-way ANOVA summary for Bray-Curtis and weighted UniFrac

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	0.009	0.005	0.41	6.66E-01	0.006	0.001	2.51	9.78E-02
Within groups	31	0.341	0.011			0.039	0.004		
Total	33	0.350				0.045			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A16c One-way ANOVA summary for Jaccard and unweighted UniFrac

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	2	0.003	0.001	0.36	7.00E-01	0.003	0.001	0.36	4.37E-01
Within groups	31	0.126	0.004			0.054	0.002		
Total	33	0.057				0.057			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A13 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst month groupings for purification station 1

Table A17a Structure-base AMOVA test purification station 1

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.62	0.21	4.38	1.00E-03	0.32	0.11	4.12	1.00E-03
Within groups	6	0.28	0.05			0.15	0.03		
Total	9	0.90				0.47			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A17b Membership-base AMOVA test purification station 1

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	1.06	0.35	1.35	1.00E-03	0.91	0.30	1.46	1.00E-03
Within groups	6	1.57	0.26			1.25	0.21		
Total	9	2.64				2.16			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; *F_{ST}*, F-statistic; *p*, p-value.

Table A17c Post-hoc pair-wise AMOVA tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	1.10E-01	1.02E-01	1.00E-01	9.90E-02
August vs. June	9.70E-02	1.12E-01	2.20E-02	1.95E-01
August vs. May	9.20E-02	8.80E-02	1.13E-02	9.90E-02
July vs. June	3.30E-01	6.59E-01	3.35E-02	3.29E-01
July vs. May	1.10E-01	1.04E-01	1.01E-01	9.50E-02
June vs. May	1.01E-01	9.50E-02	2.88E-02	2.04E-01

Table A17d Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	1.90E-01	1.00E+00	2.11E-01	2.05E-01
August vs. June	2.08E-01	1.00E+00	1.00E+00	1.00E+00
August vs. May	1.00E+00	1.00E+00	3.24E-01	2.95E-01
July vs. June	8.50E-02	6.90E-02	8.20E-02	7.70E-02
July vs. May	1.96E-01	2.15E-01	2.13E-01	1.93E-01
June vs. May	2.30E-01	1.74E-01	1.00E+00	1.90E-01

Table A14 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst month groupings for purification station 3

Table A18a Structure-base AMOVA test purification station 1

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	3	0.60	0.20	1.58	4.00E-03	0.40	0.13	0.70	3.00E-03
Within groups	8	0.98	0.12			0.31	0.04		
Total	11	1.58				0.70			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A18b Membership-base AMOVA test purification station 1

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>	<i>SS</i>	<i>MS</i>	F_{ST}	<i>p</i>
Between groups	3	0.92	0.31	1.16	4.10E-02	0.78	2.59	1.13	9.50E-02
Within groups	8	2.11	0.26			1.84	0.23		
Total	11	3.03				2.62			

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *MS*, mean square; F_{ST} , F-statistic; *p*, p-value.

Table A18c Post-hoc pair-wise AMOVA tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	1.06E-01	8.60E-02	9.10E-02	1.00E+00
August vs. June	4.96E-01	1.08E-01	2.98E-01	1.00E+00
August vs. May	2.00E-01	8.70E-02	1.09E-01	1.00E+00
July vs. June	2.90E-01	3.00E-01	2.90E-01	1.00E+00
July vs. May	1.00E-01	8.70E-02	9.10E-02	1.00E+00
June vs. May	1.10E-01	1.05E-01	3.14E-01	1.00E+00

Table A18d Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	9.60E-02	7.90E-02	6.70E-02	9.00E-02
August vs. June	1.00E+00	6.28E-01	6.11E-01	6.31E-01
August vs. May	8.30E-02	1.07E-01	1.01E-01	7.70E-02
July vs. June	6.07E-01	6.13E-01	6.11E-01	5.95E-01
July vs. May	9.30E-02	9.30E-02	8.80E-02	7.90E-02
June vs. May	6.15E-01	6.03E-01	6.10E-01	5.94E-01

Table A15 AMOVA and parsimony: Testing for differences in the prokaryotic composition amongst month groupings for purification station 3

Table A19a Structure-base AMOVA test purification station 1

	Bray-Curtis					Weighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.63	0.21	2.63	8.00E-03	0.34	0.11	3.53	7.00E-03
Within groups	8	0.64	0.08			0.26	0.03		
Total	11	1.27				0.60			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A19b Membership-base AMOVA test purification station 1

	Jaccard					Unweighted UniFrac			
	<i>df</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>	<i>SS</i>	<i>MS</i>	<i>F_{ST}</i>	<i>p</i>
Between groups	3	0.90	0.30	1.29	1.00E-03	0.77	0.26	1.27	3.00E-03
Within groups	8	1.87	0.23			1.61	0.20		
Total	11	2.77				2.38			

Abbreviations: ***df***, degrees of freedom; ***SS***, sum of squares; ***MS***, mean square; ***F_{ST}***, F-statistic; ***p***, p-value.

Table A19c Post-hoc pair-wise AMOVA tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	6.14E-01	4.84E-01	1.30E-01	3.11E-01
August vs. June	9.20E-02	9.60E-02	2.30E-02	1.01E-01
August vs. May	8.50E-02	2.13E-01	9.80E-02	1.18E-01
July vs. June	1.31E-01	1.02E-01	2.30E-02	1.84E-01
July vs. May	4.60E-02	3.01E-01	9.90E-02	1.08E-01
June vs. May	8.90E-02	1.04E-01	1.85E-01	2.13E-01

Table A19d Parsimony tests

	Structure-base diversity matrices		Membership-base diversity matrices	
	Bray-Curtis	Weighted UniFrac	Jaccard	Unweighted UniFrac
August vs. July	5.94E-01	1.00E+00	6.90E-02	8.70E-02
August vs. June	7.60E-02	8.60E-02	5.85E-01	9.60E-02
August vs. May	5.84E-01	8.10E-02	8.80E-02	8.10E-02
July vs. June	5.68E-01	6.05E-01	6.17E-01	8.40E-02
July vs. May	7.70E-02	8.70E-02	8.70E-02	8.20E-02
June vs. May	8.50E-02	6.60E-02	1.03E-01	5.74E-01

Table A20 Number of sequence reads generated by the Illumina MiSeq platform and the sequence reads retained after a processing series conducted in MOTHUR.

Sample number	Treatment sample	Plant	Illumina reads	MiSeq sequences	Sequence reads after processing
1	Sand_01		29927		26489
2	Sand_02		22690		20020
3	Sand_03		32421		28333
4	Sand_04		29220		25760
5	Sand_05		27233		24376
6	Sand_06		7277		6373
7	Sand_07		15174		13344
8	Sand_08		33066		29161
9	Sand_09		29855		26088
10	Sand_10		28620		25452
11	Sand_11		27805		24092
12	Sand_12		41746		36856
13	Sand_13		39535		35026
14	Sand_14		35208		31408
15	Sand_15		33728		30271
16	Sand_16		31906		28335
17	Sand_17		61650		40522
18	Sand_18		30720		19974
19	Sand_19		58835		40470
20	Sand_20		35859		24828
21	Sand_21		38572		26246
22	Sand_22		44477		29374
23	Sand_23		46127		32001
24	Sand_24		27885		18594
25	Sand_25		16630		11293
26	Sand_26		48351		33737
27	Sand_27		47981		31673
28	Sand_28		19287		14006
29	Sand_29		17005		10746
30	Sand_30		43011		31628
31	Sand_31		69143		49034
32	Sand_32		8802		6244
33	Sand_33		38608		26926
34	Sand_34		45366		31352
35	Sand_36		22377		15608
36	Sand_37		58882		42490
37	Sand_38		56101		40691
38	Sand_39		52247		36569
39	Sand_40		24798		17815

40	Sand_41	49481	33873
41	Sand_42	59263	41672
42	Sand_43	55884	38270
43	Sand_44	62084	44623
44	Sand_45	19149	13229
45	Sand_46	18196	12791
46	Sand_47	20776	16157
47	Sand_48	41046	28763
48	Sand_49	41009	28112
49	Sand_50	25876	18233
50	Sand_51	65426	47787
51	Sand_52	66082	48673
52	Sand_53	44882	31903
53	Sand_54	33037	23802
54	Sand_55	16274	12104
55	Sand_56	9765	6314
56	Sand_57	40967	30657
57	Sand_58	23032	16187
58	Sand_59	41592	29874
59	Sand_60	49506	36445
60	Sand_61	82620	62180
61	Sand_62	31518	23925
62	Sand_63	52061	35818
63	Sand_65	56789	39841
64	Sand_66	23921	16584
65	Sand_67	44685	31772
66	Sand_68	46952	32032
67	Sand_69	48024	35124
68	Sand_70	33852	23267
69	Sand_71	32068	22598
70	Sand_72	32232	23374
71	Sand_73	70305	49915
72	Sand_74	27158	19302
73	Sand_75	49988	31744
74	Sand_76	55564	35820
75	Sand_77	63489	41315
76	Sand_79	17786	12366
77	Sand_80	54413	33874
78	Sand_81	55656	37663
79	Sand_82	28186	17843
80	Sand_83	36734	24140
81	Sand_84	90023	59745

82	Sand_85	63482	40363
83	Sand_86	28781	18589
84	Sand_87	81457	55651
85	Sand_88	55641	38403
86	Sand_89	53594	37028
87	Sand_90	35525	24584
88	Sand_92	6965	4648
89	Sand_93	72258	53505
90	Sand_94	553	125

APPENDIX B: SUPPLEMENTARY DATA FOR CHAPTER 4

Table B1. Number of sequence reads in the drinking water distribution system samples, generated by the Illumina MiSeq platform pre- and post-quality processing, conducted in MOTHUR

Sample number	DWDS sample	Illumina sequencing reads	MiSeq	Number of sequences retained after quality processing
1	RW_1	28699		25532
2	RW_2	48740		36232
3	RW_3	73639		51877
4	RW_4	54519		39730
5	RW_5	49494		34159
6	RW_6	27959		18008
7	RW_7	1671		1406
8	RW_9	21092		17894
9	RW_10	30471		24092
10	RW_11	16927		14367
11	RW_12	16031		13882
12	FI_1	28999		25147
13	FI_2	76969		54313
14	FI_3	32270		22541
15	FI_4	35317		26518
16	FI_5	29536		21790
17	FI_6	52301		35937
18	FI_7	43515		33736
19	FI_8	9608		7996
20	FI_9	33386		26168
21	FI_10	9506		7932
22	FI_11	8534		6941
23	FI_12	28275		23354
24	Sand_1	27233		24379
25	Sand_2	38572		26254
26	Sand_3	58882		42498
27	Sand_4	66082		48688
28	Sand_5	48024		35123
29	Sand_6	90023		59754
30	Sand_7	2536		2004
31	Sand_8	43451		35882
32	Sand_9	15793		12136
33	Sand_10	43349		35737
34	Sand_11	28496		23544
35	Sand_12	14122		11585

36	FE_1	36986	32676
37	FE_2	31217	22767
38	FE_3	53267	37356
39	FE_4	63547	46404
40	FE_5	49265	34709
41	FE_6	50341	32913
42	FE_7	9201	7866
43	FE_8	46830	38736
44	FE_9	56248	46277
45	FE_10	32344	26030
46	FE_11	10231	8219
47	FE_12	8913	7272
48	CI_1	26712	13871
49	CI_2	19712	9940
50	CI_4	3273	1015
51	CI_5	36241	25259
52	CI_6	52678	28046
53	CI_7	6405	3003
54	CI_9	10210	7982
55	CI_10	2365	1359
56	CI_12	9895	5362
58	BfAm_2	10449	5071
59	BfAm_3	1926	705
60	BfAm_4	11754	7028
61	BfAm_5	82373	54327
62	BfAm_9	21377	18149
57	BfAm_11	16896	12618
63	CIAm__2	22860	13382
64	CIAm__3	3803	2334
65	CIAm__4	12499	9341
66	CIAm__5	13246	8415
67	CIAm__6	9186	5119
68	CIAm__9	5170	4351
69	DSP_1_1	7079	5943
71	DSP_1_2	57656	38429
72	DSP_1_6	55286	38835
73	DSP_1_7	2255	1754
74	DSP_1_9	7459	6477
70	DSP_1_10	3298	2738
75	DSP_2_1	10675	8902
78	DSP_2_2	23824	16336
79	DSP_2_3	29516	21206
80	DSP_2_4	72956	57953
81	DSP_2_5	78313	58657

82	DSP_2_6	13410	9385
83	DSP_2_7	1148	868
84	DSP_2_8	11950	10248
76	DSP_2_10	808	658
77	DSP_2_11	4533	3640
85	DSP_3_1	10243	8586
89	DSP_3_3	26920	19660
90	DSP_3_4	21843	15989
91	DSP_3_5	23640	15367
92	DSP_3_8	33479	27946
86	DSP_3_10	10944	8738
87	DSP_3_11	4335	3301
88	DSP_3_2	6712	4296
93	DSP_4_2	17208	11636
94	DSP_4_3	60612	44409
95	DSP_4_5	60813	39822
96	DSP_4_6	64391	46679
97	DSP_4_7	3096	1991
98	DSP_4_8	23622	19570
99	DSP_4_9	1720	1440
100	DSP_5_1	7668	6368
103	DSP_5_2	28428	19399
104	DSP_5_3	29811	21205
105	DSP_5_4	49439	36459
106	DSP_5_5	56797	38150
107	DSP_5_6	6119	4173
108	DSP_5_7	864	675
109	DSP_5_8	35086	28931
101	DSP_5_10	3408	2712
102	DSP_5_12	15398	11865

Drinking water distribution system (DWDS), source water (RW), filter influent (FI), filter effluent (FE), chlorination (Cl), before chloramination (BfAm), chloramination (ClAm), drinking system point 1 (DSP_1), drinking system point 2 (DSP_2), drinking system point 3(DSP_3), drinking system point 4 (DSP_4), drinking system point 5 (DSP_5)

Table B2. Analysis of Molecular Variance (AMOVA) data, showing no significant difference in the DWDS microbial community structure and membership using beta-diversity metrics, Bray Curtis pairwise and Weighted UniFrac as well as Jaccard pairwise and Unweighted UniFrac, respectively, according to spatial groupings

Bray Curtis dissimilarity metric					
BfAm-CI	df	SS	MS	F_{ST}	p-value
Among	1	0,54	0,54	1,56	0.08
Within	13	4,49	0,35		
Total	14	5,03			
BfAm-CIAm	df	SS	MS	F_{ST}	p-value
Among	1	0,43	0,43	1,07	0.35
Within	10	4,01	0,4		
Total	11	4,44			
CIAm-DSP2	df	SS	MS	F_{ST}	p-value
Among	1	0,5	0,5	1,46	0.09
Within	13	4,4	0,34		
Total	14	4,9			
FE-FI	df	SS	MS	F_{ST}	p-value
Among	1	0,17	0,17	1,21	0.19
Within	22	3,15	0,14		
Total	23	3,32			
Jaccard dissimilarity metric					
BfAm-CI	df	SS	MS	F_{ST}	p-value
Among	1	0,44	0,44	1,14	0.14
Within	13	4,98	0,38		
Total	14	5,42			
Weighted UniFrac metric					
BfAm-CI	df	SS	MS	F_{ST}	p-value
Among	1	0,46	0,46	2,08	0.05
Within	13	2,89	0,22		
Total	14	3,35			
BfAm-CIAm	df	SS	MS	F_{ST}	p-value
Among	1	0,34	0,34	1,2	0.24
Within	10	2,85	0,29		
Total	11	3,2			
CIAm-DSP2	df	SS	MS	F_{ST}	p-value
Among	1	0,24	0,24	0,99	0.43
Within	13	3,09	0,24		
Total	14	3,33			
DSP3-DSP5	df	SS	MS	F_{ST}	p-value
Among	1	0,18	0,18	1,34	0.19
Within	17	2,3	0,14		
Total	18	2,48			
DSP4-DSP5	df	SS	MS	F_{ST}	p-value
Among	1	0,2	0,2	1,61	0.07
Within	15	1,83	0,12		
Total	16	2,02			
FE-FI	df	SS	MS	F_{ST}	p-value
Among	1	0,1	0,1	1,14	0.30

Within	22	1,94	0,09		
Total	23	2,04			
Unweighted UniFrac metric					
BfAm-CI	df	SS	MS	F_{ST}	p-value
Among	1	0,3	0,3	0,93	0.55
Within	13	4,15	0,32		
Total	14	4,44			
BfAm-CIAm	df	SS	MS	F_{ST}	p-value
Among	1	0,35	0,35	1,14	0.15
Within	10	3,09	0,31		
Total	11	3,45			
CI-CIAm	df	SS	MS	F_{ST}	p-value
Among	1	0,4	0,4	1,33	0.05
Within	13	3,87	0,3		
Total	14	4,27			

Abbreviations: source water (RW), filter influent (FI), filter effluent (FE), chlorination (CI), before chloramination (BfAm), chloramination (CIAm), drinking system point 1 (DSP_1), drinking system point 2 (DSP_2), drinking system point 3(DSP_3), drinking system point 4 (DSP_4), drinking system point 5 (DSP_5); observed species (Sobs, richness), Shannon diversity (H', diversity) and Pielou's evenness (J, evenness), degrees of freedom (df), sum of squares (SS), mean square (MS), F-statistic (FST).

APPENDIX C: SUPPLEMENTARY DATA FOR CHAPTER 5

Table C1 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall seasonal statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	3	6099	2033.16	2.7636	0.05072
Within the groups	54	39727	735.68		
Total	57				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	3	6.092	2.03054	3.107	0.04392
Within the groups	54	35.292	0.65355		
Total	57				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	0.15763	0.052543	3.0233	0.374	0.0474
Within the groups	0.93847	0.017379			
Total	57				

Table C2 Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating seasonal statistical insignificant effect in community

	Sobs	Shannon	Pielou
Spring-Autumn	0.5496104	0.2606409	0.2936929
Summer-Autumn	0.1807409	0.2854198	0.4841075
Winter-Autumn	0.9547221	0.9338375	0.8306824
Summer-Spring	0.8646796	0.9999992	0.9920947
Winter-Spring	0.2641958	0.0806447	0.0525938
Winter-Summer	0.0628875	0.0953833	0.1223847

Table C3 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall monthly statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	11	11532	1048.38	1.4062	0.2026
Within the groups	46	34294	745.52		
Total	57				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	11	10.926	0.99329	1.5002	0.1642
Within the groups	46	30.457	0.66211		
Total	57				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	11	0.31346	0.028497	1.6749	0.1098
Within the groups	46	0.78263	0.017014		
Total	57				

Table C4: Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating monthlyl statistical insignificant effect in community

	Sobs	Shannon	Pielou
August-April	0.9997338	0.9648181	0.8698433
December-April	0.9999744	0.9649250	0.8195695
February-April	0.9678098	0.9558841	0.9245446
January-April	0.8652288	0.9458132	0.9598163
July-April	0.9999353	0.9999860	0.9999972
June-April	0.9991355	0.9999509	0.9999995
March-April	0.9997246	0.9967485	0.9556086
May-April	0.9999506	1.0000000	0.9992683
November-April	0.9999191	0.9934414	0.9703604
October-April	0.9648619	0.6893956	0.4899877
September-April	0.9999999	0.9801701	0.8364756
December-August	1.0000000	1.0000000	1.0000000
February-August	0.9999829	1.0000000	1.0000000
January-August	0.9977982	1.0000000	1.0000000
July-August	0.9514348	0.7335460	0.5837162
June-August	0.8868699	0.6860596	0.6328446
March-August	1.0000000	0.9999999	1.0000000
May-August	0.9553762	0.9862501	0.9994790
November-August	1.0000000	1.0000000	0.9999999
October-August	0.9999772	0.9999547	0.9999632
September-August	0.9999997	1.0000000	1.0000000
February-December	0.9999322	1.0000000	0.9999999
January-December	0.9961847	1.0000000	0.9999998
July-December	0.9836701	0.7535733	0.5314548
June-December	0.9527634	0.7099535	0.5779119
March-December	1.0000000	0.9999995	0.9999987
May-December	0.9853043	0.9854595	0.9975271
November-December	1.0000000	1.0000000	0.9999937
October-December	0.9999146	0.9999938	0.9999997
September-December	1.0000000	1.0000000	1.0000000
January-February	0.9999994	1.0000000	1.0000000
July-February	0.6853428	0.7053560	0.6814448
June-February	0.5478288	0.6565741	0.7277970
March-February	0.9999837	0.9999996	1.0000000
May-February	0.6967265	0.9817394	0.9999216
November-February	0.9999291	1.0000000	1.0000000
October-February	1.0000000	0.9999783	0.9997100
September-February	0.9974893	1.0000000	1.0000000
July-January	0.4840009	0.6982706	0.7833475

June-January	0.3624651	0.6520671	0.8206661
March-January	0.9978495	0.9999961	1.0000000
May-January	0.4950236	0.9750942	0.9999813
November-January	0.9954921	0.9999994	1.0000000
October-January	0.9999996	0.9999991	0.9996822
September-January	0.9689910	1.0000000	1.0000000
June-July	1.0000000	1.0000000	1.0000000
March-July	0.9508057	0.9085956	0.7554875
May-July	1.0000000	0.9998303	0.9689879
November-July	0.9688522	0.8747005	0.8004412
October-July	0.6744759	0.3248390	0.2190566
September-July	0.9960730	0.7938281	0.5352436
March-June	0.8857733	0.8797478	0.7972982
May-June	1.0000000	0.9995670	0.9794475
November-June	0.9189232	0.8403313	0.8382892
October-June	0.5365575	0.2849329	0.2517898
September-June	0.9828009	0.7504131	0.5845419
May-March	0.9547837	0.9993238	0.9999888
November-March	1.0000000	1.0000000	1.0000000
October-March	0.9999782	0.9971045	0.9989008
September-March	0.9999996	1.0000000	0.9999999
November-May	0.9716955	0.9983458	0.9999977
October-May	0.6859632	0.7875454	0.9467130
September-May	0.9966152	0.9933074	0.9988715
October-November	0.9999095	0.9987178	0.9976552
September-November	1.0000000	1.0000000	0.9999994
September-October	0.9970890	0.9998032	0.9999893

Table C5 AMOVA table for distance matrices on Bray-Curtis, unfrac weighted, Jaccard and Unifrac Unweighted on all months, showing significant differences to one another (shown with a *)

Variables	SS	DF	MS	Fs	P-value
Bray Curtis					
april-august-december-january-june-march-may-november-october-september					
Among	5.3121	11	0.482918	1.37916	<0.001*
Within	16.1071	46	0.350155		
Total	21.4192	57			
Jaccard					
april-august-december-january-june-march-may-november-october-september					
Among	4.81554	11	0.437776	1.18943	0.002*
Within	16.9306	46	0.368056		
Total	21.7461	57			
Unweighted					
april-august-december-january-june-march-may-november-october-september					
Among	4.00268	11	0.36388	1.12841	0.056
Within	14.8336	46	0.32247		
Total	18.8363	57			
Weighted					
april-august-december-january-june-march-may-november-october-september					
Among	3.63979	11	0.33089	1.34916	0.005*
Within	11.2818	46	0.245256		
Total	14.9216	57			

Table C6 AMOVA showing distance matrices on Bray-Curtis, Unifrac weighted and Jaccard on all months in relation to one another, showing where the significant difference were found (shown with a *)

	Bray-Curtis	Jaccard	Weighted
April-August	0.019*	0.082	0.167
April-December	0.142	0.308	0.243
April-February	0.488	0.172	0.533
April-January	0.146	0.354	0.511
April-July	0.792	0.075	0.895
April-June	0.503	0.228	0.479
April-March	0.437	0.622	0.585
April-May	0.195	0.32	0.282
April-November	0.499	0.368	0.739
April-October	0.05*	0.273	0.107
April-September	0.089	0.051	0.16
August-December	0.025	0.166	0.147
August-February	0.01*	0.02*	0.063
August-January	0.03*	0.108	0.09
August-July	0.045	0.059	0.079
August-June	0.166	0.149	0.256
August-March	0.006	0.085	0.01*
August-May	0.05*	0.131	0.244
August-November	0.004*	0.084	0.041
August-October	0.004*	0.371	0.033
August-September	0.182	0.684	0.459
December-February	0.281	0.086	0.5
December-January	0.709	0.34	0.736
December-July	0.151	0.036*	0.164
December-June	0.047*	0.191	0.102
December-March	0.144	0.289	0.238
December-May	0.029*	0.254	0.061
December-November	0.434	0.688	0.342
December-October	0.476	0.393	0.574
December-September	0.184	0.355	0.345
February-January	0.24	0.166	0.749
February-July	0.245	0.047*	0.196
February-June	0.163	0.053*	0.187
February-March	0.223	0.127	0.334
February-May	0.016*	0.082	0.027*
February-November	0.138	0.168	0.197
February-October	0.066	0.099	0.33
February-September	0.042*	0.06	0.179

January-July	0.109	0.042*	0.197
January-June	0.041	0.103	0.072
January-March	0.115	0.353	0.274
January-May	0.004*	0.188	0.023*
January-November	0.428	0.343	0.465
January-October	0.229	0.246	0.545
January-September	0.114	0.078	0.19
July-June	0.839	0.194	0.543
July-March	0.274	0.068	0.463
July-May	0.072	0.179	0.082
July-November	0.503	0.09	0.539
July-October	0.051	0.056	0.069
July-September	0.202	0.033*	0.125
June-March	0.145	0.092	0.156
June-May	0.283	0.439	0.195
June-November	0.341	0.301	0.29
June-October	0.021*	0.291	0.027*
June-September	0.234	0.089	0.312
March-May	0.012	0.245	0.028
March-November	0.239	0.306	0.462
March-October	0.004	0.194	0.09
March-September	0.004	0.014	0.025
May-November	0.057	0.352	0.055
May-October	0.035	0.175	0.055
May-September	0.134	0.094	0.096
November-October	0.226	0.591	0.203
November-September	0.158	0.209	0.249
October-September	0.055	0.539	0.087

Table C7 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall sample points statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	3	29596	9865.2	5.2768	0.04668
Within the groups	31	57955	1869.5		
Total	33				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	3	7.310	2.4368	2.1963	0.1084
Within the groups	31	34.395	1.1095		
Total	33				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	3	0.18725	0.062416	2.1024	0.1201
Within the groups	31	0.92033	0.029688		
Total	33				

Table C8 Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating sampling points statistical insignificant effect in community

	Sobs	Shannon	Pielou
F2-F1	0.0266413	0.7140104	0.9990850
F3-F1	0.9999446	0.8103356	0.3954658
F4-F1	0.9646192	0.6281758	0.3189042
F3-F2	0.0243856	0.2052284	0.2993300
F4-F2	0.0062728	0.1111365	0.2334687
F4-F3	0.9480934	0.9878403	0.9987050

Table C9 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall monthly statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	9	19591	2176.8	0.8008	0.6192
Within the groups	25	67960	2718.4		
Total	34				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	9	15.364	1.7071	1.6201	0.1634
Within the groups	25	26.342	1.0537		
Total	34				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	9	0.52929	0.058810	2.5425	0.03158
Within the groups	25	0.57828	0.023131		
Total	34				

Table C10 Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating monthlyl statistical insignificant effect in community

	Sobs	Shannon	Pielou
August-April	1.0000000	0.9999845	0.9944807
December-April	0.9999721	0.9945454	0.9757041
January-April	1.0000000	0.9999999	1.0000000
June-April	0.9999198	0.9998737	0.9999037
March-April	0.9996019	0.9999987	0.9999997
May-April	0.9556910	0.3513110	0.1227330
November-April	1.0000000	1.0000000	1.0000000
October-April	0.9998969	0.9999989	0.9998197
September-April	0.9854156	0.9944443	0.9973489
December-August	0.9996337	0.9309805	0.5760585
January-August	1.0000000	0.9998079	0.9932484
June-August	0.9999971	1.0000000	0.9999965
March-August	0.9999685	1.0000000	0.9996396
May-August	0.9129224	0.1781346	0.0196045
November-August	1.0000000	0.9999720	0.9945449
October-August	0.9990765	0.9985716	0.9999988
September-August	0.9953696	0.9999462	1.0000000
January-December	0.9999963	0.9999442	0.9989436

June-December	0.9893189	0.8895898	0.7960513
March-December	0.9779286	0.9578054	0.9132506
May-December	0.9976074	0.8432784	0.6191145
November-December	0.9997970	0.9982923	0.9906138
October-December	1.0000000	0.9998180	0.7729819
September-December	0.8855480	0.7530655	0.6827831
June-January	0.9999816	0.9993139	0.9996465
March-January	0.9999082	0.9999510	0.9999900
May-January	0.9868107	0.7234449	0.3928135
November-January	1.0000000	1.0000000	1.0000000
October-January	0.9999853	1.0000000	0.9994572
September-January	0.9954085	0.9904430	0.9959466
March-June	1.0000000	0.9999999	0.9999998
May-June	0.7611305	0.1436078	0.0425883
November-June	0.9999986	0.9998258	0.9998586
October-June	0.9821719	0.9955620	1.0000000
September-June	0.9998849	0.9999940	0.9999989
May-March	0.6990298	0.2138928	0.0733153
November-March	0.9999845	0.9999965	0.9999990
October-March	0.9660027	0.9995814	0.9999991
September-March	0.9999807	0.9997562	0.9998524
November-May	0.9391555	0.4746393	0.1991912
October-May	0.9988357	0.5253707	0.0389861
September-May	0.5110696	0.1013409	0.0361831
October-November	0.9994821	0.9999999	0.9997544
September-November	0.9972320	0.9944005	0.9971355
September-October	0.8549698	0.9630523	0.9999997

Table C11 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall seasonal statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	3	2792	930.71	0.3404	0.7962
Within the groups	31	84759	2734.16		
Total	33				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	3	4.369	1.4562	1.209	0.3228
Within the groups	31	37.337	1.2044		
Total	33				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	3	0.20144	0.067146	2.2971	0.09703
Within the groups	31	0.90614	0.029230		
Total	33				

Table C12 Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating seasonal statistical insignificant effect in community

	Sobs	Shannon	Pielou
Spring-Autumn	0.9600365	0.6782276	0.2764247
Summer-Autumn	0.9938473	0.9989927	0.9999470
Winter-Autumn	0.8819051	0.4148561	0.1882456
Summer-Spring	0.9072613	0.6991794	0.3908392
Winter-Spring	0.9932329	0.9596884	0.9875409
Winter-Summer	0.8173568	0.4642062	0.2821734

Table C13 AMOVA table for distance matrices Bray-Curtis, unfrac weighted, Jaccard and Unfrac Unweighted on all seasons in relation to one another, insignificant differences are seen

Variables	SS	DF	MS	Fs	P-value
Bray Curtis					
Autumn-Spring-Summer-Winter					
Among	1.54105	3	0.513682	1.17137	0.072
Within	13.5945	31	0.438531		
Total	15.1355	34			
Jaccard					
Autumn-Spring-Summer-Winter					
Among	1.29001	3	0.430005	0.998441	0.458
Within	13.351	31	0.430676		
Total	14.641	34			
Unweighted					
Autumn-Spring-Summer-Winter					
Among	1.03157	3	0.343857	0.890928	0.829
Within	11.9646	31	0.385953		
Total	12.9961	34			
Weighted					
Autumn-Spring-Summer-Winter					
Among	1.01638	3	0.338793	1.02736	0.404
Within	10.2229	31	0.329771		
Total	11.2393	34			

Table C14 AMOVA table for distance matrices Bray-Curtis, unfrac weighted, Jaccard and Unfrac Unweighted on all months in relation to one another, insignificant difference are seen

Variables	SS	DF	MS	Fs	P-value
Bray Curtis					
april-august-december-january-june-march-may-november-october-september					
Among	4.46371	9	0.495968	1.16187	0.390
Within	10.6718	25	0.426872		
Total	15.1355	34			
Jaccard					
april-august-december-january-june-march-may-november-october-september					
Among	3.66854	9	0.407615	0.928726	0.942
Within	10.9724	25	0.438897		
Total	14.641	34			
Unweighted					
april-august-december-january-june-march-may-november-october-september					
Among	3.11087	9	0.345653	0.874163	0.972
Within	9.88524	25	0.39541		
Total	12.9961	34			
Weighted					
april-august-december-january-june-march-may-november-october-september					
Among	3.21686	9	0.357429	1.11384	0.176
Within	8.02242	25	0.320897		
Total	11.2393	34			

Table C15 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall seasonal statistical insignificant effect in community

Sobs					
	DF	SS	MS	F-value	P-value
Between the groups	1	235.71	235.71	1.9828	0.1709
Within the groups	26	3090.81	118.88		
Total	27				
Shannon					
	DF	SS	MS	F-value	P-value
Between the groups	1	0.4159	0.41589	1.0362	0.3181
Within the groups	26	10.4356	0.40137		
Total	27				
Pielou					
	DF	SS	MS	F-value	P-value
Between the groups	1	0.00114	0.0011446	0.0667	0.7983
Within the groups	26	0.44642	0.0171702		
Total	27				

Table C16 Post hoc Tukey HSD P-values for Sobs, Shannon and Pielou, evaluating seasonal statistical insignificant effect in community

	Sobs	Shannon	Pielou
Winter-Spring	0.1709419	0.3180894	0.7982892

Table C17 ANOVA table and P-values for Sobs, Shannon and Pielou, evaluating an overall monthly statistical insignificant effect in community

	Sobs	Shannon	Pielou
July-August	0.9142372	0.9873752	0.9999439
June-August	0.9989863	0.9999735	1.0000000
November-August	0.8871584	0.9999836	0.9558425
October-August	0.8890957	0.8564130	0.9486079
September-August	0.9905977	0.9872428	0.9961546
June-July	0.7380253	0.9605231	0.9999303
November-July	0.9999999	0.9950657	0.9171068
October-July	0.9999982	0.9990209	0.9914613
September-July	0.9956933	0.9999995	0.9998880
November-June	0.6512060	0.9991570	0.9438331
October-June	0.6404696	0.7172120	0.9336627
September-June	0.9071642	0.9529116	0.9949449
October-November	0.9999999	0.8968365	0.4470462
September-November	0.9952215	0.9955669	0.7204065
September-October	0.9963132	0.9946918	0.9986093

Table C19 Line 2 AMOVA table for distance matrices on Bray-Curtis, unfrac weighted, Jaccard and Unifrac Unweighted on all seasons, showing significant differences to one another (shown with a *)

Variables	SS	DF	MS	Fs	P-value
Bray Curtis					
Spring-Winter					
Among					
Within	8.78942	26	0.338055		
Total	9.36347	27			
Jaccard					
Spring-Winter					
Among					
Within	9.17834	26	0.353013		
Total	9.60987	27			
Unweighted					
Spring-Winter					
Among					
Within	7.91727	26	0.30451		
Total	8.28594	27			
Weighted					
Spring-Winter					
Among					
Within	4.91058	26	0.188869		
Total	5.19565	27			

APPENDIX D: SUPPLEMENTARY DATA FOR CHAPTER 6

Table D1 OTUs classified into the relevant phyla, order and families containing potentially pathogenic bacteria based on their respective taxonomic affiliation provided by MOTHUR.

Family	Phylum	Order	OTU
Acetobacteraceae	Proteobacteria	Rhodospirillales	Otu00190
	Proteobacteria	Rhodospirillales	Otu00304
	Proteobacteria	Rhodospirillales	Otu00331
	Proteobacteria	Rhodospirillales	Otu00355
	Proteobacteria	Rhodospirillales	Otu00456
	Proteobacteria	Rhodospirillales	Otu00601
	Proteobacteria	Rhodospirillales	Otu00737
	Proteobacteria	Rhodospirillales	Otu00946
	Proteobacteria	Rhodospirillales	Otu01044
	Proteobacteria	Rhodospirillales	Otu01341
	Proteobacteria	Rhodospirillales	Otu01749
	Proteobacteria	Rhodospirillales	Otu01826
	Proteobacteria	Rhodospirillales	Otu01834
	Proteobacteria	Rhodospirillales	Otu01836
	Proteobacteria	Rhodospirillales	Otu02023
	Proteobacteria	Rhodospirillales	Otu02169
	Proteobacteria	Rhodospirillales	Otu02294
	Proteobacteria	Rhodospirillales	Otu02486
	Proteobacteria	Rhodospirillales	Otu02643
	Proteobacteria	Rhodospirillales	Otu02783
	Proteobacteria	Rhodospirillales	Otu02874
	Proteobacteria	Rhodospirillales	Otu03099
	Proteobacteria	Rhodospirillales	Otu03139

	Proteobacteria	Rhodospirillales	Otu03206
	Proteobacteria	Rhodospirillales	Otu03690
	Proteobacteria	Rhodospirillales	Otu03694
	Proteobacteria	Rhodospirillales	Otu03721
	Proteobacteria	Rhodospirillales	Otu03724
	Proteobacteria	Rhodospirillales	Otu03731
	Proteobacteria	Rhodospirillales	Otu03954
	Proteobacteria	Rhodospirillales	Otu04197
	Proteobacteria	Rhodospirillales	Otu04316
	Proteobacteria	Rhodospirillales	Otu04330
	Proteobacteria	Rhodospirillales	Otu05085
	Proteobacteria	Rhodospirillales	Otu05094
	Proteobacteria	Rhodospirillales	Otu05095
	Proteobacteria	Rhodospirillales	Otu05097
	Proteobacteria	Rhodospirillales	Otu05099
	Proteobacteria	Rhodospirillales	Otu05842
	Proteobacteria	Rhodospirillales	Otu05843
	Proteobacteria	Rhodospirillales	Otu05847
	Proteobacteria	Rhodospirillales	Otu05853
	Proteobacteria	Rhodospirillales	Otu05877
	Proteobacteria	Rhodospirillales	Otu06132
	Proteobacteria	Rhodospirillales	Otu08611
	Proteobacteria	Rhodospirillales	Otu08613
	Proteobacteria	Rhodospirillales	Otu08625
	Proteobacteria	Rhodospirillales	Otu08629
	Proteobacteria	Rhodospirillales	Otu08686
	Proteobacteria	Rhodospirillales	Otu08692
	Proteobacteria	Rhodospirillales	Otu08693
	Proteobacteria	Rhodospirillales	Otu09137
	Proteobacteria	Rhodospirillales	Otu11819

	Proteobacteria	Rhodospirillales	Otu11822
	Proteobacteria	Rhodospirillales	Otu11825
	Proteobacteria	Rhodospirillales	Otu11826
	Proteobacteria	Rhodospirillales	Otu11832
	Proteobacteria	Rhodospirillales	Otu11833
	Proteobacteria	Rhodospirillales	Otu11839
	Proteobacteria	Rhodospirillales	Otu11843
	Proteobacteria	Rhodospirillales	Otu11846
	Proteobacteria	Rhodospirillales	Otu11847
	Proteobacteria	Rhodospirillales	Otu11851
	Proteobacteria	Rhodospirillales	Otu11856
	Proteobacteria	Rhodospirillales	Otu12040
	Proteobacteria	Rhodospirillales	Otu12054
	Proteobacteria	Rhodospirillales	Otu12059
	Proteobacteria	Rhodospirillales	Otu12062
	Proteobacteria	Rhodospirillales	Otu12063
Aeromonadaceae	Proteobacteria	Aeromonadales	Otu00094
	Proteobacteria	Aeromonadales	Otu01379
Alcaligenaceae	Proteobacteria	Burkholderiales	Otu00393
	Proteobacteria	Burkholderiales	Otu00974
	Proteobacteria	Burkholderiales	Otu01997
	Proteobacteria	Burkholderiales	Otu02037
	Proteobacteria	Burkholderiales	Otu02452
	Proteobacteria	Burkholderiales	Otu06084
	Proteobacteria	Burkholderiales	Otu13236
	Proteobacteria	Burkholderiales	Otu13713
Bacillaceae	Firmicutes	Bacillales	Otu00368
	Firmicutes	Bacillales	Otu00922
	Firmicutes	Bacillales	Otu01127
	Firmicutes	Bacillales	Otu01466

	Firmicutes	Bacillales	Otu01654
	Firmicutes	Bacillales	Otu02392
	Firmicutes	Bacillales	Otu02996
	Firmicutes	Bacillales	Otu03112
	Firmicutes	Bacillales	Otu03730
	Firmicutes	Bacillales	Otu04345
	Firmicutes	Bacillales	Otu05061
	Firmicutes	Bacillales	Otu05164
	Firmicutes	Bacillales	Otu08526
	Firmicutes	Bacillales	Otu08669
	Firmicutes	Bacillales	Otu15864
	Firmicutes	Bacillales	Otu15881
	Firmicutes	Bacillales	Otu15891
	Firmicutes	Bacillales	Otu15914
	Firmicutes	Bacillales	Otu16113
	Firmicutes	Bacillales	Otu16114
	Firmicutes	Bacillales	Otu16119
Bacteroidaceae	Bacteroidetes	Bacteroidales	Otu00754
	Bacteroidetes	Bacteroidales	Otu00847
	Bacteroidetes	Bacteroidales	Otu00970
	Bacteroidetes	Bacteroidales	Otu01521
	Bacteroidetes	Bacteroidales	Otu05144
	Bacteroidetes	Bacteroidales	Otu09846
Bradyrhizobiaceae	Proteobacteria	Rhizobiales	Otu00095
	Proteobacteria	Rhizobiales	Otu00642
	Proteobacteria	Rhizobiales	Otu01445
Brevibacteriaceae	Actinobacteria	Actinomycetales	Otu03701
Burkholderiaceae	Proteobacteria	Burkholderiales	Otu00809
	Proteobacteria	Burkholderiales	Otu01172
	Proteobacteria	Burkholderiales	Otu02122

	Proteobacteria	Burkholderiales	Otu08651
	Proteobacteria	Burkholderiales	Otu08855
	Proteobacteria	Burkholderiales	Otu13673
Campylobacteraceae	Proteobacteria	Campylobacterales	Otu00314
	Proteobacteria	Campylobacterales	Otu00735
	Proteobacteria	Campylobacterales	Otu04505
	Proteobacteria	Campylobacterales	Otu08008
Caulobacteraceae	Proteobacteria	Caulobacterales	Otu00062
	Proteobacteria	Caulobacterales	Otu00172
	Proteobacteria	Caulobacterales	Otu00281
	Proteobacteria	Caulobacterales	Otu00392
	Proteobacteria	Caulobacterales	Otu00458
	Proteobacteria	Caulobacterales	Otu01150
	Proteobacteria	Caulobacterales	Otu01250
	Proteobacteria	Caulobacterales	Otu01551
	Proteobacteria	Caulobacterales	Otu01805
	Proteobacteria	Caulobacterales	Otu02837
	Proteobacteria	Caulobacterales	Otu03479
	Proteobacteria	Caulobacterales	Otu03693
	Proteobacteria	Caulobacterales	Otu04743
	Proteobacteria	Caulobacterales	Otu04744
	Proteobacteria	Caulobacterales	Otu05390
	Proteobacteria	Caulobacterales	Otu05393
	Proteobacteria	Caulobacterales	Otu09166
	Proteobacteria	Caulobacterales	Otu09170
	Proteobacteria	Caulobacterales	Otu09470
	Proteobacteria	Caulobacterales	Otu09473
	Proteobacteria	Caulobacterales	Otu09474
	Proteobacteria	Caulobacterales	Otu09479
Clostridiaceae	Firmicutes	Clostridiales	Otu01509

	Firmicutes	Clostridiales	Otu01612
	Firmicutes	Clostridiales	Otu02544
	Firmicutes	Clostridiales	Otu02720
	Firmicutes	Clostridiales	Otu03486
	Firmicutes	Clostridiales	Otu04001
	Firmicutes	Clostridiales	Otu04106
	Firmicutes	Clostridiales	Otu04814
	Firmicutes	Clostridiales	Otu05306
	Firmicutes	Clostridiales	Otu05327
	Firmicutes	Clostridiales	Otu07784
	Firmicutes	Clostridiales	Otu07791
	Firmicutes	Clostridiales	Otu08025
	Firmicutes	Clostridiales	Otu08394
	Firmicutes	Clostridiales	Otu15363
	Firmicutes	Clostridiales	Otu15458
	Firmicutes	Clostridiales	Otu15459
	Firmicutes	Clostridiales	Otu15474
Comamonadaceae	Proteobacteria	Burkholderiales	Otu00002
	Proteobacteria	Burkholderiales	Otu00059
	Proteobacteria	Burkholderiales	Otu00061
	Proteobacteria	Burkholderiales	Otu00079
	Proteobacteria	Burkholderiales	Otu00090
	Proteobacteria	Burkholderiales	Otu00100
	Proteobacteria	Burkholderiales	Otu00109
	Proteobacteria	Burkholderiales	Otu00125
	Proteobacteria	Burkholderiales	Otu00137
	Proteobacteria	Burkholderiales	Otu00159
	Proteobacteria	Burkholderiales	Otu00222
	Proteobacteria	Burkholderiales	Otu00245
	Proteobacteria	Burkholderiales	Otu00272

	Proteobacteria	Burkholderiales	Otu00330
	Proteobacteria	Burkholderiales	Otu00343
	Proteobacteria	Burkholderiales	Otu00403
	Proteobacteria	Burkholderiales	Otu00413
	Proteobacteria	Burkholderiales	Otu00533
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	Proteobacteria	Burkholderiales	Otu00694
	Proteobacteria	Burkholderiales	Otu00969
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	Proteobacteria	Burkholderiales	Otu01203
	Proteobacteria	Burkholderiales	Otu01403
	Proteobacteria	Burkholderiales	Otu01560
	Proteobacteria	Burkholderiales	Otu01602
	Proteobacteria	Burkholderiales	Otu01708
	Proteobacteria	Burkholderiales	Otu02012
	Proteobacteria	Burkholderiales	Otu02256
	Proteobacteria	Burkholderiales	Otu02322
	Proteobacteria	Burkholderiales	Otu02419
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	Proteobacteria	Burkholderiales	Otu02641
	Proteobacteria	Burkholderiales	Otu03126
	Proteobacteria	Burkholderiales	Otu03130
	Proteobacteria	Burkholderiales	Otu03484
	Proteobacteria	Burkholderiales	Otu03615
	Proteobacteria	Burkholderiales	Otu03878
	Proteobacteria	Burkholderiales	Otu03890
	Proteobacteria	Burkholderiales	Otu04766
	Proteobacteria	Burkholderiales	Otu05978
	Proteobacteria	Burkholderiales	Otu05981

	Proteobacteria	Burkholderiales	Otu06004
	Proteobacteria	Burkholderiales	Otu06014
	Proteobacteria	Burkholderiales	Otu06099
	Proteobacteria	Burkholderiales	Otu06101
	Proteobacteria	Burkholderiales	Otu06103
	Proteobacteria	Burkholderiales	Otu06750
	Proteobacteria	Burkholderiales	Otu08630
	Proteobacteria	Burkholderiales	Otu08642
	Proteobacteria	Burkholderiales	Otu08678
	Proteobacteria	Burkholderiales	Otu08733
	Proteobacteria	Burkholderiales	Otu08888
	Proteobacteria	Burkholderiales	Otu13221
	Proteobacteria	Burkholderiales	Otu13229
	Proteobacteria	Burkholderiales	Otu13231
	Proteobacteria	Burkholderiales	Otu13232
	Proteobacteria	Burkholderiales	Otu13242
	Proteobacteria	Burkholderiales	Otu13252
	Proteobacteria	Burkholderiales	Otu13253
	Proteobacteria	Burkholderiales	Otu13674
	Proteobacteria	Burkholderiales	Otu13689
	Proteobacteria	Burkholderiales	Otu13710
	Proteobacteria	Burkholderiales	Otu13717
Corynebacteriaceae	Actinobacteria	Actinomycetales	Otu00467
	Actinobacteria	Actinomycetales	Otu00517
	Actinobacteria	Actinomycetales	Otu01101
	Actinobacteria	Actinomycetales	Otu01475
	Actinobacteria	Actinomycetales	Otu02104
	Actinobacteria	Actinomycetales	Otu02684
	Actinobacteria	Actinomycetales	Otu08085
	Actinobacteria	Actinomycetales	Otu13605

Enterobacteriaceae	Proteobacteria	Enterobacteriales	Otu00136
	Proteobacteria	Enterobacteriales	Otu00250
	Proteobacteria	Enterobacteriales	Otu01284
	Proteobacteria	Enterobacteriales	Otu03093
	Proteobacteria	Enterobacteriales	Otu03768
	Proteobacteria	Enterobacteriales	Otu03937
	Proteobacteria	Enterobacteriales	Otu07459
	Proteobacteria	Enterobacteriales	Otu07464
	Proteobacteria	Enterobacteriales	Otu11371
	Proteobacteria	Enterobacteriales	Otu11372
	Proteobacteria	Enterobacteriales	Otu11378
Enterococcaceae	Firmicutes	Lactobacillales	Otu02588
	Firmicutes	Lactobacillales	Otu11666
Flavobacteriaceae	Bacteroidetes	Flavobacteriales	Otu00010
	Bacteroidetes	Flavobacteriales	Otu00030
	Bacteroidetes	Flavobacteriales	Otu00069
	Bacteroidetes	Flavobacteriales	Otu00096
	Bacteroidetes	Flavobacteriales	Otu00113
	Bacteroidetes	Flavobacteriales	Otu00117
	Bacteroidetes	Flavobacteriales	Otu00128
	Bacteroidetes	Flavobacteriales	Otu00156
	Bacteroidetes	Flavobacteriales	Otu00161
	Bacteroidetes	Flavobacteriales	Otu00163
	Bacteroidetes	Flavobacteriales	Otu00252
	Bacteroidetes	Flavobacteriales	Otu00267
	Bacteroidetes	Flavobacteriales	Otu00280
	Bacteroidetes	Flavobacteriales	Otu00437
	Bacteroidetes	Flavobacteriales	Otu00487
	Bacteroidetes	Flavobacteriales	Otu00698
	Bacteroidetes	Flavobacteriales	Otu00777

	Bacteroidetes	Flavobacteriales	Otu00896
	Bacteroidetes	Flavobacteriales	Otu00928
	Bacteroidetes	Flavobacteriales	Otu01117
	Bacteroidetes	Flavobacteriales	Otu01157
	Bacteroidetes	Flavobacteriales	Otu01300
	Bacteroidetes	Flavobacteriales	Otu01314
	Bacteroidetes	Flavobacteriales	Otu01319
	Bacteroidetes	Flavobacteriales	Otu01443
	Bacteroidetes	Flavobacteriales	Otu01776
	Bacteroidetes	Flavobacteriales	Otu01859
	Bacteroidetes	Flavobacteriales	Otu02283
	Bacteroidetes	Flavobacteriales	Otu02810
	Bacteroidetes	Flavobacteriales	Otu02827
	Bacteroidetes	Flavobacteriales	Otu03217
	Bacteroidetes	Flavobacteriales	Otu03220
	Bacteroidetes	Flavobacteriales	Otu03331
	Bacteroidetes	Flavobacteriales	Otu03685
	Bacteroidetes	Flavobacteriales	Otu03736
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	Bacteroidetes	Flavobacteriales	Otu03738
	Bacteroidetes	Flavobacteriales	Otu04338
	Bacteroidetes	Flavobacteriales	Otu04832
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	Bacteroidetes	Flavobacteriales	Otu05911
	Bacteroidetes	Flavobacteriales	Otu05913
	Bacteroidetes	Flavobacteriales	Otu06188
	Bacteroidetes	Flavobacteriales	Otu06285
	Bacteroidetes	Flavobacteriales	Otu06382
	Bacteroidetes	Flavobacteriales	Otu06388
	Bacteroidetes	Flavobacteriales	Otu06405

	Bacteroidetes	Flavobacteriales	Otu06406
	Bacteroidetes	Flavobacteriales	Otu06961
	Bacteroidetes	Flavobacteriales	Otu06981
	Bacteroidetes	Flavobacteriales	Otu06982
	Bacteroidetes	Flavobacteriales	Otu06987
	Bacteroidetes	Flavobacteriales	Otu06993
	Bacteroidetes	Flavobacteriales	Otu07160
	Bacteroidetes	Flavobacteriales	Otu07214
	Bacteroidetes	Flavobacteriales	Otu07216
	Bacteroidetes	Flavobacteriales	Otu07258
	Bacteroidetes	Flavobacteriales	Otu13298
	Bacteroidetes	Flavobacteriales	Otu13321
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	Bacteroidetes	Flavobacteriales	Otu13323
	Bacteroidetes	Flavobacteriales	Otu13327
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	Bacteroidetes	Flavobacteriales	Otu13337
	Bacteroidetes	Flavobacteriales	Otu13338
	Bacteroidetes	Flavobacteriales	Otu13371
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	Bacteroidetes	Flavobacteriales	Otu13434
	Bacteroidetes	Flavobacteriales	Otu13462
	Bacteroidetes	Flavobacteriales	Otu13463
Francisellaceae	Proteobacteria	Legionellales	Otu02662
Halomonadaceae	Proteobacteria	Oceanospirillales	Otu03719
	Proteobacteria	Oceanospirillales	Otu07580
	Proteobacteria	Oceanospirillales	Otu09656
Helicobacteraceae	Proteobacteria	Campylobacterales	Otu00806
	Proteobacteria	Campylobacterales	Otu00833

	Proteobacteria	Campylobacterales	Otu10736
Legionellaceae	Proteobacteria	Legionellales	Otu00256
	Proteobacteria	Legionellales	Otu00536
	Proteobacteria	Legionellales	Otu00641
	Proteobacteria	Legionellales	Otu00728
	Proteobacteria	Legionellales	Otu00740
	Proteobacteria	Legionellales	Otu00839
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	Proteobacteria	Legionellales	Otu00883
	Proteobacteria	Legionellales	Otu00889
	Proteobacteria	Legionellales	Otu00990
	Proteobacteria	Legionellales	Otu01182
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	Proteobacteria	Legionellales	Otu01488
	Proteobacteria	Legionellales	Otu01710
	Proteobacteria	Legionellales	Otu01733
	Proteobacteria	Legionellales	Otu01779
	Proteobacteria	Legionellales	Otu01829
	Proteobacteria	Legionellales	Otu02101
	Proteobacteria	Legionellales	Otu02128
	Proteobacteria	Legionellales	Otu02224
	Proteobacteria	Legionellales	Otu02332
	Proteobacteria	Legionellales	Otu02725
	Proteobacteria	Legionellales	Otu02726
	Proteobacteria	Legionellales	Otu02752
	Proteobacteria	Legionellales	Otu02773
	Proteobacteria	Legionellales	Otu03128
	Proteobacteria	Legionellales	Otu03354
	Proteobacteria	Legionellales	Otu03622
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	Proteobacteria	Legionellales	Otu03667
	Proteobacteria	Legionellales	Otu03868
	Proteobacteria	Legionellales	Otu03873
	Proteobacteria	Legionellales	Otu05134
	Proteobacteria	Legionellales	Otu05136
	Proteobacteria	Legionellales	Otu05159
	Proteobacteria	Legionellales	Otu05163
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	Proteobacteria	Legionellales	Otu06606
	Proteobacteria	Legionellales	Otu06669
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	Proteobacteria	Legionellales	Otu15275
	Proteobacteria	Legionellales	Otu15276
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	Proteobacteria	Legionellales	Otu15683
	Proteobacteria	Legionellales	Otu15695
	Proteobacteria	Legionellales	Otu15709
	Proteobacteria	Legionellales	Otu15716
	Proteobacteria	Legionellales	Otu15718
	Proteobacteria	Legionellales	Otu15726
	Proteobacteria	Legionellales	Otu15727
	Proteobacteria	Legionellales	Otu15728
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	Proteobacteria	Legionellales	Otu15733
	Proteobacteria	Legionellales	Otu15735
	Proteobacteria	Legionellales	Otu15738

	Proteobacteria	Legionellales	Otu15739
Leptospiraceae	Spirochaetes	Leptospirales	Otu00930
	Spirochaetes	Leptospirales	Otu01110
Methylobacteriaceae	Proteobacteria	Rhizobiales	Otu00150
	Proteobacteria	Rhizobiales	Otu00335
	Proteobacteria	Rhizobiales	Otu00479
	Proteobacteria	Rhizobiales	Otu01108
	Proteobacteria	Rhizobiales	Otu03134
	Proteobacteria	Rhizobiales	Otu03159
	Proteobacteria	Rhizobiales	Otu04167
	Proteobacteria	Rhizobiales	Otu14066
	Proteobacteria	Rhizobiales	Otu14081
Microbacteriaceae	Actinobacteria	Actinomycetales	Otu00105
	Actinobacteria	Actinomycetales	Otu00158
	Actinobacteria	Actinomycetales	Otu00524
	Actinobacteria	Actinomycetales	Otu00571
	Actinobacteria	Actinomycetales	Otu00873
	Actinobacteria	Actinomycetales	Otu02413
	Actinobacteria	Actinomycetales	Otu02566
	Actinobacteria	Actinomycetales	Otu03464
	Actinobacteria	Actinomycetales	Otu06110
	Actinobacteria	Actinomycetales	Otu13467
	Actinobacteria	Actinomycetales	Otu13737
Micrococcaceae	Actinobacteria	Actinomycetales	Otu00257
	Actinobacteria	Actinomycetales	Otu00457
	Actinobacteria	Actinomycetales	Otu00747
	Actinobacteria	Actinomycetales	Otu00917
	Actinobacteria	Actinomycetales	Otu01401
	Actinobacteria	Actinomycetales	Otu13486
	Actinobacteria	Actinomycetales	Otu13735

Moraxellaceae	Proteobacteria	Pseudomonadales	Otu00007
	Proteobacteria	Pseudomonadales	Otu00282
	Proteobacteria	Pseudomonadales	Otu00284
	Proteobacteria	Pseudomonadales	Otu00318
	Proteobacteria	Pseudomonadales	Otu00383
	Proteobacteria	Pseudomonadales	Otu00386
	Proteobacteria	Pseudomonadales	Otu00454
	Proteobacteria	Pseudomonadales	Otu00474
	Proteobacteria	Pseudomonadales	Otu00598
	Proteobacteria	Pseudomonadales	Otu00878
	Proteobacteria	Pseudomonadales	Otu01210
	Proteobacteria	Pseudomonadales	Otu01565
	Proteobacteria	Pseudomonadales	Otu02240
	Proteobacteria	Pseudomonadales	Otu12247
Mycobacteriaceae	Actinobacteria	Actinomycetales	Otu00076
	Actinobacteria	Actinomycetales	Otu00296
	Actinobacteria	Actinomycetales	Otu01406
	Actinobacteria	Actinomycetales	Otu13499
	Actinobacteria	Actinomycetales	Otu13539
	Actinobacteria	Actinomycetales	Otu13658
	Actinobacteria	Actinomycetales	Otu13709
	Actinobacteria	Actinomycetales	Otu13754
Neisseriaceae	Proteobacteria	Neisseriales	Otu00146
	Proteobacteria	Neisseriales	Otu00406
	Proteobacteria	Neisseriales	Otu00537
	Proteobacteria	Neisseriales	Otu00961
	Proteobacteria	Neisseriales	Otu00976
	Proteobacteria	Neisseriales	Otu01305
	Proteobacteria	Neisseriales	Otu02042
	Proteobacteria	Neisseriales	Otu02806

	Proteobacteria	Neisseriales	Otu04196
	Proteobacteria	Neisseriales	Otu05068
	Proteobacteria	Neisseriales	Otu05069
	Proteobacteria	Neisseriales	Otu05257
	Proteobacteria	Neisseriales	Otu08511
	Proteobacteria	Neisseriales	Otu08519
	Proteobacteria	Neisseriales	Otu08536
	Proteobacteria	Neisseriales	Otu10339
	Proteobacteria	Neisseriales	Otu10341
Nocardiaceae	Actinobacteria	Actinomycetales	Otu02287
	Actinobacteria	Actinomycetales	Otu04830
	Actinobacteria	Actinomycetales	Otu05991
	Actinobacteria	Actinomycetales	Otu08410
	Actinobacteria	Actinomycetales	Otu13542
	Actinobacteria	Actinomycetales	Otu13547
Paenibacillaceae	Firmicutes	Bacillales	Otu00707
	Firmicutes	Bacillales	Otu01469
	Firmicutes	Bacillales	Otu02032
	Firmicutes	Bacillales	Otu02070
	Firmicutes	Bacillales	Otu03702
	Firmicutes	Bacillales	Otu04364
	Firmicutes	Bacillales	Otu08503
	Firmicutes	Bacillales	Otu08514
	Firmicutes	Bacillales	Otu08521
	Firmicutes	Bacillales	Otu08549
	Firmicutes	Bacillales	Otu08655
	Firmicutes	Bacillales	Otu08660
	Firmicutes	Bacillales	Otu08663
	Firmicutes	Bacillales	Otu15845
	Firmicutes	Bacillales	Otu15876

	Firmicutes	Bacillales	Otu15883
	Firmicutes	Bacillales	Otu15884
	Firmicutes	Bacillales	Otu15885
	Firmicutes	Bacillales	Otu15886
	Firmicutes	Bacillales	Otu15915
	Firmicutes	Bacillales	Otu16110
Pasteurellaceae	Proteobacteria	Pasteurellales	Otu00258
Promicromonosporaceae	Actinobacteria	Actinomycetales	Otu04826
Pseudomonadaceae	Proteobacteria	Pseudomonadales	Otu00004
	Proteobacteria	Pseudomonadales	Otu00005
	Proteobacteria	Pseudomonadales	Otu00071
	Proteobacteria	Pseudomonadales	Otu00145
	Proteobacteria	Pseudomonadales	Otu00483
	Proteobacteria	Pseudomonadales	Otu01302
	Proteobacteria	Pseudomonadales	Otu02174
	Proteobacteria	Pseudomonadales	Otu02634
	Proteobacteria	Pseudomonadales	Otu02673
	Proteobacteria	Pseudomonadales	Otu06002
	Proteobacteria	Pseudomonadales	Otu06005
	Proteobacteria	Pseudomonadales	Otu06108
	Proteobacteria	Pseudomonadales	Otu06116
	Proteobacteria	Pseudomonadales	Otu06126
	Proteobacteria	Pseudomonadales	Otu06770
	Proteobacteria	Pseudomonadales	Otu06777
	Proteobacteria	Pseudomonadales	Otu06779
	Proteobacteria	Pseudomonadales	Otu06823
	Proteobacteria	Pseudomonadales	Otu06824
	Proteobacteria	Pseudomonadales	Otu12138
	Proteobacteria	Pseudomonadales	Otu12240
	Proteobacteria	Pseudomonadales	Otu12244

	Proteobacteria	Pseudomonadales	Otu12260
	Proteobacteria	Pseudomonadales	Otu12279
	Proteobacteria	Pseudomonadales	Otu12280
Shewanellaceae	Proteobacteria	Alteromonadales	Otu00724
Sphingobacteriaceae	Bacteroidetes	Sphingobacteriales	Otu00135
	Bacteroidetes	Sphingobacteriales	Otu00177
	Bacteroidetes	Sphingobacteriales	Otu00837
	Bacteroidetes	Sphingobacteriales	Otu01293
	Bacteroidetes	Sphingobacteriales	Otu01545
	Bacteroidetes	Sphingobacteriales	Otu01669
	Bacteroidetes	Sphingobacteriales	Otu01824
	Bacteroidetes	Sphingobacteriales	Otu01957
	Bacteroidetes	Sphingobacteriales	Otu02339
	Bacteroidetes	Sphingobacteriales	Otu02707
	Bacteroidetes	Sphingobacteriales	Otu02935
	Bacteroidetes	Sphingobacteriales	Otu03125
	Bacteroidetes	Sphingobacteriales	Otu03457
	Bacteroidetes	Sphingobacteriales	Otu03499
	Bacteroidetes	Sphingobacteriales	Otu03668
	Bacteroidetes	Sphingobacteriales	Otu03676
	Bacteroidetes	Sphingobacteriales	Otu04059
	Bacteroidetes	Sphingobacteriales	Otu04084
	Bacteroidetes	Sphingobacteriales	Otu04758
	Bacteroidetes	Sphingobacteriales	Otu04767
	Bacteroidetes	Sphingobacteriales	Otu04768
	Bacteroidetes	Sphingobacteriales	Otu04770
	Bacteroidetes	Sphingobacteriales	Otu04774
	Bacteroidetes	Sphingobacteriales	Otu05402
	Bacteroidetes	Sphingobacteriales	Otu05404
	Bacteroidetes	Sphingobacteriales	Otu08618

	Bacteroidetes	Sphingobacteriales	Otu08626
	Bacteroidetes	Sphingobacteriales	Otu08627
	Bacteroidetes	Sphingobacteriales	Otu15178
	Bacteroidetes	Sphingobacteriales	Otu15179
	Bacteroidetes	Sphingobacteriales	Otu15180
	Bacteroidetes	Sphingobacteriales	Otu15181
	Bacteroidetes	Sphingobacteriales	Otu15182
	Bacteroidetes	Sphingobacteriales	Otu15183
	Bacteroidetes	Sphingobacteriales	Otu15184
	Bacteroidetes	Sphingobacteriales	Otu15191
	Bacteroidetes	Sphingobacteriales	Otu15192
	Bacteroidetes	Sphingobacteriales	Otu15194
	Bacteroidetes	Sphingobacteriales	Otu15195
	Bacteroidetes	Sphingobacteriales	Otu15230
	Bacteroidetes	Sphingobacteriales	Otu15300
	Bacteroidetes	Sphingobacteriales	Otu15302
Sphingomonadaceae	Proteobacteria	Sphingomonadales	Otu00012
	Proteobacteria	Sphingomonadales	Otu00039
	Proteobacteria	Sphingomonadales	Otu00081
	Proteobacteria	Sphingomonadales	Otu00119
	Proteobacteria	Sphingomonadales	Otu00124
	Proteobacteria	Sphingomonadales	Otu00129
	Proteobacteria	Sphingomonadales	Otu00239
	Proteobacteria	Sphingomonadales	Otu00251
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	Proteobacteria	Sphingomonadales	Otu00273
	Proteobacteria	Sphingomonadales	Otu00401
	Proteobacteria	Sphingomonadales	Otu00583
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	Proteobacteria	Sphingomonadales	Otu01253
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	Proteobacteria	Sphingomonadales	Otu01426
	Proteobacteria	Sphingomonadales	Otu01484
	Proteobacteria	Sphingomonadales	Otu01549
	Proteobacteria	Sphingomonadales	Otu01763
	Proteobacteria	Sphingomonadales	Otu01771
	Proteobacteria	Sphingomonadales	Otu01823
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	Proteobacteria	Sphingomonadales	Otu04658
	Proteobacteria	Sphingomonadales	Otu07333
	Proteobacteria	Sphingomonadales	Otu07339
	Proteobacteria	Sphingomonadales	Otu07345
	Proteobacteria	Sphingomonadales	Otu07347
	Proteobacteria	Sphingomonadales	Otu07361
	Proteobacteria	Sphingomonadales	Otu07443
	Proteobacteria	Sphingomonadales	Otu07456
	Proteobacteria	Sphingomonadales	Otu07460
	Proteobacteria	Sphingomonadales	Otu07473
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	Proteobacteria	Sphingomonadales	Otu13980
	Proteobacteria	Sphingomonadales	Otu13983
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	Proteobacteria	Sphingomonadales	Otu13986
	Proteobacteria	Sphingomonadales	Otu13989
	Proteobacteria	Sphingomonadales	Otu13991
	Proteobacteria	Sphingomonadales	Otu13993
	Proteobacteria	Sphingomonadales	Otu13995
	Proteobacteria	Sphingomonadales	Otu13996
	Proteobacteria	Sphingomonadales	Otu14009
	Proteobacteria	Sphingomonadales	Otu14038
	Proteobacteria	Sphingomonadales	Otu14047
	Proteobacteria	Sphingomonadales	Otu14114

	Proteobacteria	Sphingomonadales	Otu14119
Staphylococcaceae	Firmicutes	Bacillales	Otu00108
	Firmicutes	Bacillales	Otu15849
	Firmicutes	Bacillales	Otu15878
	Firmicutes	Bacillales	Otu15896
	Firmicutes	Bacillales	Otu15900
	Firmicutes	Bacillales	Otu15907
	Firmicutes	Bacillales	Otu16122
Streptococcaceae	Firmicutes	Lactobacillales	Otu00168
	Firmicutes	Lactobacillales	Otu00444
	Firmicutes	Lactobacillales	Otu00465
	Firmicutes	Lactobacillales	Otu00559
	Firmicutes	Lactobacillales	Otu07622
Vibrionaceae	Proteobacteria	Vibrionales	Otu09583
Xanthomonadaceae	Proteobacteria	Xanthomonadales	Otu00037
	Proteobacteria	Xanthomonadales	Otu00085
	Proteobacteria	Xanthomonadales	Otu00131
	Proteobacteria	Xanthomonadales	Otu00157
	Proteobacteria	Xanthomonadales	Otu00362
	Proteobacteria	Xanthomonadales	Otu00365
	Proteobacteria	Xanthomonadales	Otu00423
	Proteobacteria	Xanthomonadales	Otu00424
	Proteobacteria	Xanthomonadales	Otu00637
	Proteobacteria	Xanthomonadales	Otu00836
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	Proteobacteria	Xanthomonadales	Otu01213
	Proteobacteria	Xanthomonadales	Otu01464
	Proteobacteria	Xanthomonadales	Otu02029
	Proteobacteria	Xanthomonadales	Otu02234
	Proteobacteria	Xanthomonadales	Otu02271

	Proteobacteria	Xanthomonadales	Otu02314
	Proteobacteria	Xanthomonadales	Otu02708
	Proteobacteria	Xanthomonadales	Otu03103
	Proteobacteria	Xanthomonadales	Otu03446
	Proteobacteria	Xanthomonadales	Otu03993
	Proteobacteria	Xanthomonadales	Otu04480
	Proteobacteria	Xanthomonadales	Otu04519
	Proteobacteria	Xanthomonadales	Otu06332
	Proteobacteria	Xanthomonadales	Otu08238
	Proteobacteria	Xanthomonadales	Otu08253
	Proteobacteria	Xanthomonadales	Otu08290
	Proteobacteria	Xanthomonadales	Otu12469
	Proteobacteria	Xanthomonadales	Otu12472
	Proteobacteria	Xanthomonadales	Otu12498
	Proteobacteria	Xanthomonadales	Otu12501
	Proteobacteria	Xanthomonadales	Otu12504
	Proteobacteria	Xanthomonadales	Otu12505
	Proteobacteria	Xanthomonadales	Otu12518
	Proteobacteria	Xanthomonadales	Otu12519
	Proteobacteria	Xanthomonadales	Otu12520
	Proteobacteria	Xanthomonadales	Otu12522
	Proteobacteria	Xanthomonadales	Otu12524
	Proteobacteria	Xanthomonadales	Otu12525
	Proteobacteria	Xanthomonadales	Otu12528

Table D2: OTUs classified into the relevant phyla, order, families and genera containing potentially pathogenic bacteria based on their respective taxonomic affiliation provided by MOTHUR.

Family	Genus	Phylum	Order	OTU
Brevibacteriaceae	Brevibacterium	Actinobacteria	Actinomycetales	Otu03701
Corynebacteriaceae	Corynebacterium	Actinobacteria	Actinomycetales	Otu00467
	Corynebacterium	Actinobacteria	Actinomycetales	Otu00517
	Corynebacterium	Actinobacteria	Actinomycetales	Otu01101
	Corynebacterium	Actinobacteria	Actinomycetales	Otu01475
	Corynebacterium	Actinobacteria	Actinomycetales	Otu02104
	Corynebacterium	Actinobacteria	Actinomycetales	Otu02684
	Corynebacterium	Actinobacteria	Actinomycetales	Otu08085
	Corynebacterium	Actinobacteria	Actinomycetales	Otu13605
Micrococcaceae	Micrococcus	Actinobacteria	Actinomycetales	Otu00747
	Kocuria	Actinobacteria	Actinomycetales	Otu13486
Mycobacteriaceae	Mycobacterium	Actinobacteria	Actinomycetales	Otu00076
	Mycobacterium	Actinobacteria	Actinomycetales	Otu00296
	Mycobacterium	Actinobacteria	Actinomycetales	Otu01406
	Mycobacterium	Actinobacteria	Actinomycetales	Otu13499
	Mycobacterium	Actinobacteria	Actinomycetales	Otu13539
	Mycobacterium	Actinobacteria	Actinomycetales	Otu13658
	Mycobacterium	Actinobacteria	Actinomycetales	Otu13709
	Mycobacterium	Actinobacteria	Actinomycetales	Otu13754
Nocardiaceae	Rhodococcus	Actinobacteria	Actinomycetales	Otu02287
	Rhodococcus	Actinobacteria	Actinomycetales	Otu04830
	Rhodococcus	Actinobacteria	Actinomycetales	Otu05991
	Nocardia	Actinobacteria	Actinomycetales	Otu13542
	Nocardia	Actinobacteria	Actinomycetales	Otu13547
Bacillaceae	Bacillus	Firmicutes	Bacillales	Otu00368
	Bacillus	Firmicutes	Bacillales	Otu00922
	Bacillus	Firmicutes	Bacillales	Otu01127

	Bacillus	Firmicutes	Bacillales	Otu01466
	Bacillus	Firmicutes	Bacillales	Otu01654
	Bacillus	Firmicutes	Bacillales	Otu03730
	Bacillus	Firmicutes	Bacillales	Otu04345
	Bacillus	Firmicutes	Bacillales	Otu08669
	Bacillus	Firmicutes	Bacillales	Otu15864
	Bacillus	Firmicutes	Bacillales	Otu15914
Clostridiaceae	Clostridium	Firmicutes	Clostridiales	Otu02720
	Clostridium	Firmicutes	Clostridiales	Otu03486
	Clostridium	Firmicutes	Clostridiales	Otu04001
	Clostridium	Firmicutes	Clostridiales	Otu04106
	Clostridium	Firmicutes	Clostridiales	Otu05327
	Clostridium	Firmicutes	Clostridiales	Otu07784
	Clostridium	Firmicutes	Clostridiales	Otu08025
	Clostridium	Firmicutes	Clostridiales	Otu08394
	Clostridium	Firmicutes	Clostridiales	Otu15363
	Clostridium	Firmicutes	Clostridiales	Otu15459
	Clostridium	Firmicutes	Clostridiales	Otu15474
Enterococcaceae	Enterococcus	Firmicutes	Lactobacillales	Otu02588
	Enterococcus	Firmicutes	Lactobacillales	Otu11666
Paenibacillaceae	Paenibacillus	Firmicutes	Bacillales	Otu00707
	Paenibacillus	Firmicutes	Bacillales	Otu01469
	Paenibacillus	Firmicutes	Bacillales	Otu02032
	Paenibacillus	Firmicutes	Bacillales	Otu02070
	Paenibacillus	Firmicutes	Bacillales	Otu03702
	Paenibacillus	Firmicutes	Bacillales	Otu08514
	Paenibacillus	Firmicutes	Bacillales	Otu08521
	Paenibacillus	Firmicutes	Bacillales	Otu08549
	Paenibacillus	Firmicutes	Bacillales	Otu08655
	Paenibacillus	Firmicutes	Bacillales	Otu08660

	Paenibacillus	Firmicutes	Bacillales	Otu08663
	Paenibacillus	Firmicutes	Bacillales	Otu15845
	Paenibacillus	Firmicutes	Bacillales	Otu15876
	Paenibacillus	Firmicutes	Bacillales	Otu15883
	Paenibacillus	Firmicutes	Bacillales	Otu15884
	Paenibacillus	Firmicutes	Bacillales	Otu15885
	Paenibacillus	Firmicutes	Bacillales	Otu15886
	Paenibacillus	Firmicutes	Bacillales	Otu15915
	Paenibacillus	Firmicutes	Bacillales	Otu16110
Staphylococcaceae	Staphylococcus	Firmicutes	Bacillales	Otu00108
	Staphylococcus	Firmicutes	Bacillales	Otu15849
	Staphylococcus	Firmicutes	Bacillales	Otu15878
	Staphylococcus	Firmicutes	Bacillales	Otu15896
	Staphylococcus	Firmicutes	Bacillales	Otu15900
	Staphylococcus	Firmicutes	Bacillales	Otu15907
	Staphylococcus	Firmicutes	Bacillales	Otu16122
Streptococcaceae	Streptococcus	Firmicutes	Lactobacillales	Otu00168
	Streptococcus	Firmicutes	Lactobacillales	Otu00444
	Streptococcus	Firmicutes	Lactobacillales	Otu00559
	Streptococcus	Firmicutes	Lactobacillales	Otu07622
Bacteroidaceae	Bacteroides	Bacteroidetes	Bacteroidales	Otu00754
	Bacteroides	Bacteroidetes	Bacteroidales	Otu00847
	Bacteroides	Bacteroidetes	Bacteroidales	Otu00970
	Bacteroides	Bacteroidetes	Bacteroidales	Otu01521
	Bacteroides	Bacteroidetes	Bacteroidales	Otu05144
	Bacteroides	Bacteroidetes	Bacteroidales	Otu09846
Flavobacteriaceae	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00010
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00069
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00096
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00113

	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00117
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00128
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00156
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00161
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00163
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00252
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00267
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00280
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00437
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00487
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00698
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00777
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00896
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu00928
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01117
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01300
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01314
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01319
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01776
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu01859
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu02283
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu02810
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu02827
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu03220
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu03685
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu04338
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu04832
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu04843
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu05911
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu05913

	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06188
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06388
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06406
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06961
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06981
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu06987
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13298
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13322
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13323
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13327
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13337
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13433
	Flavobacterium	Bacteroidetes	Flavobacteriales	Otu13462
Sphingobacteriaceae	Sphingobacterium	Bacteroidetes	Sphingobacteriales	Otu01669
	Sphingobacterium	Bacteroidetes	Sphingobacteriales	Otu15194
Bradyrhizobiaceae	Bosea	Proteobacteria	Rhizobiales	Otu01445
Caulobacteraceae	Caulobacter	Proteobacteria	Caulobacterales	Otu00392
	Caulobacter	Proteobacteria	Caulobacterales	Otu00458
	Brevundimonas	Proteobacteria	Caulobacterales	Otu01250
Methylobacteriaceae	Methylobacterium	Proteobacteria	Rhizobiales	Otu00150
	Methylobacterium	Proteobacteria	Rhizobiales	Otu01108
	Methylobacterium	Proteobacteria	Rhizobiales	Otu03134
	Methylobacterium	Proteobacteria	Rhizobiales	Otu14066
	Methylobacterium	Proteobacteria	Rhizobiales	Otu14081
Sphingomonadaceae	Novosphingobium	Proteobacteria	Sphingomonadales	Otu00012
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu00039
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu00273
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu00583
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu00708
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu01115

	Novosphingobium	Proteobacteria	Sphingomonadales	Otu01301
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu01771
	Novosphingobium	Proteobacteria	Sphingomonadales	Otu02300
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu02470
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu02520
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu02632
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu03836
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu03839
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu04317
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu04641
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu04643
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu04652
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu04658
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu07347
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu07456
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13973
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13985
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13991
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13993
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13995
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu13996
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu14009
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu14038
	Sphingomonas	Proteobacteria	Sphingomonadales	Otu14114
Acetobacteraceae	Roseomonas	Proteobacteria	Rhodospirillales	Otu00355
	Roseomonas	Proteobacteria	Rhodospirillales	Otu00601
	Roseomonas	Proteobacteria	Rhodospirillales	Otu03099
	Roseomonas	Proteobacteria	Rhodospirillales	Otu05099
	Roseomonas	Proteobacteria	Rhodospirillales	Otu12040
Comamonadaceae	Acidovorax	Proteobacteria	Burkholderiales	Otu08642

Alcaligenaceae	Alcaligenes	Proteobacteria	Burkholderiales	Otu01997
Burkholderiaceae	Burkholderia	Proteobacteria	Burkholderiales	Otu00809
	Burkholderia	Proteobacteria	Burkholderiales	Otu01172
	Burkholderia	Proteobacteria	Burkholderiales	Otu02122
	Burkholderia	Proteobacteria	Burkholderiales	Otu08651
	Burkholderia	Proteobacteria	Burkholderiales	Otu13673
Neisseriaceae	Eikenella	Proteobacteria	Neisseriales	Otu02042
	Chromobacterium	Proteobacteria	Neisseriales	Otu02806
Moraxellaceae	Acinetobacter	Proteobacteria	Pseudomonadales	Otu00007
	Acinetobacter	Proteobacteria	Pseudomonadales	Otu00386
	Acinetobacter	Proteobacteria	Pseudomonadales	Otu00454
	Acinetobacter	Proteobacteria	Pseudomonadales	Otu00598
	Acinetobacter	Proteobacteria	Pseudomonadales	Otu01565
Aeromonadaceae	Aeromonas	Proteobacteria	Aeromonadales	Otu00094
Pseudomonadaceae	Pseudomonas	Proteobacteria	Pseudomonadales	Otu00004
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu00005
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu00071
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu00145
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu02174
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu02634
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu02673
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06002
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06005
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06116
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06126
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06770
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06777
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06779
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06823
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu06824

	Pseudomonas	Proteobacteria	Pseudomonadales	Otu12240
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu12244
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu12260
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu12279
	Pseudomonas	Proteobacteria	Pseudomonadales	Otu12280
Enterobacteriaceae	Escherichia	Proteobacteria	Enterobacteriales	Otu00136
	Yersinia	Proteobacteria	Enterobacteriales	Otu01284
Halomonadaceae	Halomonas	Proteobacteria	Oceanospirillales	Otu03719
	Halomonas	Proteobacteria	Oceanospirillales	Otu07580
	Halomonas	Proteobacteria	Oceanospirillales	Otu09656
Legionellaceae	Legionella	Proteobacteria	Legionellales	Otu00536
	Legionella	Proteobacteria	Legionellales	Otu00641
	Legionella	Proteobacteria	Legionellales	Otu00728
	Legionella	Proteobacteria	Legionellales	Otu00990
	Legionella	Proteobacteria	Legionellales	Otu01326
	Legionella	Proteobacteria	Legionellales	Otu01829
	Legionella	Proteobacteria	Legionellales	Otu02332
	Legionella	Proteobacteria	Legionellales	Otu02725
	Legionella	Proteobacteria	Legionellales	Otu02752
	Legionella	Proteobacteria	Legionellales	Otu03128
	Legionella	Proteobacteria	Legionellales	Otu03654
	Legionella	Proteobacteria	Legionellales	Otu03868
	Legionella	Proteobacteria	Legionellales	Otu05134
	Legionella	Proteobacteria	Legionellales	Otu05136
	Legionella	Proteobacteria	Legionellales	Otu06606
	Legionella	Proteobacteria	Legionellales	Otu06669
	Legionella	Proteobacteria	Legionellales	Otu06734
	Legionella	Proteobacteria	Legionellales	Otu15679
	Legionella	Proteobacteria	Legionellales	Otu15716
	Legionella	Proteobacteria	Legionellales	Otu15735

	Legionella	Proteobacteria	Legionellales	Otu15738
	Legionella	Proteobacteria	Legionellales	Otu15739
Shewanellaceae	Shewanella	Proteobacteria	Alteromonadales	Otu00724
Xanthomonadaceae	Stenotrophomonas	Proteobacteria	Xanthomonadales	Otu00037
	Stenotrophomonas	Proteobacteria	Xanthomonadales	Otu01213
	Stenotrophomonas	Proteobacteria	Xanthomonadales	Otu12498
	Stenotrophomonas	Proteobacteria	Xanthomonadales	Otu12522
Vibrionaceae	Vibrio	Proteobacteria	Vibrionales	Otu09583
Campylobacteraceae	Arcobacter	Proteobacteria	Campylobacterales	Otu00314
	Arcobacter	Proteobacteria	Campylobacterales	Otu00735
	Campylobacter	Proteobacteria	Campylobacterales	Otu04505
	Campylobacter	Proteobacteria	Campylobacterales	Otu08008

Table D3: OTUs classified into the relevant phyla, order, families and genera closely related to the potentially pathogenic bacterial strains.

Family	Phylum	Genus	Species	OTU
Acetobacteraceae	Proteobacteria	unclassified	unclassified	Otu01044
Aeromonadaceae	Proteobacteria	Aeromonas	unclassified	Otu00094
Alcaligenaceae	Proteobacteria	Alcaligenes	faecalis	Otu01997
Bacillaceae	Firmicutes	Bacillus	unclassified	Otu01654
Bacteroidaceae	Bacteroidetes	Bacteroides	unclassified	Otu00754
	Bacteroidetes	Bacteroides	ovatus	Otu00970
	Bacteroidetes	Bacteroides	unclassified	Otu05144

Burkholderiaceae	Proteobacteria	Burkholderia	bryophila	Otu00809
	Proteobacteria	Burkholderia	unclassified	Otu01172
Caulobacteraceae	Proteobacteria	Caulobacter	vibrioides	Otu00392
Comamonadaceae	Proteobacteria	unclassified	unclassified	Otu00002
	Proteobacteria	unclassified	unclassified	Otu03484
Corynebacteriaceae	Actinobacteria	Corynebacterium	unclassified	Otu01101
	Actinobacteria	Corynebacterium	unclassified	Otu00517
Enterobacteriaceae	Proteobacteria	Escherichia	coli	Otu00136
	Proteobacteria	unclassified	unclassified	Otu00250
	Proteobacteria	Yersinia	unclassified	Otu01284
Enterococcaceae	Firmicutes	Enterococcus	unclassified	Otu02588
Legionellaceae	Proteobacteria	Legionella	unclassified	Otu02725
Methylobacteriaceae	Proteobacteria	Methylobacterium	hispanicum	Otu00150
	Proteobacteria	Magnetospirillum	magnetotacticum	Otu00479
Microbacteriaceae	Actinobacteria	unclassified	unclassified	Otu00873
Micrococcaceae	Actinobacteria	Micrococcus	luteus	Otu00747
Moraxellaceae	Proteobacteria	Enhydrobacter	unclassified	Otu00282
	Proteobacteria	Acinetobacter	lwoffii	Otu00598
Mycobacteriaceae	Actinobacteria	Mycobacterium	unclassified	Otu00076
	Actinobacteria	Mycobacterium	unclassified	Otu01406
Neisseriaceae	Proteobacteria	Eikenella	unclassified	Otu02042
	Proteobacteria	Chromobacterium	unclassified	Otu02806
Paenibacillaceae	Firmicutes	Paenibacillus	lautus	Otu15845
Pseudomonadaceae	Proteobacteria	Pseudomonas	unclassified	Otu00071
	Proteobacteria	Pseudomonas	stutzeri	Otu02634
Shewanellaceae	Proteobacteria	Shewanella	unclassified	Otu00724
Sphingobacteriaceae	Bacteroidetes	Sphingobacterium	multivorum	Otu01669
Sphingomonadaceae	Proteobacteria	Novosphingobium	unclassified	Otu00039
	Proteobacteria	unclassified	unclassified	Otu01823
	Proteobacteria	Sphingomonas	unclassified	Otu04658

Staphylococcaceae	Firmicutes	Staphylococcus	unclassified	Otu00108
Streptococcaceae	Firmicutes	Streptococcus	infantis	Otu00168
Xanthomonadaceae	Proteobacteria	Stenotrophomonas	geniculata	Otu12498

Table D4: OTUs which are potential bacterial pathogens.

OUT	MOTHUR Taxonomy Classification- Phylum/ Family/ Genus/ Species	Strain/s closely related to in combined phylogenetic tree	LTPs Accession number	Pathogenic strain/s closely related to in phylogenetic sub-trees	Accession number	Reference
Otu00039	Proteobacteria/ Sphingomonadacea e/ Novosphingobium	<i>Novosphingobium aromaticivorans</i>	CP000248	<i>Novosphingobium aromaticivorans</i>	CP000248	2007 Kampfer <i>et al.</i> , 2010 Zhang <i>et al.</i> , 2013 Abraham <i>et al.</i> , 2013 Glaeser <i>et al.</i> , 2014 Feng <i>et al.</i> , 2014 Han <i>et al.</i> , 2014 Huang <i>et al.</i> , 2014 Lee <i>et al.</i> , 2014 Kampfer <i>et al.</i> , 2016 Chen <i>et al.</i> , 2016 Feng <i>et al.</i> , 2016 Sheu <i>et al.</i> , 2016 Zhang <i>et al.</i>

Otu00094	Proteobacteria/ Aeromonadaceae/ Aeromonas	<i>Aeromonas caviae</i> ; <i>Aeromonas veronii</i> ; <i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ; <i>Aeromonas jandaei</i>	X74674; X60414; DQ207728; X60413	<i>Aeromonas caviae</i>, <i>Aeromonas veronii</i>; <i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i>; <i>Aeromonas jandaei</i>	X74674, X60410	1993 Collins <i>et al.</i> , 2003 Huys <i>et al.</i> , 2004 Minana-galbis <i>et al.</i> , 2006 Saha <i>et al.</i> , 2007 Nhung <i>et al.</i> , 2010 Alperi <i>et al.</i> , 2011 Figueras <i>et al.</i> , 2013 Aravena-roman <i>et al.</i>
Otu00108	Firmicutes/ Staphylococcaceae/ Staphylococcus	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ; <i>Staphylococcus capitis</i> subsp. <i>capitis</i> ; <i>Staphylococcus epidermis</i> ; <i>Staphylococcus lugdunensis</i> ; <i>Staphylococcus warneri</i>	L36472; L37599; D83363; AB009941; L37603	<i>Staphylococcus warneri</i>, <i>Staphylococcus lugdunensis</i>, <i>Staphylococcus epidermidis</i>, <i>Staphylococcus capitis</i> subsp. <i>capitis</i>, <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	L37603, AB009941, D83363, L37599, L36472	2005 Devriese <i>et al.</i> , 2010 Masalma <i>et al.</i> , 2010 Novakova <i>et al.</i> , 2010 Riesen <i>et al.</i> , 2010 Supre <i>et al.</i> , 2013 de Bel <i>et al.</i> , 2015 Svec <i>et al.</i>
Otu00136	Proteobacteria/ Enterobacteriaceae/ Escherichia/ coli	<i>Escherichia coli</i> ; <i>Escherichia fergusonii</i> ; <i>Shigella sonnei</i> ; <i>Shigella flexneri</i>	X80725; AF530475; FR870445; X96963	<i>Escherichia coli</i>, <i>Escherichia fergusonii</i>, <i>Shigella sonnei</i>, <i>Shigella flexneri</i>	AJ508775, X80725, AF530475, FR870445, X96963	2013 Lagier <i>et al.</i> , 2014 Gu <i>et al.</i> , 2015 Kampfer <i>et al.</i> , 2015 Liu <i>et al.</i> , 2016 Doijad <i>et al.</i>
Otu00150	Proteobacteria/ Methylobacteriaceae/ Methylobacterium/ hispanicum	<i>Methylobacterium mesophilicum</i> ; <i>Methylobacterium radiotolerans</i>	AB175636; D32227	<i>Methylobacterium radiotolerans</i>, <i>Methylobacterium mesophilicum</i>	AB175649, D32227	2011 Chauer <i>et al.</i> , 2012 Tani <i>et al.</i> , 2013 Tani <i>et al.</i> , 2013 Veyisoglu <i>et al.</i> , 2013 Wellner <i>et al.</i> , 2014 Madhaiyan <i>et al.</i>

Otu00168	Firmicutes/ Streptococcaceae/ Streptococcus/ infantis	<i>Streptococcus parasanguinis</i>	AF003933	<i>Streptococcus parasanguinis</i>	AF003933	2002 Woo <i>et al.</i> , 2008 Takada <i>et al.</i> , 2014 Saito <i>et al.</i> , 2015 Nomoto <i>et al.</i> , 2015 Vela <i>et al.</i> , 2016 Saito <i>et al.</i>
Otu00250	Proteobacteria/ Enterobacteriaceae	<i>Klebsiella pneumoniae subsp. pneumoniae</i> ; <i>Enterobacter intermedius</i> ; <i>Enterobacterhorma echei</i> ; <i>Enterobacter cancerogenus</i> ; <i>Enterobacter aerogenes</i> ; <i>Enterobacter asburiae</i>	X87276; AF310217; AJ508302; Z96078; AB004750; AB004744	<i>Klebsiella pneumoniae subsp. pneumoniae</i> ; <i>Enterobacter intermedius</i> ; <i>Enterobacter hormaechei</i> ; <i>Enterobacter cancerogenus</i> ; <i>Enterobacter aerogenes</i> ; <i>Enterobacter asburiae</i>	X87276, Y17657	2010 Xu <i>et al.</i>
Otu00282	Proteobacteria/ Moraxellaceae/ Enhydrobacter	<i>Moraxella osloensis</i>	JN175341	<i>Moraxella osloensis</i>	JN175341	2005 Xie <i>et al.</i> , 2007 Angelos <i>et al.</i> , 2009 Hennessee <i>et al.</i> , 2010 Vela <i>et al.</i> , 2014 Abbas <i>et al.</i> , 2014 Feng <i>et al.</i> , 2014 Li <i>et al.</i> , 2014 Smet <i>et al.</i> , 2015 Krizova <i>et al.</i> , 2015 Li <i>et al.</i> , 2016 Poppel <i>et al.</i>
Otu00479	Proteobacteria/ Methylobacteriaceae/ Magnetospirillum/ magnetotacticum	<i>Methylobacterium aminovorans</i>	AB175629	<i>Methylobacterium aminovorans</i>	D32224, AB175629	2011 Chauer <i>et al.</i> , 2012 Tani <i>et al.</i> , 2013 Tani <i>et al.</i> , 2013 Veyisoglu <i>et al.</i> , 2013 Wellner <i>et al.</i> , 2014 Madhaiyan <i>et al.</i>
Otu00517	Actinobacteria/ Corynebacteriaceae / Corynebacterium	<i>Corynebacterium tuberculostearicum</i>	AJ438050	<i>Corynebacterium tuberculostearicum</i>	AJ438050	2004 Feurer <i>et al.</i> , 2011 Wu <i>et al.</i> , 2013 Wiertz <i>et al.</i> , 2015 Baumgardt <i>et al.</i> , 2015 Kampfer <i>et al.</i>

Otu00747	Actinobacteria/ Micrococcaceae/ Micrococcus/ luteus	<i>Micrococcus luteus</i>	AJ536198	<i>Micrococcus luteus</i>	AJ536198, KF524364	1995 Stackerbrandt <i>et al.</i> , 2000 Liu <i>et al.</i> , 2003 Tang <i>et al.</i> , 2007 Liu <i>et al.</i> , 2009 Chen <i>et al.</i> , 2009 Zhao <i>et al.</i> , 2013 Rieser <i>et al.</i>
Otu00754	Bacteroidetes/ Bacteroidaceae/ Bacteroides	<i>Bacteroides vulgatus</i>	AJ867050	<i>Bacteroides vulgatus</i>	AJ867050	2005 Whitehead <i>et al.</i> , 2006 Thi ngoc lan <i>et al.</i> , 2010 Kim <i>et al.</i> , 2010 Sakamoto <i>et al.</i> , 2010 Watanabe <i>et al.</i> , 2011 Ueki <i>et al.</i> , 2012 Sakamoto <i>et al.</i> , 2014 Hatamoto <i>et al.</i> , 2015 Saptura <i>et al.</i>
Otu01172	Proteobacteria/ Burkholderiaceae/ Burkholderia	<i>Burkholderia pseudomallei</i>	DQ108392	<i>Burkholderia pseudomallei</i>	DQ108392, U96931	1998 Brett <i>et al.</i> , 2006 Glass <i>et al.</i> , 2010 Aizawa <i>et al.</i> , 2011 Otsuka., 2015 Smet <i>et al.</i> , 2016 Peeters <i>et al.</i>
Otu01284	Proteobacteria/ Enterobacteriaceae/ Yersinia	<i>Yersinia enterocolitica</i> <i>subsp. enterocolitica</i> ; <i>Serratia liquefaciens</i> ; <i>Serratia plymuthica</i>	AF366378; AJ306725; AJ233433	<i>Yersinia enterocolitica</i> <i>subsp. enterocolitica</i>, <i>Serratia liquefaciens</i>, <i>Serratia plymuthica</i>	AF366378, AF366376	2008 Merhej <i>et al.</i> , 2008 Sprague <i>et al.</i> , 2011 Hurst <i>et al.</i> , 2011 Murros-kontinen <i>et al.</i>
Otu01406	Actinobacteria/ Mycobacteriaceae/ Mycobacterium	<i>Mycobacterium lentiflavum</i> ; <i>Mycobacterium genavense</i> ; <i>Mycobacterium montefiorensis</i> ; <i>Mycobacterium simiae</i>	AF480583; X60070; AF330038; X52931	<i>Mycobacterium simiae</i>, <i>Mycobacterium montefiorensis</i>, <i>Mycobacterium lentiflavum</i>, <i>Mycobacterium genavense</i>	AJ616230, X52931, AF330038, AF480583, X60070	2003 Levi <i>et al.</i> , 2005 Tortoli <i>et al.</i> , 2011 Tortoli <i>et al.</i> , 2013 Kim <i>et al.</i> , 2013 Shojaei <i>et al.</i> , 2013 Zhang <i>et al.</i> , 2014 Kim <i>et al.</i>
Otu01654	Firmicutes/ Bacillaceae/ Bacillus	<i>Bacillus cereus</i>	AE016877	<i>Bacillus cereus</i>	AE016877, AB190217	1998 Nakamura <i>et al.</i> , 2006 Shivaji <i>et al.</i> , 2007 Peak <i>et al.</i> , 2012 Seiler <i>et al.</i> , 2013 Guinebreiere <i>et al.</i> , 2016 Liu <i>et al.</i> , 2016 Miller <i>et al.</i>

Otu01997	Proteobacteria/ Alcaligenaceae/ Alcaligenes/ faecalis	<i>Alcaligenes faecalis</i> <i>subsp. faecalis</i>	D88008	<i>Alcaligenes faecalis subsp. faecalis</i>	D88008	2005 van Trappen <i>et al.</i>
Otu02588	Firmicutes/ Enterococcaceae/ Enterococcus	<i>Enterococcus</i> <i>durans</i> ; <i>Enterococcus</i> <i>faecalis</i> ; <i>Enterococcus</i> <i>faecium</i> ; <i>Enterococcus</i> <i>hirae</i>	AJ276354; AB012212; AJ301830; Y17302	<i>Enterococcus durans</i>; <i>Enterococcus faecalis</i>; <i>Enterococcus faecium</i>; <i>Enterococcus hirae</i>	AJ276354; AB012212; AJ301830; Y17302	2003 de Graef <i>et al.</i> , 2005 Naser <i>et al.</i> , 2005 Svec <i>et al.</i> , 2006 Cavalho <i>et al.</i> , 2007 Sukontasing <i>et al.</i> , 2013 Chen <i>et al.</i> , 2013 Frolkova <i>et al.</i> , 2013 Kim <i>et al.</i> , 2013 van Leeuwenhoek <i>et al.</i> , 2014 Li <i>et al.</i> , 2014 Lucena-padros <i>et al.</i>