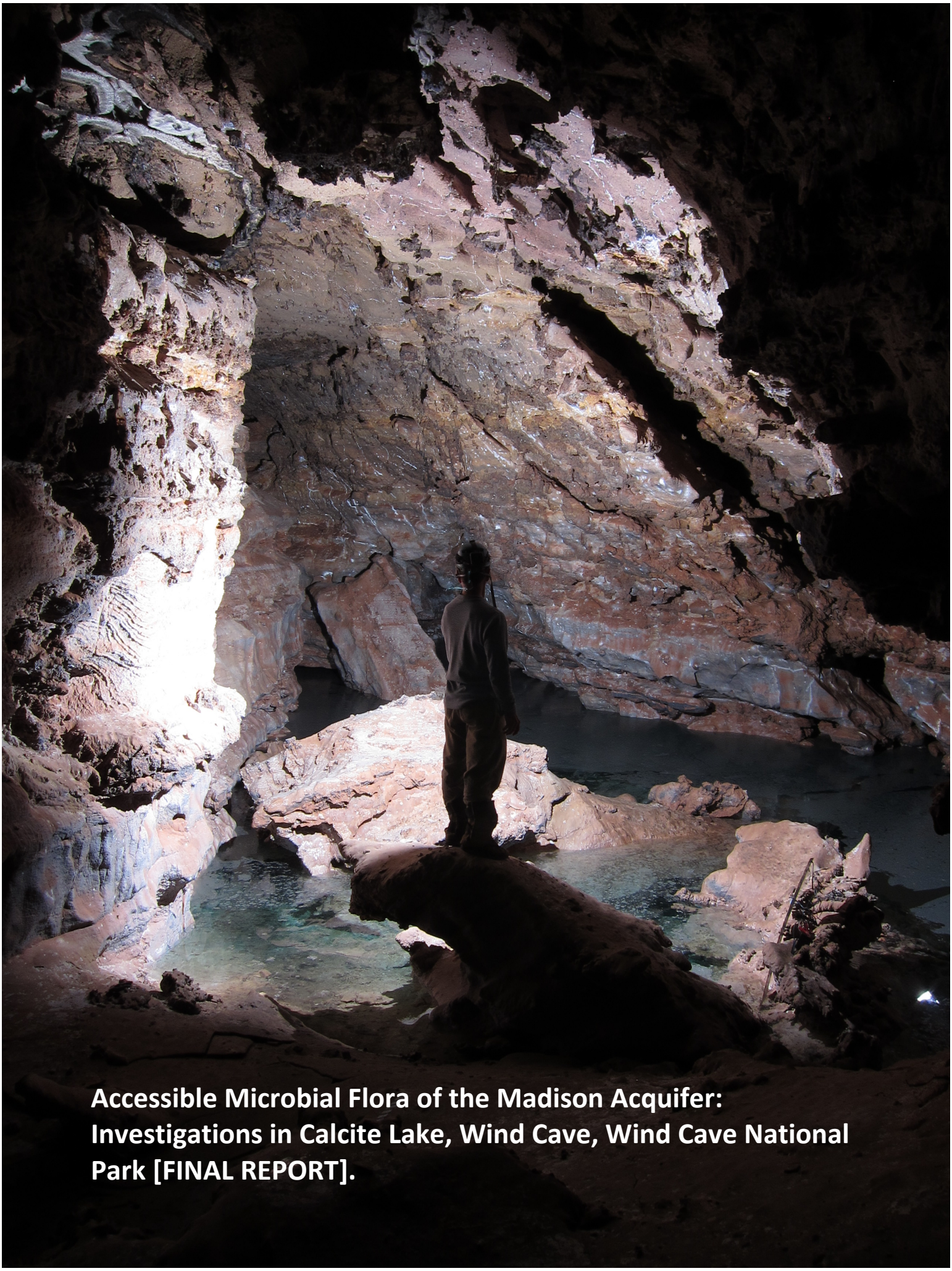


Accessible Microbial Flora of the Madison Acquifer: Investigations in Calcite Lake, Wind Cave, Wind Cave National Park [FINAL REPORT].

October 31, 2011
Amended June 23, 2012
Report to the NPS Water Sources Division

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ACKNOWLEDGEMENTS

This report describes something quite remarkable: under the difficult conditions of a cave, with size, power and weight limitations, we have been able to filter 200 L of water to examine one of the most unique microbial environments on Earth. It could not have been done without the work of Andrew Wallace, Juan Giarrizzo, Michael Barton, Michael Johnston, and the support of the staff at Wind Cave National Park, particularly Marc Ohms (who made things work, when the logistics seemed insurmountable) and Rod Horrocks for valuable maps and data. Finally, none of this would have happened without the perseverance of Jeff Hughes, hydrologist for the National Park Service. From in-cave assistance to magic money when we needed it the most, Jeff was always there. Thanks Jeff.

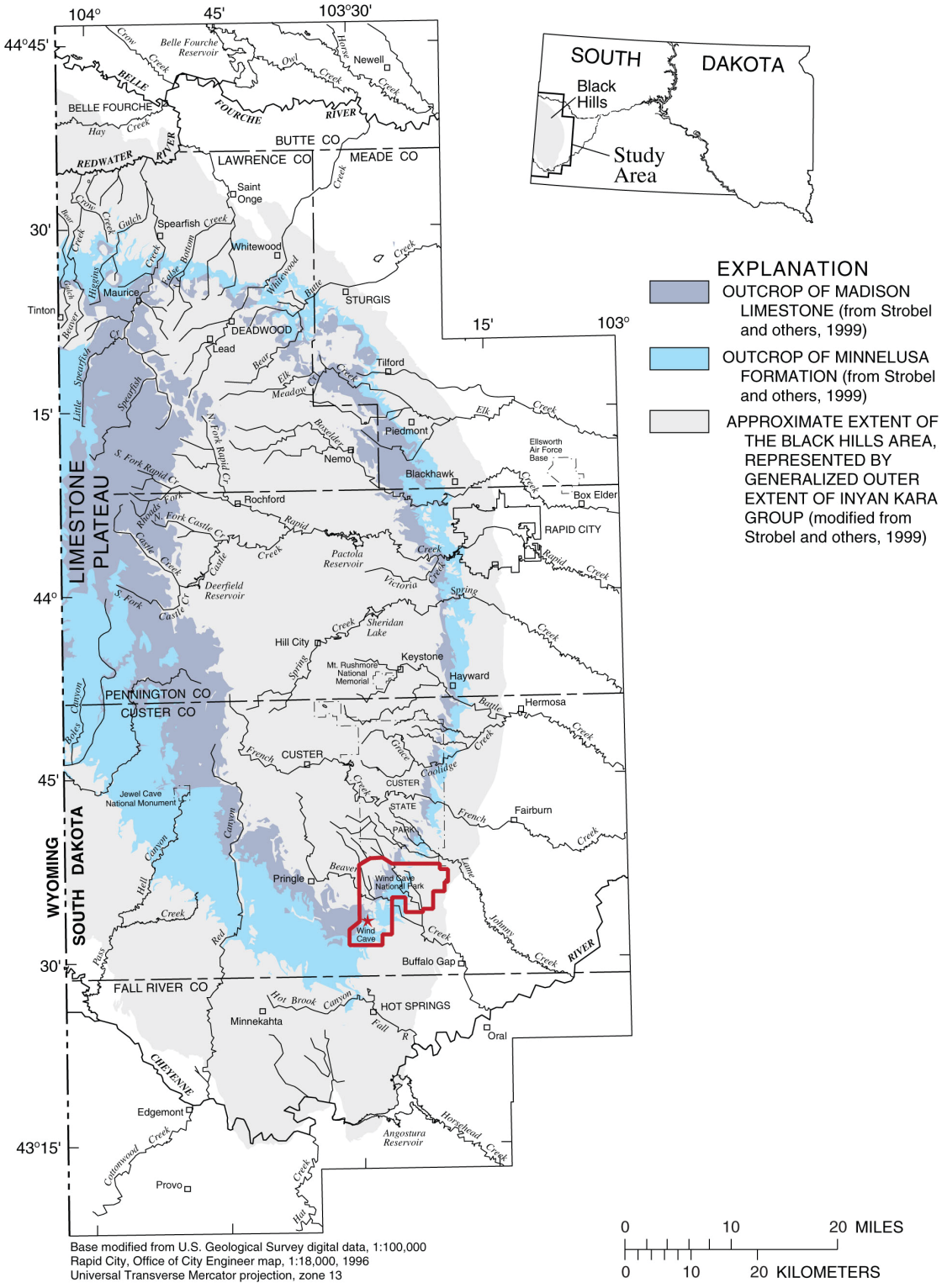


Figure 1. Generalized geology of the Black Hills area surrounding Wind Cave National Park, including the approximate location of the Madison and Minnelusa outcrops. The location of the park is show (in red) as is the location of Wind Cave (red star). From Naus, Driscoll and Carter 2001).

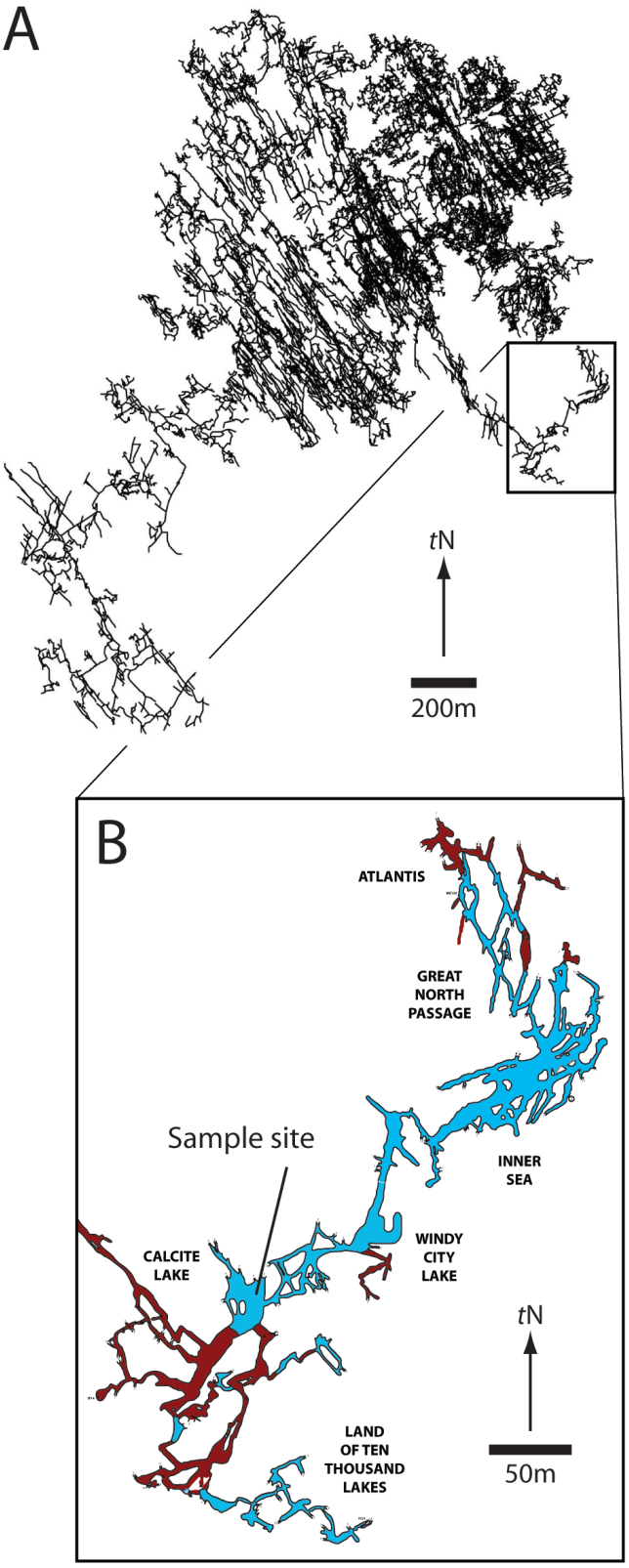


Figure 2. Line plot of Wind Cave (A) and relative location of the lakes complex (B). The location of the lakes sampling site is shown (B) (maps courtesy of Rod Horrocks, Marc Ohms, and Wind Cave National Park).

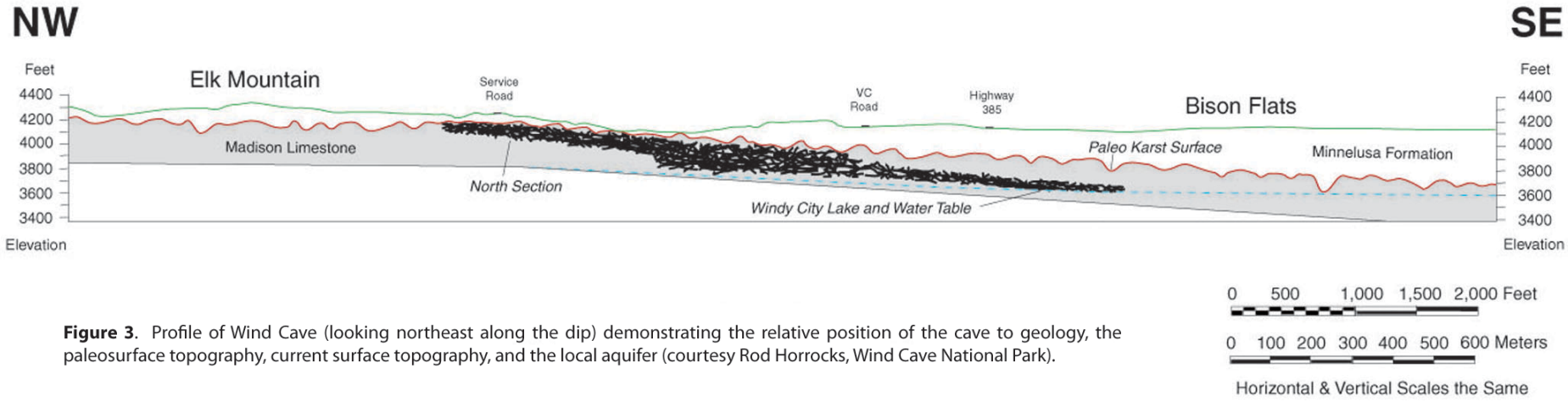


Figure 3. Profile of Wind Cave (looking northeast along the dip) demonstrating the relative position of the cave to geology, the paleosurface topography, current surface topography, and the local aquifer (courtesy Rod Horrocks, Wind Cave National Park).

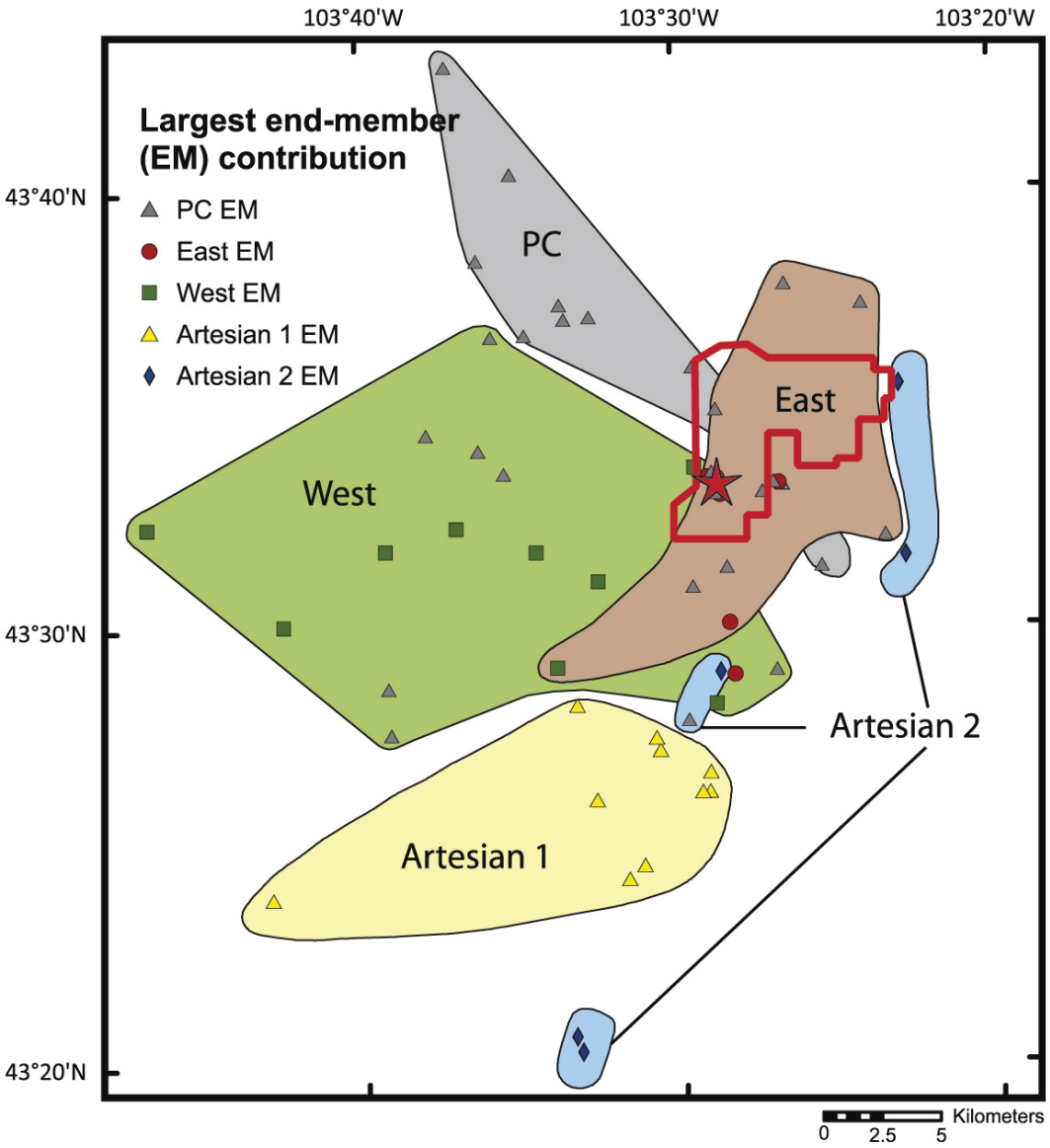


Figure 4. Generalized location of aquifers around the Wind Cave National Park region. The West, Artesian 1 and Artesian 2 represent the Madison aquifer regional flow, while PC represents waters recharging the aquifer from the Precambrian rocks of the central Black Hills and the East represents a locally recharged aquifer (from Long and Vader 2011).

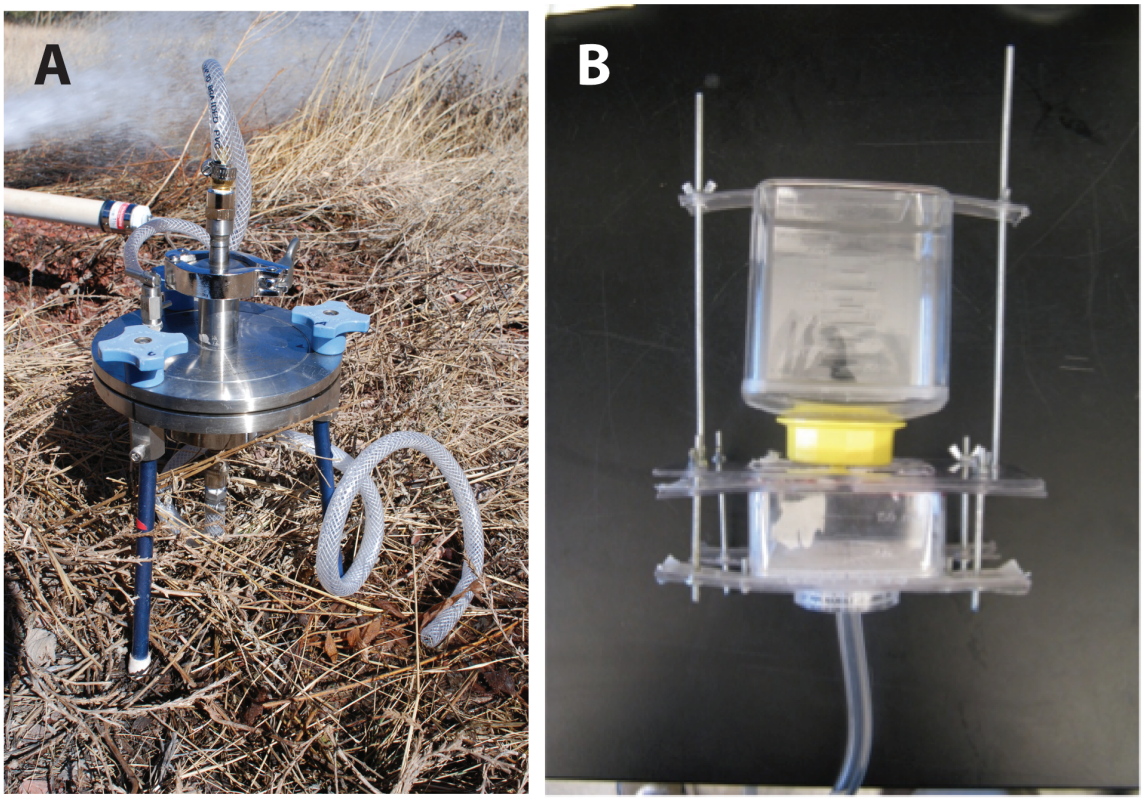


Figure 5. (A) The high-pressure filter device that was used to filter PW2 and STR. Hydrostatic pressure from each well was used to push material through a 142 mm Durapore (0.1 μm) membrane. (B) The J-unit device that was successfully used to isolate sufficient biomass from the Wind Cave Lakes (WCL).

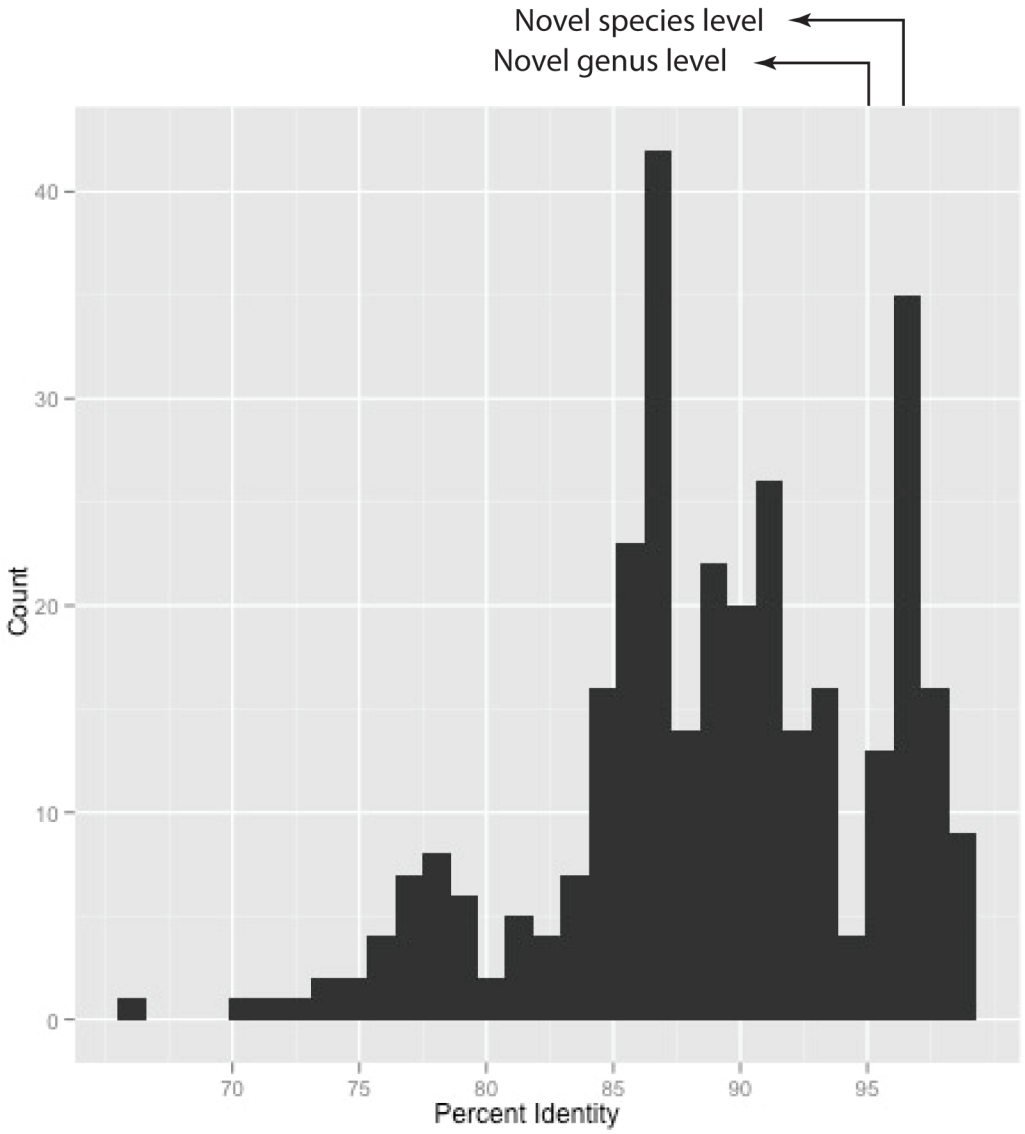


Figure 6. The comparative distribution of WCL phylotype identities at the nucleotide level to similar sequences within the NCBI Genbank database. Generally similarity >97% demonstrates identity at the species , <95% demonstrates identity at the genus level and <85% demonstrates identity at the phylum level.

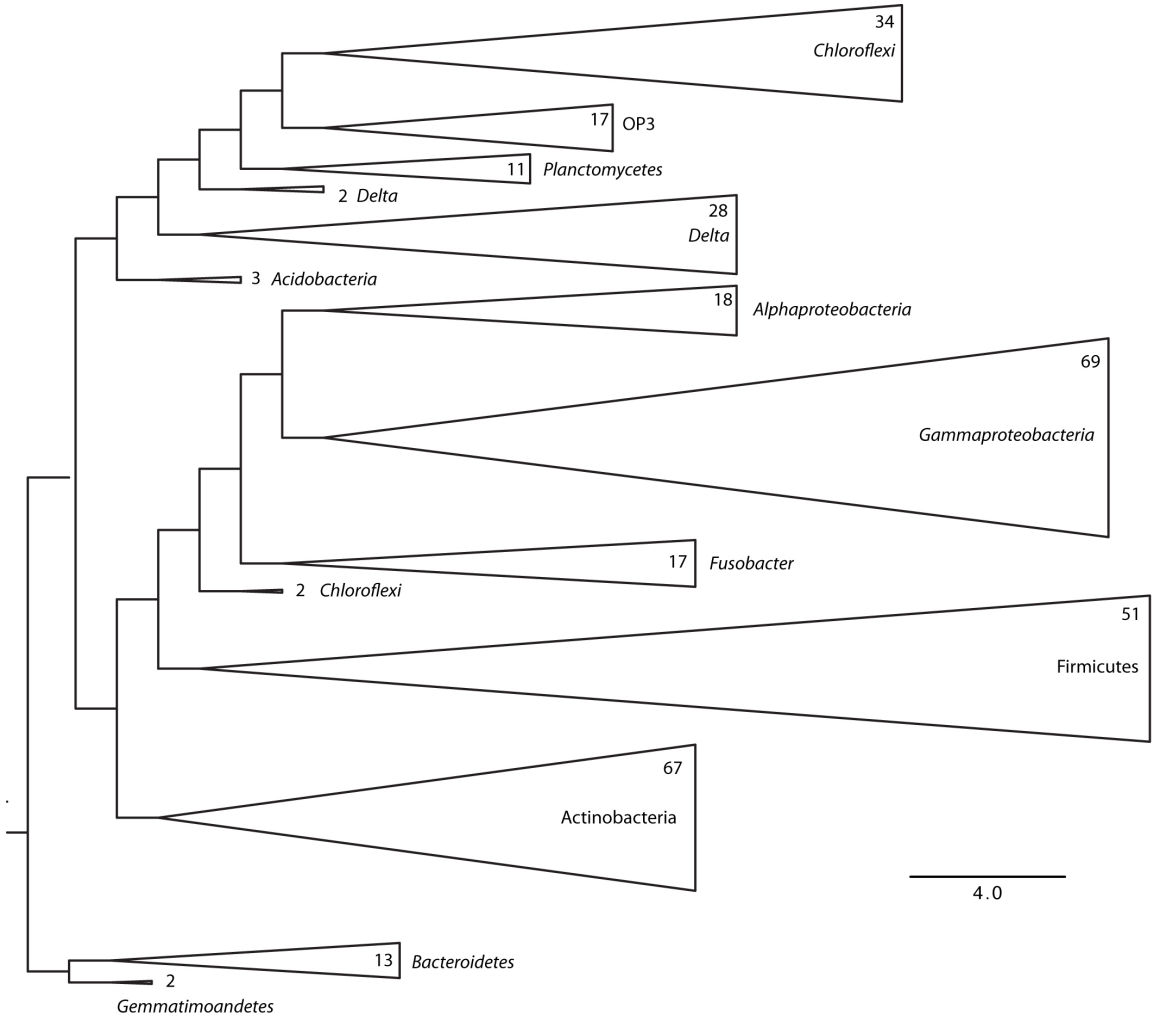


Figure 7. Evolutionary distance cladogram demostrating the relative distribution of phylotypes identified within WCL. The scale bar indicates the relative distance for 4 changes/site within the nucleotide sequence (this cladogram demonstrates the distribution across the entire Bacteria). No outgroup was used in this construction.

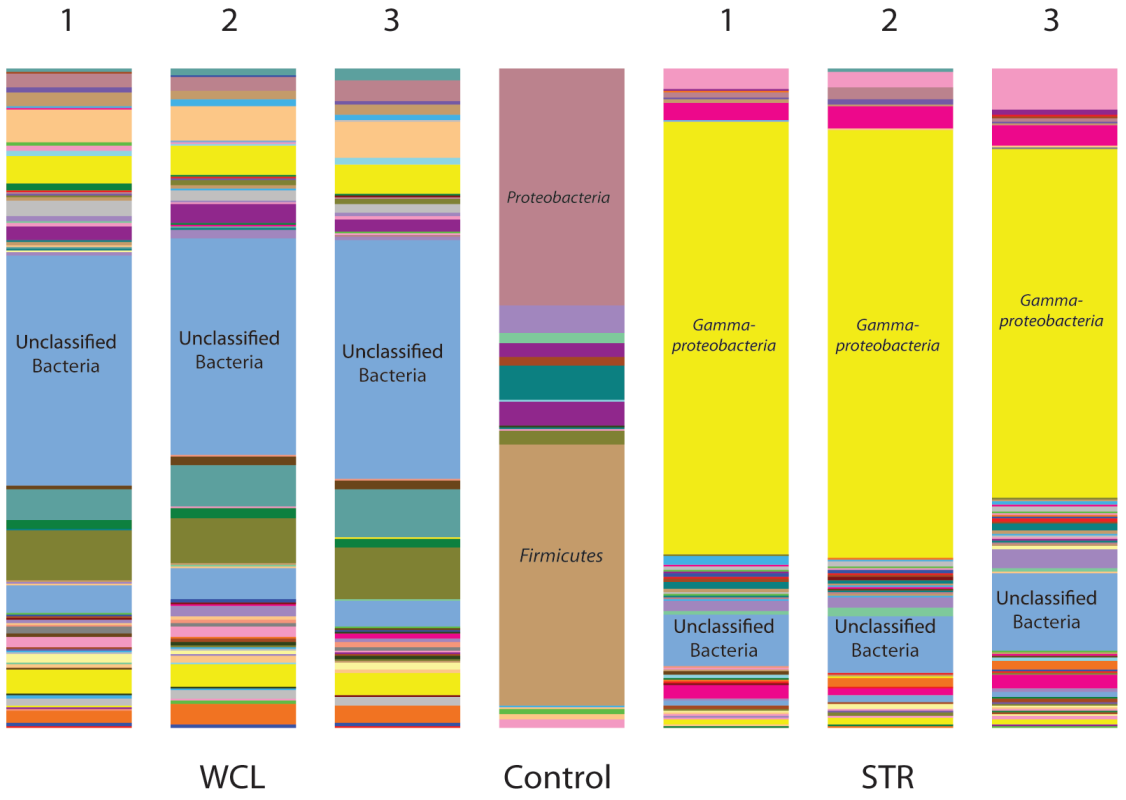


Figure 8. Distribution of the 454 sequence data at the genus level (each color demonstrates the relative contribution of each genera to the overal diversity of each sample). The three separate PCR amplifications for WCL and STR are shown, along with the preparation control (CTL).

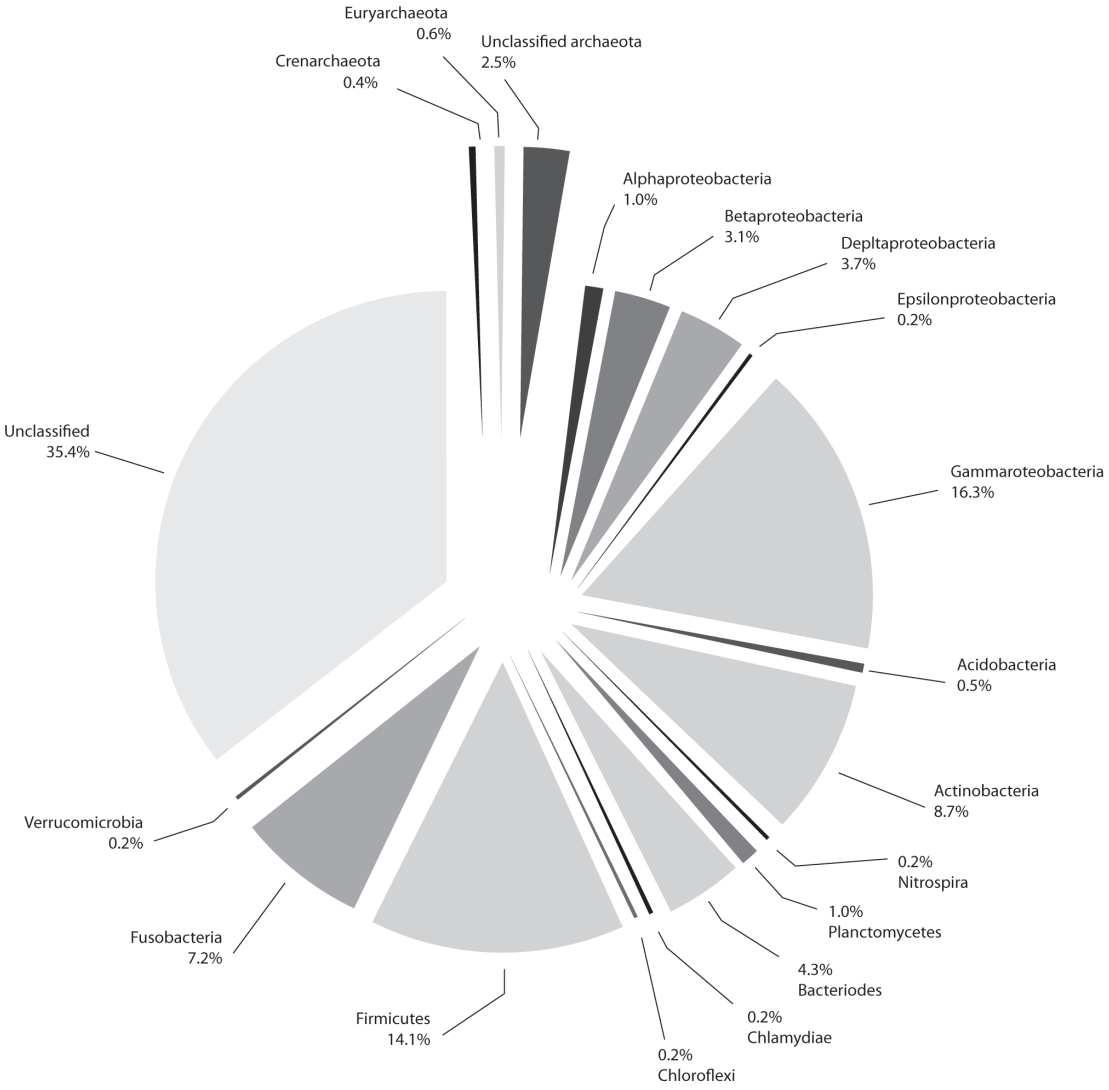


Figure 9. Distribution of binned 454-tag sequences from WCL within the respective Bacterial phyla.

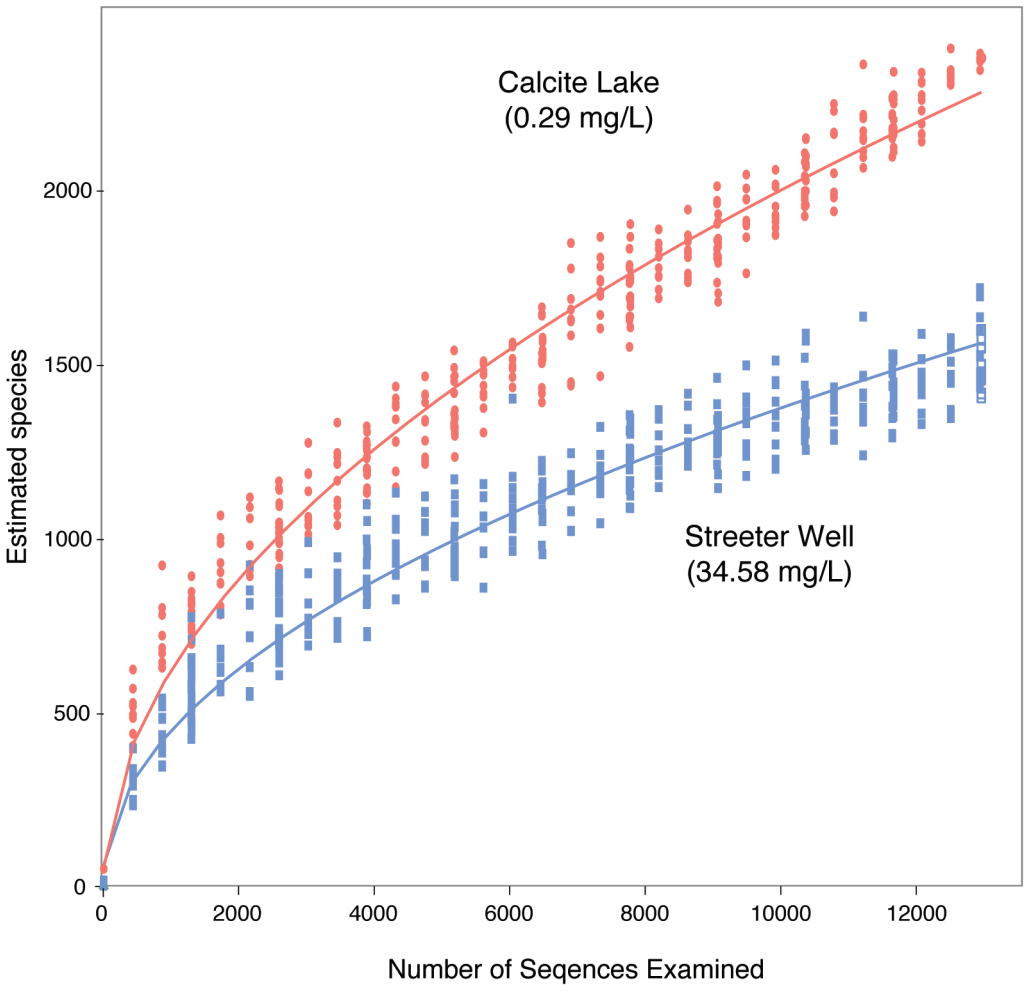


Figure 10. Rarefaction curves comparing the microbial species diveristy at the Wind Cave Lakes (red) with Streeter Well (blue). A leveling off of the curve would indicate the full diversity of the site had been explored. The amount of dissolved organic carbon at each site is indicated. AChao1 non-parametric estimator was used.

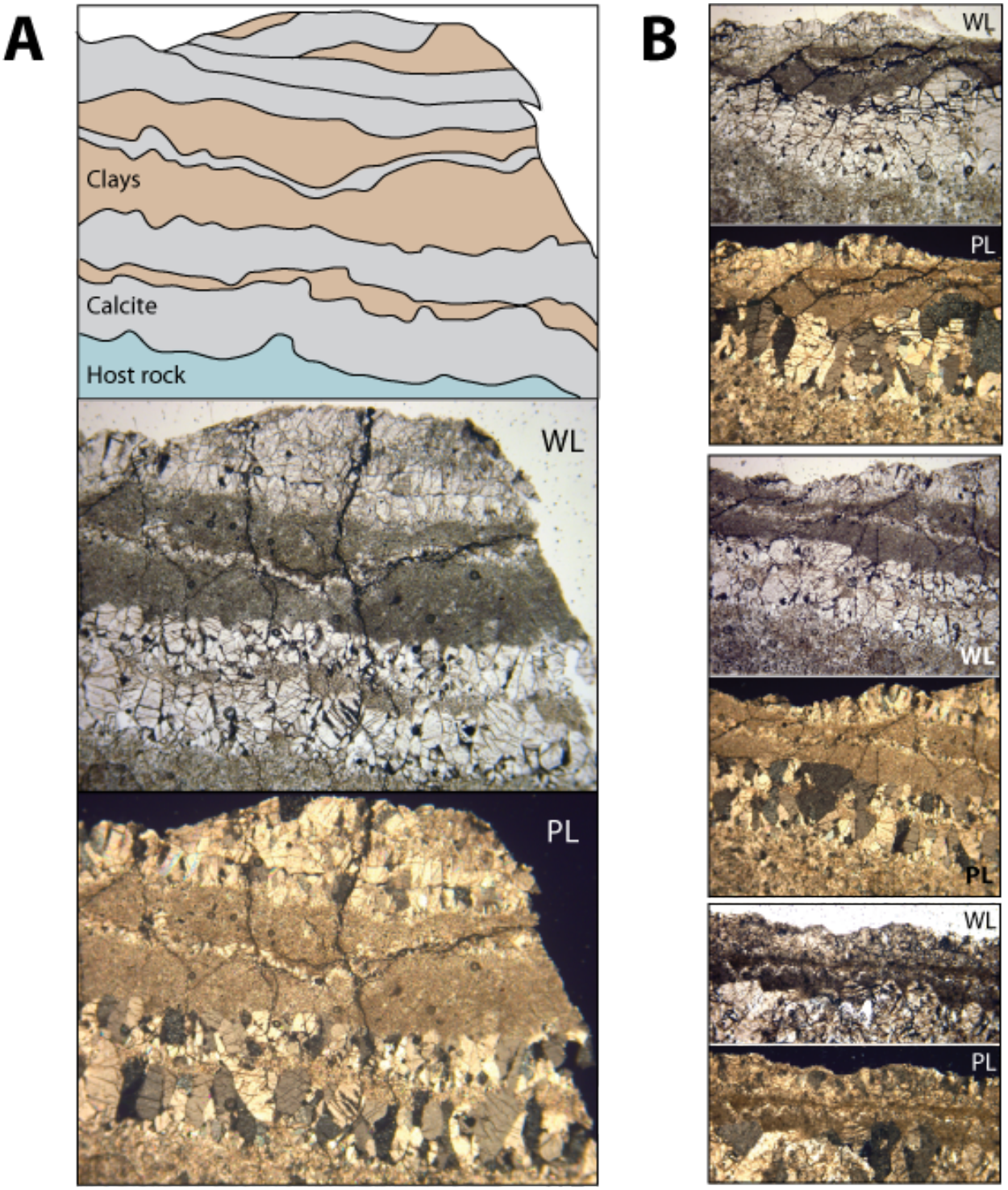


Figure 11. Laminated bedrock surfaces found at the Wind Cave Lakes. **A)** Detail demonstrating the lamination of the host rock surface with calcite and clay-like deposits. The upper image demonstrates mapping of the respective layers, including white light (WL) and polarized light (PL) images of the same thin section. **B)** Demonstrates representative thin sections from wall surfaces around the Lakes. Again, WL and PL correspond to white light and polarized light.

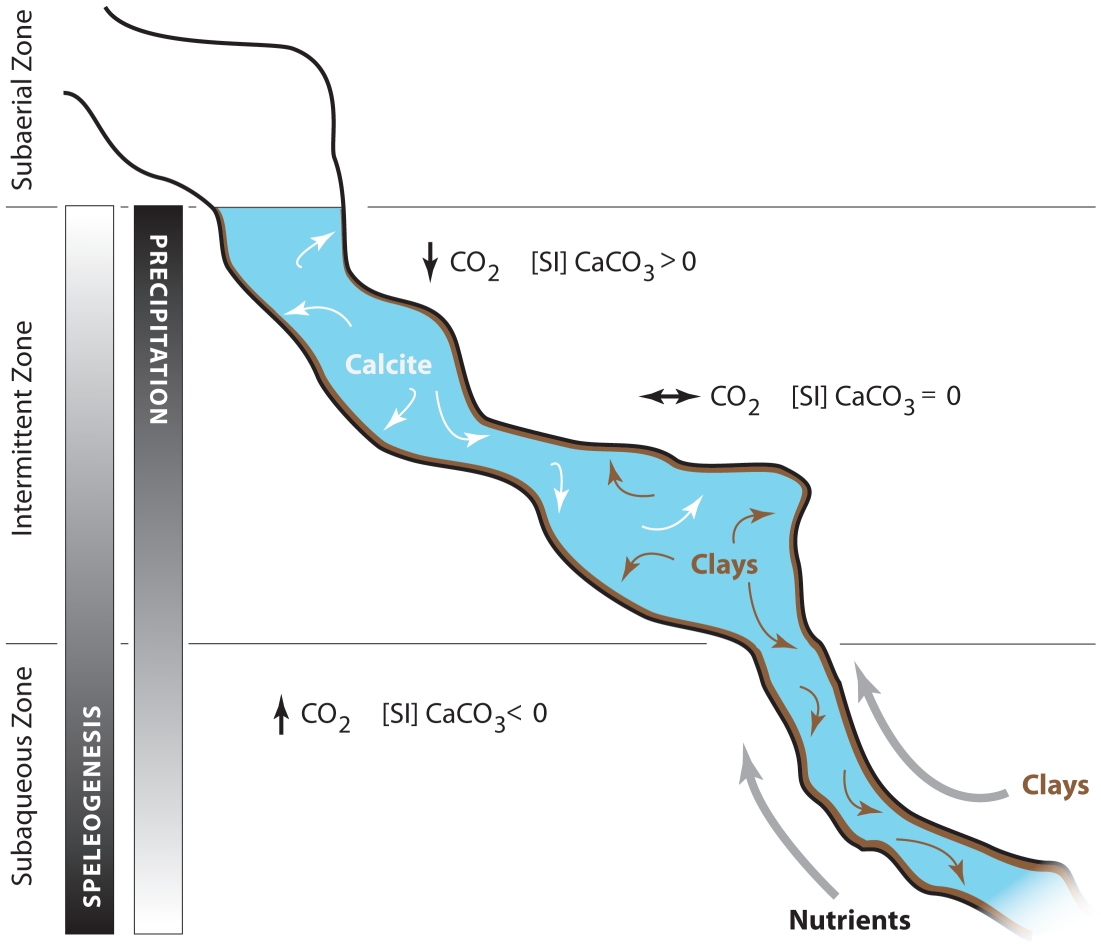


Figure 12. Model of proposed speleogenesis within the Wind Cave Lakes. In the subaqueous zone, the input of nutrients leads to biofilm formation. At the contact between the biofilm and the host rock, local acidic conditions promote dissolution, while microbial heterotrophic growth increases CO_2 and leads to a drop in the saturation index for $CaCO_2$. Together, these promote speleogenesis. At the same time, suspended clays within the water stick to biofilm, leading to clay-like deposits. In the dry zone, the loss of water leads to death of the biofilm and an absence of dissolution. In the intermittent zone between the subaqeuous and dry zones, fluctuating water levels cause biofilm formation to be transient. In regions where the biofilm tends to predominate, a combination of CO_2 production and local acidic conditions allows dissolution to predominate. In regions where the biofilm is less well developed, there is no CO_2 production, allowing the saturation index for $CaCO_2$ to remain high and lead to calcite precipitation.

Table 1. Comparative total cell numbers for the sites included in this study.

Sample	Treatment	Mag	Microscope Factor	Fields of View	Bacteria/FOV	Avg. Bact/FOV	Std. Dev./FOV	Volume Counted	Total cells/mL	Std Dev (%)
July 26, 2010										
CTL	None	63 circle	4318	200	12	0.06	0.02	5	$5.2x10^{1}$	28.8
PW2	None	63 grid	16230	100	573	5.73	0.24	1	$9.3x10^{4}$	4.2
STR	None	63 circle	4318	100	147	1.47	0.12	1	$6.3x10^{3}$	12.1
WCL	None	63 circle	4318	100	68	0.68	0.08	1	**$2.9x10^{3}$**	8.2
June 6, 2011										
WCL	None	100 circle	4096	100	85	0.85	0.09	1	**$3.48x10^{3}$**	10.8
WCL	None	100 circle	4096	100	36	0.36	0.06	1	**$1.47x10^{3}$**	16.7
WCL	US	100 grid	20106	50	17	0.34	0.08	1	**$6.84x10^{3}$**	24.3
WCL	US	100 circle	4096	100	46	0.46	0.07	1	**$1.88x10^{3}$**	14.7
WCL	US	100 circle	4096	100	38	0.38	0.06	1	**$1.56x10^{3}$**	16.2
WCL	Det. Mix	100 grid	20106	50	23	0.46	0.10	1	**$9.25x10^{3}$**	20.9
WCL	Det. Mix	100 grid	20106	50	22	0.44	0.09	1	**$8.85x10^{3}$**	21.3
WCL	Det. Mix + US	100 grid	20106	50	17	0.34	0.08	1	**$6.84x10^{3}$**	24.3
WCL	Det. Mix + US	100 grid	20106	50	21	0.42	0.09	1	**$8.44x10^{3}$**	21.8

Table 2: Water chemistry of the sample sites used within this study. TOC data was collected in 2010. All inorganic water chemistry measurements were taken in 2009 (except N and P from 2007) were compiled from raw NPS data and Back (2011).

Site	pH	TOC (mg/L)	Endotoxin (EU/mL)	Glucan (pg/mL)	DO (mg/L)	Ca (mg/L)	Mg (mg/L)	Na (mg/L)	HCO_3 (mg/L)	Cl (mg/L)	SO_4 (mg/L)	NO_2+NO_3 (mg/L)	P (mg/L)
BCS	7.3	38.80	-	-	6.2	443	73.3	27.4	217	32.9	1290.0	0.39	-
PW2	7.8	-	-	-	3.9	27.3	13.7	78.5	223	17.4	38.4	0.21	3.37
STR	7.6	34.58	-	-	7.4	40.3	14.3	9.0	166	2.6	11.4	0.51	2.44
WCL	7.75	0.29[a]	77.3[a]	ND[b]	-	35.8	19.6	7.21	162	4.22	9.57	-	-

[a] Average values for two separate samples
[b] ND – none detected

DESCRIPTION OF STUDY AREA

In terms of structural and developmental diversity, Wind Cave is one of the most complex caves in the world. The cave is found within the Mississippian age limestone of the Madison Formation along the eastern flank of the Black Hills, South Dakota (Figure 1), which is regionally 90 – 320 m thick and is capped by quartz sandstones of the Minnelusa Formation (Redden and DeWitt 2008). Wind Cave is also one of the oldest caves in the world, with initial karstification occurring during exposure of the Madison limestone within the mid-Carboniferous period (Palmer and Palmer 2000). Multiple speleogenetic events, including filling, burial, uplift and subsequent erosion, have generated the cave morphology as observed today -- a complex maze cave exceeding 200 Km in length (Figure 2; Palmer and Palmer 2000).

The morphology of Wind Cave owes little to current surface topography, rather the structure of the cave is related to the layered bedding of the Madison Formation (interbedded limestone and dolomite separated by chert beds) and the primary speleogenetic events that occurred during the Paleocene and Eocene, generating the fractures that control the structure of the deeper dolomitic layers (Figure 2; Palmer and Palmer 2000). The most recent speleogenetic processes began during the Eocene Epoch, after the early Tertiary uplift of the Black Hills had tilted the local ~5° toward the southeast, causing recharge water from both the exposed Madison and Precambian rocks of the Black Hills to begin flowing through the paleocave, leading to passage enlargement. As a result, surface features are not indicative of subsurface cave features and the entrances were formed when erosion and down cutting excavated existing cave passage (Palmer and Palmer 2000).

Wind Cave is not alone within the Madison Formation and the Black Hills contain 340 known caves, including the massive (~250 Km) Jewel Cave, but Wind Cave is unique in its depth (194 m), which allows access to the aquifer within the Madison Formation (all other access points are via drilled well or discharge springs) (Figure 3). This aquifer is found via a series of lakes in the deepest sections of Wind Cave, ~ 137 m underground (Figures 2 and 3). The highest of these lakes (What-the-Hell Lake; WTH) receives local recharge water (Back 2011, Long and Valder 2011), which drains into the nearby Wind Cave Lakes (WCL) complex. The age of this local recharge water when it reaches WTH has been estimated at ~ 25 years (Back 2011). The WCL complex consists primarily of local recharge water (96%), although the regional and local groundwater flow paths that impact Wind Cave area create a complex aquifer pattern (Long and Valder 2011) and the cave itself is impacted by both local recharge and regional groundwater flow (Figure 4). Due to its complex speleogenesis, it is likely that the deeper passages pre-date current groundwater levels with extant cave passages existing below the surface of the current aquifer. Nonetheless, the speleogenesis of the cave likely remains tied to this aquifer (Palmer and Palmer 2000).

The aim of this study was to examine the microfauna of Calcite Lake as a representative community of microorganisms living within this unique mixed aquifer. In addition to sampling water within WCL, we also examined microbial communities in wells that we also believe to be in the same aquifer, including: Beaver Creek Spring (BCS), Park Well #2 (PW2) and Streeter Well

(STR). Our results represent the most comprehensive examination of a microbial community within a cave environment to date, including microscopic, phylogenetic, culture and biogeochemical techniques. The generated data suggest that the microfauna of WCL represents a unique microbial community, with a highly diverse microbial community despite cell numbers well below those previously observed in freshwater environments. The energy sources driving the growth of these microorganisms and suggest that they may play a role in speleogenesis.

MATERIALS AND METHODS

Sampling

One of the most challenging aspects of this project was related to collecting samples for microbiological analysis. Environmental microorganisms are extremely difficult to cultivate in the laboratory, especially those that are found within extreme environments where <0.1% of organisms can be cultivated using standard techniques (Amann et al. 1996). Therefore, to identify these organisms it is necessary to use molecular techniques, which allow us to identify the entirety of a community even when many are unculturable (Pace 1997). To do this, we must isolate enough total DNA to allow amplification of the 16S ribosomal RNA gene sequences for the entire community. Due to the efficiency of DNA extraction techniques, we require at least 2 μg of DNA from the environment (an average bacterium contains 3 femtograms of DNA) equivalent to 6.6×10^8 cells.

Generally this would not be a difficult; karst aquifers are anticipated to have microbial cell numbers equivalent to other oligotrophic freshwater sources of approximately 2×10^6 cells/mL (compared to the open oceans of 1.5×10^7 cells/mL) (Farnleitner et al. 2005, Newton et al. 2011). It would therefore be anticipated that to obtain the minimal biomass for analysis within the Wind Cave Lakes would require ~20 L of water, compared to 45 mL from seawater. Our initial collection attempts were therefore made on this assumed number.

SAMPLING

November 2, 2008

During our first reconnaissance trip we filtered water for microbial analyses from both BCS and STR using the 0.22 μm Sterivex filtration (Millipore #SVGV010RS) technique, which works well for sampling environmental waters. In order to filter 20 L of water over a short time period we constructed a portable water pump based around a Turboject 200-C fuel pump designed for model aircraft. This pump can generate 20 psi of pressure and pump up to 600 mL/min. With this pump placed down-stream of the filter it was possible to draw water rapidly. Upon processing these initial samples we determined that the sterivex filters became rapidly clogged with clay and iron oxide particles (these filters are easily clogged by 1 μm particles) and the maximum volume we were able to collect with our portable filtration pump was 10 L.

While the water chemistry of BCS provides information regarding the aquifer, our preliminary reconnaissance indicated that there was a tremendous amount of fecal matter from the fact that the spring was used to water cattle. Despite numerous attempts to filter material within the spring, all PCR and cultivation techniques revealed the presence of bacteria normally associated with the rumen of cattle. We therefore decided that BCS would not serve as a viable site for a microbiological investigation. During this trip we were unable to sample at PW2 as

the flow of the well could not be reduced to levels sufficient to stop blowing our equipment across the road. Logistical considerations prevented access to WCL.

July 26 2010

In order to overcome some of the problems we had previously with filters clogging with these geological samples, a new approach was used at PW2 and STR. Samples were collected with a large diameter, high-pressure sampling device (Figure 5A) using the hydrostatic pressure of the well at STR, while PW2 was sampled using the pressure of the installed well pump. In order to sample at STR and PW2 it is necessary to removed three well volumes of water before sampling the aquifer (Zara Environmental standard protocol). As a result, ~2100 litres of water was allowed to flow out of each well before sampling. Even though the stainless steel filter allows much greater surface area of the filters (113 cm^2) and pressures (60 psi) on each filter, again the sediment particles at both of these wells led to filter clogging. At PW2 the problem was quite dramatic and it was only possible to filter ~20 L of material before backpressure in the pump caused the seals to blow out explosively. At STR it was possible for 60 L of water to be filtered before the pump gave out. Despite obtaining lower filtrate volumes than anticipated, the filters were collected, preserved in 70% ethanol and the biomass collected for sampling. On preparation in the lab, the STR sample did not contain sufficient DNA to allow amplification using PCR. The PW2 sample was destroyed during processing and no DNA was collected. Samples were successfully collected for cultivation, water chemistry and cell numbers.

Given the difficulty in generating high pressures and carrying the large filter equipment (Figure 5A) within Wind Cave, we used an alternative approach. To increase the potential DNA yield/sample we used the portable Turbojet C-200 pump along with 0.2 μm aluminum oxide Anodisc filters (Whatman #6809-6022), which can be crushed directly into extraction buffers. Within the cave we attempted to pull 20 L of water through the filter using the pump downstream of the filter; however the filter pump was unable to generate enough suction to pull sufficient water through as the filter began to clog with sediment. We therefore changed the position of the pump to be upstream of the filter, allowing enough force to be generated to continue to push water though the filter. Once again, as the filter became clogged with sediment, the backpressure of the pump built up until the water pressure blew a hole directly through the Anodisc filter. This flooded the pump and effectively ending the experiment. Samples were successfully collected for cultivation, water chemistry and cell numbers.

December 14 2010

The July sampling trip gave us a clear idea of the total cell numbers within the Wind Cave Lakes (~1.13×10^3 cells/mL). Thus we were able to determine that we would need to filter 200 – 300 L of water to collect 2 μg of DNA (300 - 500 L). To move this volume of water through a filter required a much larger pump and filter diameter so that backpressure would not create a problem. Nothing like this has been used to sample microorganisms from water environments before and required a complete redesign of such sampling equipment. The pump used was a Global Water SP200 variable speed peristaltic pump, which can pump up to 2 L/min. This

filtration unit was designed by Juan Giarrizzo and was based on a Nalgene disposable 0.22 μm filter (Figure 5B). This had the advantage of being a sterile, Gamma-radiated device that could remain open to avoid backpressure problems. A sterile gauze pre-filter was added to the device to remove the particles that have previously blocked the membranes [http://www.youtube.com/ watch?v=G04p0lFesG4]. This pump was allowed to run for 3.5 hours in the cave and ~ 200 L of water was filtered through the 0.22 μm membrane, which allowed successful DNA extraction for amplification. The device was similarly used at STR to collect amplifiable DNA, while a preparation control device that was carried into the cave failed to yield amplifiable DNA.

June 6 2011

No DNA sampling was carried out during the June collection trip, however samples were collected to confirm cell numbers and for fluorescent *in situ* hybridization techniques.

MOLECULAR TECHNIQUES

16S rDNA Community Analysis

Unless stated otherwise, all chemicals were obtained from Sigma-Aldrich, while all DNA protocols were carried out in a laminar-flow hood using aerosol resistant pipette tips to reduce the likelihood of contamination. Genomic DNA was extracted from filter using a low biomass bead beating protocol (Barton et al. 2006) and negative control isolations were carried out in parallel to measure any contamination of the final samples. Community 16S ribosomal RNA gene sequence libraries for Bacteria were prepared from extracted DNA by amplification using the universal forward primer 8F (5′-AGA GTT TGA TCC TGG CTC AG-3′) and the bacterial-specific reverse primer 805R (5′- GAC TAC CAG GGT ATC TAA T-3′). PCR amplification was carried out with a hot start at 94 °C for 8 minutes, followed by a minute at 94 °C, 45 seconds at 58 °C and one minute at 72 °C for 42 cycles. For an Archaeal library, the archaea-specific primer 333Fa (5′ – TCC AGG CCC TAC GGG – 3′) was used in combination with 1391R across a range of annealing temperatures (55 – 65°C). Purified PCR products were cloned into a pTOPO-TA Cloning Vector (Invitrogen Corp., Carlsbad, CA) according to the manufacturer's recommended protocol and representative clones were sequenced at the University of Kentucky Advanced Genetic Technologies Center (UK-AGTC; http://www.uky.edu/Centers/AGTC). Partial sequences of each 16S rRNA gene were compiled using DNA Baser Sequence Assembler (Heracle Software Co., Germany) and compared to the NCBI database by BLAST (http://www.ncbi.nlm.nih.gov) (Altschul et al. 1997). The compiled sequences were aligned using the Greengenes NAST alignment algorithm (http://greengenes.lbl.gov/cgi-bin/nph-NAST_align.cgi) (DeSantis et al. 2006) and potential chimeric sequences were identified for removal using Bellerophone software (http://comp-bio.anu.edu.au/bellerophon/bellerophon.pl) (Huber et al. 2004). Contigs were assembled together using the DNA baser software. Assembled sequences were aligned with manual corrections in the ARB Software Package (http://mpi-bremen.de/molecol/arb) and trimmed using Seaview 2.2 to generated sequences with the same length in order to prevent artificial grouping. For evolutionary distance calculations, a

maximum likelihood algorithm using a general time reversal (GTR) substitution model was carried out in RAxML 7.2.7 with 1000 bootstrap replicates.

16S Identification of Cultures

To identify each isolate, the genomic DNA was extracted using a ZR Fungal/Bacterial DNA Kit (Zymo Research, Orange, CA) and the 16S ribosomal RNA gene sequence identified as previously described. Sequences that were difficult to identify in this manner were cloned into a pTOPO-TA Cloning Vector (Invitrogen Corp., Carlsbad, CA) before sequencing, whereupon sequencing and identification were carried out as described.

Community 454-tag Pyrosequencing

Environmental DNA was extracted and amplified using PCR with the universal primers 515F and 806R (Walters *et al.,* 2011) in three separate reactions. Each sample was labeled by including a unique molecular barcode in the primer for each sample site and the amplified DNA sequenced using a Roche/454 by Research Testing Services (Lubbock, TX). The resulting read data generated 41,400 tag sequences which were analyzed using the QIIME software (Caporaso *et al.,* 2010). Nucleotide sequences from each site were separated using the PCR-encoded barcode and poor quality reads filtered out using Denoiser (Reeder and Knight, 2010). Operational taxonomic units (OTUs) were identified using uclust (Edgar *et al.,* 2011) and the taxonomy of each OTU was classified using RDP (Cole *et al.,* 2009). Chimeric OTUs were subsequently identified and excluded using ChimeraSlayer (Haas *et al.,* 2011), generating 24,623 unique tag sequences. The control sample was PCR amplified in a single reaction, generating 25,907 reads, which were similarly processed to generate 14,250 tag sequences. Alpha rarefaction curves were generated for the remaining OTUs in QIIME.

CELL COUNTING

During each sampling campaign three 15 mL samples of water were collected using aseptic technique and immediately preserved in 2% formaldehyde. For cell enumeration 1 ml of water was filtered onto 0.2 µm pore size membrane filters (Whatman Anodisc or Whatman Cyclopore) and the cells stained with SYBR Green I (Sigma-Aldrich, St. Louis, MO). Total cell counts were carried out using epifluorescence microscopy (Leica DMZ2500 with 63x and 100x objectives, Filterset I5). Blank counts were determined at the beginning and the end of each working day. The average blank value (52 cells ml^{-1}) was subtracted from each cell count. Between 50 and 200 fields of view were inspected in order to achieve a total count of at least 20 cells. Aggregation of cells or formation of biofilms may reduce the number of visible cells, therefore the samples were treated in four different ways: (1) filtering the untreated sample straight onto the membrane, (2) immersing the sample vial into a sonication bath (Bandelin Sonorex, 10 min at 640 W) prior to filtration, (3) adding a detergent solution (100 mM disodium EDTA dihydrate, 100 mM sodium pyrophosphate decahydrate, 1 % vol/vol Tween 80) and methanol (1) to the sample and vortexing it for 30 minutes to dissolve extracellular polymers, and (4) a combination of methods 2 and 3. The results from all four treatments vary by a factor

of ~6, from 1.56 to 9.25 x 10^3 cells ml^{-1}, with untreated and sonicated samples being rather on the low end of the spectrum and detergent mix and detergent mix/ultrasonic treated samples on the high end.

GEOCHEMISTRY

Total organic carbon (TOC) analysis was carried out by WATERS laboratories (Western Kentucky University, Kentucky, USA) using high temperature combustion method (SM5310B) in a Shimadzu total organic carbon analyzer TOC-V series. Endotoxin (LPS) and (1,3)-β-D-glucan determination was carried out by Associates of Cape Cod, Inc. (East Falmouth, MA). LPS testing was carried out via a turbidimetric method using the Pyrotell-T reagent in a Pyros® Kinetix Kinetic Tube Reader at 37°C, while Glucan testing was carried out via a chromogenic method using the Glucatell reagent in a BioTek ELx808 microplate reader. Results were pooled from sampling in 2010 and 2011. All inorganic water chemistry measurements were taken in 2009 (except N and P from 2007) and compiled from raw National Park Service (USA) data and Back (2011). To prepare thin sections, rock samples were collected using a hammer and chisel, dried at 100˚ C and impregnated with Petropoxy. After curing for 24-48 hours, cut samples were ground and polished on a lap wheel to approximately 30 μm. Thin sections were photographed under plane polarized light using a Nikon E400Pol polarizing microscope

RESULTS

The most profound finding from this study was the extremely low cell numbers encountered in the Wind Cave Lakes (Table 1). These numbers were remarkable and initially caused us to think that our counting estimates had been incorrect. We therefore collected additional samples and sent them to Dr. Jens Kallmeyer at the University of Potsdam, Germany, an international expert on the enumeration of pelagic bacteria in nutrient-limited waters. Dr. Kallmeyer's numbers agreed with our own at ~2.3 – 2.9 x 10^3 cells/mL. The water in WCL has extremely low biomass, far below any encountered for any karst environment, aquifer or other studied body of water (Farnleitner et al. 2005, Goldscheider et al. 2006, Newton et al. 2011, Pederson et al. 2008, Pronk et al. 2009, Redden and DeWitt 2008, Shabarova and Pernthaler 2010, Urbach et al. 2001, Walters et al. 2011). With such a low cell number count, additional water samples were collected that allowed disruption of potential biofilms, which is caused by the clumping together of bacterial cells to survive extreme conditions (Poli et al. 2010). Repeating cell number analyses with samples collected 11 months apart, using a variety of separation techniques revealed that low cell numbers are consistent at 2.48 x 10^3 cells/mL, although a slightly higher number of cells can be counted following biofilm disruption at 7.64 x 10^3 cells/mL (Table 1). Examination of other wells and spring surrounding Wind Cave, including STR and PW2, also demonstrated low cell numbers of 6.3 x 10^3 and 9.3 x 10^4 cells/mL, respectively.

In order to confirm the extremely low cell numbers observed in WCL we used an additional assay based on the lipopolysaccharide (LPS) content of Gram negative bacteria. These bacteria contain LPS as part of their outer member, which can act as a surrogate for the total number of these organisms within water (Priscu et al. 1999), where 1 endotoxin unit ≅10^5 Gram negative (*Escherichia coli*) cells. We examined the LPS content of the water at WCL as 77.3 EU/mL (Table 2). This is equivalent to ~8.1 x 10^3 cells mL^{-1}, a value higher than the cell numbers counted within these water samples (Table 1); however, we used a nitrocellulose membrane filter in the collection of this water, which can artificially inflate the LPS values. LPS can sometimes be inflated by the presence of other bacterial polymers, such as exopolysaccharide (EPS), which is responsible for biofilm formation. We therefore tested the water for total (1,3)-β-D-glucan, one of the most common polysaccharides associated with EPS in both Gram negative and Gram-positive bacteria. Our results (Table 2) demonstrated that EPS values were below the detection level (<31 ng/mL) of this assay. A number consistent with low cell numbers and the absence of significant biofilm particles in the water, which can artificially reduce measured cell numbers.

With such a low number of cells in the WCL, filtering enough water to obtain biomass for a phylogenetic assessment of microbial community structure was a challenge (as described in the materials and methods). Nonetheless, we were able to filter ~ 200 L of water from both WCL and STR to extract amplifiable DNA. PW2 became unavailable at this time as the well was shut off; however, given the high sulfate levels in this well (Table 2) it is unlikely that the microbial community there would have provided valuable insight into community dynamics within the WCL local aquifer.

We undertook a comprehensive phylogenetic analysis of the microbial community within WCL and STR, with both full length 16S rRNA gene sequence analysis and tag-pyrosequencing. Two 16S clone libraries were constructed as part of this project. The first clone library was generated from the Anodisc filtration experiment carried out in July 2010, where the backpressure of the pump destroyed the filter. While the filter was destroyed during this filtration attempt, we collected the fragments and isolated any DNA present. A PCR product was generated from this trace DNA, which was used to construct an 88-member bacterial clone library, but analysis suggested that this library was dominated by oil-degrading microbial species. These data suggest that we cannot rule out pump flooding contaminating the sample.

The second clone library was constructed from the cells collected during December 2010. Despite numerous attempts under a variety of conditions we were unable to generate a PCR product for the Archaeal primers, suggesting that there were insufficient numbers of these organisms to allow amplification. PCR of the Bacteria was more successful and we generated a 384-member clone library (Supplemental Table S1). Of this library, 30 sequences were removed as either chimeric or incomplete sequences. What was remarkable about this library was the low identity of phylotypes to current sequences within the Genbank database (www.ncbi.nlm.nih.gov/nucleotide). The distribution of these phylotypes suggested that many of them represent previous undescribed organisms at both the genus and species level (Figure 6), with some representing new phyla. Nonetheless, the phylogenetic reconstruction of these phyla to confirm their identity is outside the scope of this study.

While the WCL 16S phylotypes demonstrated a remarkable distribution of Phyla (Figure 7) quite distinct from previously described freshwater communities (Farnleitner et al. 2005, Kallmeyer et al. 2008, Newton et al. 2011, Pederson et al. 2008, Priscu et al. 1999, Pronk et al. 2009, Shabarova and Pernthaler 2010, Urbach et al. 2001), the most remarkable observation in this community was the lack of dominance of the *Alpha*- and *Betaproteobacteria;* these phyla tend to predominate in other water and karst environments (Farnleitner et al. 2005, Newton et al. 2011, Shabarova and Pernthaler 2010). Members of this group are generally associated with nitrogen fixing activities in nutrient limited systems, although the geochemical data of WCL (Table 2) suggest that nitrogen may not be limiting in these environments. There is also a predominance of *Gammaproteobacteria,* which are normally associated with the breakdown of complex organic matter. Therefore, to determine whether organic carbon was contributing to community growth at WCL we examined the total organic carbon (TOC) content of WCL, which was very low at 0.29 mg TOC/L (Table 2). The low levels of organic carbon supports the long residence time of infiltrating waters (> 25 yrs), where the water is stripped of available organic carbon during its long residence time *en route* to the lake (Naus et al. 2001).

The only microbial community that demonstrates any structural similarity to the WCL sample is that extracted from pools deep within (-735 m) a Swiss Cave (Shabarova and Pernthaler 2010), which also demonstrates a high number of representatives of the OP3 division (Hugenholtz et al. 1998). Members of the OP3 are widely distributed in the environment (Glockner et al. 2010), but their lack of cultivation makes it difficult to determine their role, although recent work

suggests these species are involved in the production of magnetite and greigite (Kolinko et al. 2011). The presence of the OP3 and other phylotypes related to iron oxidizing and reducing species suggest that iron may play a role in energy generating mechanisms within WCL. Microscopic examination of thin-sections from rocks surrounding the lakes did indicate the presence of oxidized iron deposits, supporting this hypothesis.

In order to further examine the rare microbial biosphere at WCL, we carried out a tag-pyrosequencing analysis of three separate PCR amplifications. The results (Figure 8 and Supplemental Table S2) support the observed diversity in WCL, including a high proportion of bacterial sequences that cannot be reliably classified within the current phylogenetic framework (Figure 9). Most notable within this data is that we were able to detect the presence of Archaea, including members of the *Crenarchaeota* and *Euryarchaeota.* While the contribution of these organisms was minor (0.3% and 0.6%, respectively) their presence at low numbers explains our inability to detect them via PCR analysis. Within the Bacteria there was again a predominance of the *Gammaproteobacteria, Actinobacteria* and *Firmicutes* (Figures 7 and 9). The 454 sequencing data also revealed the presence of representatives of the *Alpha-* and *Betaproteobacteria,* although still at much lower levels than normally seen in cave environments (Figure 9). Other significant Phyla observed include the *Epsiloproteobacteria,* which are normally associated with sulfate reduction, the *Nitrospira* which are involved in nitrogen cycling and the *Chlamydiae*, which have previously identified in Lechuguilla Cave pools (D. Northup, personal communication, 2006). Of note was the presence of the predatory genera *Bdvellvibrio, Myxococcus* and *Ensifer,* which may play an important role in carbon turnover (Supplemental Table S2).

One of the questions that this study has brought up is whether Streeter Well (STR), which has a high level of geochemical similarity to the Wind Cave Lakes (WCL) represents a site to sample the microbial community present within this aquifer. To determine the similarity between these sites we also carried out tag-pyrosequencing analysis of three separate PCR amplifications at STR. The results demonstrated a remarkable difference in the community profile between STR and WCL (Figure 8), with almost a complete absence of the Archaea. Instead the STR community is dominated (65%) by members of the *Gammaproteobacteria* (Figure 8) and more closely resemble microbial communities associated with corroded concrete pipes, suggesting that this community may resemble adherent bacterial species from the well casings (Vincke et al. 2001).

In a comparative analysis between the WCL and STR samples, we looked at community diversity using the Chao 1 non-parametric estimator. This estimator can determine whether the sampling technique has provided sufficient depth of coverage to adequately describe the resident community in an ecosystem. Our results (Figure 10) demonstrate that the WCL community is significantly more diverse than STR. The estimator also suggests that WCL contains thousands of unique microbial species and that a sample size of 25,000 phylotypes is insufficient to describe the full species diversity of this ecosystem.

In our final analysis, we wanted to examine how the geochemistry of the cave environment could be influencing microbial community structure. We therefore examined the thin sections of wall rock surrounding the WCL (Figure 2). These thin-sections demonstrated that a complex geochemical system is associated with the lakes, with what appears to be fluctuating periods of calcium deposition followed by a more complex period of deposition, presumably of clay-like material (Figure 11). This generates the laminated pattern observed in the calcite coatings (Figure 11). While we cannot directly ascribe a microbial origin for this lamination without a more detailed geochemical analysis, the data would be consistent with a fluctuating lake level leading to periods of bacterial growth and loss (Figure 12).

CONCLUSIONS

Over recent decades molecular biology has revolutionized microbiology, allowing us to examine microorganisms in diverse environments without the need for cultivation. Such techniques have dramatically increased our understanding of the ability for microorganisms to survive in the extremes of temperature, chemistry, radioactivity, and have even opened up the possibility for life under other planetary conditions (McKay and Smith, 2005). In this study, we examined the lakes at Wind Cave, a geologically isolated, ultra-oligotrophic subterannean lake ecosystem. Despite the extremel nutrient limitation of this environment, we identified a microbial community with a remarkably high level of diversity.

Repeated sampling over a two year period revealed that the WCL contained a remarkably low biomass, between 1.56 - 9.25 X 10^3 cells mL^{-1} (Table 1). This number is 2 – 3 orders of magnitude lower than previously observed for any other waters examined, including oligotrophic seawater (~10^5 cells mL^{-1}) (Rowe *et al.*, 2011), freshwater (~10^6 cells mL^{-1}) (Urbach *et al.,* 2001), and other karst aquifers (~10^6 cells mL^{-1}) (Farnleitner *et al.,* 2005, Goldscheider *et al.,* 2006, Sharbarova and Pernthaler, 2010). Indeed these numbers are below total cell numbers for any previously examined environment, other than the accretion ice of Lake Vostok (~10^2 - 10^3 cells mL^{-1}; Karl *et al.,* 1999, Priscu *et al.,* 1999). To determine whether this microbial community is unique, we compared it with the nearby Park Well #2 (PW2) and Streeter Well (STR), which presumably intercept the same aquifer. Cell numbers at these sites were considered low for water, but higher than the numbers observed at WCL. The water at PW2 contained more cells than STR or WCL, which may be related to the presence of sulfates within this water (Table 2). Sulfate may contribute to higher cell numbers at this site, where sulfate can serve as an electron donor for autotrophic growth under the low oxygen conditions observed in this spring. Such sulfate has been associated with higher cell numbers in similar deep-subsurface aquifer sites. It was also noted that the PW2 water contained a far greater amount of suspended particles than any other sample site, which might reflect suspended clay particles of the Minnelusa.

In order to examine the community structure of the lake, we filtered >200 L of lake water for community profiling using molecular techniques. Direct PCR analysis was unable to detect archaeal and eukaryal DNA from the sample (data not shown), while pyrosequencing generated 24,623 universal tag sequences that included members of both the Bacteria and Archaea. No eukaryotic species were detected via microscopy, PCR or pyrosequencing within WCL; however, scant filamentous fungi were detected via cultivation. Full-length 16S rRNA sequencing provides ~1600 nt of information on the phylogenetic placement of the identified phylotype, allowing a more robust analysis of community structure. Tag-pyrosequencing, with a much smaller ~400 nt sequence does not provide statistically significant data for phylogenetic analysis; however it does allow deep sequencing of the site, often revealing the rare biosphere (Kysela et al. 2005, Ley et al. 2006, Sogin et al. 2006). Both analyses in concert are considered the gold standard for examining the complete profile of microbial communities. The pyrosequencing data suggests that the Wind Cave lakes contain a diverse community dominated by bacteria (Figure 8). This community was more diverse and distinct from STR

microbial community, which is dominated by the *Gammaproteobacteria.* These data are consistent with the geochemical analyses of Back and Long (Back 2011, Long and Valder 2011), which suggests that STR is hydrologically connected to the water at WCL. A comparative analysis of the microorganisms at STR and WCL sites suggests that the community sampled at STR actually represents a biofilm community residing along the concrete casing of the well itself. Concrete contains numerous chemicals that can promote microbial growth and, despite draining three well volumes to remove this residual community before sampling, it appears that this approach was unsuccessful. Therefore, the only mechanism to effectively reach the unique biome of the Wind Cave Lakes appears to be via travel through the cave.

To determine what factors could be driving the observed bacterial diversity within WCL, we examined the water chemistry (Table S2). The results demonstrate that while nitrogen and phosphorous are available, carbon for heterotrophic growth is limited (0.29 mg/L organic carbon). The complexity of the carbon, presumably containing soil fulvic and humic acids, may be responsible for driving the dominance of the Gammaproteobacteria seen in both the 16S and pyrosequencing libraries. The predominance of soild-derived organic carbon is also indicated by the presence of a large number of phylotypes associated with soil and deep ocean sedimens (Supplemental Table 1). In addition, we saw some evidence that iron oxidation was taking place, both in the presence of iron-oxidizing species (Supplemental Table 1) and the precipitation of iron oxides within the laminated deposits. We did not determine if the water contained iron, although the presence of reduced iron could indicate another energy source for the system. While the current WCL sample site is within the shallower regions of Calcite Lake, deeper samples may support the role of regional flow in community growth (J. Back, personal communication, 2011), although we did not examine the potential for hydrocarbons from the Powder River Basin to be driving community growth; however, in support of this possibility, we did identify phylotypes that are associated with hydrocarbon-contaminated aquifers (Supplemental Table 1). Unfortunately, without cultures to demonstrate such a phenotype, the role of hydrocarbons remains speculative.

In addition to species growth, there must be species death and carbon turnover, particularly in this nutrient-limited ecosystem. The fact that we weren't able to observe any eukaryotic predators suggests that bacteria bay be playing an important role in turnover, supported by the presence of three genera known to be involved in predation: *Bdellvibrio, Myxococcus* and *Enisfer* (Supplemental Table 2). Such species could therefore be playing an important role in carbon turnover in this system, thus driving up diversity. One question we were unable to address in this study was the role of bacteriophage in driving diversity. Given the lack of eukaryotic predation in the system, but high diversity, it is likely that bacteriophage are limiting the growth of *k*-type species. Given that bacteriophage diversity can often exceed prokaryotic diversity by an order of magnitude, the WCL therefore demonstrate a unique habit in which to examine such processes.

One observation we made during cell counting was the occasional appearance of clumped cells, often containing upwards of 100 bacterial cells. While our EPS data rule out a significant contribution of biofilms to the planktonic community in the lake, it does not rule out a

microbial biofilm lining the basin of the lakes. Indeed, our phylogenetic analyses and the laminated structure of the wall rock may even support the presence of this biofilm, lining the rock surfaces and serving as a source for the planktonic cells seen in the water. Further, we postulate that the appearance of laminated structures in the thin sections suggests that these biofilms may be driving speleogenesis (Figure 11). In this model, microbial heterotrophic growth from the input of organic nutrients increases dissolved CO_2 levels, reducing the saturation index for $CaCO_3$ in the water. This drives dissolution of the surrounding host rock. Microbial growth presumably leads to the accumulation of biofilms on the surface of the rock. At the interface between the biofilm and the rock, local chemical conditions can be dramatically different, generally leading to acidic conditions that also rapidly promote dissolution. The charged polysaccharides of the biofilm will also attract charged clay molecules in the water, leading to their accumulation on these surfaces. This scenario is true for all areas inundated by the water; however, the variability in water level contributes to the observed laminated structure of the rock. As the water level drops, biofilm structures are exposed and quickly die. When the water rises and this area is once again submerged, there is no significant microbial activity at first to generate CO_2 and calcite begins to precipitate. After a time, the microbial community becomes re-established and dissolution begins again. The timing of such activities will dictate the type and pattern of such events (Figure 11) and whether dissolution exceeds precipitation, leading to speleogenesis.

SUMMARY

Microbial ecologists have argued that microbial diversity can be driven through niche differentiation, dispersion, competition, and disturbance; however, the static nature of the Wind Cave environment (constant temperature, no seasonal/diurnal variation, limited water dynamics) and the apparent absence of eukaryotic predation argue against these models. Rather, the Wind Cave lakes appear to contain a bacterially dominated ecosystem where bacteria and their viruses may represent the top predators. This isolated but humanly accessible environment may therefore provide a test bed for developing techniques to study other planktonic, low biomass environments, such as Lake Vostok. And even those with potentially low biomass, such as the moons Europa and Enceladus. This study suggests that the lakes in Wind Cave represent a unique microbial biome unlike any previously described. The cell numbers observed suggest that the lakes contain fewer microbial cells that any current body of water on Earth and even compete with Antarctic accretion ice for extremely low biomass (Priscu et al. 1999). The importance of this microbial community, in its ability to allow us to understand extremely ancient microbial ecosystems, cannot be overstated.

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Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P1A03	Uncultured deep-sea bacterium	93%	Deep-sea surface sediments	Unclassified
P1A04	Mesorhizobium albiziae strain	95%	Subtropical region of China	Alpha
P1A05	Uncultured OP3 clone W50mContig13	85%	Low temperature ultramafic rocks	OP3
P1A07	*Streptococcus salivarius*	99%	Endotracheal tube biofilm	Firmicutes
P1A08	uncultured Actinomyces	99%	Endotracheal tube biofilm	Actinobacteria
P1A09	Uncultured organism clone	79%		Unclassified
P1A10	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P1A11	*Fusobacterium* sp. oral clone	99%	tongue dorsa	Fusobacteria
P1A12	Uncultured *Anaerolineae* bacterium	99%	aliphatic hydrocarbon-contaminated soil	Chloroflexi
P1B02	Uncultured bacterium clone	99%		Unclassified
P1B03	Uncultured bacterium clone	87%	Eleveted soil CO2	Unclassified
P1B04	Uncultured deep-sea bacterium	93%		Unclassified
P1B06	Uncultured bacterium clone (62% query)	96%	Human skin microbiota	Unclassified
P1B07	Uncultured *Gemella* clone	99%	Clean room environment	Firmicutes
P1B08	Uncultured bacterium clone		Endotracheal tube biofilm	Unclassified
P1B10	Uncultured bacterium clone	90%	uranium and technetium bioimmobilization	Unclassified
P1B11	Uncultured bacterium clone	96%	soil bacterial and archaeal community	Unclassified
P1B12	Uncultured bacterium clone	92%	Ridge flank crustal fluids	Unclassified
P1C01	Uncultured bacterium clone	90%	monochlorobenzene contaminated groundwat	Unclassified
P1C03	Uncultured bacterium clone	99%		Unclassified
P1C04	Uncultured *Cellvibrio*	99%	Soil	Proteobacteria
P1C07	Uncultured bacterium clone	94%	Natural asphalts	Unclassified
P1C08	Uncultured bacterium clone (77% query)	99%		Unclassified
P1C09	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P1C10	Uncultured bacterium clone	99%	Bartonella-positive fleas	Unclassified
P1C11	Uncultured deep-sea bacterium	92%	Deep-sea surface sediments	Unclassified
P1D01	*Abiotrophia paradiacens*	99%	Endotracheal tube biofilm	Firmicutes
P1D02	Uncultured deep-sea bacterium	94%	deep-sea surface sediments	Unclassified
P1D03	Uncultured bacterium clone	99%	patients with P. aeruginosa	Unclassified
P1D04	*Rothia mucilaginosa*	99%	human skin microbiota	Actinobacteria
P1D05	*Actinomyces lingnae*	78%	Endotracheal tube biofilm	Actinobacteria
P1D06	*Sphingopyxis witflariensis*	98%	activated sludge	Proteobacteria
P1D07	Uncultured bacterium clone(Streptococcus sali	99%	gut microbiome	Firmicutes
P1D08	Uncultured *Acidimicrobiales* bacterium	97%	hydrocarbon-contaminated soil	Actinobacteria
P1D09	Uncultured bacterium clone	99%	aquifer biofilms	Planctomycetes

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P1D10	Uncultured planctomycete gene	90%	Subseafloor	Planctomycetes
P1D11	Uncultured bacterium clone	95%	Soil	Unclassified
P1D12	Uncultured actinobacterium clone	94%	potash-polluted marsh	Actinobacteria
P1E01	*Paenibacillus sp.*	99%	Nodulation in black locust	Firmicutes
P1E02	Uncultured bacterium clone	97%	Endotracheal tube biofilm	Acidobacteria
P1E03	Uncultured *Acidobacteria* bacterium	94%	subsurface sediments	Acidobacteria
P1E04	Uncultured *Acidimicrobiales* bacterium	98%	hydrocarbon-contaminated soil	Actinobacteria
P1E05	Uncultured *Agrobacterium*	94%	low-biomass carbonate rock	Proteobacteria
P1E07	Uncultured *Rhodocyclaceae* bacterium	97%	CO2 affected soil	Proteobacteria
P1E09	Uncultured deep-sea bacterium	94%	deep-sea surface sediments	Unclassified
P1E10	Uncultured *Chloroflexi* bacterium	92%	deep Arctic Ocean	Chloroflexi
P1E11	Uncultured bacterium clone	99%	Human gut	Unclassified
P1E12	Uncultured bacterium clone	93%	CO2 affected soil	Unclassified
P1F01	Uncultured *Fusobacterium*	99%	Stomach microbiota	Fusobacteria
P1F05	Uncultured deep-sea bacterium	93%	deep-sea surface sediments	Unclassified
P1F06	Uncultured *Rhodocyclaceae* bacterium		CO2 affected soil	Proteobacteria
P1F07	Uncultured bacterium partial	96%	active fermenters in earthworm gut	Unclassified
P1F08	Uncultured bacterium partial	92%	active fermenters in earthworm gut	Unclassified
P1F09	Uncultured bacterium clone	89%	Lake Washington Sediments	Unclassified
P1F10	*Fusobacterium periodonticum*	99%	Humans with periodontal disease	Fusobacteria
P1F11	Uncultured bacterium clone	99%	low-level-radioactive-waste site	Unclassified
P1F12	Uncultured *Actinobacterium*	95%	Dolomite rock from the Alps	Actinobacteria
P1G02	Uncultured bacterium clone(69% query)	98%	Endotracheal tube biofilm	Unclassified
P1G03	*Capnocytophaga sp*. oral clone	99%	human subgingival plaque	Unclassified
P1G04	Uncultured bacterium clone	90%	Urban aerosols harbor	Unclassified
P1G08	Actinomyces sp(52% query)	91%	tongue dorsa	Actinobacteria
P1G09	Uncultured *Nitrospirales* bacterium clone	99%	Karstic cave in Slovenia	Nitrospirae
P1G10	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P1G12	*Actinomyces* sp. oral clone	99%	tongue dorsa	Actinobacteria
P1H01	Uncultured deep-sea bacterium	99%	deep-sea surface sediments	Unclassified
P1H02	Uncultured bacterium clone	95%	dredged river sediments	Unclassified
P1H03	*Lachnospiraceae* bacterium	99%	Human Oral Microbiome	Firmicutes
P1H04	Uncultured deep-sea bacterium	94%	deep-sea surface sediments	Unclassified
P1H05	Uncultured bacterium clone(77% query)	99%	Endotracheal tube biofilm	Unclassified
P1H06	Uncultured bacterium clone	96%	dredged river sediments	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P1H07	Uncultured bacterium clone	85%	water distribution system	Unclassified
P1H08	Uncultured deep-sea bacterium	83%	deep-sea surface sediments	Unclassified
P1H09	*Pseudomonas* sp.	99%	Kartchner Caverns, Arizona	Gamma
P1H10	*Pseudomonas* sp.	98%	Kartchner Caverns, Arizona	Gamma
P1H11	Uncultured deep-sea bacterium	94%	deep-sea surface sediments	Unclassified
P1H12	Leptotrichia sp. oral clone(70% query)	95%	tongue dorsa	Fusobacteria
P2A02	Uncultured bacterium clone	86%	rare members of the soil	Unclassified
P2A03	Uncultured bacterium clone	99%	Groundwater	Unclassified
P2A04	Uncultured *Gammaproteobacterium*	97%	Antarctic terrestrial habitats	Gamma
P2A05	Uncultured bacterium clone(71% query)	95%	Antarctica soils	Unclassified
P2A06	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2A07	Uncultured soil bacterium clone	87%	Arizona soil	Unclassified
P2A08	Unidentified bacterium	87%	Nullarbor caves, Australia	Unclassified
P2A09	Pseudomonas sp.	99%		Gamma
P2A10	Uncultured *Burkholderiaceae* bacterium	96%	hydrocarbon-contaminated soil	Gamma
P2A11	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2A12	Uncultured bacterium clone	99%	patients with P. aeruginosa	Unclassified
P2B02	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P2B03	Uncultured bacterium clone	95%	Soil	Unclassified
P2B04	Uncultured organism clone(89% query)	91%		Unclassified
P2B05	Uncultured *Gammaproteobacterium*	92%	Drinking water microflora	Gamma
P2B06	Uncultured bacterium clone(69% query)	99%	Endotracheal tube biofilm	Unclassified
P2B07	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P2B10	Uncultured *Planctomycetacia* bacterium	91%	hydrocarbon-contaminated soi	Planctomycetes
P2B11	Uncultured bacterium clone	95%	Soil	Unclassified
P2B12	Uncultured bacterium clone	87%	variable soil profile	Unclassified
P2C01	Uncultured bacterium clone	94%	ephemeral desert stream sediment	Unclassified
P2C02	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P2C03	Pseudomonas sp.(67% query)	97%	Epiphytic microorganisms	Proteobacteria
P2C04	*Leptotrichia wadei* strain	99%	Human oral microbiome	Fusobacteria
P2C05	Uncultured *Fusobacterium* sp. Clone	99%	stomach microbiota	Fusobacteria
P2C07	*Streptococcus mitis*	99%	Oral microbiome	Firmicutes
P2C08	*Pseudomonas* sp.	99%	Epiphytic microorganisms	Gamma
P2C10	Uncultured bacterium clone	99%	Soil	Unclassified
P2C11	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P2C12	Uncultured bacterium clone	89%	groundwater	Unclassified
P2D02	Uncultured bacterium clone	99%	Intestine	Unclassified
P2D03	Uncultured bacterium clone	89%	Soil	Unclassified
P2D05	Uncultured bacterium clone	95%	Soil	Unclassified
P2D06	*Amycolatopsis marina* strain	98%	ocean sediment	Actinobacteria
P2D07	Uncultured bacterium clone	99%	patients with P. aeruginosa	Unclassified
P2D08	Uncultured *Gammaproteobacterium*	97%	Antarctic	Gamma
P2D09	Uncultured soil bacterium clone	94%	Soil	Unclassified
P2D10	Uncultured bacterium clone	93%	Namibian upwelling system	Unclassified
P2D12	Uncultured bacterium clone	90%	equine fecal contamination	Unclassified
P2E01	Uncultured *Gemmatimonadaceae*	91%	pyrosequenced amplicons	Gemmatimonadete
P2E03	Uncultured *Chloroflexi* bacterium clone	90%	North Pacific Subtropical Gyre	Chloroflexi
P2E04	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P2E05	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2E07	Uncultured sulfur-oxidizing symbiont bacterium	98%	hydrocarbon-contaminated soil	Unclassified
P2E09	Uncultured bacterium clone	99%	Subsurface ecosystem	Unclassified
P2E10	*Cellvibrio* sp.	98%	natural cellulosic fibres	Proteobacteria
P2E11	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2E12	Uncultured bacterium clone	93%	heavily oil-contaminated and pristine soils	Unclassified
P2F01	Uncultured bacterium clone	95%	soil of the former lake Texcoco (Mexico)	Unclassified
P2F02	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P2F03	*Streptococcus oralis*	99%	Streptococcus genome	Firmicutes
P2F04	Uncultured *Proteobacterium* clone	96%	Ocean soil	Proteobacteria
P2F05	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2F07	Uncultured *Rhodocyclaceae* bacterium clone	96%	CO2 affected soil	Proteobacteria
P2F08	Uncultured bacterium clone	99%	human skin microbiota	Unclassified
P2F09	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2F12	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P2G01	Uncultured *Actinobacterium* gene	95%	dolomite rock	Actinobacteria
P2G02	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2G03	Uncultured bacterium clone	96%	Mammal gut microbe	Unclassified
P2G04	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P2G05	*Pseudomonas* sp.	99%	Leaf surfaces	Gamma
P2G07	Uncultured deep-sea bacterium	89%	Atlantic ocean deep-sea sediments	Unclassified
P2G08	Uncultured deep-sea bacterium	89%	Atlantic ocean deep-sea sediments	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P2G09	*Mesorhizobium albiziae*	95%	subtropical region of China	Alpha
P2G11	*Pseudomonas* sp.	99%	Leaf surfaces	Unclassified
P2G12	Uncultured bacterium clone(78% query)	83%	high-elevation landscape Andes	Unclassified
P2H01	*Streptomyces sodiiphilus*	96%	novel alkaliphilic actinomycete	Actinobacteria
P2H02	Uncultured *Actinobacterium* gene	95%	dolomite rock	Actinobacteria
P2H03	Uncultured *Rhodocyclaceae* bacterium clone	96%	CO2 affected soil	Proteobacteria
P2H04	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2H05	Uncultured *Gammaproteobacterium*	92%	Oil contaminate coastal sediment	Gamma
P2H06	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P2H07	Uncultured bacterium clone	97%	dredged river sediments	Unclassified
P2H08	Uncultured *Deltaproteobacterium*		Karstic cave Slovenia	Delta
P2H10	Uncultured bacterium clone	93%	environmental surveys	Unclassified
P2H12	Uncultured bacterium clone	89%	Soil biosphere	Unclassified
P3A02	Uncultured deep-sea bacterium	94%	Atlantic ocean deep-sea sediments	Unclassified
P3A03	*Steroidobacter denitrificans* strain	92%	Hormone degrading gammaproteobacterium	Proteobacteria
P3A04	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3A05	Uncultured bacterium clone	94%	recently-deglaciated soil	Unclassified
P3A08	Uncultured bacterium clone	94%	natural asphalts	Unclassified
P3A09	Uncultured bacterium clone(60% query	98%	human skin microbiome	Unclassified
P3A11	Uncultured bacterium clone	98%	dredged river sediments	Unclassified
P3A12	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P3B03	Uncultured *Rhodocyclaceae* bacterium clone	96%	CO2 affected soil	Proteobacteria
P3B04	Uncultured bacterium clone	94%	recently-deglaciated soil	Unclassified
P3B05	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P3B06	Uncultured bacterium clone	100%	Endotracheal tube biofilm	Unclassified
P3B08	Uncultured bacterium clone	80%	water distribution system	Unclassified
P3B09	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3B10	*Abiotrophia paradiacens*	99%	Abiotrophia	Firmicutes
P3C01	Uncultured bacterium clone	99%	human skin microbiome	Unclassified
P3C02	*Myxobacterium* clone	86%	e donors for anaerobic respiration	Proteobacteria
P3C04	Uncultured *Alphaproteobacterium*	94%	Dolomite rock in the Alps	Alpha
P3C05	Uncultured bacterium clone(65% query)	99%	Endotracheal tube biofilm	Unclassified
P3C06	*Mesorhizobium albiziae* strain	95%	subtropical region of China	Alpha
P3C08	Uncultured bacterium clone	99%	Intestinal microbiota	Unclassified
P3C09	Uncultured bacterium clone	100%	Endotracheal tube biofilm	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P3C10	Uncultured bacterium clone	99%	soil profile	Unclassified
P3C12	Uncultured bacterium clone	91%	recently-deglaciated soil	Unclassified
P3D01	Uncultured bacterium clone	99%	human skin microbiome	Unclassified
P3D02	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3D03	Uncultured bacterium clone(78% query)	92%	soil	
P3D04	Uncultured bacterium clone	92%	soil	Unclassified
P3D05	Uncultured bacterium clone	94%	recently-deglaciated soil	Unclassified
P3D08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3D09	Uncultured bacterium clone	87%	soil	Unclassified
P3D10	Uncultured bacterium clone(70% query)	96%	Human lung	
P3D12	Uncultured bacterium clone	93%	soil profile	Unclassified
P3E01	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P3E02	Uncultured bacterium clone	91%	recently-deglaciated soil	Unclassified
P3E03	Uncultured bacterium clone	99%	Intestinal microbiota	Unclassified
P3E04	Uncultured *Alphaproteobacterium*	99%	Dolomite rock in the Alps	Alpha
P3E05	Uncultured bacterium clone	92%	sediment of Lake Washington	Unclassified
P3E06	Uncultured bacterium clone	99%	Intestinal microbiota	Unclassified
P3E07	Uncultured bacterium clone	89%	CO2 affected soil	Unclassified
P3E08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3E09	Uncultured bacterium clone(65% query)	100%	Intestinal microbiota	Unclassified
P3E11	*Pseudomonas* sp	99%	Kartchner Caverns, Arizona	Gamma
P3E12	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3F01	Uncultured bacterium clone	84%	Manganese- and iron-dependent marine meth	Unclassified
P3F02	*Nocardia* sp.	98%	shallow water sediments	Actinobacteria
P3F03	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P3F04	Uncultured bacterium clone	99%	Intestinal microbiota	Unclassified
P3F05	Uncultured bacterium clone	95%	Soil	Unclassified
P3F06	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3F07	Uncultured bacterium clone	98%	Endotracheal tube biofilm	Unclassified
P3F08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3F09	Uncultured bacterium clone	97%	Socompa Volcano	Unclassified
P3F10	Uncultured bacterium clone	99%	groundwater	Unclassified
P3F11	*Pseudomonas* sp	99%	Leaf structures	Gamma
P3F12	Uncultured *Actinobacterium*	95%	Dolomite rock in the Alps	Actinobacteria
P3G01	Uncultured bacterium clone		Soil in Antarctica	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P3G02	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P3G03	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3G04	Leptotrichia buccalis(73% query)	99%	Leptotrichia buccalis genome	Fusobacteria
P3G05	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3G06	Uncultured deep-sea bacterium	94%	Atlantic ocean deep-sea sediments	Unclassified
P3G07	Uncultured bacterium clone	99%	Intestinal microbiota	Unclassified
P3G08	Uncultured bacterium clone	89%	groundwater	Unclassified
P3G09	*Myxobacterium* sp.	86%	e donors for anaerobic respiration	Actinobacteria
P3G10	Uncultured bacterium clone	99%	human skin microbiome	Unclassified
P3G11	Uncultured bacterium clone	94%	California grassland soil	Unclassified
P3G12	Uncultured bacterium clone	99%	ow-level-radioactive-waste site	Unclassified
P3H01	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P3H02	Uncultured bacterium clone	99%	Human gut microbe	Unclassified
P3H04	Uncultured bacterium clone	99%	Human gut microbe	Unclassified
P3H05	Uncultured *Gammaproteobacterium*	87%	Wadi An Natrun Lake, Egypt	Gamma
P3H06	Uncultured bacterium clone	88%	drinking water distribution system	Unclassified
P3H07	Uncultured bacterium clone	99%	human skin microbiome	Unclassified
P3H08	Uncultured bacterium clone(63% query)	97%	Canadian high Arctic Ice Core	Unclassified
P3H09	Actinophytocola sp.(65% query)	93%	Selective isolation	
P3H10	Uncultured bacterium clone	94%	shower curtain biofilm	Unclassified
P3H11	Uncultured bacterium clone	90%	drinking water distribution system	Unclassified
P3H12	*Actinomyces* sp.	98%	Tongue dorsa	Actinobacteria
P4A02	Uncultured bacterium clone	99%	Groundwater	Unclassified
P4A03	Uncultured bacterium clone	90%	Drinking water distribution system	Unclassified
P4A04	*Myceligenerans crystallogenes*	97%	Roman catacombs	Actinobacteria
P4A05	Uncultured bacterium clone	97%	microbial communities	Unclassified
P4A07	Uncultured bacterium clone(67% query)	99%	Endotracheal tube biofilm	Unclassified
P4A08	*Pseudomonas* sp.	99%	leaf surfaces	Gamma
P4A09	*Pseudomonas* sp.(69% query)	99%	leaf surfaces	Gamma
P4A10	Uncultured *Actinobacterium*	95%	Dolomite rock from the Alps	Actinobacteria
P4A11	Uncultured bacterium clone	99%	intestinal microbiota	Unclassified
P4A12	Uncultured bacterium clone		human skin microbiota	Unclassified
P4B02	Uncultured *Alphaproteobacterium*	98%	Microbial communities	Alpha
P4B03	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P4B04	Uncultured bacterium clone	86%	Soil	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

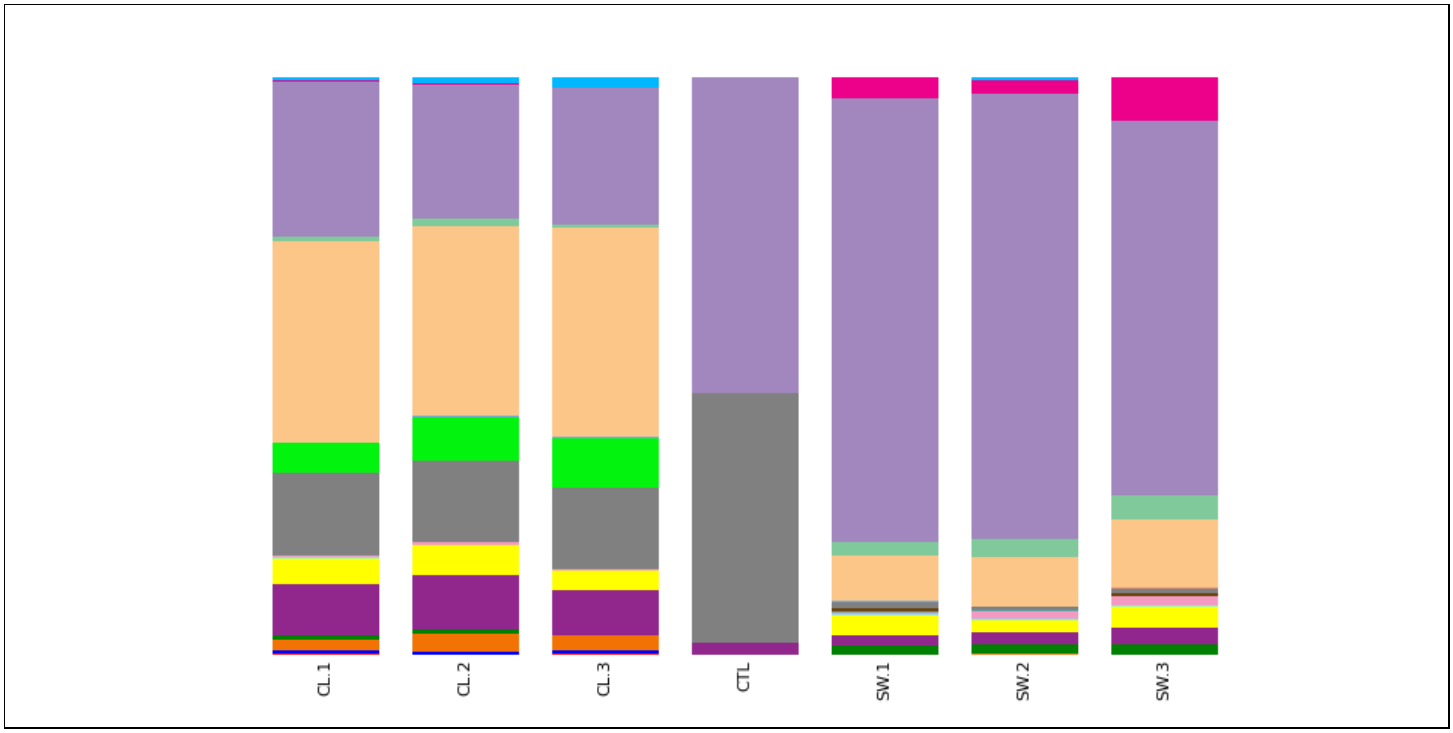
Sample ID	16S ID	%ID	Origin	Division
P4B07	Uncultured *Actinobacterium*	94%	Dolomite rock from the Alps	Actinobacteria
P4B08	Uncultured bacterium clone	97%	Dredged river sediments	Unclassified
P4B09	Uncultured bacterium clone	97%	Dredged river sediments	Unclassified
P4B10	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4B11	Uncultured bacterium clone	99%	Human Gut	Unclassified
P4B12	Uncultured bacterium clone(56% query)	87%	Chinese rice field	
P4C01	Uncultured *Actinobacterium* clone	96%	Salmonid gill bacteria	Actinobacteria
P4C02	Uncultured bacterium clone	89%	Soil	Unclassified
P4C03	*Streptococcus mitis*	99%	Human Oral Microbiome	Actinobacteria
P4C04	Uncultured bacterium clone	99%	Groundwater	Unclassified
P4C05	Uncultured *Rhodocyclaceae* clone	97%	CO2 affected soil	Proteobacteria
P4C06	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P4C08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4C09	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4C10	*Sinobacter flavus* strain	94%	Description of Sinobacter flavus gen	Actinobacteria
P4C11	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4D01	Uncultured bacterium clone(76% query)	99%	Intestinal microbiota	Unclassified
P4D03	*Nocardiopsis* sp.	98%	Marine Nocardiopsis species	Actinobacteria
P4D04	Uncultured bacterium clone	91%	Soil	Unclassified
P4D05	Mesorhizobium albiziae strain	95%	subtropical region of China	Alpha
P4D06	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4D07	*Streptococcus mitis*	99%	Human Oral Microbiome	Actinobacteria
P4D08	Uncultured bacterium clone	96%	gut microbes	Unclassified
P4D09	Uncultured bacterium clone	96%	gut microbes	Unclassified
P4D10	*Pseudomonas* sp.	99%	leaf surfaces	Gamma
P4D11	Uncultured bacterium clone	85%	water distribution system	Unclassified
P4D12	Uncultured *Alphaproteobacterium*(80% query)	93%	Dolomite rock from the Alps	Alpha
P4E01	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4E02	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4E03	Uncultured bacterium clone	93%	soil profile	Unclassified
P4E04	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4E05	Euzebya tangerina gene	94%	sea cucumber Holothuria edulis	
P4E06	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4E07	Uncultured bacterium clone	90%	California grassland	Unclassified
P4E08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified

Supplemental Table S1: Clone Library Phylotypes Obtained From December 2010

Sample ID	16S ID	%ID	Origin	Division
P4E11	Uncultured bacterium clone	94%	Dredged river sediments	Unclassified
P4E12	Uncultured bacterium clone	87%	Soil	Unclassified
P4F01	Uncultured bacterium clone(76% query)	99%	Endotracheal tube biofilm	Unclassified
P4F02	Uncultured bacterium clone	98%	Dredged river sediments	Unclassified
P4F03	Uncultured bacterium clone	89%	Groundwater	Unclassified
P4F04	Uncultured bacterium clone	93%	Soil	Unclassified
P4F05	Uncultured bacterium clone	87%	Soil	Unclassified
P4F06	Uncultured bacterium clone	92%	CO2 affected soil	Unclassified
P4F07	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4F08	Uncultured bacterium clone	98%	anoxic river sediment	Unclassified
P4F09	Uncultured bacterium clone	98%	anoxic river sediment	Unclassified
P4F10	Uncultured bacterium clone	89%	stratified hypersaline microbial mat	Unclassified
P4F11	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P4F12	*Afipia* sp.	98%	water treatment filters	Proteobacteria
P4G01	Uncultured bacterium clone	99%	human skin microbiota	Unclassified
P4G02	Uncultured deep-sea bacterium	92%	Atlantic ocean deep-sea sediments	Unclassified
P4G03	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4G07	Uncultured bacterium clone	97%	Dredged river sediments	Unclassified
P4G08	Uncultured bacterium clone	86%	Soil	Unclassified
P4G09	Uncultured bacterium clone	86%	Soil	Unclassified
P4G10	*Bacillus herbersteinensis*	98%	*Bacillus herbersteinensis*	Firmicutes
P4G11	Uncultured bacterium clone		water distribution system	Unclassified
P4H01	Uncultured deep-sea bacterium	93%	Atlantic ocean deep-sea sediments	Unclassified
P4H02	*Paenibacillus* sp.	99%	Alaskan tundra	Firmicutes
P4H03	Uncultured soil bacterium clone	92%	Soil	Unclassified
P4H05	Uncultured bacterium clone	99%	Human skin microbiota	Unclassified
P4H06	*Sinorhizobium fredii*	96%		Proteobacteria
P4H07	Uncultured bacterium clone	86%	Soil	Unclassified
P4H08	Uncultured bacterium clone	99%	Endotracheal tube biofilm	Unclassified
P4H09	Uncultured bacterium clone(51% query)	99%	Endotracheal tube biofilm	Unclassified
P4H11	Uncultured bacterium clone	93%	waste activated sludge	Unclassified

Taxonomy Summary. Current Level:

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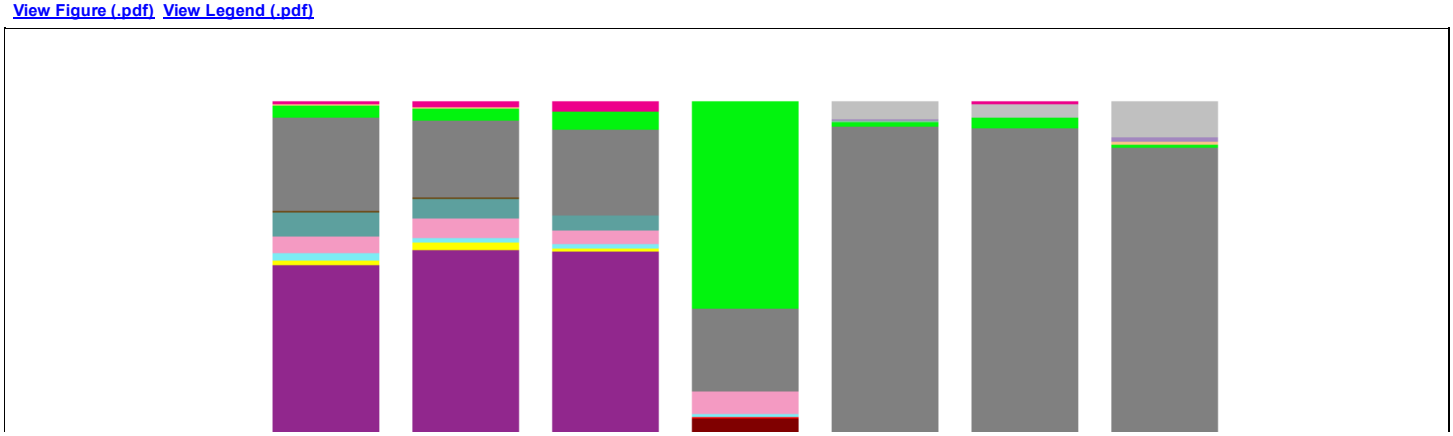


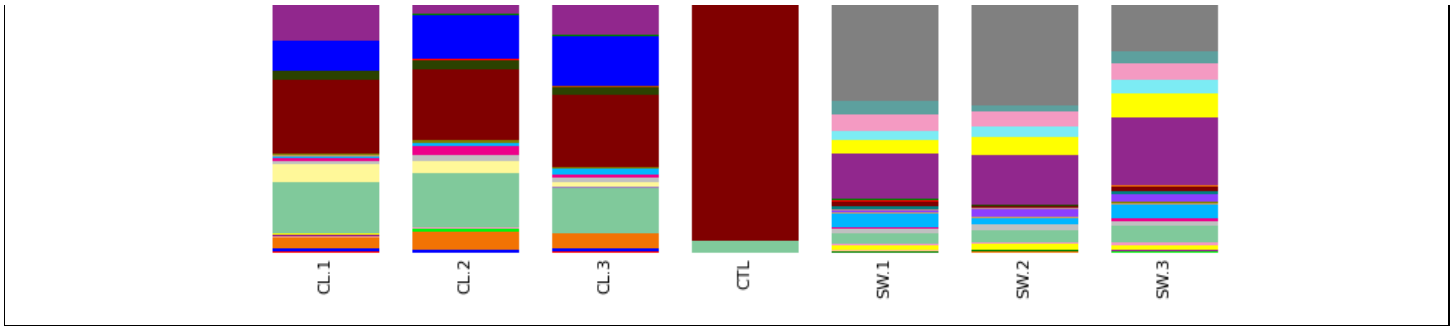
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		Total		CL.1	CL.2	CL.3	CTL	SW.1	SW.2	SW.3
Legend	Taxonomy	count	%	%	%	%	%	%	%	%
	Archaea;Crenarchaeota	0	0.2%	0.4%	0.2%	0.5%	0.0%	0.0%	0.0%	0.1%
	Archaea;Euryarchaeota	0	0.3%	0.5%	0.6%	0.6%	0.0%	0.0%	0.1%	0.0%
	Archaea;Other	0	1.2%	2.0%	3.2%	2.4%	0.0%	0.2%	0.6%	0.2%
	Bacteria;Acidobacteria	0	0.9%	0.7%	0.6%	0.2%	0.0%	1.7%	1.5%	1.8%
	Bacteria;Actinobacteria	0	5.0%	8.9%	9.4%	7.7%	2.3%	1.7%	2.1%	2.7%
	Bacteria;Bacteroidetes	0	3.2%	4.3%	5.1%	3.4%	0.1%	3.4%	2.1%	3.8%
	Bacteria;Chlamydiae	0	0.2%	0.4%	0.2%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi	0	0.6%	0.2%	0.3%	0.1%	0.0%	0.4%	1.4%	1.5%
	Bacteria;Cyanobacteria	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.2%	0.1%
	Bacteria;Deinococcus-Thermus	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.5%	0.1%	0.5%
	Bacteria;Firmicutes	1	12.5%	14.3%	14.0%	14.0%	43.1%	0.9%	0.4%	0.8%
	Bacteria;Fusobacteria	0	3.1%	5.2%	7.6%	8.7%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Gemmatimonadetes	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Nitrospira	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Other	1	18.8%	34.7%	32.6%	36.1%	0.2%	7.9%	8.6%	11.7%
	Bacteria;Planctomycetes	0	1.8%	0.8%	1.5%	0.7%	0.0%	2.3%	3.1%	4.3%
	Bacteria;Proteobacteria	3	49.5%	26.9%	23.0%	23.5%	54.3%	76.9%	77.1%	64.8%
	Bacteria;SR1	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;TM7	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia	0	1.9%	0.2%	0.3%	0.1%	0.0%	3.3%	2.5%	7.1%
	Unclassified;Other	0	0.4%	0.3%	0.8%	1.5%	0.0%	0.1%	0.1%	0.1%

Taxonomy Summary. Current Level:

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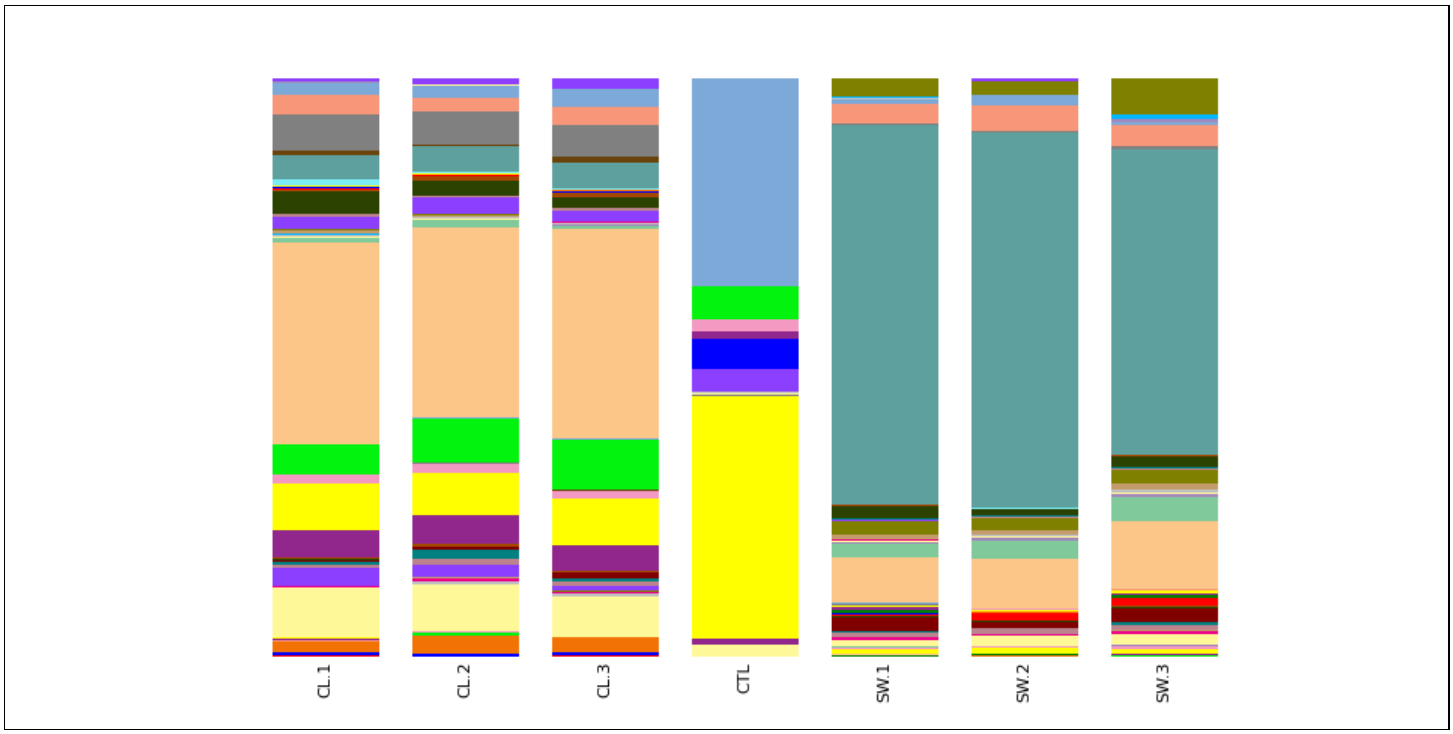


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Legend	Taxonomy	Total count	Total %	CL.1 %	CL.2 %	CL.3 %	CTL %	SW.1 %	SW.2 %	SW.3 %
	Archaea;Crenarchaeota;Thermoprotei	0	0.2%	0.4%	0.2%	0.5%	0.0%	0.0%	0.0%	0.1%
	Archaea;Euryarchaeota;Other	0	0.3%	0.5%	0.6%	0.6%	0.0%	0.0%	0.1%	0.0%
	Archaea;Other;Other	0	1.2%	2.0%	3.2%	2.4%	0.0%	0.2%	0.6%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp1	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp10	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp16	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp17	0	0.1%	0.1%	0.3%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp18	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp22	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp25	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp3	0	0.1%	0.5%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp4	0	0.4%	0.1%	0.1%	0.0%	0.0%	0.7%	1.1%	0.9%
	Bacteria;Acidobacteria;Acidobacteria_Gp5	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp6	0	0.2%	0.0%	0.1%	0.0%	0.0%	0.4%	0.3%	0.4%
	Bacteria;Acidobacteria;Acidobacteria_Gp7	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria	0	5.0%	8.9%	9.4%	7.7%	2.3%	1.7%	2.1%	2.7%
	Bacteria;Bacteroidetes;Bacteroidetes_incertae_sedis	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia	0	0.9%	3.2%	2.1%	0.9%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria	0	0.7%	0.3%	1.2%	0.9%	0.1%	0.7%	0.9%	1.0%
	Bacteria;Bacteroidetes;Other	0	0.5%	0.5%	1.5%	0.5%	0.0%	0.3%	0.1%	0.4%
	Bacteria;Bacteroidetes;Sphingobacteria	0	1.1%	0.2%	0.4%	1.0%	0.0%	2.4%	1.1%	2.4%
	Bacteria;Chlamydiae;Chlamydiae	0	0.2%	0.4%	0.2%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Anaerolineae	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Other	0	0.4%	0.0%	0.0%	0.0%	0.0%	0.3%	1.4%	1.3%
	Bacteria;Cyanobacteria;Cyanobacteria	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.2%	0.1%
	Bacteria;Deinococcus-Thermus;Deinococci	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.5%	0.1%	0.5%
	Bacteria;Firmicutes;Bacilli	1	11.8%	12.8%	12.3%	12.5%	43.0%	0.8%	0.3%	0.7%
	Bacteria;Firmicutes;Clostridia	0	0.7%	1.5%	1.5%	1.5%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Firmicutes;Erysipelotrichi	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Other	0	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria	0	3.1%	5.2%	7.6%	8.7%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Gemmatimonadetes;Gemmatimonadetes	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Nitrospira;Nitrospira	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Other;Other	1	18.8%	34.7%	32.6%	36.1%	0.2%	7.9%	8.6%	11.7%
	Bacteria;Planctomycetes;Planctomycetacia	0	1.8%	0.8%	1.5%	0.7%	0.0%	2.3%	3.1%	4.3%
	Bacteria;Proteobacteria;Alphaproteobacteria	0	1.3%	1.4%	0.7%	0.6%	0.5%	1.7%	1.9%	2.3%
	Bacteria;Proteobacteria;Betaproteobacteria	0	2.9%	2.7%	3.5%	2.3%	3.7%	2.8%	2.5%	2.8%
	Bacteria;Proteobacteria;Deltaproteobacteria	0	2.2%	4.2%	3.4%	2.7%	0.0%	2.4%	1.0%	2.0%
	Bacteria;Proteobacteria;Epsilonproteobacteria	0	0.1%	0.4%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria	3	36.4%	16.1%	13.3%	14.9%	14.3%	69.3%	69.9%	57.1%
	Bacteria;Proteobacteria;Other	0	6.6%	2.2%	2.0%	3.0%	35.8%	0.9%	1.7%	0.6%
	Bacteria;SR1;SR1_genera_incertae_sedis	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;TM7;TM7_genera_incertae_sedis	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Opitutae	0	0.1%	0.1%	0.2%	0.1%	0.0%	0.1%	0.0%	0.5%
	Bacteria;Verrucomicrobia;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Verrucomicrobia;Spartobacteria	0	0.1%	0.1%	0.0%	0.0%	0.0%	0.3%	0.0%	0.7%
	Bacteria;Verrucomicrobia;Subdivision3	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Verrucomicrobiae	0	1.6%	0.0%	0.0%	0.0%	0.0%	2.8%	2.5%	5.9%
	Unclassified;Other;Other	0	0.4%	0.3%	0.8%	1.5%	0.0%	0.1%	0.1%	0.1%

Taxonomy Summary. Current Level:

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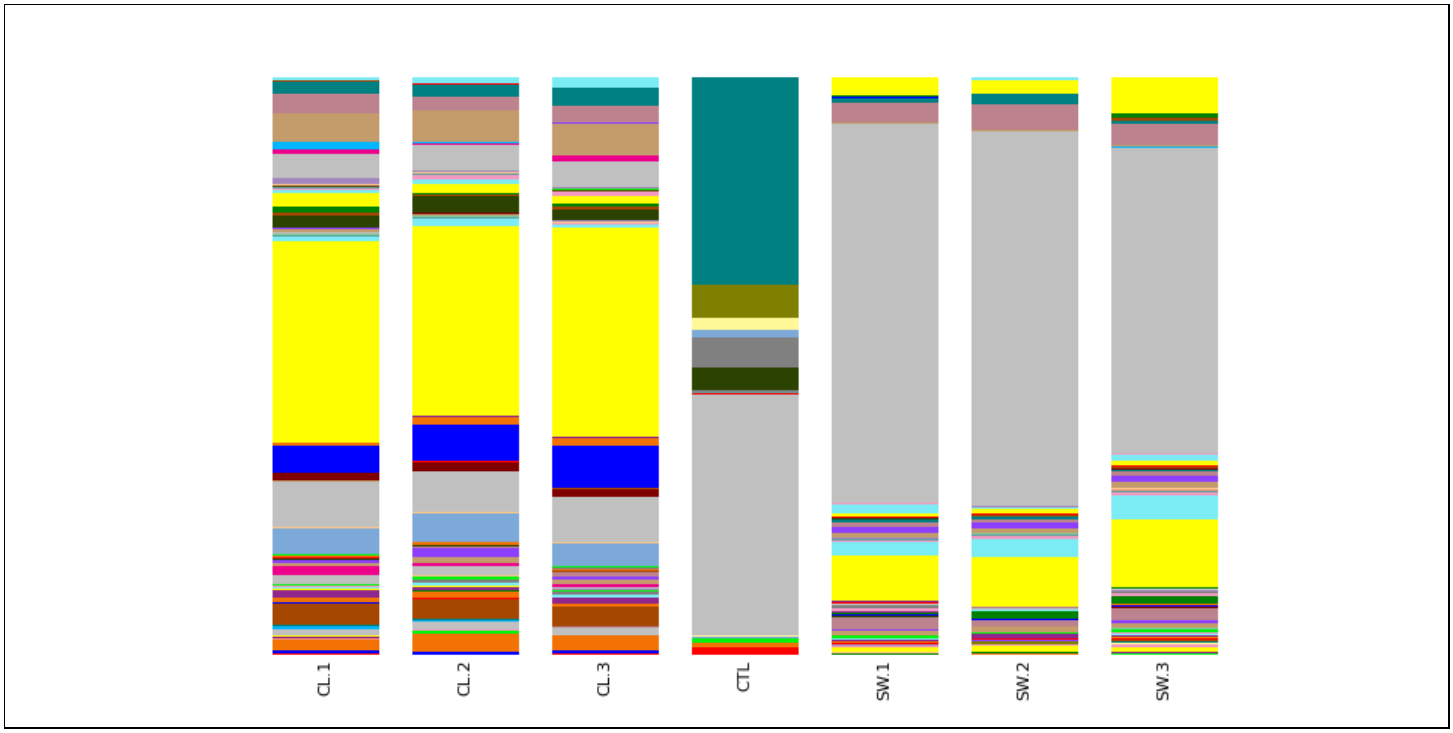
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		Total		CL.1	CL.2	CL.3	CTL	SW.1	SW.2	SW.3
Legend	Taxonomy	count	%	%	%	%	%	%	%	%
	Archaea;Crenarchaeota;Thermoprotei;Other	0	0.2%	0.4%	0.2%	0.5%	0.0%	0.0%	0.0%	0.1%
	Archaea;Euryarchaeota;Other;Other	0	0.3%	0.5%	0.6%	0.6%	0.0%	0.0%	0.1%	0.0%
	Archaea;Other;Other;Other	0	1.2%	2.0%	3.2%	2.4%	0.0%	0.2%	0.6%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp1;Gp1	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp10;Gp10	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp16;Gp16	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp17;Gp17	0	0.1%	0.1%	0.3%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp18;Gp18	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp22;Gp22	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp25;Gp25	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp3;Gp3	0	0.1%	0.5%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp4;Gp4	0	0.4%	0.1%	0.1%	0.0%	0.0%	0.7%	1.1%	0.9%
	Bacteria;Acidobacteria;Acidobacteria_Gp5;Gp5	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp6;Gp6	0	0.2%	0.0%	0.1%	0.0%	0.0%	0.4%	0.3%	0.4%
	Bacteria;Acidobacteria;Acidobacteria_Gp7;Gp7	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobidae_incertae_sedis	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales	0	4.4%	8.5%	8.0%	7.0%	2.3%	1.2%	1.8%	1.8%
	Bacteria;Actinobacteria;Actinobacteria;Nitriliruptorales	0	0.1%	0.1%	0.5%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Other	0	0.4%	0.3%	0.7%	0.4%	0.0%	0.4%	0.2%	0.6%
	Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Bacteroidetes;Bacteroidetes_incertae_sedis;Fulvivirga	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales	0	0.9%	3.2%	2.1%	0.9%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales	0	0.7%	0.3%	1.2%	0.9%	0.1%	0.7%	0.9%	1.0%
	Bacteria;Bacteroidetes;Other;Other	0	0.5%	0.5%	1.5%	0.5%	0.0%	0.3%	0.1%	0.4%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales	0	1.1%	0.2%	0.4%	1.0%	0.0%	2.4%	1.1%	2.4%
	Bacteria;Chlamydiae;Chlamydiae;Chlamydiales	0	0.2%	0.4%	0.2%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Other;Other	0	0.4%	0.0%	0.0%	0.0%	0.0%	0.3%	1.4%	1.3%
	Bacteria;Cyanobacteria;Cyanobacteria;Chloroplast	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%
	Bacteria;Cyanobacteria;Cyanobacteria;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.5%	0.1%	0.5%
	Bacteria;Firmicutes;Bacilli;Bacillales	0	2.2%	4.6%	4.8%	4.5%	1.0%	0.5%	0.0%	0.3%
	Bacteria;Firmicutes;Bacilli;Lactobacillales	1	9.5%	8.2%	7.5%	7.9%	41.9%	0.3%	0.3%	0.3%
	Bacteria;Firmicutes;Bacilli;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales	0	0.7%	1.5%	1.5%	1.5%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Firmicutes;Clostridia;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%

	Bacteria;Firmicutes;Other;Other	0	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales	0	3.1%	5.2%	7.6%	8.7%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Nitrospira;Nitrospira;Nitrospirales	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Other;Other;Other	1	18.8%	34.7%	32.6%	36.1%	0.2%	7.9%	8.6%	11.7%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales	0	1.8%	0.8%	1.5%	0.7%	0.0%	2.3%	3.1%	4.3%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales	0	0.2%	0.0%	0.1%	0.1%	0.0%	0.4%	0.5%	0.5%
	Bacteria;Proteobacteria;Alphaproteobacteria;Other	0	0.2%	0.2%	0.2%	0.1%	0.1%	0.2%	0.3%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales	0	0.3%	0.5%	0.2%	0.4%	0.3%	0.1%	0.1%	0.4%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales	0	0.5%	0.7%	0.1%	0.0%	0.0%	0.8%	0.8%	1.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales	0	1.1%	0.3%	0.2%	0.1%	0.1%	2.5%	2.1%	2.2%
	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales	0	1.5%	2.0%	2.9%	1.9%	3.7%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Other	0	0.3%	0.4%	0.4%	0.3%	0.0%	0.2%	0.1%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.3%	0.2%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales	0	1.9%	4.0%	2.5%	1.8%	0.0%	2.2%	1.0%	1.7%
	Bacteria;Proteobacteria;Deltaproteobacteria;Other	0	0.3%	0.2%	0.9%	0.8%	0.0%	0.2%	0.0%	0.3%
	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales	0	0.1%	0.4%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales	0	0.9%	0.2%	0.1%	0.4%	5.4%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Cardiobacteriales	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales	0	0.2%	0.0%	0.0%	0.1%	1.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria_incertae_sedis	0	0.1%	0.3%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales	0	0.2%	0.9%	0.1%	0.2%	0.0%	0.1%	0.3%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales	0	0.3%	0.0%	0.0%	0.0%	2.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Other	2	28.0%	4.3%	4.4%	4.5%	0.0%	65.5%	64.8%	52.8%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales	0	0.3%	0.8%	0.5%	0.8%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales	0	2.6%	6.2%	5.6%	5.6%	0.0%	0.3%	0.2%	0.3%
	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales	0	0.8%	0.0%	0.0%	0.0%	5.5%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales	0	2.9%	3.4%	2.3%	3.1%	0.0%	3.3%	4.6%	3.7%
	Bacteria;Proteobacteria;Other;Other	0	6.6%	2.2%	2.0%	3.0%	35.8%	0.9%	1.7%	0.6%
	Bacteria;SR1;SR1_genera_incertae_sedis;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;TM7;TM7_genera_incertae_sedis;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Opitutae;Opitutales	0	0.1%	0.1%	0.2%	0.0%	0.0%	0.1%	0.0%	0.5%
	Bacteria;Verrucomicrobia;Opitutae;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Verrucomicrobia;Spartobacteria;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Spartobacteria;Spartobacteria_genera_incertae_sedis	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.7%
	Bacteria;Verrucomicrobia;Subdivision3;Subdivision3_genera_incertae_sedis	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales	0	1.6%	0.0%	0.0%	0.0%	0.0%	2.8%	2.5%	5.9%
	Unclassified;Other;Other;Other	0	0.4%	0.3%	0.8%	1.5%	0.0%	0.1%	0.1%	0.1%

Taxonomy Summary. Current Level:

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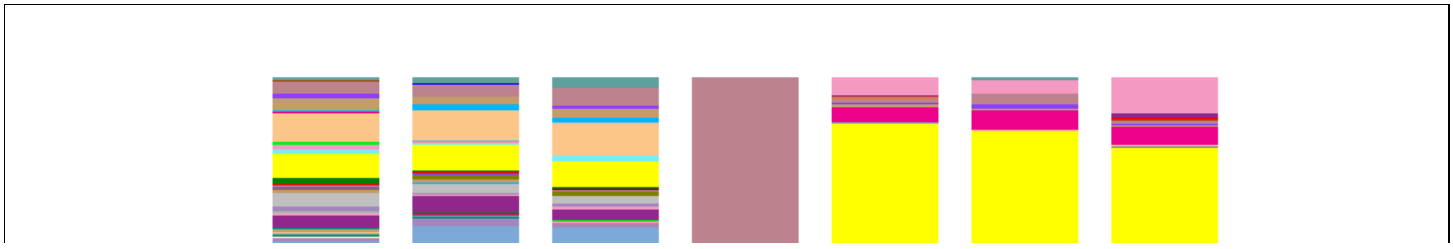
		Total		CL.1	CL.2	CL.3	CTL	SW.1	SW.2	SW.3
Legend	Taxonomy	count	%	%	%	%	%	%	%	%

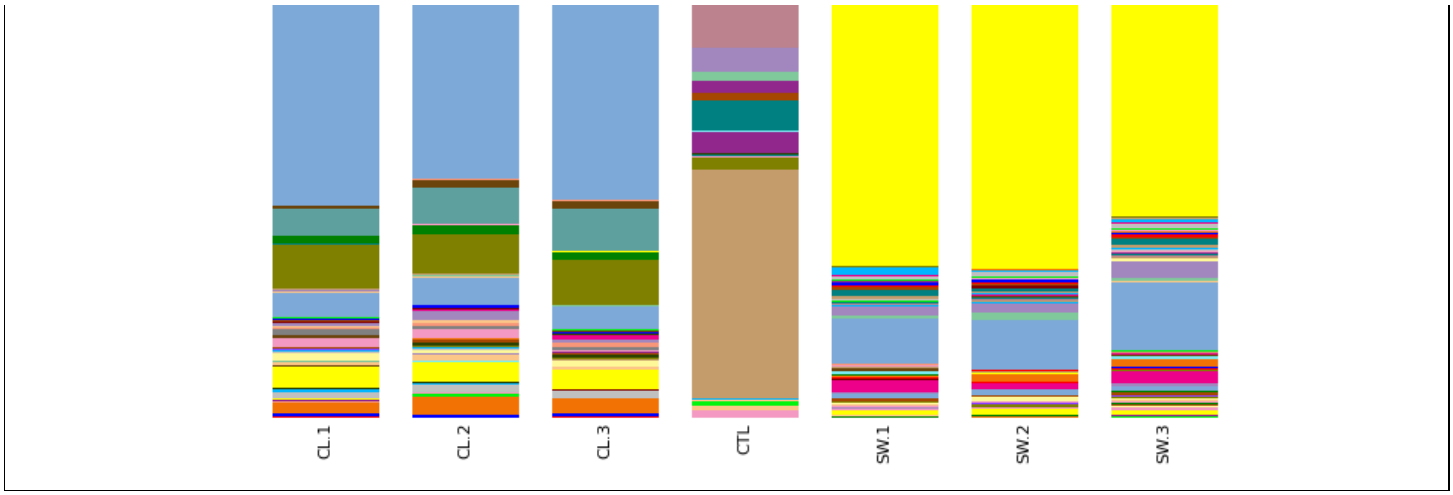
	Archaea;Crenarchaeota;Thermoprotei;Other;Other	0	0.2%	0.4%	0.2%	0.5%	0.0%	0.0%	0.0%	0.1%
	Archaea;Euryarchaeota;Other;Other;Other	0	0.3%	0.5%	0.6%	0.6%	0.0%	0.0%	0.1%	0.0%
	Archaea;Other;Other;Other;Other	0	1.2%	2.0%	3.2%	2.4%	0.0%	0.2%	0.6%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp1;Gp1;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp10;Gp10;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp16;Gp16;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp17;Gp17;Other	0	0.1%	0.1%	0.3%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp18;Gp18;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp22;Gp22;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp25;Gp25;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp3;Gp3;Other	0	0.1%	0.5%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp4;Gp4;Other	0	0.4%	0.1%	0.1%	0.0%	0.0%	0.7%	1.1%	0.9%
	Bacteria;Acidobacteria;Acidobacteria_Gp5;Gp5;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp6;Gp6;Other	0	0.2%	0.0%	0.1%	0.0%	0.0%	0.4%	0.3%	0.4%
	Bacteria;Acidobacteria;Acidobacteria_Gp7;Gp7;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Iamiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobidae_incertae_sedis;Ilumatobacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae	0	0.5%	1.2%	1.4%	1.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae	0	0.1%	0.5%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dietziaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.2%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Glycomycetaceae	0	0.0%	0.0%	0.1%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae	0	0.1%	0.0%	0.2%	0.1%	0.2%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae	0	1.5%	3.6%	3.5%	3.2%	0.0%	0.1%	0.0%	0.3%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae	0	0.3%	0.0%	0.0%	0.1%	1.4%	0.1%	0.2%	0.2%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae	0	0.1%	0.3%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae	0	0.5%	0.7%	1.0%	0.5%	0.6%	0.2%	0.0%	0.2%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiopsaceae	0	0.1%	0.1%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Other	0	0.6%	1.4%	0.7%	0.9%	0.0%	0.2%	0.9%	0.3%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae	0	0.1%	0.2%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae	0	0.3%	0.3%	0.4%	0.6%	0.0%	0.3%	0.0%	0.5%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptosporangiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Nitriliruptorales;Nitriliruptoraceae	0	0.1%	0.1%	0.5%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Other;Other	0	0.4%	0.3%	0.7%	0.4%	0.0%	0.4%	0.2%	0.6%
	Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Conexibacteraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidetes_incertae_sedis;Fulvivirga;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae	0	0.5%	1.7%	1.5%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae	0	0.4%	1.5%	0.5%	0.6%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	0	0.7%	0.3%	1.1%	0.9%	0.1%	0.7%	0.9%	1.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Other;Other;Other	0	0.5%	0.5%	1.5%	0.5%	0.0%	0.3%	0.1%	0.4%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae	0	0.9%	0.2%	0.2%	0.6%	0.0%	2.1%	1.1%	2.2%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cyclobacteriaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Other	0	0.1%	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%	0.1%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae	0	0.1%	0.0%	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Other	0	0.1%	0.4%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Other;Other;Other	0	0.4%	0.0%	0.0%	0.0%	0.0%	0.3%	1.4%	1.3%
	Bacteria;Cyanobacteria;Cyanobacteria;Chloroplast;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%
	Bacteria;Cyanobacteria;Cyanobacteria;Chloroplast;Streptophyta	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Cyanobacteria;Cyanobacteria;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Deinococcaceae	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.4%	0.1%	0.5%
	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Other	0	0.2%	0.0%	0.0%	0.3%	0.0%	0.4%	0.0%	0.3%
	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae	0	0.2%	0.1%	0.1%	0.1%	0.8%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae	0	1.9%	4.4%	4.8%	4.1%	0.3%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae	0	0.1%	0.3%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae	0	0.1%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.2%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Other	0	0.0%	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	1	9.3%	7.8%	7.0%	7.8%	41.8%	0.2%	0.3%	0.1%
	Bacteria;Firmicutes;Bacilli;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI	0	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%

	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Veillonellaceae	0	0.6%	1.2%	1.4%	1.5%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Other;Other;Other	0	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae	0	2.6%	4.8%	6.4%	7.3%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae	0	0.4%	0.4%	1.2%	1.5%	0.0%	0.0%	0.0%
	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Other;Other;Other;Other	1	18.8%	34.7%	32.6%	36.1%	0.2%	7.9%	8.6%	11.7%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae	0	1.8%	0.8%	1.5%	0.7%	0.0%	2.3%	3.1%	4.3%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae	0	0.2%	0.0%	0.1%	0.1%	0.0%	0.4%	0.5%	0.5%
	Bacteria;Proteobacteria;Alphaproteobacteria;Other;Other	0	0.2%	0.2%	0.2%	0.1%	0.1%	0.2%	0.3%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Aurantimonadaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae	0	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae	0	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae	0	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Other	0	0.1%	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae	0	0.1%	0.3%	0.2%	0.2%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	0	0.5%	0.7%	0.1%	0.0%	0.0%	0.8%	0.8%	0.9%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae	0	0.0%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis	0	0.5%	0.1%	0.1%	0.0%	0.0%	1.1%	1.0%	1.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae	0	0.3%	0.1%	0.0%	0.0%	0.0%	0.8%	0.6%	0.7%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Other	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.4%	0.4%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae	0	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.2%	0.1%
	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae	0	1.5%	2.0%	2.9%	1.9%	3.7%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Other;Other	0	0.3%	0.4%	0.4%	0.3%	0.0%	0.2%	0.1%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.3%	0.2%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae	0	0.3%	1.3%	0.2%	0.5%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Nannocystaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Other	0	1.0%	2.3%	1.5%	1.3%	0.0%	0.5%	0.8%	0.9%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae	0	0.5%	0.5%	0.8%	0.0%	0.0%	1.5%	0.2%	0.8%
	Bacteria;Proteobacteria;Deltaproteobacteria;Other;Other	0	0.3%	0.2%	0.9%	0.8%	0.0%	0.2%	0.0%	0.3%
	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae	0	0.1%	0.4%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae	0	0.1%	0.2%	0.1%	0.4%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Other	0	0.8%	0.0%	0.0%	0.0%	5.4%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Cardiobacteriales;Cardiobacteriaceae	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	0	0.2%	0.0%	0.0%	0.1%	1.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria_incertae_sedis;Solimonas	0	0.1%	0.3%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae	0	0.2%	0.9%	0.1%	0.2%	0.0%	0.0%	0.3%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae	0	0.3%	0.0%	0.0%	0.0%	2.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Other;Other	2	28.0%	4.3%	4.4%	4.5%	0.0%	65.5%	64.8%	52.8%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae	0	0.3%	0.8%	0.5%	0.8%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	0	0.3%	1.2%	0.1%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae	0	2.3%	5.0%	5.5%	5.6%	0.0%	0.1%	0.1%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae	0	0.8%	0.0%	0.0%	0.0%	5.5%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae	0	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae	0	2.9%	3.3%	2.2%	3.0%	0.0%	3.2%	4.6%	3.7%
	Bacteria;Proteobacteria;Other;Other;Other	0	6.6%	2.2%	2.0%	3.0%	35.8%	0.9%	1.7%	0.6%
	Bacteria;SR1;SR1_genera_incertae_sedis;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;TM7;TM7_genera_incertae_sedis;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae	0	0.1%	0.1%	0.2%	0.0%	0.0%	0.1%	0.0%	0.5%
	Bacteria;Verrucomicrobia;Opitutae;Other;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Verrucomicrobia;Spartobacteria;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Spartobacteria;Spartobacteria_genera_incertae_sedis;Other	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.7%
	Bacteria;Verrucomicrobia;Subdivision3;Subdivision3_genera_incertae_sedis;Other	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae	0	1.6%	0.0%	0.0%	0.0%	0.0%	2.8%	2.5%	5.9%
	Unclassified;Other;Other;Other;Other	0	0.4%	0.3%	0.8%	1.5%	0.0%	0.1%	0.1%	0.1%

Taxonomy Summary. Current Level:

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		Total		CL.1	CL.2	CL.3	CTL	SW.1	SW.2	SW.3
Legend	Taxonomy	count	%	%	%	%	%	%	%	%
	Archaea;Crenarchaeota;Thermoprotei;Other;Other;Other	0	0.2%	0.4%	0.2%	0.5%	0.0%	0.0%	0.0%	0.1%
	Archaea;Euryarchaeota;Other;Other;Other;Other	0	0.3%	0.5%	0.6%	0.6%	0.0%	0.0%	0.1%	0.0%
	Archaea;Other;Other;Other;Other;Other	0	1.2%	2.0%	3.2%	2.4%	0.0%	0.2%	0.6%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp1;Gp1;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp10;Gp10;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp16;Gp16;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp17;Gp17;Other;Other	0	0.1%	0.1%	0.3%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Acidobacteria;Acidobacteria_Gp18;Gp18;Other;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp22;Gp22;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp25;Gp25;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp3;Gp3;Other;Other	0	0.1%	0.5%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Acidobacteria;Acidobacteria_Gp4;Gp4;Other;Other	0	0.4%	0.1%	0.1%	0.0%	0.0%	0.7%	1.1%	0.9%
	Bacteria;Acidobacteria;Acidobacteria_Gp5;Gp5;Other;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Acidobacteria;Acidobacteria_Gp6;Gp6;Other;Other	0	0.2%	0.0%	0.1%	0.0%	0.0%	0.4%	0.3%	0.4%
	Bacteria;Acidobacteria;Acidobacteria_Gp7;Gp7;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Iamiaceae;Iamia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobiales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Acidimicrobidae_incertae_sedis;Ilumatobacter;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces	0	0.5%	1.2%	1.4%	1.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Cellulomonadaceae;Cellulomonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	0	0.1%	0.5%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dermabacteraceae;Brachybacterium	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Dietziaceae;Dietzia	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Blastococcus	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.2%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Geodermatophilus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Glycomycetaceae;Glycomyces	0	0.0%	0.0%	0.1%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;Ornithinicoccus	0	0.0%	0.0%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineosporia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Agromyces	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Arthrobacter	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Kocuria	0	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Rothia	0	1.5%	3.5%	3.4%	3.2%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Catelliglobosispora	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Other	0	0.3%	0.0%	0.0%	0.0%	1.4%	0.0%	0.2%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Virgisporangium	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;Nocardia	0	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;Rhodococcus	0	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Actinopolymorpha	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Kribbella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Nocardioides	0	0.4%	0.6%	1.0%	0.5%	0.6%	0.2%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardioidaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Nocardiopsaceae;Nocardiopsis	0	0.1%	0.1%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Other;Other	0	0.6%	1.4%	0.7%	0.9%	0.0%	0.2%	0.9%	0.3%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Myceligenerans	0	0.1%	0.2%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Promicromonosporaceae;Promicromonospora	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;Amycolatopsis	0	0.1%	0.1%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Pseudonocardiaceae;Pseudonocardia	0	0.2%	0.2%	0.2%	0.5%	0.0%	0.2%	0.0%	0.3%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptomycetaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Streptosporangiaceae;Nonomuraea	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae;Actinocorallia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Thermomonosporaceae;Actinomadura	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Nitriliruptorales;Nitriliruptoraceae;Nitriliruptor	0	0.1%	0.1%	0.5%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Other;Other;Other	0	0.4%	0.3%	0.7%	0.4%	0.0%	0.4%	0.2%	0.6%

	Bacteria;Actinobacteria;Actinobacteria;Rubrobacterales;Rubrobacteraceae;Rubrobacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Conexibacteraceae;Conexibacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Other;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Actinobacteria;Actinobacteria;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidetes_incertae_sedis;Fulvivirga;Other;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Porphyromonas	0	0.5%	1.6%	1.5%	0.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Tannerella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Other	0	0.1%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella	0	0.3%	1.3%	0.4%	0.6%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Fluviicola	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Capnocytophaga	0	0.2%	0.2%	0.6%	0.7%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0	0.4%	0.0%	0.0%	0.0%	0.1%	0.7%	0.9%	1.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Other	0	0.1%	0.1%	0.5%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Other;Other;Other;Other	0	0.5%	0.5%	1.5%	0.5%	0.0%	0.3%	0.1%	0.4%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Ferruginibacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Flavisolibacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Chitinophagaceae;Other	0	0.9%	0.2%	0.2%	0.6%	0.0%	2.0%	1.1%	2.2%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cyclobacteriaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Adhaeribacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Arcicella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Emticicia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Hymenobacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Spirosoma	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Other;Other	0	0.1%	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%	0.1%
	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedobacter	0	0.1%	0.0%	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Other;Other	0	0.1%	0.4%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Parachlamydiaceae;Other	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Other	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.2%	0.0%	0.2%
	Bacteria;Chloroflexi;Other;Other;Other;Other	0	0.4%	0.0%	0.0%	0.0%	0.0%	0.3%	1.4%	1.3%
	Bacteria;Cyanobacteria;Cyanobacteria;Chloroplast;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%
	Bacteria;Cyanobacteria;Cyanobacteria;Chloroplast;Streptophyta;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Cyanobacteria;Cyanobacteria;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Deinococcaceae;Deinococcus	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.4%	0.1%	0.5%
	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Oceanobacillus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Other;Other	0	0.2%	0.0%	0.0%	0.3%	0.0%	0.4%	0.0%	0.3%
	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus	0	0.1%	0.1%	0.1%	0.1%	0.8%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Planococcaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Gemella	0	1.9%	4.3%	4.8%	4.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	0	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Abiotrophia	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Aerococcus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Atopostipes	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Pediococcus	0	0.1%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.2%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Other;Other	0	0.0%	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Other	0	5.8%	0.1%	0.1%	0.0%	39.8%	0.2%	0.3%	0.1%
	Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	0	3.5%	7.7%	6.9%	7.8%	2.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Bacilli;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI;Anaerococcus	0	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Oribacterium	0	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Desulfosporosinus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Filifactor	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	0	0.6%	1.2%	1.4%	1.5%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Clostridia;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Solobacterium	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Firmicutes;Other;Other;Other;Other	0	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae;Fusobacterium	0	2.6%	4.8%	6.4%	7.3%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Leptotrichia	0	0.4%	0.4%	1.2%	1.4%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Fusobacteria;Fusobacteria;Fusobacteriales;Leptotrichiaceae;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Nitrospira;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	0	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Other;Other;Other;Other;Other	1	18.8%	34.7%	32.6%	36.1%	0.2%	7.9%	8.6%	11.7%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Blastopirellula	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Gemmata	0	0.4%	0.0%	0.1%	0.0%	0.0%	0.5%	1.3%	0.7%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Other	0	1.2%	0.6%	1.3%	0.6%	0.0%	1.6%	1.7%	2.7%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Pirellula	0	0.1%	0.2%	0.0%	0.0%	0.0%	0.1%	0.0%	0.5%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Planctomyces	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Singulisphaera	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Zavarzinella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0	0.1%	0.0%	0.0%	0.1%	0.0%	0.1%	0.4%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.3%

	Bacteria;Proteobacteria;Alphaproteobacteria;Other;Other;Other	0	0.2%	0.2%	0.2%	0.1%	0.1%	0.2%	0.3%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Aurantimonadaceae;Aurantimonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Chelatococcus	0	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bosea	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Rhodopseudomonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Devosia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Pedomicrobium	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methylobacteriaceae;Methylobacterium	0	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Other;Other	0	0.1%	0.0%	0.0%	0.2%	0.0%	0.1%	0.0%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Hoeflea	0	0.1%	0.3%	0.1%	0.2%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Mesorhizobium	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Other	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Craurococcus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Inquilinus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.3%	0.1%	0.2%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.5%	0.1%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	0	0.3%	0.6%	0.1%	0.0%	0.0%	0.4%	0.2%	0.6%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingosinicella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Other	0	0.0%	0.1%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	0	0.3%	0.0%	0.1%	0.0%	0.0%	0.9%	0.4%	0.9%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Other	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.6%	0.1%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pseudorhodoferax	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.3%	0.2%	0.3%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.5%	0.4%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Other;Other	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.4%	0.4%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia	0	0.1%	0.1%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%
	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Neisseria	0	1.5%	2.0%	2.9%	1.9%	3.5%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Uruburuella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Other;Other;Other	0	0.3%	0.4%	0.4%	0.3%	0.0%	0.2%	0.1%	0.4%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechloromonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Zoogloea	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.3%	0.2%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;Peredibacter	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Cystobacter	0	0.1%	0.5%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacteraceae;Other	0	0.2%	0.8%	0.2%	0.5%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Nannocystaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Other;Other	0	1.0%	2.3%	1.5%	1.3%	0.0%	0.5%	0.8%	0.9%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Byssovorax	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Chondromyces	0	0.4%	0.0%	0.2%	0.0%	0.0%	1.4%	0.2%	0.7%
	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Other	0	0.2%	0.4%	0.6%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Deltaproteobacteria;Other;Other;Other	0	0.3%	0.2%	0.9%	0.8%	0.0%	0.2%	0.0%	0.3%
	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Campylobacter	0	0.1%	0.4%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter	0	0.1%	0.2%	0.1%	0.4%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Other;Other	0	0.8%	0.0%	0.0%	0.0%	5.4%	0.0%	0.0%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Cardiobacteriales;Cardiobacteriaceae;Cardiobacterium	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Other	0	0.2%	0.0%	0.0%	0.1%	1.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Gammaproteobacteria_incertae_sedis;Solimonas;Other	0	0.1%	0.3%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Aquicella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Other	0	0.2%	0.9%	0.1%	0.2%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas	0	0.3%	0.0%	0.0%	0.0%	2.2%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Other;Other;Other	2	28.0%	4.3%	4.4%	4.5%	0.0%	65.5%	64.8%	52.8%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Other	0	0.3%	0.8%	0.5%	0.8%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0	0.1%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Alkanindiges	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Perlucidibaca	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.1%	0.2%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter	0	0.1%	0.5%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Cellvibrio	0	0.1%	0.1%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0	2.3%	4.8%	5.3%	5.5%	0.0%	0.0%	0.1%	0.1%
	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Other	0	0.2%	0.0%	0.0%	0.0%	1.6%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio	0	0.6%	0.0%	0.0%	0.0%	4.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae;Other	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae;Steroidobacter	0	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Luteimonas	0	1.3%	0.0%	0.0%	0.0%	0.0%	2.7%	3.5%	3.2%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter	0	0.3%	0.4%	0.8%	1.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Other	0	0.8%	2.1%	1.3%	1.4%	0.0%	0.4%	0.2%	0.2%

	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0	0.4%	0.7%	0.0%	0.6%	0.0%	0.2%	1.0%	0.3%
	Bacteria;Proteobacteria;Other;Other;Other;Other	0	6.6%	2.2%	2.0%	3.0%	35.8%	0.9%	1.7%	0.6%
	Bacteria;SR1;SR1_genera_incertae_sedis;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;TM7;TM7_genera_incertae_sedis;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Alterococcus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0	0.1%	0.1%	0.2%	0.0%	0.0%	0.0%	0.0%	0.2%
	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%
	Bacteria;Verrucomicrobia;Opitutae;Other;Other;Other	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Other;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Bacteria;Verrucomicrobia;Spartobacteria;Other;Other;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Spartobacteria;Spartobacteria_genera_incertae_sedis;Other;Other	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.7%
	Bacteria;Verrucomicrobia;Subdivision3;Subdivision3_genera_incertae_sedis;Other;Other	0	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Prosthecobacter	0	1.6%	0.0%	0.0%	0.0%	0.0%	2.8%	2.5%	5.9%
	Unclassified;Other;Other;Other;Other;Other	0	0.4%	0.3%	0.8%	1.5%	0.0%	0.1%	0.1%	0.1%