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Relating functional microbial diversity to eastern Iowa alluvial aquifer groundwater chemistry

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RELATING FUNCTIONAL MICROBIAL DIVERSITY TO EASTERN IOWA ALLUVIAL AQUIFER GROUNDWATER CHEMISTRY

by

Kendra Marie Markland

A thesis submitted in partial fulfillment
of the requirements for the Master of Science
degree in Civil and Environmental Engineering in the
Graduate College of
The University of Iowa

May 2018

Thesis Supervisor: Assistant Professor Craig Just

Graduate College
The University of Iowa
Iowa City, Iowa

CERTIFICATE OF APPROVAL

MASTER'S THESIS

This is to certify that the Master's thesis of

Kendra Marie Markland

has been approved by the Examining Committee for
the thesis requirement for the Master of Science degree
in Civil and Environmental Engineering at the May 2018 graduation.

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ABSTRACT

Alluvial aquifers are important sources of drinking water for Eastern Iowans. However, alluvial aquifers are particularly susceptible to contamination from surface activities due to their shallow depth, permeable material, and close connection to surface waters. Domestic wells and monitoring wells located in alluvial aquifers within the Eastern Iowa Basins study unit, which covers 19,500 square miles, were sampled. The study unit includes the Wapsipinicon, Cedar, Iowa, and Skunk River basins, all of which drain to the Mississippi River. During the summer of 2017, a sampling effort of twelve domestic, twenty-four monitoring, and two municipal wells within the Eastern Iowa Basins study unit was conducted. Water quality data, including dissolved oxygen, nitrate, ammonia, dissolved organic carbon, iron, and sulfate concentrations, was collected. Additionally, microbial DNA samples were collected via filtration of alluvial groundwater. We tested the hypotheses that microbial species richness would decrease with increasing NO_3^--N concentrations and that differences in groundwater chemistry would be associated with differences in microbial community taxonomy. Overall, the current state of microbial populations in alluvial aquifers was studied, where the risk of groundwater contamination is high.

PUBLIC ABSTRACT

Groundwater is an important natural resource throughout the world. In Eastern Iowa, much of our groundwater comes from alluvial aquifers. These aquifers are located directly below and adjacent to rivers and streams. Because they are shallow and closely connected to surface waters, alluvial aquifers are susceptible to contamination from activities on the land surface. This study involved the sampling of thirty-eight wells within the Eastern Iowa Basins study unit, which includes the Wapsipinicon, Cedar, Iowa, and Skunk River basins, during the summer of 2017. Water quality data and microbial DNA samples were collected to help us understand how the aquifer water chemistry is related to the microorganisms present. Because microorganisms play crucial roles in transforming contaminants in groundwater, it is important to include microbial community assessments in water quality monitoring. We concluded that wells with differing water chemistry were in fact inhabited by different microbial communities.

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INTRODUCTION

The concentration of nutrients and other chemical constituents in groundwater is regularly monitored in Iowa and throughout the world. However, additional focus should be placed on the microbiological communities and their associations with groundwater constituents. Since microbial communities often govern nutrient cycling and contaminant biodegradation, it is important to understand the relationship between microbial community structure and groundwater geochemistry. Alluvial aquifers are of particular importance because they often carry a high risk of contamination and frequently serve as drinking water sources. This study explores various relationships between groundwater geochemistry and functional microbial diversity in alluvial aquifers in Eastern Iowa.

Alluvial aquifers

Alluvial aquifers are shallow deposits of sand and gravel located along river valleys (Figure 1). The alluvial deposits originate from the historical flows of the river and the materials deposited via the river over time. Alluvial materials are thus quite variable due to their dependence on historical river flows. The makeup of the alluvium is an important aspect in the infiltration of water into the shallow aquifer. Alluvium consisting of fine-grained materials, such as silt and clay, can restrict water flow to the aquifer. However, larger, coarse-grained materials more easily allow for water flow [3].

Overall, alluvial aquifers are highly productive and located at relatively shallow well depths. The water table is typically located five to twenty feet below the land surface [5]. Their shallow depths and close proximity to rivers renders the alluvial groundwater levels highly variable as functions of drought or flood conditions. During times of severe drought, groundwater contributions from alluvial systems can help maintain river flow. Because of the direct connection between alluvial aquifers and the land surface, alluvial groundwater has been in the subsurface for the shortest period of time when compared to all other groundwater [3]. Land surface contributions to alluvial aquifers also make them extremely susceptible to contamination. Groundwater in alluvial aquifers generally has similar water quality to its adjoining river system [3]. It is mainly recharged via infiltration of rain water through the overlying land surface. In some instances, nearby bedrock aquifers can also interact with alluvial aquifers by receiving or contributing water via groundwater flow [5].

In Iowa, alluvial aquifers underlie much of the land surface (Figure 2). The aquifers of Iowa's larger interior rivers range in thickness from thirty to seventy feet. Alluvial aquifers, despite their high risk for contamination, are greatly utilized as a source of drinking water for people living close to the river. According to the Iowa Geological Survey, nearly thirty percent of Iowa's drinking water supplies come from alluvial aquifers (Figure 3) [3]. Alluvial wells have shallow well depths and are productive water sources, making them ideal for many people's needs. Their widespread use as a drinking water source and their susceptibility to contamination make alluvial aquifers an important natural resource requiring extensive monitoring.

Nitrogen contamination in aquifers

Nitrogen is a necessary element for all forms of life because it is needed to build proteins, DNA, RNA, and many other cellular components. Nitrogen exists in a variety of oxidation states and makes up eighty percent of the earth's atmosphere in the form of nitrogen gas. Nitrogen gas must be converted to a more available form, such as ammonia (NH_3-N), nitrate (NO_3^--N), or organic nitrogen, before it can be utilized by life forms (Figure 4). The natural process of nitrogen fixation has been greatly altered due to the development of the Haber-Bosch method in the early 1900s. The Haber-Bosch process allows for the production of nitrogen fertilizers directly from nitrogen gas in the atmosphere. The nitrogen fertilizers are then applied to agricultural land to increase crop yields [9].

In intensive agriculture settings, the nitrogen cycle is greatly altered by a variety of factors, especially the addition of large amounts of inorganic nitrogen in the form of fertilizer. The inorganic nitrogen is easily mobilized and lost, if not taken up by the target crop [10]. Fertilizers are often applied prior to the spring planting season. Due to the extensive rainfall often experienced during that time of the year, tremendous amounts of nitrogen are lost from agriculture fields [4]. Additionally, the nitrogen cycle is greatly affected by the loss of nutrients with the harvest of the crop at the end of the growing season. Alterations in soil structure may also affect the cycling of nitrogen because organic matter in the soil is no longer the main source of slowly released nutrients. As large fluxes of nutrients are applied to the soil, soil microorganisms are unable to accommodate them. Much of the applied nitrogen is thus lost to the surrounding surface water and groundwater in the form of nitrate (Figure 4) [10].

As the result of nitrogen loss to shallow groundwater, nitrate is the most common chemical contaminant of groundwater [11]. In natural ecosystems, nitrate remains at low, stable concentrations. Natural nitrate concentrations are generally defined as less than 3 mg/L of NO_3^--N. Concentrations exceeding the background level of 3 mg/L are usually due to anthropogenic sources [12]. Examples of anthropogenic sources include the application of nitrogen fertilizer and animal manure containing large amounts of nitrogen [13]. In areas of intensive agriculture where these practices are common, the risk of shallow groundwater contamination can be extremely high (Figure 5).

Many health concerns are associated with nitrogen-contaminated groundwater. Excessive nitrate in drinking water has been linked to methemoglobinemia, also known as “blue baby syndrome,” in young children [14]. This association led to the 10 mg/L of NO_3^--N standard passed by the U.S. Environmental Protection Agency. Other health effects are also of great concern, including possible carcinogenic effects associated with the formation of N-nitroso compounds in the body. These compounds, which include both nitrosamines and nitrosamides, have been shown to cause tumors in numerous organs throughout the body [15]. Recent research has shown long-term ingestion of drinking water with elevated nitrate concentrations is associated with an increased risk of several birth defects [16], as well as ovarian cancer and bladder cancer in postmenopausal women [17] [18].

Microbial populations in aquifers

The vast majority of the world’s unfrozen freshwater is stored in inland aquifers [19]. However, we know immensely more about the ecology of inland lakes and streams than we do about the ecology of the aquifers containing the freshwater many populations rely on [20]. Based on what we do know about aquifer ecology, aquifers can often contain rare microorganisms that are not widely distributed [21]. Microorganisms are present in aquifers as either attached to aquifer material or suspended in the groundwater

[22]. They can be resident microorganisms, which are permanently established in the aquifer, or they can be transported microorganisms, which are originally from surface waters or soils that now exist in the aquifer due to groundwater recharge [23]. Aerobic and anaerobic microorganisms are known to inhabit aquifers [24], and their metabolisms play a crucial role in the biogeochemical processes of the subsurface [25]. Microbial communities present in aquifers are influenced by groundwater geochemistry and recharge, terminal electron acceptors present, and a variety of environmental parameters [26].

Generally, aquifers are colonized by heterotrophic bacteria with the ability to survive in nutrient-poor conditions with little available organic carbon [27]. These microorganisms are crucial for the cycling of nutrients and the biological transformation of contaminants [28] [29]. Because they are well adapted to nutrient-poor conditions, fluctuations in the environment are difficult challenges for the bacterial communities to address. Thus, it is crucial to assess how humans have and may continue to impact the microorganisms in aquifers, which are important to innumerable biogeochemical processes of the subsurface [30].

The ecosystem services and processes performed by the bacterial communities in the aquifers are tied to the groundwater microbial diversity. Thus, any changes in microbial diversity may result in alterations of those processes in the subsurface [31]. Microbial diversity has been shown to be responsive to changes in overlying land practices [32]. Inputs to aquifers, such as organic carbon and nutrients, in moderate amounts may lead to increases in microbial diversity. However, excessive increases of these inputs can result in decreased microbial diversity [30]. Highly disturbed or contaminated aquifers are associated with less diverse microbial communities because the community has adapted to the altered aquifer conditions [26].

Protection of microbial diversity is a critical task because of the bacterial communities' role in groundwater quality. Microbial diversity provides a potential source of contaminant degradation and nutrient transformation abilities, which may be necessary now and in the future [30]. It is important to determine how environmental factors affect groundwater microbial populations and their biodiversity in order to properly manage groundwater resources and the ecosystem services they provide [33]. As we become more concerned about groundwater quality and recharge, the need for research in the area of groundwater ecosystems has become glaringly apparent [34]. Little attention is given to the ecosystem that exists within these important freshwater sources, and assessing the bacterial communities in groundwater is an often ignored aspect of aquifer assessment [25]. The lack of information on groundwater ecology limits the ability to address a need for the conservation of groundwater microbiota [35], and this is a concerning fact because of the critical role microbial communities play in the biogeochemical cycles of the subsurface [25].

The study of the distribution and diversity of subsurface microorganisms is necessary for more complete evaluations of aquifers. Bacterial populations inhabiting aquifers can be sampled via groundwater and/or sediment sampling, with attention to both allowing for the most complete description of the aquifer [22]. However, the collection of groundwater, rather than sediment, is a much simpler procedure requiring less time and equipment. For groundwater sample collection, wells may need to be purged of at least two or three well casing volumes to ensure sampling of aquifer water.

Purging is necessary to obtain a sample representative of the aquifer itself, rather than the artificial environment associated with the constructed well being used to access the groundwater [23]. Samples collected from well water, rather than aquifer water, provide an incomplete representation of the microbial community and its functional abilities [36].

After a sampling well is purged, pre-sterilized equipment should be used to avoid contamination between sites and from the equipment. Microbial samples can then be collected via water collection or filtration. Because of the lower abundance of microorganisms in groundwater, filtration is often the preferred sample collection method. Filtration in the field, rather than in the laboratory, may also be preferred to avoid the transport of large volumes of water to the laboratory.

Microbial metabolisms in aquifers

Groundwater systems contain microorganisms capable of a variety of metabolic pathways (Figure 6). These pathways couple endergonic and exergonic reactions to enable microorganisms to obtain energy and grow. In aerobic groundwater, the reduction of oxygen is coupled to the oxidation of organic material, which releases the most possible energy of any electron donor/acceptor pair. Some aerobic microorganisms can also perform anaerobic fermentation. However, respiration is always preferred, as it releases the most energy [37].

In anaerobic groundwater environments, a variety of electron donors and acceptors can be utilized, depending on the microorganisms present and the environmental conditions. A potentially important energy-releasing pathway in anaerobic groundwater environments is methanogenic respiration. This process can occur via two different pathways – carbon dioxide reduction or acetate reduction. Neither of these pathways is very thermodynamically favorable; however, methanogenic respiration can be a predominant process in environments with few other inorganic electron acceptors [37].

In the presence of sulfate as an electron acceptor, anaerobic groundwater environments can contain microorganisms capable of sulfate reduction. Sulfate-reducing bacteria depend on bacteria capable of fermentation to supply them with simple electron donor compounds, such as hydrogen, lactate, and acetate. The sulfate reduction pathway linked to the utilization of lactate is the best studied pathway. Of all the possible pathways, though, sulfate acts as the terminal electron acceptor, once it is activated by ATP [37].

Fe(III) reduction is also of great importance in groundwater biogeochemistry [37]. Many iron-reducing microorganisms are capable of acquiring energy by oxidizing organic compounds to carbon dioxide via Fe(III) reduction to Fe(II). The organic compounds utilized as electron donors can often be organic contaminants found in contaminated aquifers. Some iron-reducing microorganisms can reduce other metals as well, such as uranium and chromium. Overall, the reduction of Fe(III) to Fe(II) is a widespread microbial process that draws great attention due to its role in the mobilization of iron in aquifers [38].

An even wider variety of microorganisms are capable of coupling the oxidation of organic matter to the reduction of nitrate. Research has shown that nitrate reduction is an important pathway in groundwater affected by human activities. On the other hand, pristine groundwater systems do not normally rely on nitrate as a terminal electron acceptor. Nitrate reduction resulting in the production of nitrogen gas is termed denitrification. Denitrification is inhibited in groundwater containing oxygen, thus allowing for the accumulation of nitrate in aerobic subsurface environments. Nitrate does not tend to accumulate in anaerobic groundwater environments due to the activity of denitrifying microorganisms [37].

In systems with available nitrate, denitrification rates are governed by the amount of available dissolved organic carbon (DOC). In the absence of enough DOC, reduced iron may be utilized as an electron donor via autotrophic denitrification [6]. This process can be abiotic or biotic, being performed by organisms such as *Gallionella ferruginea*. Autotrophic denitrification is noted in situations where aquifers with Fe(II) do not normally have nitrate accumulations [8]. Biotic reduction of nitrate can also occur via the oxidation of reduced sulfur, by organisms such as *Thiobacillus denitrificans* [6]. Additional pathways are also possible, such as anaerobic ammonia oxidation (anammox) and nitrite-dependent anaerobic oxidation of methane (n-damo).

Of all of the possible energy-releasing pathways, a single redox situation may not exist throughout an entire aquifer. Rather, a variety of redox reactions may occur within the aquifer, depending upon more localized conditions [39]. Groundwater is subject to many biotic and abiotic processes [40], and the water chemistry conditions of the aquifer are intrinsically tied to the microorganisms present in the aquifer and their metabolic properties [37]. Identifying and understanding the microorganisms responsible for nutrient cycling in aquifers is crucial to the study of groundwater resources and their future use. In order to sustainably utilize our groundwater resources, we must study all aspects of aquifer biogeochemical cycling.

The objective of this research study was to evaluate the relationship between water chemistry of alluvial aquifers in Eastern Iowa and the bacterial populations present in the aquifers. We wanted to include bacterial diversity in the assessment of alluvial aquifer water quality in Eastern Iowa because of the crucial role microorganisms play in the global cycle of nutrients. We hypothesized that the microbial species richness would decrease with increasing nitrate concentrations in alluvial groundwater. Additionally, we hypothesized that differences in groundwater chemistry would be associated with differences in microbial community taxonomy. Ultimately, microbial communities would be coupled to the availability of electron donors and accepters in alluvial aquifer groundwater.

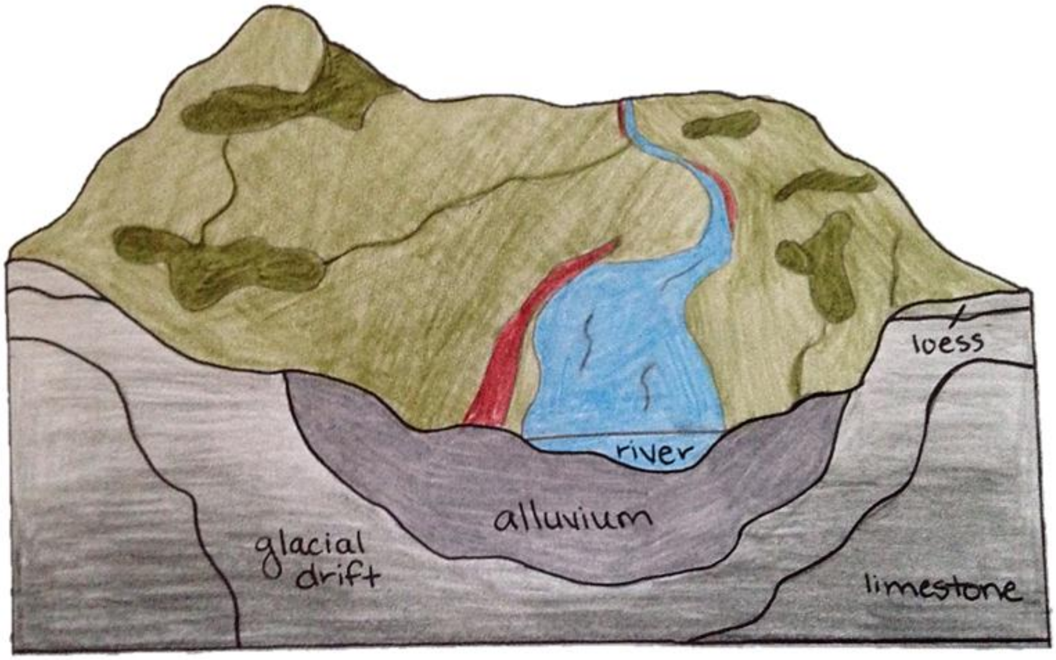


Figure 1 General depiction of an alluvial aquifer and its surroundings. Adapted from [2].

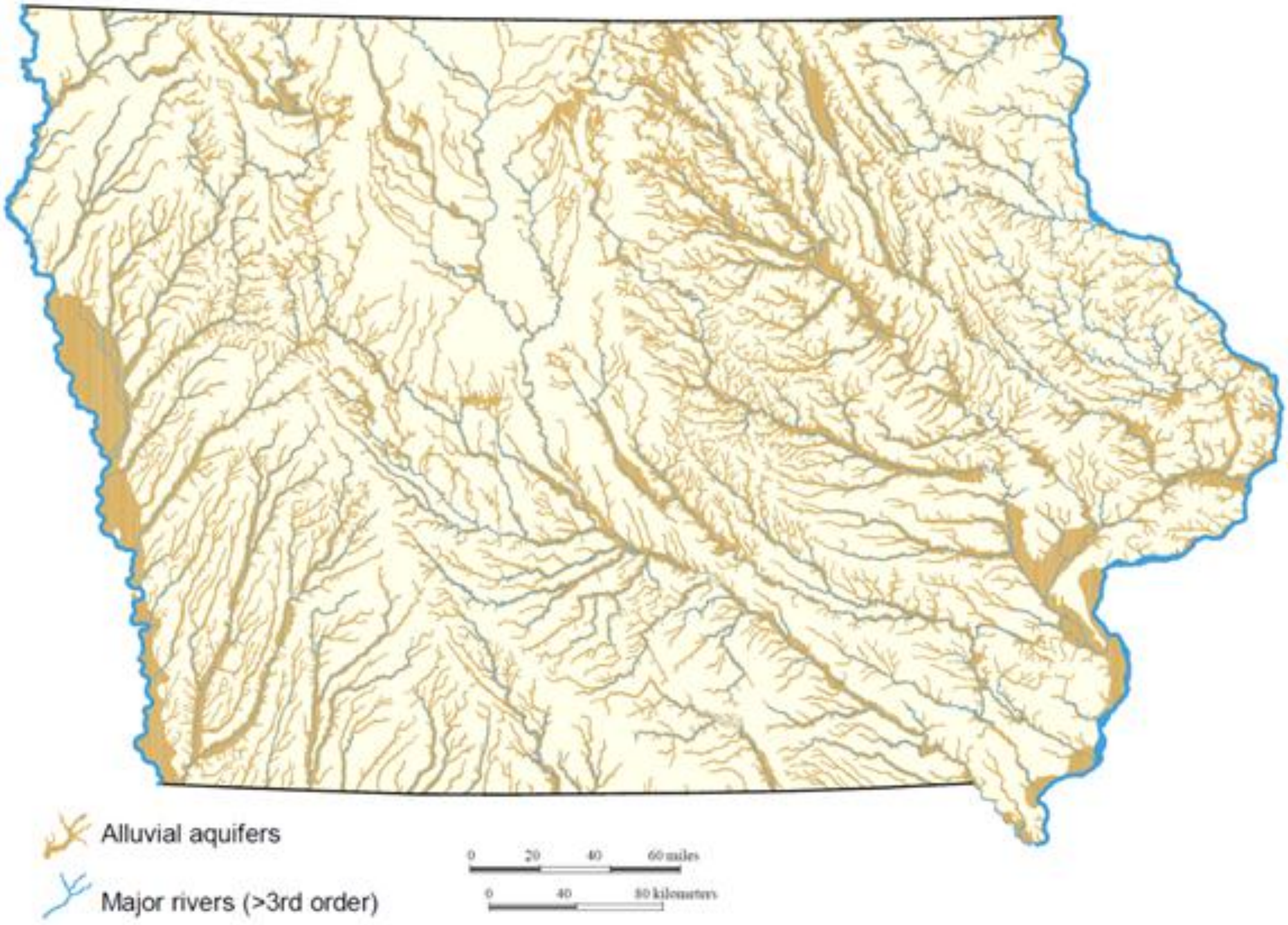


Figure 2 Map of the alluvial aquifers and major rivers of Iowa, from the Iowa Department of Natural Resources [1].

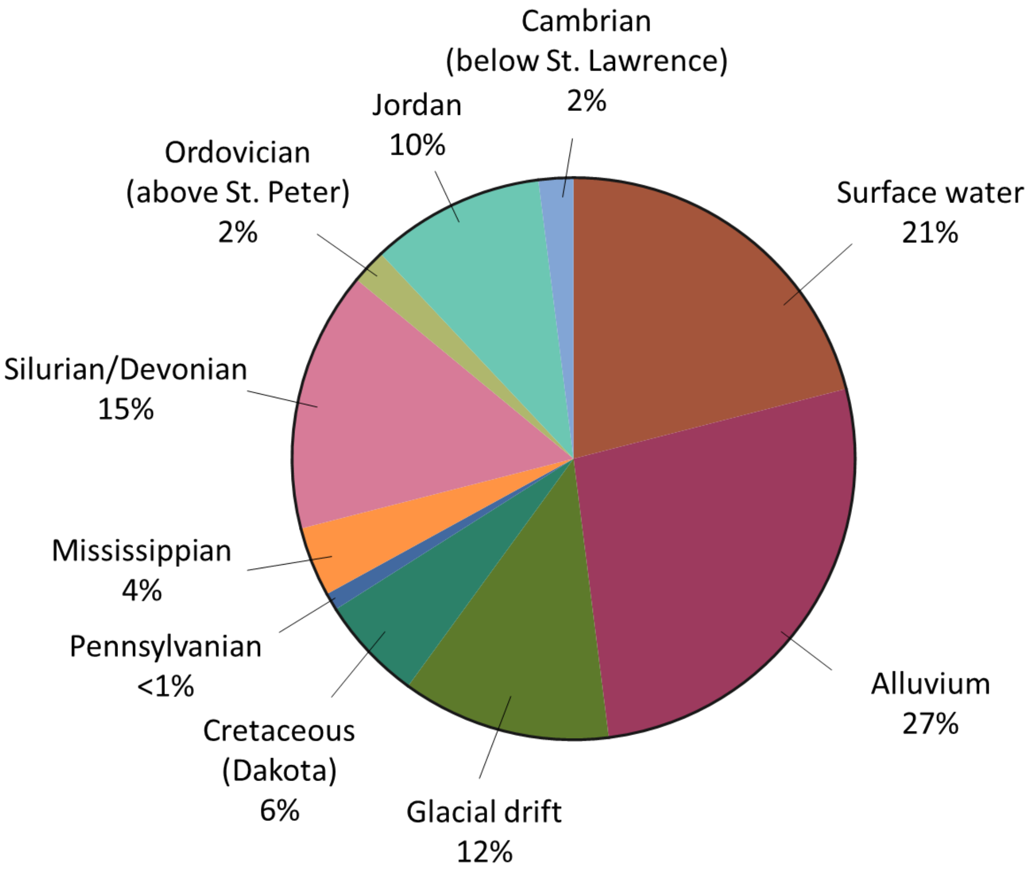


Figure 3 Drinking water supplies in Iowa by water source. Adapted from [3].

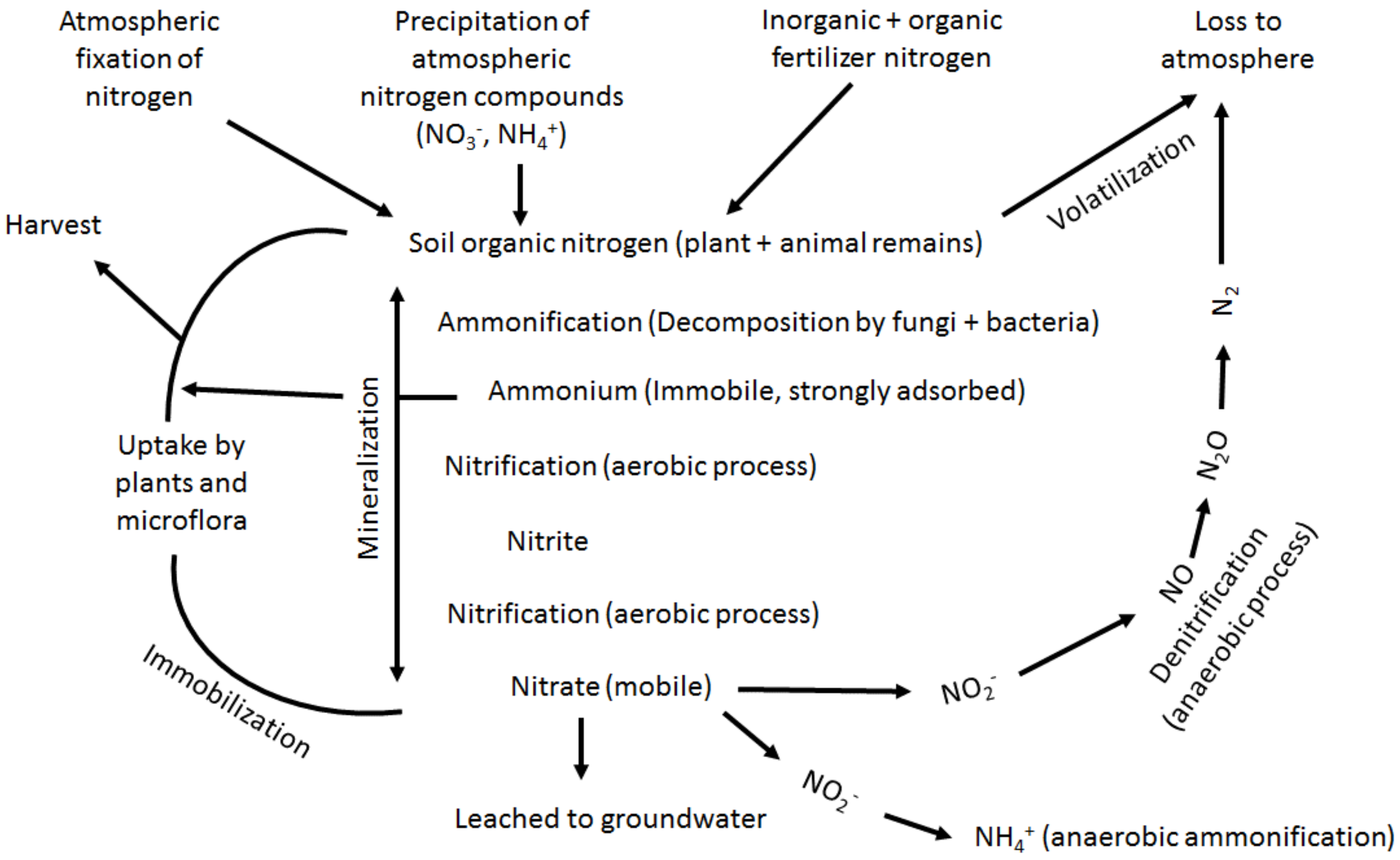


Figure 4 The nitrogen cycle and the fate of nitrogen that is incorporated into the soil. Nitrogen not utilized by plants or microorganisms has the potential to leach into the underlying groundwater. Adapted from [4].

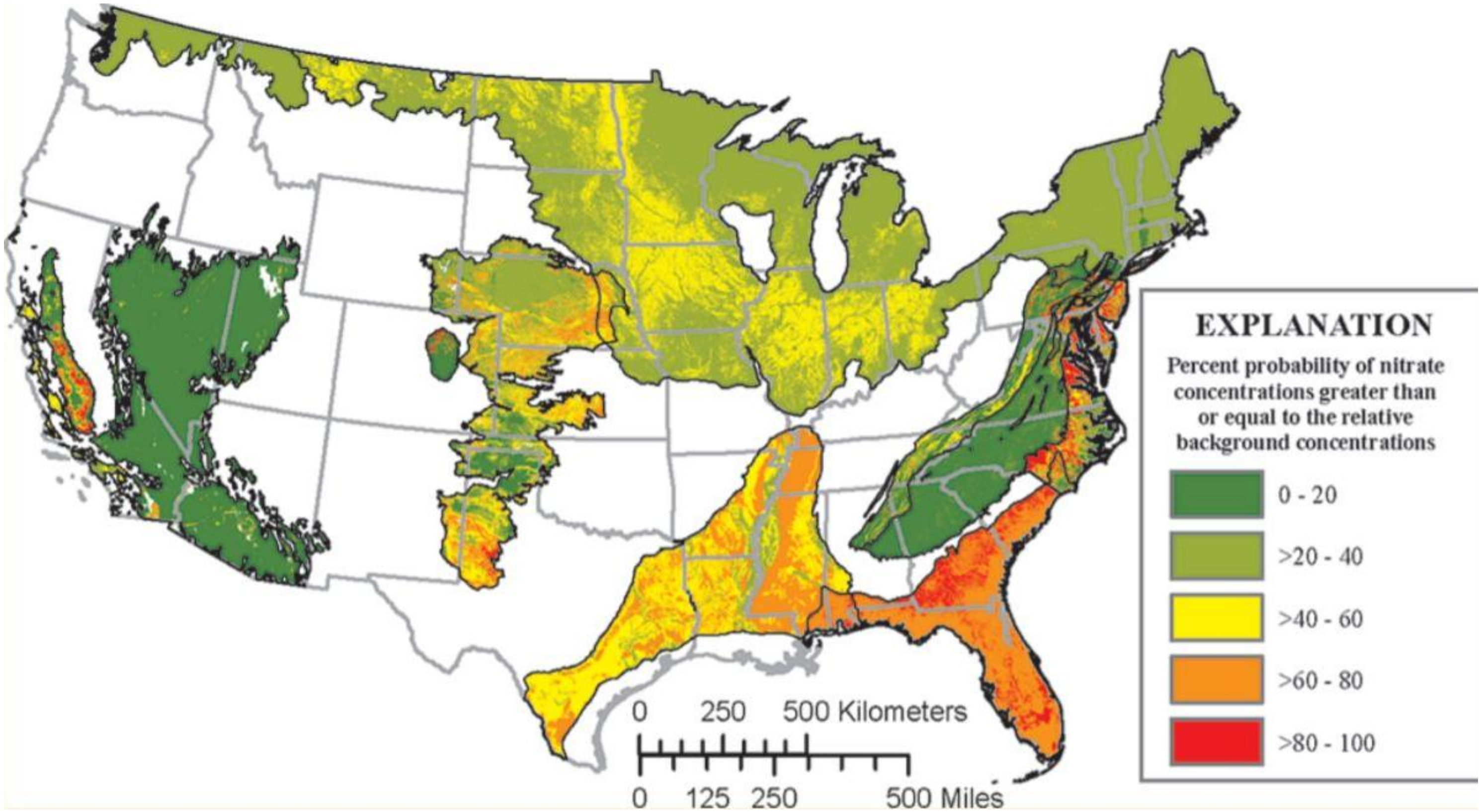
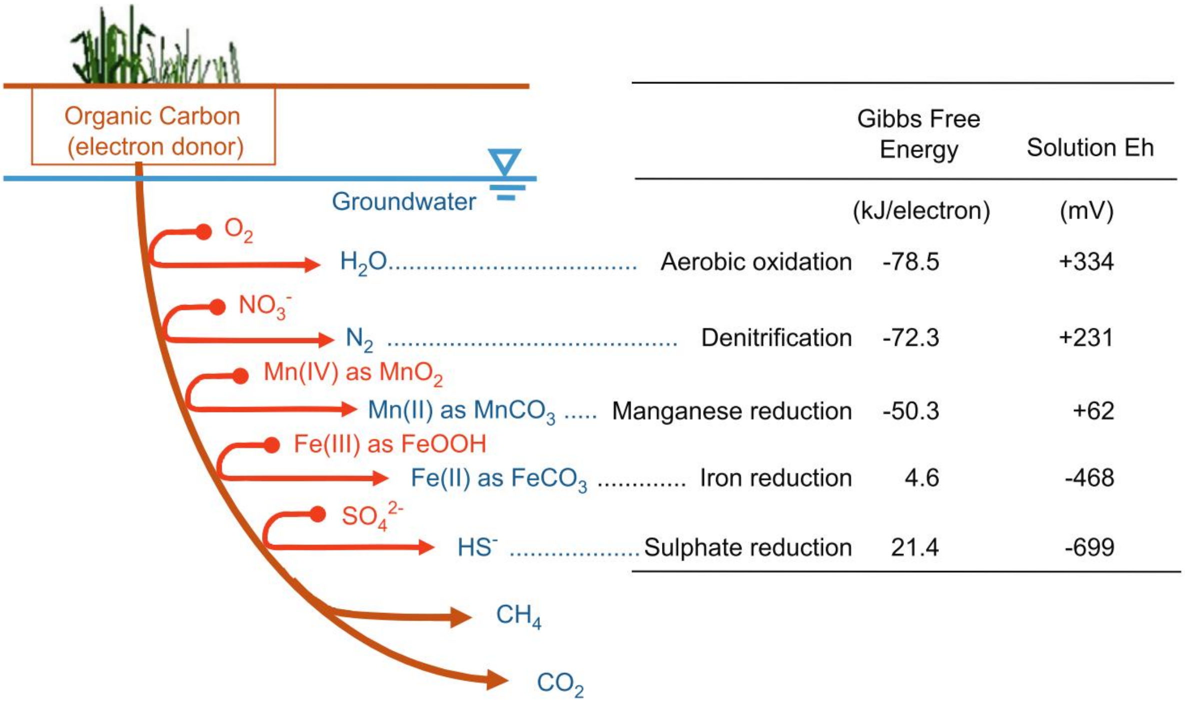


Figure 5 Map of nitrate contamination risk of recently recharged groundwater in the United States. Adapted from [7].



	Gibbs Free Energy (kJ/electron)	Solution Eh (mV)
Aerobic oxidation	-78.5	+334
Denitrification	-72.3	+231
Manganese reduction	-50.3	+62
Iron reduction	4.6	-468
Sulphate reduction	21.4	-699

Figure 6 The thermodynamic values associated with the oxidation of organic carbon via different electron acceptors in the saturated zone. From [6], adapted from [8].

MATERIALS AND METHODS

Site selection

All samples were obtained within the U.S. Geological Survey's Eastern Iowa Basins study unit, which includes the Wapsipinicon, Cedar, Iowa, and Skunk River basins (Figure 7). The study unit covers 19,500 square miles, and alluvial aquifers underlie twenty-two percent, or 4,260 square miles, of the unit. The major land use is agriculture [41]. The study sites sampled for this project included twenty-four monitoring wells, twelve domestic wells, and two municipal wells. The two municipal wells were not a part of the original study unit. Rather, they were sampled in addition to the study unit, specifically for this project.

The monitoring and domestic wells were previously chosen by the U.S. Geological Survey via a stratified random selection process. Alternate sampling sites were also chosen in the same manner, which were then utilized if the originally chosen sites did not meet the selection criteria [42]. The selection criteria for the domestic groundwater wells were as follows: 1) well is used for domestic use, 2) well is in an alluvial aquifer, 3) sampling permission could be obtained, 4) well depth is known, 5) well is currently equipped with a submersible pump, and 6) a sample could be obtained before any treatment systems [41]. The selection criteria for the agriculture monitoring well sites were as follows: 1) presence of selected land use and hydrogeologic setting, 2) no known points of contamination near the site, 3) accessible to drill rig, and 4) permission for the well installation could be obtained. Alternative locations were utilized when a suitable site was not available at the primary location [5].

The agriculture monitoring wells were previously installed using a 4.25-inch inside-diameter continuous-flight hollow-stem auger. The auger was left in the borehole during well construction to prevent collapse of the borehole. The wells were constructed of 2-inch outside-diameter flush-threaded polyvinyl-chloride (PVC) pipe and 5 feet of 0.2-inch slotted PVC screen at the base of the well. During the removal of the auger, alluvial material was used to fill the space around and above the screen. In wells with fine-grained material next to the screen, a sand-filter pack was placed around the screen instead. A bentonite annular seal was placed above the sand-filter, and the rest of the borehole was filled with native material, within a few feet below the land surface. A steel casing was cemented at the land surface to protect the well casing and to prevent the flow of surface water down the borehole. The borehole drilling equipment was cleaned between each site [5].

Sample collection and processing

Groundwater samples were obtained from the twelve domestic, twenty-four monitoring, and two municipal wells from May to August 2017 (Figure 8, Figure 9). Samples were collected following the U.S. Geological Survey National Water Quality Program sampling protocol [43]. Water depth measurements were obtained using an electric tape before and after pumping. On-site values for pH, dissolved oxygen (DO), specific conductance, water temperature, and turbidity were recorded using a Eureka Manta+ water probe (Eureka Water Probes, Austin, TX). A total of five values were recorded for each parameter, with five minutes in between recordings. Most wells were also purged of three well-casing volumes before sample collection.

Domestic and municipal well water samples were obtained by direct connection to a spigot. Monitoring well water samples were obtained via a submersible gear pump (Fultz Pumps, Inc., Lewistown, PA). Samples for major ions, nutrients, trace metals, DOC, alkalinity, tritium, and radon were collected at all sites. Some sites were more extensively sampled for additional analytes, such as pharmaceuticals, pesticides, hormones, coliform, *E. coli*, enterocci, coliphage, dissolved gases, noble gases, volatile organic carbon, stable isotopes, carbon 13/12, and carbon 14, but were not considered for this study. All samples were analyzed at the U.S. Geological Survey's National Water Quality Laboratory (NWQL) or a laboratory contracted by the USGS. Nutrient, alkalinity, DOC, and common ion samples were filtered with a 0.45-micron pore-size capsule filter (Versapor® High Capacity, Pall Corporation, Port Washington, NY), and samples were acidified prior to overnight shipping to the USGS's NWQL in Denver, Colorado [43]. All water quality and water level data is publically available via the U.S. Geological Survey's National Water Information System Web Interface (https://waterdata.usgs.gov/nwis).

All sample analyses were performed according to methods set by the U.S. Geological Survey. Method detection limits (MDLs) were established by the NWQL. The MDL was defined as "the minimum concentration of the substance that could be identified, measured, and reported with 99 percent confidence that the analyte concentration is greater than zero [5]". Quality control samples were also collected throughout the sampling timeframe, including equipment blanks, field blanks, replicates, and field spikes.

An additional bacterial sample, specifically for this project, was collected at each well. Autoclaved tubing (C-Flex®, 0.25 inch inner diameter, Cole Parmer, Vernon Hills, IL) was attached to the sterilized spigot or the pump outlet. The sample was collected by filtering one liter of groundwater through a 0.22 µm filter (Sterivex^{TM}-GP Sterile Vented Filter Unit, Millipore Sigma, St. Louis, MO). Smaller volumes were filtered at sites with turbid water. A sterile 10 mL syringe filled with air was then used to remove excess water from the filter unit before capping with Luer Lock™ plugs. The capped filter cartridge was labeled and placed in a 50 mL conical centrifuge tube (Falcon™, Thermo Fisher Scientific, Waltham, MA) for storage and transport. The tube was then placed in a plastic bag and stored on ice before returning to the lab. Filters were stored at -20°C until further processing.

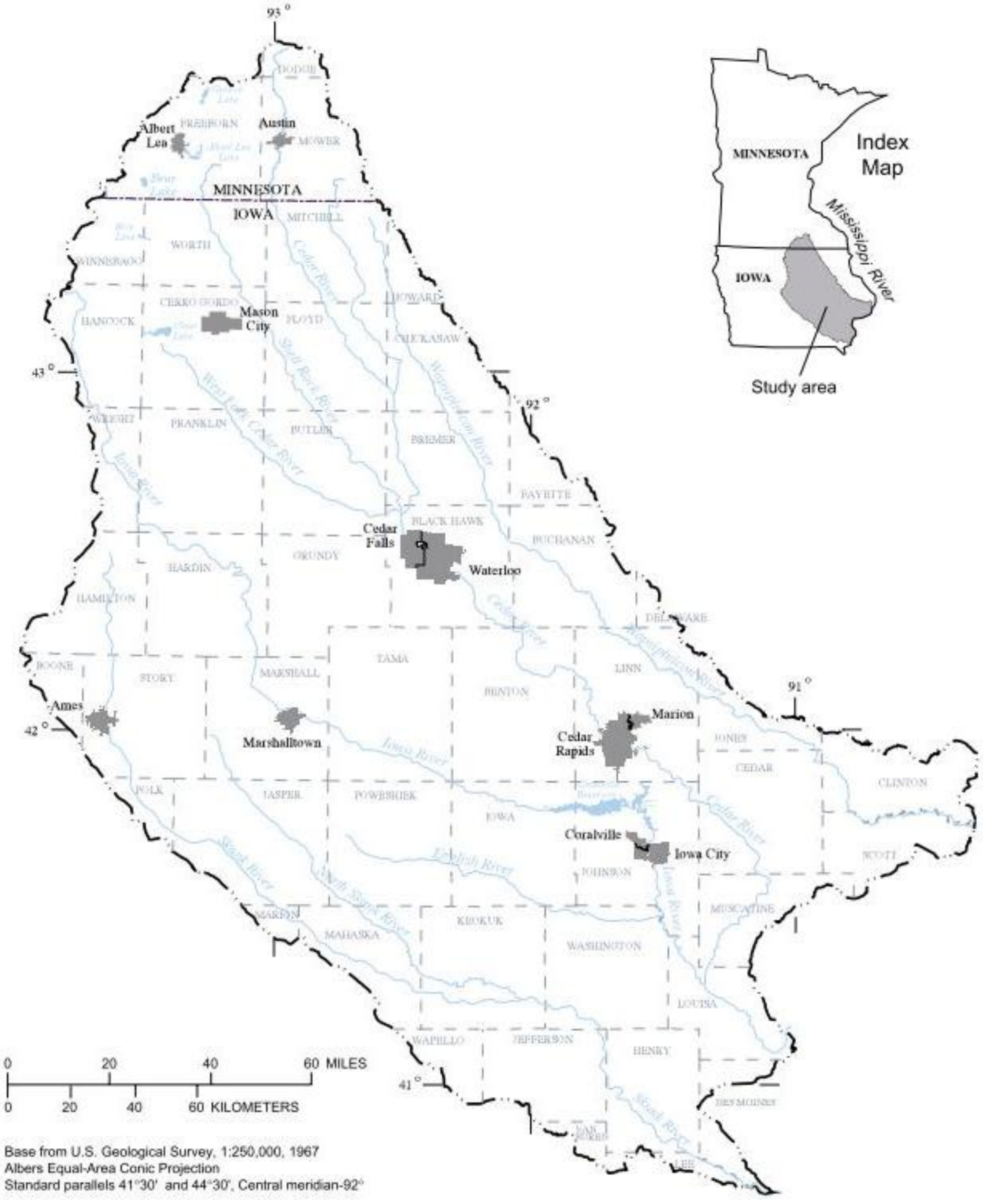
To extract the DNA from the Sterivex™ filters, the filters were thawed on ice prior to DNA isolation. DNA was isolated from the filters using the DNeasy PowerWater Sterivex Kit (Qiagen, Germantown, MD), according to the manufacturer's instructions. Briefly, cells were lysed by vortexing, heating, and bead beating. Inhibitors were removed, and DNA was eluted from the filter. DNA was stored at -20°C until further use. The isolated DNA (1-50 ng/ µL, 20 µL) was shipped to Argonne National Laboratory, Environmental Sample Preparation and Sequencing Facility (ESPSF), following the Earth Microbiome Project protocol (http://press.igsb.anl.gov/earthmicrobiome/protocols-and-standards/shipping/).

The v4 region of the prokaryotic 16S rRNA gene (515F-806R) was amplified to prepare the amplicon libraries. Each PCR reaction mixture contained 9.5 µL of MO BIO PCR DNA-free water, 12.5 µL of QuantaBio's AccuStart II PCR ToughMix (1x final concentration), 1 µL of Golay barcode tagged forward primer (200 pM final concentration), 1 µL reverse primer (200 pM final concentration), and 1 µL of template DNA. The following conditions were utilized for the PCR reaction: 94°C for 3 minutes to denature the DNA, 35 cycles at 94°C for 45 seconds, 50°C for 60 seconds, and 72°C for 90 seconds, with a final extension time of 10 minutes at 72°C. The amplicon libraries were then quantified using PicoGreen (Invitrogen, Waltham, MA) and a plate reader (Infinite® 200 PRO, Tecan, Switzerland). The amplicons were then pooled into a single tube, with each amplicon represented in equimolar amounts. The pooled samples were cleaned using AMPure XP Beads (Beckman Coulter, Brea, CA) and quantified with a fluorimeter (Qubit, Invitrogen, Waltham, MA). The pool was then diluted to 2nM, denatured, and diluted to a final concentration of 6.75 pM with a 10% PhiX spike. Amplicons were sequenced on a 151bp x 12bp x 151bp Illumina MiSeq run [44] [45], and the sequences were uploaded to NCBI (BioProject ID: SRP134927).

Data analysis

Historic Eastern Iowa Basins water chemistry data was downloaded from NWIS, and the medians, means, 10th and 90th percentiles, and outliers were plotted (GraphPad Prism 7.03, GraphPad Software, La Jolla, CA) for visual comparison to the 2017 data. The Mann-Whitney test ($p < 0.05$) was used to test differences between historical and current data. A k-means clustering, with features of well depth, DO, NO_3^--N, ammonia (NH_3-N), DOC, iron (Fe), and sulfate (SO_4^{2-}), was performed iteratively in a spreadsheet (Excel, Microsoft Corporation, Redmond, WA) until the sum of the standard error of the means for all variables was minimized.

The default Quantitative Insights in Microbial Ecology (QIIME) open-reference pipeline was utilized to assign the operational taxonomic units (OTUs) to the non-targeted 16S rRNA gene amplicon reads [46]. The basics of the QIIME open-reference pipeline include the joining, demultiplexing, filtering, and clustering with uclust of the paired-end reads provided as input [47]. The representative OTU sequences were aligned to GreenGenes 13.5 reference database [48] with a 97% similarity threshold using RDP classifier [49] for taxonomy assignment and PyNAST [50] for multiple sequence alignment. Alpha diversity values (observed OTUs) were calculated with the QIIME script, “Alpha_diversity.py”. A principle coordinate analysis (PCoA) based on the weighted OTU abundances [51] was also created using the QIIME script “beta_diversity.py” and visualized with “beta_diversity_through_plots.py”. Additional analysis of the OTU assignments was completed by calculating the median relative abundances of taxonomic assignments from the QIIME open reference picking OTU table. Select relative abundance counts for assigned clusters with differing water chemistry were tested using the Mann-Whitney test ($p < 0.05$).



Base from U.S. Geological Survey, 1:250,000, 1967
Albers Equal-Area Conic Projection
Standard parallels 41°30′ and 44°30′, Central meridian-92°

Figure 7 The U.S. Geological Survey's Eastern Iowa Basins study unit, encompassing the Wapsipinicon, Cedar, Iowa, and Skunk River basins [5].

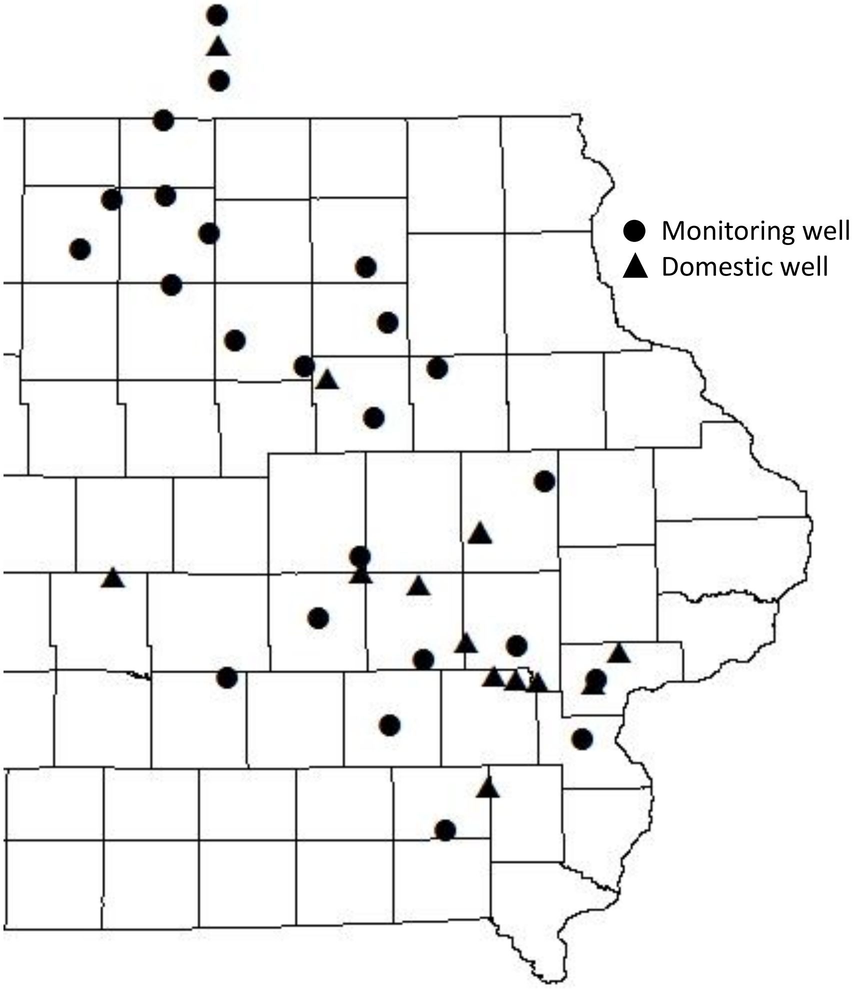


Figure 8 The domestic and monitoring wells, within the Eastern Iowa Basins study unit, sampled for this study.

Figure 9 Photographs of examples of an agriculture monitoring well (left) and a domestic well (right) sampled for this project. The agriculture monitoring well shown is also equipped with groundwater level monitoring equipment. Photos by Kymm Barnes, Hydrologist, U.S. Geological Survey.

Figure 10 Example of a USGS agriculture monitoring well water quality sampling setup using a submersible gear pump. Photo by Kymm Barnes, Hydrologist, U.S. Geological Survey.

Figure 11 A photo of me collecting water quality samples from an agriculture monitoring well, following USGS sampling protocol. Photo by Kymm Barnes, Hydrologist, U.S. Geological Survey.

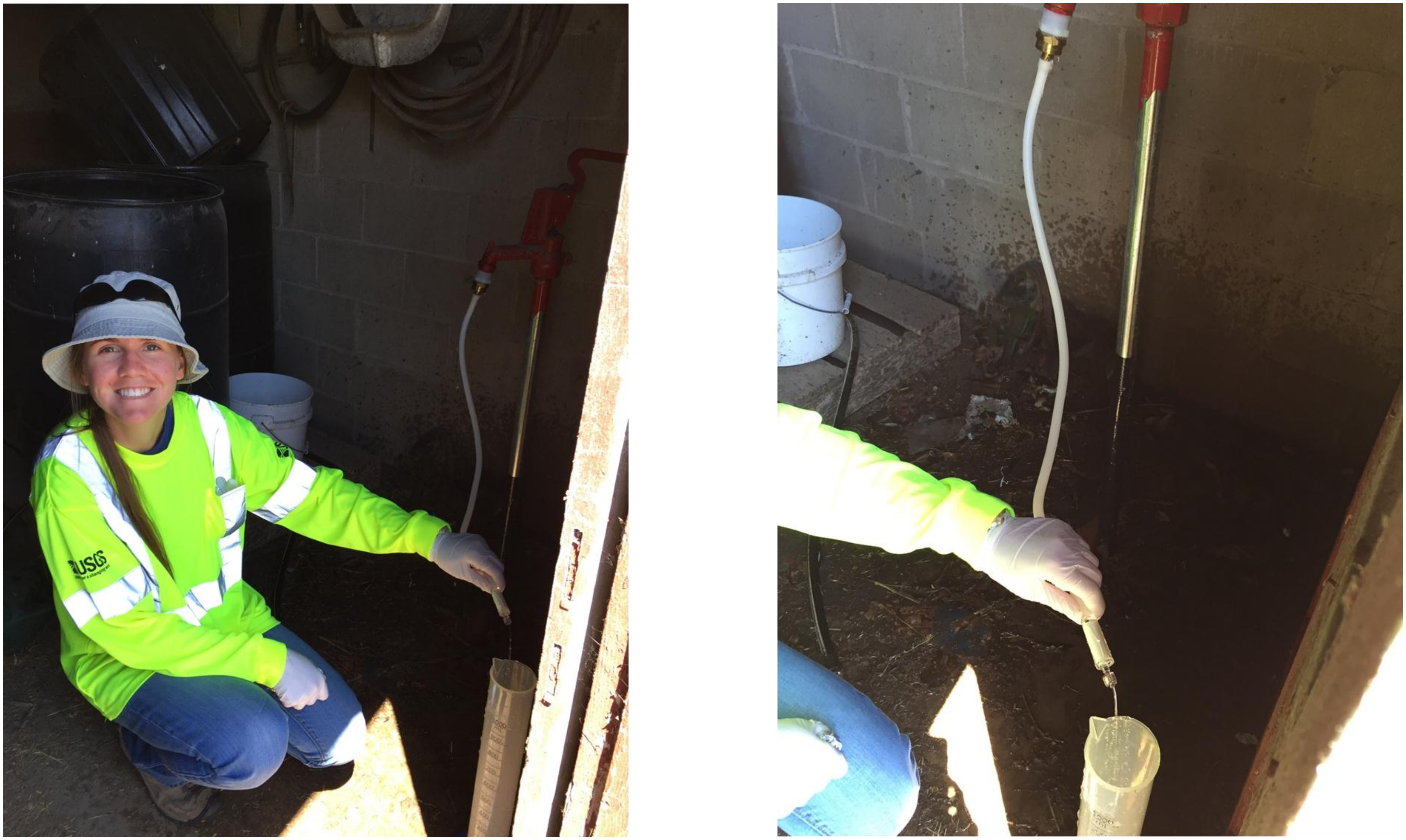


Figure 12 Photos of me collecting my additional microbial DNA sample via filtration from a domestic well. Photo by Kymm Barnes, Hydrologist, U.S. Geological Survey.

RESULTS AND DISCUSSION

Water chemistry

The historic median water chemistry concentrations, measured in 1997-98 and 2007, were similar to those from 2017 (Figure 13). A comparison of these data showed no significant differences for the concentrations of NO_3^--N, DO, DOC, and SO_4^{2-}. The historical and 2017 concentrations of NH_3-N and Fe were significantly different (p-values <0.0001 and 0.0014, respectively), but the differences can be attributed changes in detections limits for these parameters. The 2017 concentration maxima for NO_3^--N (33.2 mg/L), DO (10 mg/L), NH_3-N (4.31 mg/L), Fe (9.45 mg/L), DOC (4.21 mg/L), and SO_4^{2-} (60.3 mg/L) were similar to previous years.

Shallow wells (< 15 meters deep) contained higher concentrations of NO_3^--N and DO and often non-detectable concentrations of NH_3-N and Fe (Figure 14). Wells containing abundant DO facilitate the accumulation of oxidized nitrogen species like NO_3^--N, as well as nitrification of NH_3-N entering the groundwater. The connections between well depth, NO_3^--N, and DO were further explored (Figure 15). Nitrate was likely more persistent in the fully oxygenated shallow wells due to the inhibition of the nitrate reductase enzyme required for denitrification [52]. Additionally, wells with the highest NO_3^--N concentrations generally had less available DOC (Figure 16), making them less favorable for denitrification due to the lack of an organic electron donor [52].

The deeper wells (> 15 meters deep) contained higher concentrations of NH_3-N and Fe, with often non-detectable NO_3^--N, and low DO concentrations. During the 1997-1998 sampling period, NH_3-N was more prevalent in the deeper urban wells compared to the more shallow agricultural monitoring wells. The higher NH_3-N concentrations may be attributed to the release of NH_3-N via microbial breakdown of organic material and low DO [53]. Anaerobic conditions and the availability of DOC would also favor denitrification in the deeper wells. The lower NO_3^--N concentrations could be further explained by Fe^{2+} acting as an abiotic or biotic electron donor [6], which has been shown in previous groundwater studies [8] [54] [55].

A k-means cluster analysis was used to examine centroid feature values in the water chemistry data to qualitatively create groups based on feature similarities. This analysis identified well depth and DO as principle data features (Figure 17) and identified SO_4^{2-} as a secondary feature useful to further distinguish Cluster 1 and Cluster 3 (Figure 18). Cluster 1 was comprised of shallow wells with variable DO concentrations and lower SO_4^{2-} concentrations (Table 1). Cluster 2 included shallower wells with higher SO_4^{2-} concentrations and variable DO concentrations. The deeper wells were in Cluster 3, which had lower DO and variable SO_4^{2-} concentrations.

Microbial diversity

Alluvial groundwater DNA samples contained a variety of bacterial and archaeal phyla, with Proteobacteria, Acidobacteria, and Nitrospirae as some of the most abundant phyla (Figure 19). The species richness (measured as observed OTUs) ranged from 174 to 1673 (Figure 20), which was similar (125 to 1,341 OTUs) to the range for a variety of environmental habitats [56], but lower than the 794 to 3,632 bacterial OTUs measured in a study of 550 soil samples [57]. The variability in species richness for our study could not be associated with differences in well depth or concentrations of NO_3^--N, DOC, DO, PO_4^{3-}-P, and SO_4^{2-} (Figure 21).

The clusters were associated with different median relative abundances of microbial classes (Table 2). Cluster 1 was mostly comprised of unassigned classes (18%) and the classes *koll11* (7.6%), *Deltaproteobacteria* (6.8%), and *Betaproteobacteria* (6.2%). Cluster 2 wells were inhabited by *Betaproteobacteria* (21%), *Gammaproteobacteria* (16%), unassigned classes (7.3%), *Alphaproteobacteria* (6.2%), and *Deltaproteobacteria* (6.0%), while Cluster 3 was comprised of *Betaproteobacteria* (16%), unassigned classes (9.5%), and *Alphaproteobacteria* (8.9%). Cluster 1, with high NO_3^--N and high DO, showed a higher relative abundance of class *koll11* organisms, which are known to inhabit groundwater with oxidized conditions [58]. The class *Betaproteobacteria*, which was most abundant in Cluster 2, can exhibit a wide variety of metabolisms. Some genera within this class can derive carbon autotrophically and utilize reduced inorganic substrates as electron donors [59]. Possible reduced electron donors generally available in Cluster 2 included reduced Fe and NH_3-N. At the genus level of classification, *Crenothrix* (6.8%), capable of methane oxidation, and *Gallionella* (2.9%), an iron oxidizer, were relatively abundant in Cluster 2. The class *Deltaproteobacteria*, which is comprised of aerobic and anaerobic microorganisms, was similarly abundant across all clusters reflecting an ability to thrive in a variety of conditions.

Additional analysis from the QIIME PCoA, based on the abundance and distribution of the various OTUs, provided additional evidence of microbial diversity clustering (Figure 22). The k-means clusters assigned solely on water chemistry were similar to the results of visual clustering from the QIIME PCoA output. Visual clustering of the samples resulted in QIIME Cluster 1 being characterized by wells with higher NH_3-N, higher Fe, and lower NO_3^--N concentrations (Table 3). QIIME Cluster 2 was characterized by non-descript water chemistries at intermediate concentrations and was not subject to further analysis. QIIME Cluster 3 was characterized by shallow wells (< 9 meters) with lower NH_3-N, lower Fe, and higher NO_3^--N concentrations. QIIME Cluster 1 and QIIME Cluster 3 differed in the median distribution of taxonomic classes that made up at least 1% of the relative abundances (Table 4). The major classes representing QIIME Cluster 1 were *Betaproteobacteria* (22%), *Gammaproteobacteria* (18%), *Alphaproteobacteria* (9.6%), and *Deltaproteobacteria* (5.7%). QIIME Cluster 3 consisted mostly of unassigned classes (15%), *koll11* (7.0%), *Deltaproteobacteria* (6.5%), *Betaproteobacteria* (6.4%), and *Nitrospira* (5.2%). Similar associations between aquifer conditions and relative abundance of microbial classes were observed with this analysis.

More specific taxonomic assignments showed similarities and differences between QIIME Cluster 1 and QIIME Cluster 3 microbial communities with respect to genera with identifiable metabolic characteristics. QIIME Cluster 1 wells had significantly higher relative abundances of Fe oxidizers (*Gallionella*, p-value < 0.001) and Fe reducers (*Geobacter*, p-value = 0.0028). Sulfate reducers, including genera *GOUTA19* and *BD2-6*, in the family *Thermodesulfibrionaceae* and the family *Desulfobulbaceae*, were also significantly more abundant (all p-values < 0.001). The genus *Crenothrix*, a methane oxidizer, was significantly more abundant in Cluster 1 as well (p-value = 0.0040).

Differences in water chemistry between the well clusters were associated with differential abundances of bacterial and archaeal groups. In QIIME Cluster 1, significantly higher concentrations of Fe (p-value = 0.0016) were associated with an increased prevalence of microorganisms capable of utilizing Fe as an electron donor or acceptor. Additionally, the increased abundance of methane oxidizers in QIIME Cluster 1 corresponded with plentiful DOC. It is possible that methane, which was not tested in this study, may have been present from the breakdown of organic matter in the wells [60], thus leading to an increased abundance of methane-oxidizing bacteria. The general lack of more energetically favorable terminal electron acceptors in QIIME Cluster 1 wells, such as NO_3^--N and DO, may also explain the increased presence of SO_4^{2-} reducing populations. Select QIIME Cluster 1 wells deviated from the overall trends, such as Well KM34. This well contained abundant NH_3-N (0.96 mg/L) and DO (7.1 mg/L), while 5.36% of its microbial community was classified as the ammonia-oxidizing genus *Nitrospira*, which could thrive in such conditions. In contrast to QIIME Cluster 1, QIIME Cluster 3 wells contained significantly higher concentrations of NO_3^--N (p-value < 0.0001) and were more oxygenated. Aerobic microorganisms most likely dominated these aquifers. Due to the available DO, NO_3^--N reduction would not be favorable. Denitrifying organisms would be inhibited in this group, thus allowing for the accumulation of NO_3^--N in QIIME Cluster 3 wells.

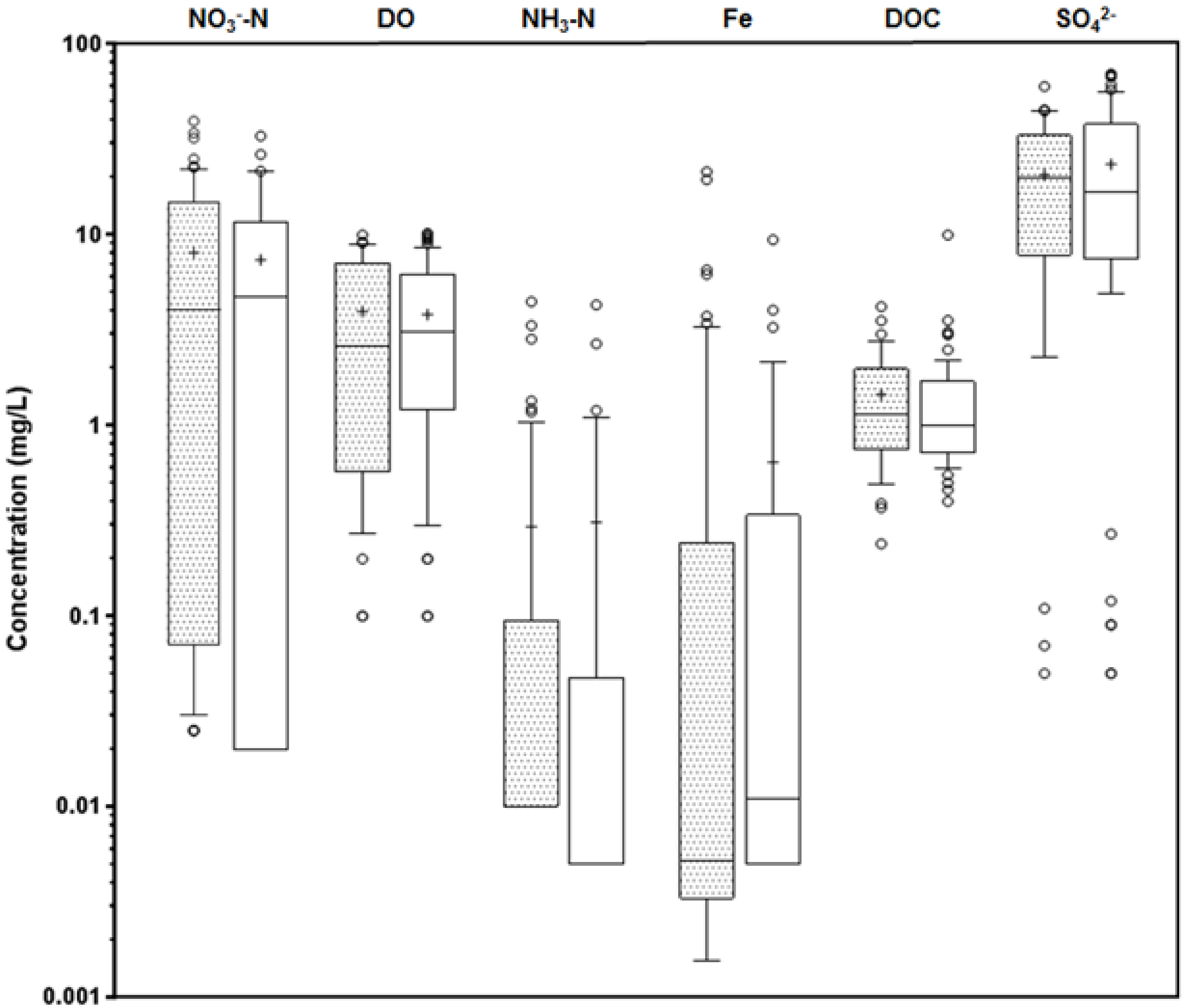


Figure 13 Historical (1997-98 and 2007; shaded boxes) and recent (2017; clear boxes) concentrations of NO_3^--N, DO, NH_3-N, Fe, DOC, and SO_4^{2-} in alluvial aquifer wells. Median values are shown as horizontal lines within the boxes, mean values are shown as "+" signs, and whiskers depict the 10th and 90th percentiles.

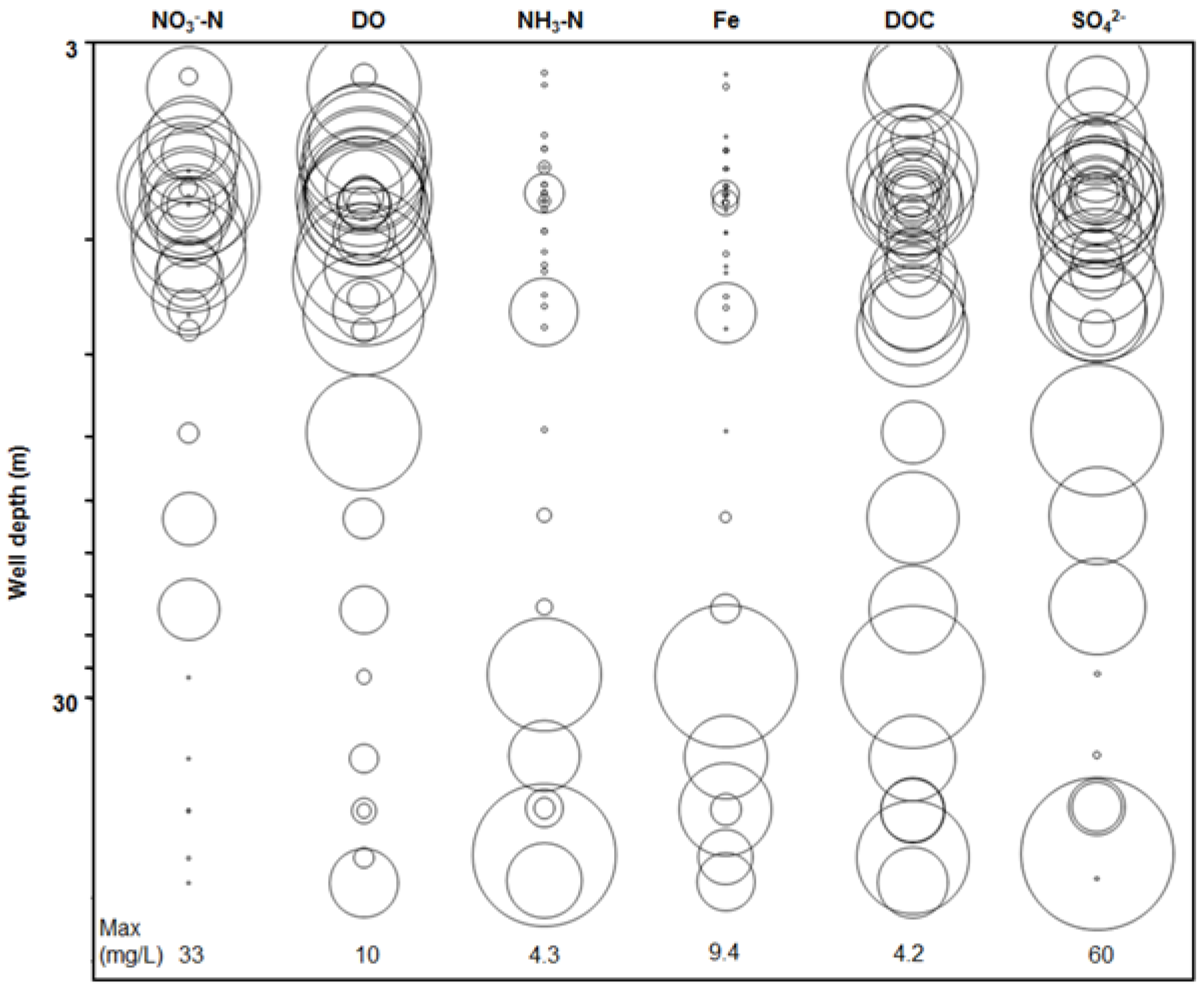


Figure 14 The relationships between well depth and NO_3^--N, DO, NH_3-N, Fe, DOC, and SO_4^{2-} concentrations in alluvial aquifer wells in 2017. The maximum concentration for any given parameter is depicted by the largest circle area which becomes proportionally smaller as concentration decreases.

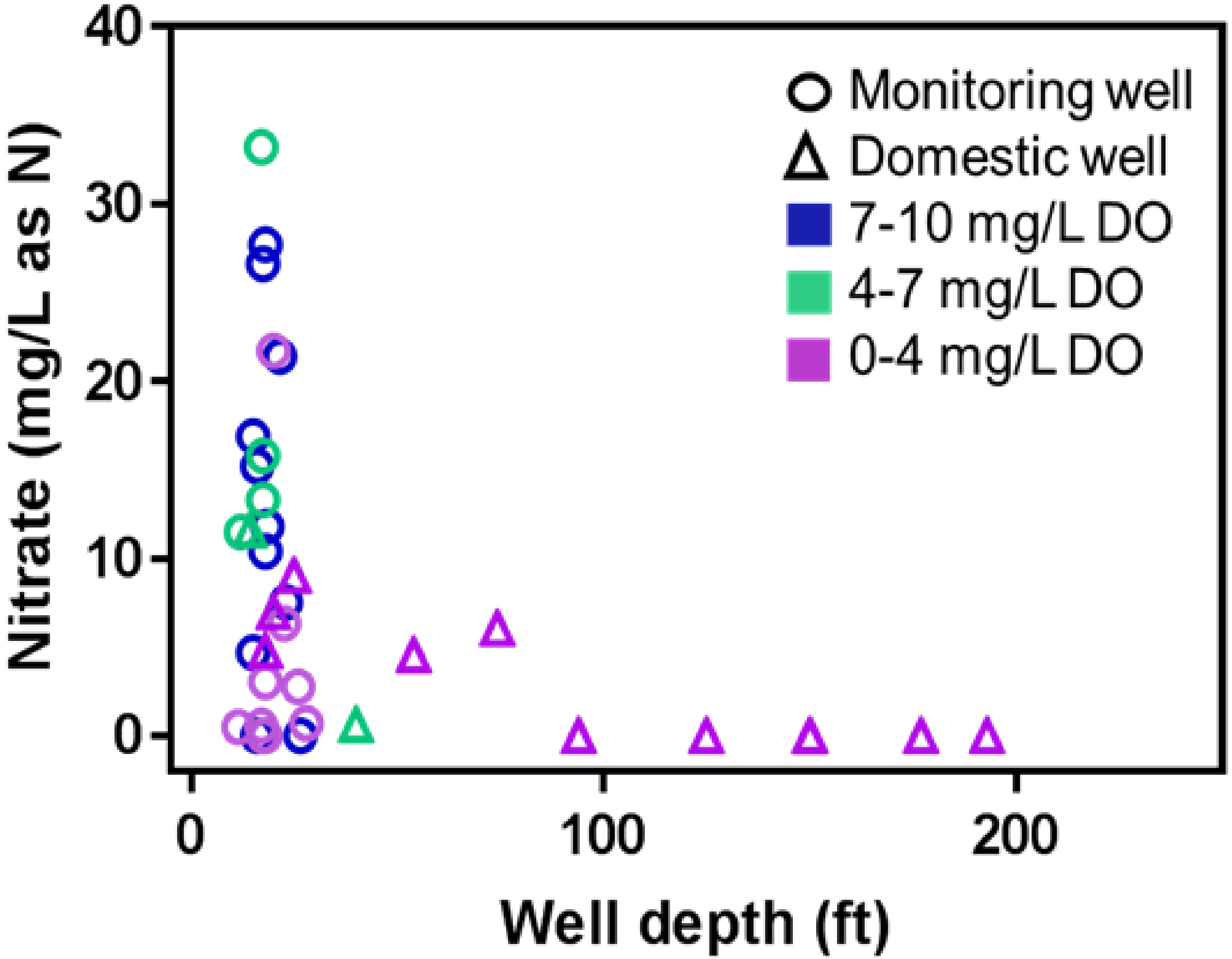


Figure 15 The relationship between NO_3^--N and DO concentrations in wells of various depths.

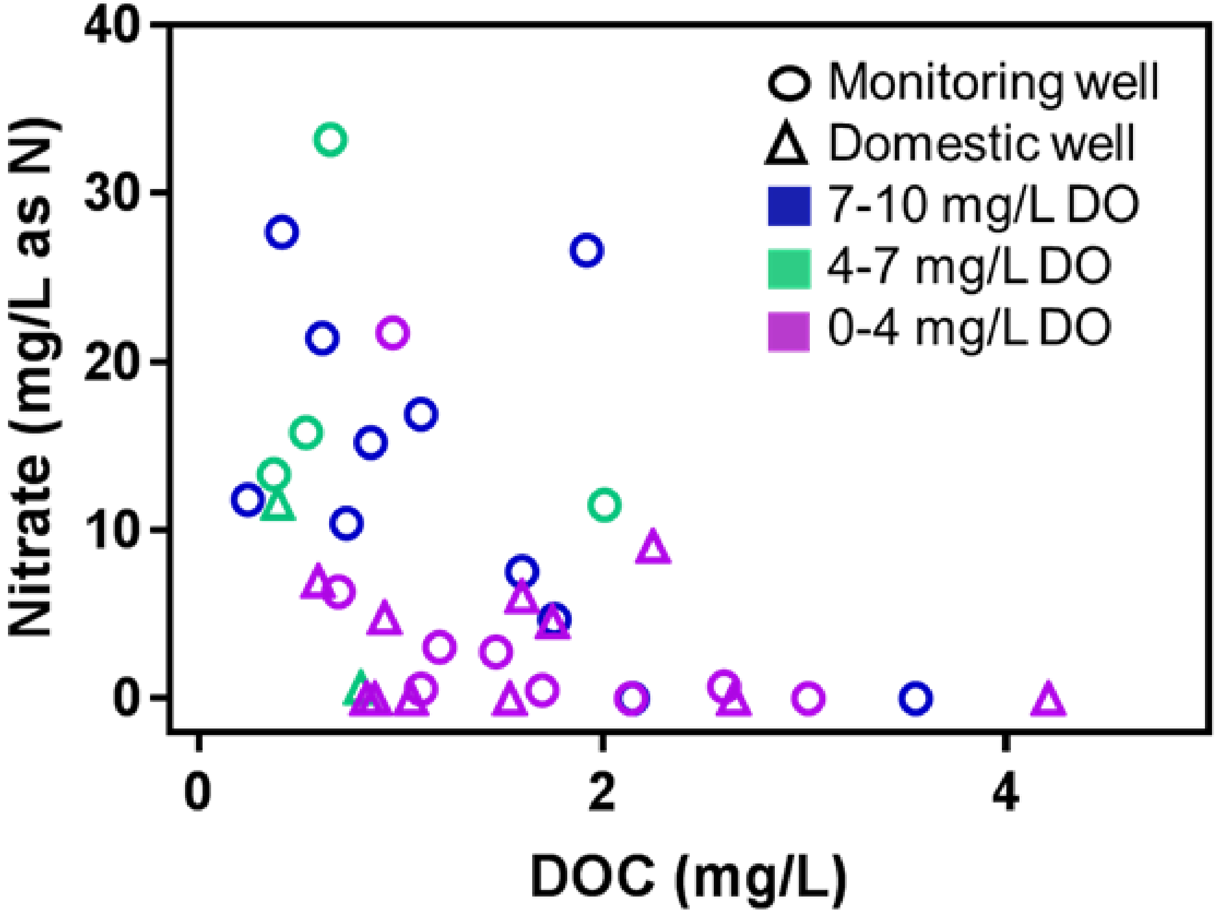


Figure 16 The relationship between NO_3^--N, DOC, and DO concentrations in domestic and monitoring wells.

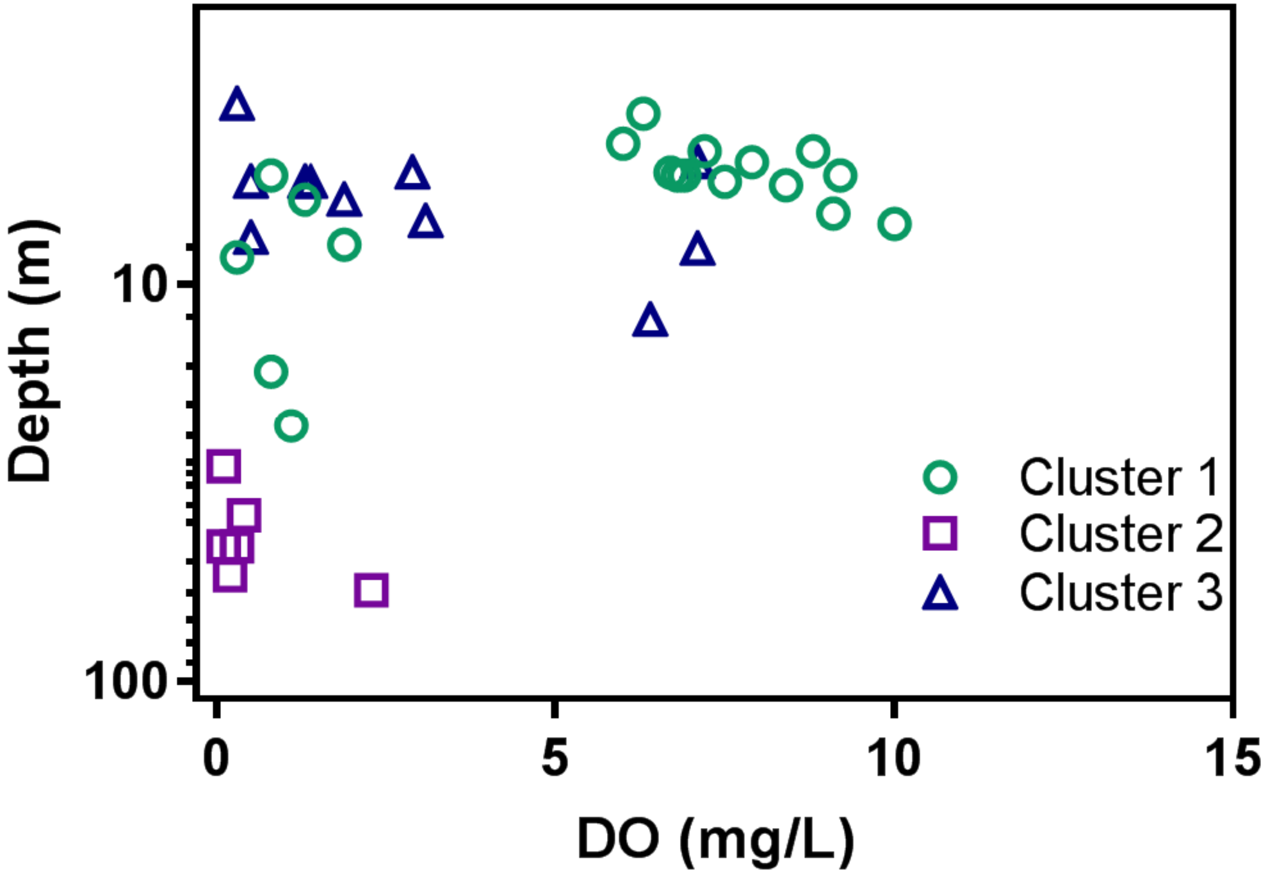


Figure 17 Groupings from the k-means cluster analysis displayed as functions of well depth and DO.

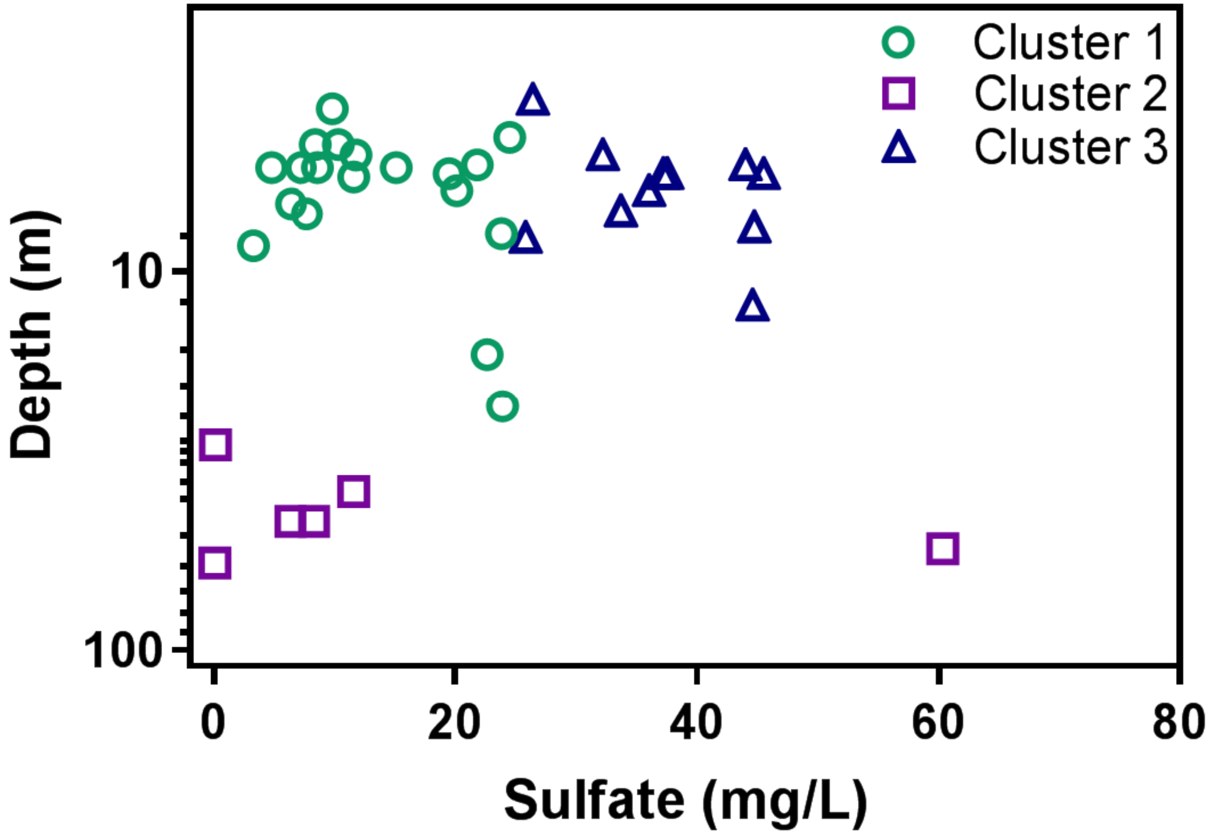


Figure 18 Groupings from the k-means cluster analysis displayed as functions of well depth and SO_4^{2-}.

Table 1 Mean water chemistry values associated with the cluster assignments.

Cluster	**Well depth (m)**	**NO_3^--N (mg/L)**	**DO (mg/L)**	**NH_3-N (mg/L)**	**Fe (mg/L)**	**DOC (mg/L)**	**SO_4^{2-} (mg/L)**
1	**7.1**	**11.6**	**5.6**	**0.028**	**0.065**	**1.4**	**13.7**
2	**45.2**	**<0.04**	**0.57**	**1.6**	**3.36**	**1.9**	**12.5**
3	**6.4**	**4.29**	**3.0**	**0.094**	**0.18**	**1.3**	**37.1**

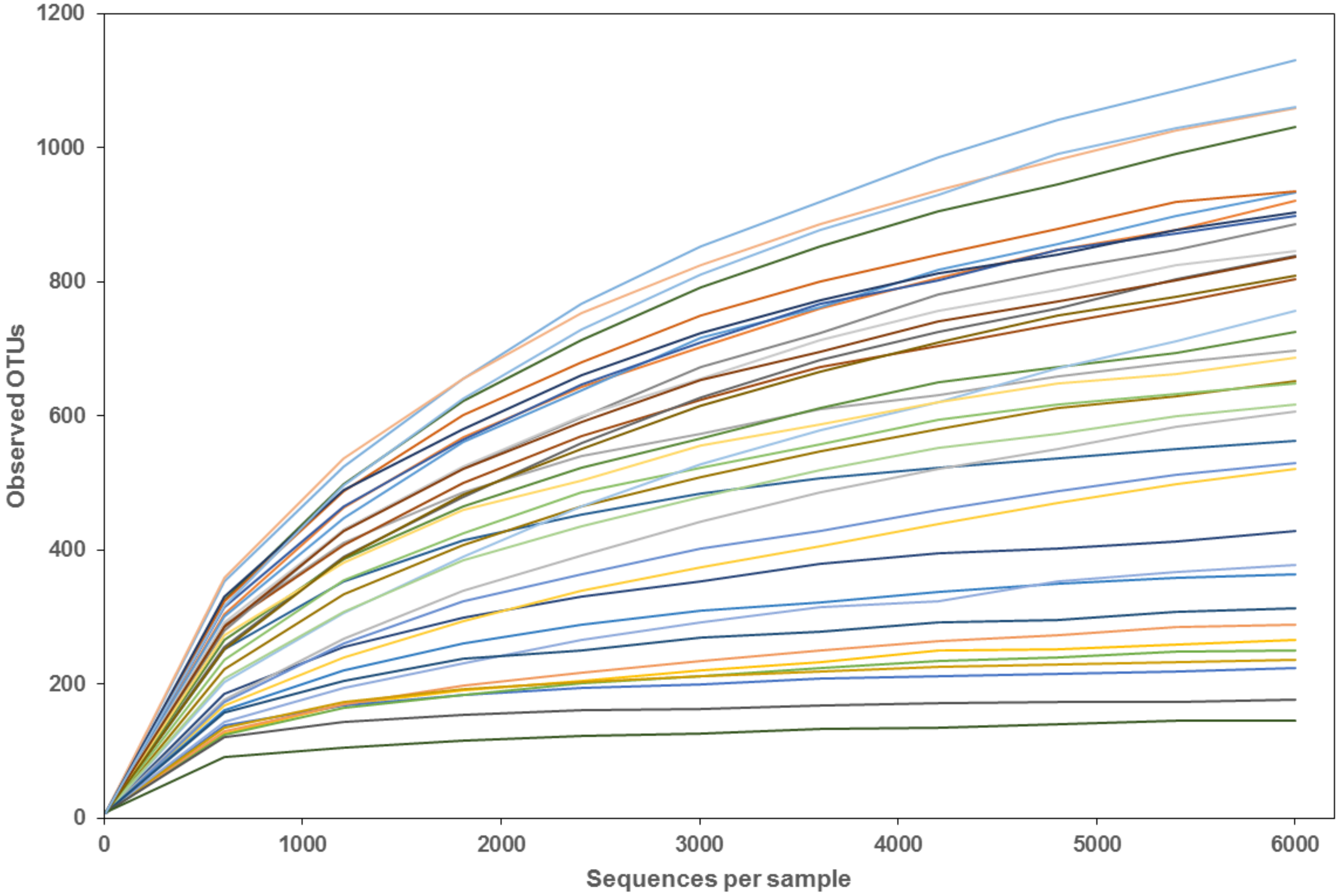


Figure 19 Rarefaction curve for all samples based on observed OTUs and sequences observed for all alluvial groundwater samples, with a threshold of 6000 sequences.

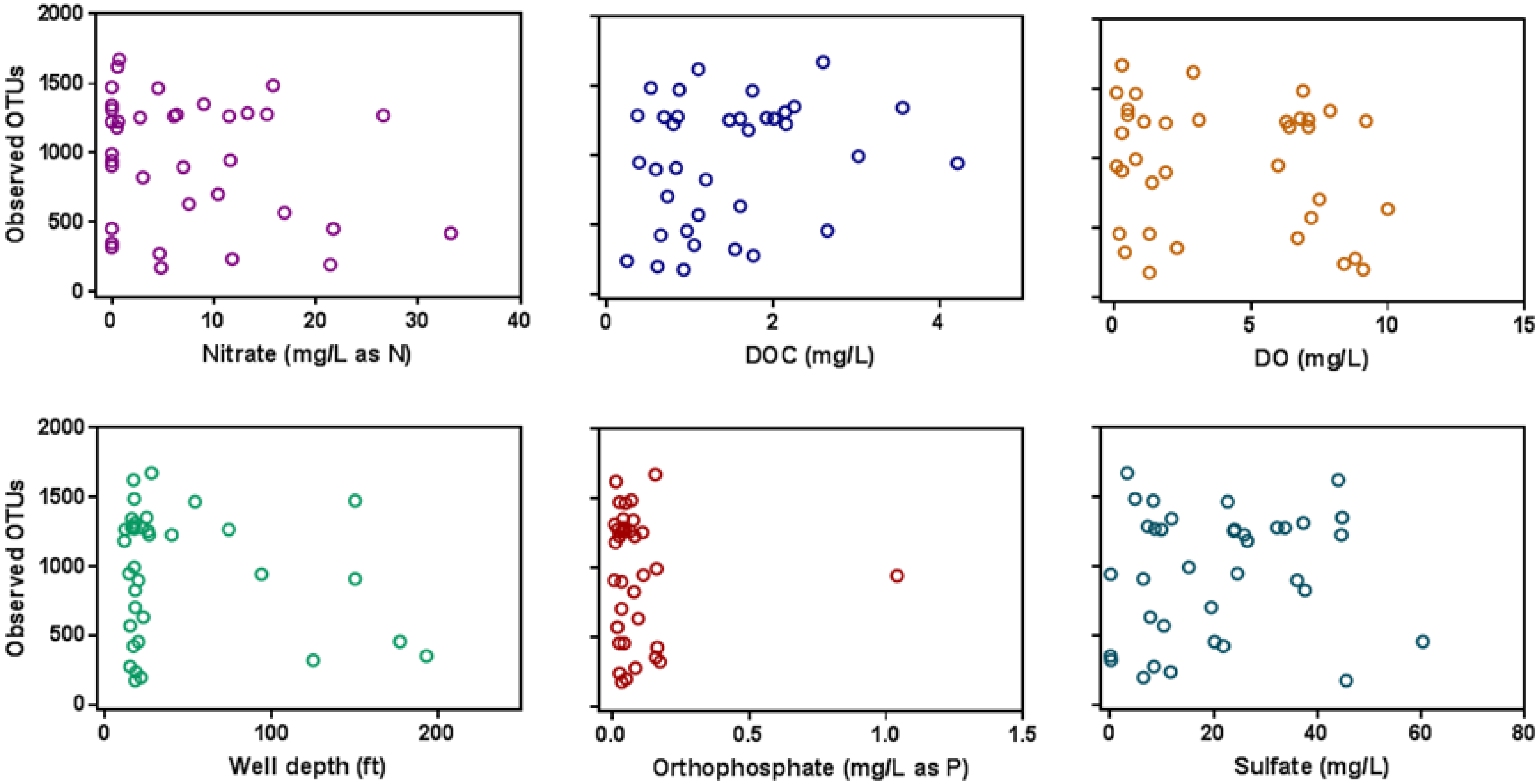


Figure 20 Correlation between various water chemistry parameters, including well depth and concentrations of NO_3^--N, DOC, DO, PO_4^{3-}, and SO_4^{2-}, and the number of observed OTUs in alluvial aquifer wells.

Table 2 Microbial classes with the highest median relative abundances in each of the clusters.

Kingdom	**Phylum**	**Class**	**Median relative abundance (%)**
Cluster 1			
Unassigned	Unassigned	Unassigned	18
Bacteria	OP3	koll11	7.6
Bacteria	Proteobacteria	Deltaproteobacteria	6.8
Bacteria	Proteobacteria	Betaproteobacteria	6.2
Bacteria	Nitrospirae	Nitrospira	5.1
Cluster 2			
Bacteria	Proteobacteria	Betaproteobacteria	21
Bacteria	Proteobacteria	Gammaproteobacteria	16
Unassigned	Unassigned	Unassigned	7.3
Bacteria	Proteobacteria	Alphaproteobacteria	6.2
Bacteria	Proteobacteria	Deltaproteobacteria	6.0
Cluster 3			
Bacteria	Proteobacteria	Betaproteobacteria	16
Unassigned	Unassigned	Unassigned	9.5
Bacteria	Proteobacteria	Alphaproteobacteria	8.9
Bacteria	Proteobacteria	Gammaproteobacteria	7.1
Bacteria	Proteobacteria	Deltaproteobacteria	5.6

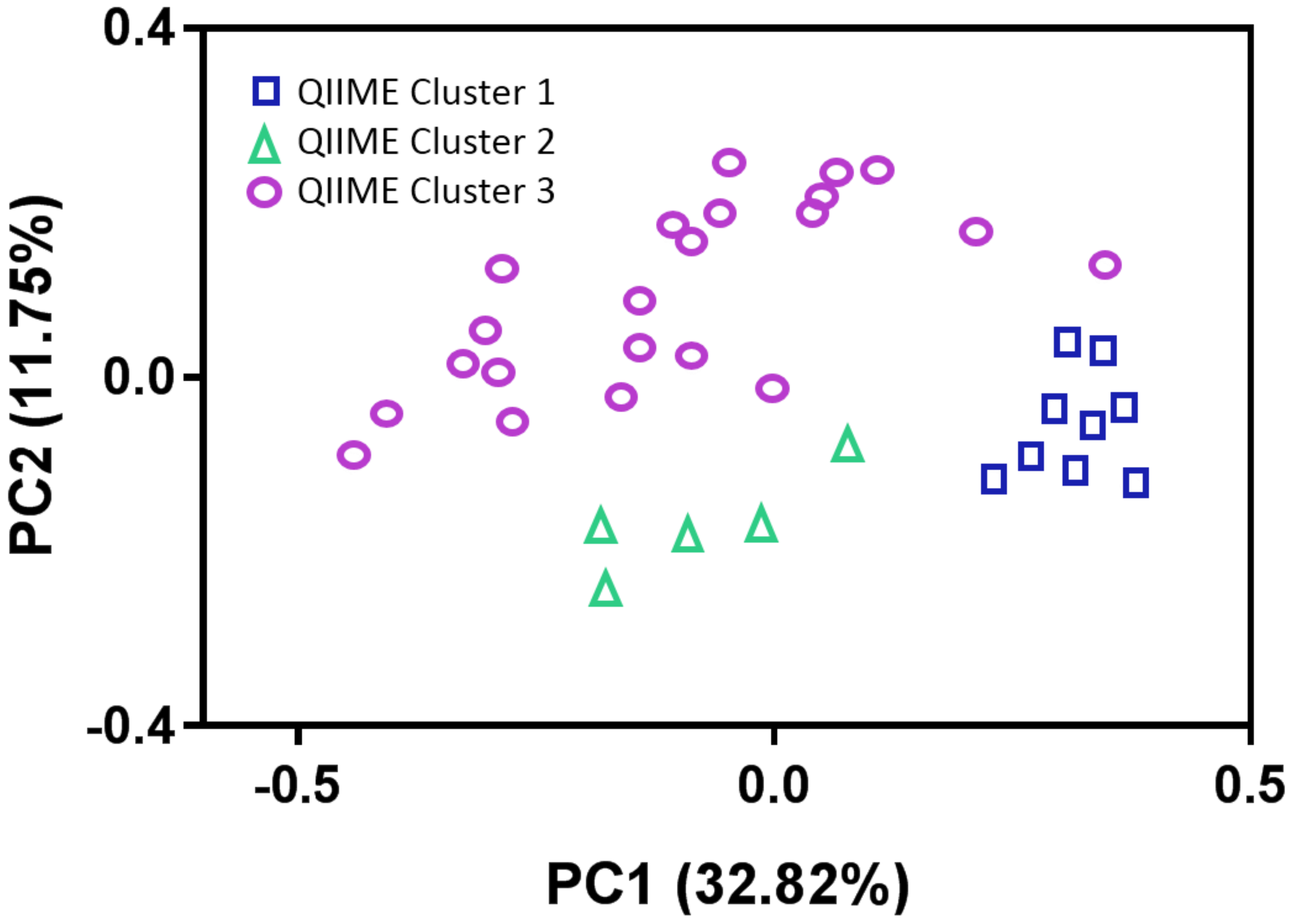


Figure 21 Principle coordinate analysis with visual clustering based on water chemistry and the distribution and abundance of OTUs.

Table 3 Water chemistry of alluvial aquifer with median values associated with QIIME PCoA clusters.

USGS Site ID	Well	Depth (m)	DO (mg/L)	[NO_3^--N] (mg/L)	[NH_3-N] (mg/L)	DOC (mg/L)	[PO_4^{3-}-P] (mg/L)	[Fe] (µg/L)	[SO_4^{2-}] (mg/L)
QIIME Cluster 1									
412711091122401	KM5	58.8	2.3	<0.040	1.2	1.05	0.16	1540	0.05
412916091405101	KM7	38.1	0.4	<0.040	1.06	1.54	0.175	3280	11.6
413634091484301	KM15	53.9	0.2	<0.040	4.31	2.65	0.026	1410	60.3
423409092283001	KM20	45.7	0.3	<0.040	0.09	0.83	0.008	443	6.32
430525093023501	KM26	3.5	0.3	0.496	<0.01	1.7	0.012	<10	26.4
423557091560501	KM30	5.3	0.8	<0.040	0.33	3.02	0.162	353	15.1
412748091285101	KM32	28.7	0.1	<0.037	2.69	4.21	1.04	9450	0.07
430159093403201	KM34	8.1	7.1	<0.040	0.96	2.15	0.082	1660	25.8
414914092024001	KM37	12.2	6.4	0.632	<0.01	0.8	0.026	<10	44.6
Median		28.7	0.4	<0.040	0.96	1.70	0.082	1410	15.1
QIIME Cluster 2									
420036091444001	KM1	22.6	1.1	6.07	0.05	1.6	0.065	685	23.9
420013091442000	KM2	16.5	0.8	4.55	0.04	1.75	0.049	55.5	22.6
412755091114101	KM10	5.5	0.5	<0.040	0.03	2.14	0.01	294	37.2
433815093000001	KM22	4.9	7.9	<0.040	0.03	3.55	0.077	10.6	11.8
434556093003501	KM23	45.7	0.1	<0.040	0.29	0.87	0.027	4040	8.28
Median		16.5	0.8	<0.040	0.04	1.75	0.049	294	22.6
QIIME Cluster 3									
412808091345001	KM4	6.1	1.9	6.99	<0.01	0.59	0.034	<10	36
411511091155101	KM6	5.6	8.4	11.8	<0.01	0.24	0.027	<10	11.6
414208092312601	KM8	5.5	7.5	10.4	<0.01	0.73	0.034	15.7	19.5
411843092105101	KM9	7.9	1.9	2.78	<0.01	1.47	0.111	11.1	23.8
413338091045601	KM11	4.4	6	11.6	<0.01	0.39	0.114	<10	24.5
424548092101701	KM12	4.6	7.2	16.9	<0.01	1.1	0.019	<10	10.3
422518092144701	KM13	5.3	6.9	15.8	<0.01	0.53	0.07	<10	4.74

Table 3 continued

USGS Site ID	Well	Depth (m)	DO (mg/L)	[NO$_3^-$-N] (mg/L)	[NH$_3$-N] (mg/L)	DOC (mg/L)	[PO$_4^{3-}$-P] (mg/L)	[Fe] (µg/L)	[SO$_4^{2-}$] (mg/L)
413540091341201	KM14	5.2	2.9	0.555	<0.01	1.1	0.014	<10	44
415139092190801	KM16	7.6	0.5	9.03	<0.01	2.25	0.04	11.1	44.7
415527092190301	KM17	6.9	3.1	6.35	<0.01	0.69	0.04	<10	33.7
405601091551901	KM19	5.5	1.4	3.05	<0.01	1.19	0.08	17.4	37.5
425401093135201	KM21	6.1	1.3	21.7	<0.01	0.96	0.043	<10	20.1
435221093001901	KM24	4.6	8.8	4.69	<0.01	1.76	0.085	11.1	8.4
425756092162401	KM25	4.9	7.1	15.2	<0.01	0.85	0.021	<10	32.2
431339093155901	KM27	3.7	6.3	11.5	<0.01	2.01	0.036	14.1	9.81
432946093161901	KM28	8.5	0.3	0.725	<0.01	2.6	0.158	<10	3.23
423639092350901	KM29	5.3	9.2	26.6	<0.01	1.92	0.047	<10	8.6
421115091250501	KM31	7.0	10	7.54	<0.01	1.6	0.095	<10	7.68
412927092575201	KM33	5.2	6.7	33.2	<0.01	0.65	0.165	10.7	21.8
431222093313301	KM35	6.6	9.1	21.4	<0.01	0.61	0.051	13.3	6.38
424203092551301	KM36	5.3	6.8	13.3	<0.01	0.37	0.041	16.7	7.16
410513091430401	KM38	5.5	1.3	4.82	<0.01	0.92	0.035	19.2	45.5
Median		5.49	6.5	10.95	<0.01	0.94	0.042	<10	19.8

Table 4 Median relative abundances of bacterial and archaeal classes in QIIME Cluster 1 and QIIME Cluster 3. Only classes with greater than one percent of the relative abundance in at least one sample are shown.

Kingdom	**Phylum**	**Class**	**Median relative abundance (%)**
QIIME Cluster 1			
Bacteria	Proteobacteria	Betaproteobacteria	22
Bacteria	Proteobacteria	Gammaproteobacteria	18
Bacteria	Proteobacteria	Alphaproteobacteria	9.6
Bacteria	Proteobacteria	Deltaproteobacteria	5.7
Unassigned	Unassigned	Unassigned	4.9
Bacteria	Nitrospirae	Nitrospira	2.7
Bacteria	OP3	koll11	1.6
Bacteria	Chloroflexi	Anaerolineae	1.5
Bacteria	Planctomycetes	Brocadiae	1.2
Bacteria	Planctomycetes	Phycisphaerae	1.0
QIIME Cluster 3			
Unassigned	Unassigned	Unassigned	15.2
Bacteria	OP3	koll11	7.0
Bacteria	Proteobacteria	Deltaproteobacteria	6.5
Bacteria	Proteobacteria	Betaproteobacteria	6.4
Bacteria	Nitrospirae	Nitrospira	5.2
Bacteria	Proteobacteria	Alphaproteobacteria	4.2
Bacteria	Proteobacteria	Gammaproteobacteria	3.8
Bacteria	Acidobacteria	Acidobacteria-6	2.8
Bacteria	OP3	PBS-25	2.4
Archaea	Crenarchaeota	Thaumarchaeota	2.2
Archaea	Parvarchaeota	Parvarchaea	1.8
Bacteria	Verrucomicrobia	Pedosphaerae	1.4

CONCLUSIONS

Connections between groundwater chemistry data and non-targeted 16S rRNA sequences of groundwater microbial populations were revealed in Eastern Iowa alluvial aquifers. Water chemistry data from 2017 was comparable to historical data (1997-98 and 2017). Shallower wells contained higher concentrations of NO_3^--N and DO but lower concentrations of NH_3-N and Fe. In contrast, deeper wells contained higher concentrations of NH_3-N and Fe, with low DO and NO_3^--N concentrations often below detection. A k-means cluster analysis showed well depth and DO as main components, with SO_4^{2-} as a secondary component, to distinguish groupings from one another. A PCoA reflecting the distribution and abundance of OTUs in the samples also exhibited clustering with respect to water chemistry. The clusters exhibited different median relative abundances of microbial taxonomic classes and select genera, which were related to the environmental conditions of the aquifers.

This study revealed relationships between groundwater quality and the microbial communities present in alluvial aquifers in Eastern Iowa. The information obtained from the non-targeted 16S rRNA sequencing and analysis provides preliminary information about the microbial communities present in aquifers with variable groundwater chemistry characteristics. Due to the difficulty associated with assigning specific metabolic traits to organisms identified via non-targeted16S rRNA sequencing, further investigation via shotgun metagenome sequencing could reveal a wealth of information about specific genes present in the DNA samples. The presence and abundance of genes associated with the nutrient cycling microorganisms, such as denitrifers and iron oxidizers, could be further explored. This information would allow for a better understanding of the role bacterial communities play in the water chemistry of alluvial aquifers, which are continually exposed to contaminants and nutrients due to their connectivity to the land surface and surface water.

The connection between groundwater chemistry and the microbial communities present in aquifers is of great interest due to our ever increasing concern about groundwater quality. Alluvial aquifers, which are frequently utilized as drinking water sources, are extremely susceptible to contamination from the land surface. The ability of alluvial aquifer ecosystems to transform nutrient or contaminant inputs is crucial for the conservation of groundwater resources, now and in the future. Microbial diversity in aquifers is intrinsically tied to groundwater quality, and we must continue to study how microbial environmental services may be affected by the changing inputs aquifers are receiving, especially in regions of intensive agriculture.

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APPENDIX: QIIME TAXONOMY INFORMATION

Table A1 Taxonomic QIIME results at the genus level by sample (KM1-KM7).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 1**	**KM 2**	**KM 4**	**KM 5**	**KM 6**	**KM 7**
Unassigned	Other	Other	Other	Other	Other	24.56	17.94	21.69	4.87	3.14	17.28
Archaea	Crenarchaeota	MBGA				0.00	0.00	0.06	0.00	0.00	0.00
Archaea	Crenarchaeota	MBGA	NRP-J			0.00	0.00	0.57	0.00	0.55	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.00	0.00	0.24	0.00	0.67	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.17	0.12	0.12	0.00	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	2.33	1.35	0.01	0.00	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		0.01	0.02	1.33	0.00	3.53	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.00	0.00	0.00	0.00	0.00	0.06
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.00	0.00	0.00	0.00	0.26
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.00	0.00	0.06	0.00	0.37
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.81
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.58
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.03	0.00	0.41	0.00	2.32
Archaea	Euryarchaeota	Thermoplasmata	E2			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.00	0.00	0.50	0.00	0.16	0.00
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			1.11	0.14	0.00	0.00	0.00	0.00
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.81	0.50	0.08	0.64	0.00	0.08
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			1.24	0.93	3.34	0.00	0.00	0.00
Bacteria						0.00	0.00	0.00	0.00	0.00	0.19
Bacteria	AC1					0.00	0.01	0.08	0.00	0.00	0.00
Bacteria	AC1	HDBW-WB69				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria					0.83	0.74	0.07	0.17	0.83	0.00
Bacteria	Acidobacteria	Acidobacteria-5				0.07	0.14	0.41	0.00	1.89	0.00
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.00	0.01	0.03	0.00	0.02	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			3.16	1.80	2.34	0.02	6.70	0.06
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.17	0.04	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.05	0.02	0.00	0.02	0.00	0.03
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		0.00	0.02	0.15	0.00	1.37	0.00
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	BPC102				0.13	0.07	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	BPC102	MVS-40			0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.02	0.02	0.02	0.00	0.00	0.00

Table A1 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 1**	**KM 2**	**KM 4**	**KM 5**	**KM 6**	**KM 7**
Bacteria	Acidobacteria	DA052	Ellin6513			0.03	0.10	0.21	0.00	0.32	0.00
Bacteria	Acidobacteria	EC1113				0.03	0.07	0.24	0.00	0.80	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.01	0.00	0.00	0.71	0.00	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.09	0.00	0.04	0.01	0.01	0.09
Bacteria	Acidobacteria	RB25				0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.00	0.00	0.10	0.00	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.00	0.00	0.03	0.00	0.26	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.07	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	0.00	0.00	0.00	0.00	0.11
Bacteria	Acidobacteria	TM1				0.00	0.00	0.13	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.00	0.00	0.01	0.00	0.39	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.00	0.00	0.06	0.00	0.25	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	iii1-8	32-20			0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.00	0.00	0.37	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.07	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.02	0.71	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.00	0.01	0.00	0.21	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.00	0.01	0.00	0.07	0.69	0.04
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.00	0.00	0.91	0.02	0.00	0.20
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.00	0.00	1.41	0.02	0.14	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.40	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.00	0.00	0.06	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.15	0.00	0.00	0.00	1.10
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.00	0.00	0.28	0.00	0.22	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.10	0.00	0.00	0.63
Bacteria	Actinobacteria	Thermoleophilia				0.01	0.00	0.00	3.50	0.00	0.01
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.00	0.00	0.00	0.00	0.00	0.00

Table A1 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 1**	**KM 2**	**KM 4**	**KM 5**	**KM 6**	**KM 7**
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		0.11	0.03	0.02	0.00	0.57	0.00
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.00	0.01	2.08	0.14	0.04	0.00
Bacteria	AncK6					0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Armatimonadetes	0319-6E2				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	BHI80-139					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.10	0.15	0.07	1.34	0.00	0.02
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.02	0.00	0.16	0.00	0.01	0.01
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.00	0.01	0.00	0.01	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.06	0.18	0.00	0.10	0.01	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			0.36	0.64	0.33	0.00	0.00	0.09
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.01	0.01	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.00	0.00	0.00	0.14	0.00	0.16
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.00	0.01	0.06	0.00	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.10	0.04	0.29	0.01	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.01	0.00	0.01	0.35	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.11	0.03	0.00	0.11	0.00	0.47
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.01	0.00	0.03	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			0.08	0.06	0.01	0.00	0.09	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.05	0.01	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.10	0.07	0.00	0.01	0.00	0.00
Bacteria	Chlorobi	BSV26				0.00	0.00	0.13	0.00	0.00	0.00
Bacteria	Chlorobi	BSV26	A89			0.04	0.02	0.06	0.58	0.46	0.22
Bacteria	Chlorobi	BSV26	C20			0.19	0.05	0.01	0.00	0.04	0.00
Bacteria	Chlorobi	BSV26	PK329			0.00	0.01	0.00	0.00	0.00	1.52
Bacteria	Chlorobi	BSV26	VC38			0.06	0.05	0.05	0.54	0.00	0.02
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.02	0.00	0.00	0.00	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.06	0.01	0.00	0.45	0.00	0.25
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.30	0.01	0.02	0.00	0.00	0.00
Bacteria	Chlorobi	OPB56				0.00	0.00	0.01	0.00	0.00	0.05
Bacteria	Chlorobi	SJA-28				0.00	0.00	0.00	0.27	0.00	0.00
Bacteria	Chloroflexi	Other	Other	Other	Other	0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31			0.21	0.08	0.03	0.00	0.00	0.03
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.26	0.17	0.13	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.73	0.04	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.95	0.62	0.44	4.52	0.68	4.07
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.23	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.11	0.07	0.01	0.23	0.00	0.87
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.01	0.08	0.04	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.10	0.40	0.00	0.07	0.00	0.00
Bacteria	Chloroflexi	Ellin6529				0.10	0.01	0.03	0.00	0.00	0.02
Bacteria	Chloroflexi	Gitt-GS-136				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	P2-11E				0.01	0.03	0.05	0.00	0.78	0.00
Bacteria	Chloroflexi	S085				0.08	0.05	0.07	0.33	0.01	0.06
Bacteria	Chloroflexi	SAR202				0.21	0.56	0.44	0.00	0.40	0.00
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.02	0.00	0.33	0.00	0.17	0.00
Bacteria	Chloroflexi	TK17				0.02	0.01	0.02	0.00	0.00	0.00
Bacteria	Chloroflexi	TK17	mle1-48			0.00	0.00	0.00	0.00	0.13	0.00
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.09	0.02	0.43	0.00	0.00	0.10
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			0.17	0.20	2.08	0.00	0.54	0.00
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			0.00	0.00	0.02	0.00	0.00	0.01
Bacteria	Cyanobacteria	ML635J-21				0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.01	0.00	0.00	0.00	0.57	0.06
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia				0.00	0.00	0.17	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			0.29	0.32	0.33	0.00	0.00	0.14
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.21	0.32	0.04	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.11	0.04	0.06	0.00	1.22	0.00
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.00	0.03	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Endomicrobia				0.94	1.18	0.28	0.00	0.00	0.00
Bacteria	FBP					0.00	0.00	0.10	0.00	0.00	0.00
Bacteria	FCPU426					0.00	0.00	0.02	0.00	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Fibrobacteres					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.00	0.00	0.00	0.02	0.00	0.08
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.00	0.01	0.00	0.00	0.09	0.03
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.00	0.00	0.00	1.18	0.00	0.20
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	0.00	0.00	0.02	0.00	0.02
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	0.00	0.00	0.00	0.00	0.05	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.00	0.00	0.00	0.00	0.00	0.07
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.00	0.00	0.00	0.03	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.00	0.00	0.00	0.49	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	OPB54			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	3BR-5F				1.03	0.21	0.08	0.00	0.00	0.00
Bacteria	GN02	BB34				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	GN02	GKS2-174				0.60	0.15	0.00	0.00	0.00	0.00
Bacteria	GN02	GN07				0.03	0.02	0.00	0.00	0.00	0.00
Bacteria	GN04					0.06	0.04	0.00	0.01	0.00	0.02
Bacteria	GN04	GN15				0.02	0.00	0.00	0.09	0.00	0.78
Bacteria	GN04	MSB-5A5				0.00	0.01	0.03	0.00	0.03	0.00
Bacteria	Gemmatimonadetes	Gemm-1				0.05	0.18	0.16	0.00	0.17	0.08
Bacteria	Gemmatimonadetes	Gemm-2				0.07	0.03	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.02	0.03	0.09	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.04	0.01	0.01	0.00	0.00	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.00	0.04	0.00	0.00	0.00	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.03	0.16	0.00	0.00	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	MVS-104					0.00	0.00	0.00	0.10	0.00	0.00
Bacteria	NC10	24-Dec	JH-WHS47			0.03	0.34	0.91	0.00	0.79	0.00
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	0.14	1.22	0.10	0.00	0.48	0.00
Bacteria	NC10	wb1-A12				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	NKB19					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.23	0.63	0.07	0.00	0.27	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		1.25	1.70	2.70	0.02	10.76	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.32	1.50	1.92	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.01	0.20	0.00	0.26	0.00	0.10
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.03	0.13	0.11	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	0.00	0.05	0.17	0.00	0.21	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	1.80	0.92	0.81	0.22	0.14	0.91
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		0.05	0.01	0.44	0.00	0.22	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.01	0.02	0.00	0.43	0.00	0.07
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.20	0.05	0.00	0.05	0.00	0.60
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.09	0.18	0.03	1.47	0.00	2.80
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.02	0.00	0.00	0.13	0.00	1.55
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.00	0.12	0.00	0.00
Bacteria	OC31					0.00	0.00	0.00	0.66	0.00	0.00
Bacteria	OD1					0.72	0.72	1.21	0.05	0.00	0.00
Bacteria	OD1	ABY1				0.24	0.17	0.23	0.00	0.00	0.00
Bacteria	OD1	Mb-NB09				0.04	0.04	0.00	0.00	0.00	0.00
Bacteria	OD1	SM2F11				0.04	0.02	0.01	0.08	0.00	0.00
Bacteria	OD1	ZB2				1.30	1.43	0.13	0.00	0.00	0.00
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.00	0.00	0.11	0.00	0.00	0.00
Bacteria	OP11	OP11-4				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OP3					0.45	1.05	0.22	0.03	0.00	0.04
Bacteria	OP3	BD4-9				1.22	2.57	0.48	0.10	0.00	0.25
Bacteria	OP3	PBS-25				5.68	7.66	3.83	0.00	1.73	0.08
Bacteria	OP3	koll11				6.11	4.98	18.01	0.04	5.22	0.00
Bacteria	OP3	koll11	GIF10			0.92	3.57	0.36	0.79	0.00	6.97
Bacteria	OP3	koll11	GIF10	kpj58rc		0.60	0.36	0.53	0.00	0.00	0.00
Bacteria	PAUC34f					0.20	0.17	0.01	0.00	1.44	0.05
Bacteria	Planctomycetes					0.03	0.01	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	BD7-11				0.06	0.02	0.01	0.00	0.72	0.00
Bacteria	Planctomycetes	C6	MVS-107			0.11	0.15	0.02	0.00	0.00	0.00
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190				0.00	0.00	0.00	0.00	0.11	0.00
Bacteria	Planctomycetes	OM190	CL500-15			0.28	0.05	0.00	0.29	0.00	0.00
Bacteria	Planctomycetes	OM190	agg27			0.06	0.02	0.00	0.18	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.40	0.64	0.23	1.35	0.01	0.06
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.00	0.00	0.05	0.00	0.04
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.03	0.01	0.00	0.75	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.43	0.00	0.00
Bacteria	Planctomycetes	Pla4				0.00	0.00	0.27	0.00	0.05	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.23	0.03	0.15	0.00	1.06	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.00	0.00	0.02	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.37	0.08	0.02	0.00	5.54	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.07	0.01	0.05	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.09	0.81	0.01	7.81	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.49	3.59	0.21	0.00	0.00	0.02
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.01	0.71	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.03	0.22	0.24	0.00	0.00	0.00
Bacteria	Proteobacteria					3.30	3.48	1.44	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.17	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.10	0.07	0.09	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.02	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.00	0.00	0.02	0.08	0.00	0.22
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.02	0.00	0.00	0.17	0.00	0.08
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.00	0.00	0.14	0.00	0.07	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.08	0.00	0.15	0.06	0.24	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.01	0.00	0.04	0.53	0.01	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.00	0.00	0.04	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.02	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	1.58	0.98	0.17	3.87	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.05	0.03	0.35	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.66	0.25	0.14	0.51	1.40	0.08
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.06	0.00	0.01	0.08	0.61	0.11
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.01	0.00	0.00	0.10	0.00	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.00	0.00	0.00	0.03	0.00	0.00

Table A1 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 1**	**KM 2**	**KM 4**	**KM 5**	**KM 6**	**KM 7**
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.00	0.00	0.00	0.05	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.14	0.06	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		1.29	1.12	0.29	0.33	0.12	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.00	0.00	0.00	0.30	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	0.00	0.00	0.00	0.00	1.42	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			0.24	0.20	0.14	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.08	0.03	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.00	0.03	0.19	0.17	0.00	0.17
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.02	0.00	1.34	0.00	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.01	0.00	0.00	0.03	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.07	0.01	0.00	0.05	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.00	0.00	1.38	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.01	0.00	0.00	4.65	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.00	0.01	0.00	0.03	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.00	0.00	0.00	0.11	0.00	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.10	0.09	0.14	0.09	0.00	0.10
Bacteria	Proteobacteria	Betaproteobacteria				2.01	2.87	0.48	1.18	0.24	1.33
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.01	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.06	0.02	0.00	0.10	0.00	0.03
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		0.23	0.06	0.05	2.26	0.14	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.00	0.00	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.06	0.00	0.11	0.00	0.00	0.27
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.00	0.00	0.02	0.02	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.00	0.05	0.00	0.02	0.05	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.00	0.01	0.00	0.01	1.37	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.03	0.10	0.21	0.24	4.29	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.00	0.00	0.00	0.01	0.03	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.06	0.02	0.00	0.16	0.00	4.26
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	8.29	1.25	0.69	3.75	0.42	1.14
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.00	0.81	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.07	0.19	0.10	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	MND1			0.43	0.71	0.32	0.16	8.10	0.06
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.13	0.01	0.17	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.01	0.00	0.00	4.21	3.85	3.49
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.00	0.01	0.00	0.05	0.17	0.52
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.00	0.00	0.00	0.00	0.40	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			0.00	0.00	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.03	0.03	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.18	0.05	0.00	0.06	0.00	0.05
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	0.03	0.02	0.08	6.24	0.00	1.38
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		0.09	0.03	0.04	2.29	0.11	1.75
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.00	0.00	0.00	0.13	0.00	0.18
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.00	0.01	0.07	0.16	0.00	0.31
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.00	0.00	0.00	0.00	0.00	0.22
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.28	0.01	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.00	0.00	0.00	0.02	0.00	0.17
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	1.67	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			1.42	0.62	0.09	2.91	0.01	12.09
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.05	0.02	0.05	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.00	0.00	0.08	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria				0.32	0.42	2.99	2.37	0.00	0.10
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.01	0.00	0.00	0.13	0.00	0.17
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.03	0.25	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.14	0.06	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.74	2.66	0.08	0.71	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.01	0.00	0.00	0.37	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.00	0.02	0.00	0.46	0.00	0.08
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.00	0.00	0.00	0.22	0.00	1.18
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		1.94	0.59	0.00	0.37	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.37	0.23	0.00	0.00	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.01	0.07	0.00	0.71	0.00	0.74
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.09	0.06	0.14	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.39	0.46	0.26	0.39	1.38	0.54
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.08	0.05	0.00	0.00	0.24	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.15	0.52	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.06	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.00	0.05	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.00	0.00	0.18	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.02	0.08	1.46	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.07	0.15	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.00	0.02	0.00	0.00	0.68	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.03	0.09	0.00	0.00	0.00	0.10
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.00	0.00	0.01	0.00	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.03	0.00	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		1.49	2.82	2.44	0.20	2.80	0.39
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.16	0.44	0.00	0.35	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		0.06	0.01	0.36	0.00	1.68	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.10	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria				0.10	0.00	2.40	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.00	0.00	0.00	0.00	0.00	0.83
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.01	0.04	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			0.04	0.05	0.12	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.02	0.02	0.00	0.01	0.00	0.00

Table A1 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 1	KM 2	KM 4	KM 5	KM 6	KM 7
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.84	0.30	0.06	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		0.52	0.23	0.23	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	0.34	0.11	0.20	0.00	0.17	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.14	0.06	0.06	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.17	0.09	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.81	9.49	0.01	15.82	0.00	18.79
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.01	0.00	1.48	0.00	0.05
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	0.19	0.07	0.58	0.14	5.76	0.48
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.34	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.01	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.12	0.01	0.00	0.14	0.11	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.01	0.03	0.01	0.00	0.00	0.04
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.11	0.06	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.00	0.00	0.06	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.01	0.00	0.00	0.00	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	SBR1093					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	SR1					0.00	0.02	0.04	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.00	0.00	0.00	0.05	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4	Other	Other	Other	0.00	0.05	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4				0.07	0.08	0.00	0.00	0.00	0.00
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.00	0.04	0.06	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		0.13	0.04	0.07	0.03	0.00	0.04

Table A1 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 1**	**KM 2**	**KM 4**	**KM 5**	**KM 6**	**KM 7**
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.31	0.16	0.00	0.09	0.68	0.02
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.01	0.00	0.00	0.23	0.00	0.08
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.01	0.04	0.22	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.31	0.18	0.29	0.28	2.82	0.21
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.00	0.00	0.07	0.00	0.36	0.08
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.00	0.00	0.06	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.36	0.19	0.00	0.85	0.00	0.12
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	WS3	PRR-12				0.16	0.01	0.05	0.00	0.00	0.00
Bacteria	WS3	PRR-12	Sediment-1			0.00	0.00	0.00	0.00	0.39	0.00
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.08	0.11	0.18	0.03	1.70	0.00

Table A2 Taxonomic QIIME results at the genus level by sample (KM8-KM13).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Unassigned	Other	Other	Other	Other	Other	9.83	16.38	20.48	15.65	19.90	12.70
Archaea	Crenarchaeota	MBGA				0.04	0.00	0.00	0.00	0.00	0.00
Archaea	Crenarchaeota	MBGA	NRP-J			0.06	0.02	0.00	0.05	0.02	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.00	0.00	0.00	0.03	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.42	0.03	0.00	0.05	0.00	0.08
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.00	2.23	0.01	0.65	0.01	0.44
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	0.28	1.72	0.32	0.00	0.00	2.01
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		5.45	0.86	0.03	0.16	2.10	0.85
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.00	0.00	0.00	0.00	0.00	0.12
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2			0.23	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.07	0.00	0.00	0.05	0.00	0.04
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			0.00	0.03	0.35	0.07	0.00	0.00
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.00	0.27	0.54	0.04	0.10	0.17
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			1.50	1.51	0.83	2.04	0.33	1.54
Bacteria						0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	AC1					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	AC1	HDBW-WB69				0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Acidobacteria					0.33	0.23	0.17	0.01	0.02	0.31
Bacteria	Acidobacteria	Acidobacteria-5				0.22	1.93	0.10	0.02	15.90	0.85
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.06	0.04	0.01	0.00	0.00	0.06
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			3.73	14.17	0.86	0.47	5.18	7.83
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.00	0.10	0.11	0.01	0.01	0.29
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.00	0.12	0.01	0.00	0.00	0.19
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		2.91	0.83	0.01	0.03	7.49	0.02
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.06	0.03	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	BPC102				0.00	0.48	0.01	0.02	0.09	0.01
Bacteria	Acidobacteria	BPC102	MVS-40			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.41	0.01	0.00	0.00	0.00	0.00

Table A2 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Bacteria	Acidobacteria	DA052	Ellin6513			1.24	0.22	0.11	0.14	2.05	0.17
Bacteria	Acidobacteria	EC1113				0.76	0.21	0.03	0.01	0.28	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.13	0.09	0.04	0.00	0.05	0.04
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.00	0.02	0.03	0.00	0.00	0.00
Bacteria	Acidobacteria	RB25				0.39	0.01	0.02	0.00	0.00	0.04
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.24	0.15	0.02	0.00	11.57	0.01
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.00	0.01	0.00	0.00	0.01
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.00	0.01	0.00	0.02	0.01	0.04
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.00	0.02	0.01	0.01	0.00	0.01
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	TM1				0.34	0.62	0.02	0.00	1.70	0.02
Bacteria	Acidobacteria	[Chloracidobacteria]				0.00	0.00	0.00	0.16	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.10	0.07	0.00	0.30	0.07	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.00	0.02	0.03	0.00	0.00	0.90
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.31	0.10	0.01	0.04	0.39	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.00	0.01	0.00	0.01	0.00	0.18
Bacteria	Acidobacteria	iii1-8	32-20			0.00	0.00	0.01	0.01	0.00	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.04	0.02	0.00	0.00	0.20	0.01
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.09	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.01	0.02	0.00	0.00	0.01
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.01	0.00	0.00	0.00	0.05
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.10	0.03	0.00	0.02	0.01	0.23
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.00	0.03	0.02	34.65	0.12	0.23
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.13	0.00	0.00	0.00	0.00	0.22
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.14	0.00	0.00	0.00	0.00	0.29
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.26	0.09	0.01	0.00	0.01	0.22
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.01	0.00	0.00	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.00	0.02	0.00	0.00	0.00	0.44
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.00	0.11	0.00	0.00	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.26	0.09	0.00	0.16	0.13	0.08
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Actinobacteria	Thermoleophilia				0.00	0.00	0.11	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.20	0.04	0.00	0.00	0.01	0.00

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		1.00	0.13	0.01	0.03	0.01	0.31
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.23	0.00	0.10	0.10	0.16	0.12
Bacteria	AncK6					0.00	0.31	0.00	0.00	0.00	0.00
Bacteria	Armatimonadetes	0319-6E2				0.07	0.00	0.00	0.00	0.00	0.01
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.16	0.00	0.00	0.00	0.00	0.00
Bacteria	BHI80-139					0.10	0.00	0.00	0.00	0.00	0.02
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.00	0.06	0.11	0.03	0.00	0.06
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.00	0.05	0.04	1.92	0.00	0.23
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.26	0.00	0.02	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.00	0.02	0.00	0.00	0.00	0.05
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	6.01	0.00	0.01	0.00	0.00	0.12
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			0.23	0.64	0.27	0.16	0.09	1.22
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.10	0.02	0.00	0.00	0.00	0.01
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	1.61	0.04	0.00	0.00	0.00	0.04
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.02	0.09	0.07	0.08	0.04	0.41
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.00	0.01	0.02	0.36	0.05	0.04
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.00	0.00	0.03	0.00	0.00	0.01
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			0.02	0.57	0.23	0.12	0.00	0.05
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.00	0.01	0.05	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.00	0.29	0.10	0.01	0.00	0.06
Bacteria	Chlorobi	BSV26				0.12	0.01	0.00	0.03	0.00	0.09
Bacteria	Chlorobi	BSV26	A89			0.61	0.48	0.22	0.02	0.00	0.14
Bacteria	Chlorobi	BSV26	C20			0.21	0.06	0.03	0.02	0.07	0.08
Bacteria	Chlorobi	BSV26	PK329			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Chlorobi	BSV26	VC38			0.00	0.02	0.12	0.00	0.01	0.07
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.00	0.00	0.12	0.00	0.00	0.01
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.00	0.00	0.02	0.00	0.00	0.00
Bacteria	Chlorobi	OPB56				0.00	0.10	0.01	0.00	0.00	0.01
Bacteria	Chlorobi	SJA-28				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Chloroflexi	Other	Other	Other	Other	0.00	0.06	0.00	0.00	0.00	0.02
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31			0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.00	0.00	0.00	0.00	0.00	0.22
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.53	0.04	1.13	0.13	0.00	0.31
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.00	0.03	0.24	0.02	0.00	0.03
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.00	0.00	0.15	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.00	0.00	0.24	0.01	0.00	0.00
Bacteria	Chloroflexi	Ellin6529				0.29	0.11	0.10	0.01	0.03	0.11
Bacteria	Chloroflexi	Gitt-GS-136				0.08	0.04	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.00	0.00	0.30	0.00
Bacteria	Chloroflexi	P2-11E				0.14	0.07	0.00	0.01	0.64	0.01
Bacteria	Chloroflexi	S085				1.64	0.13	0.04	0.06	0.05	0.08
Bacteria	Chloroflexi	SAR202				0.98	0.97	0.30	0.71	0.35	1.10
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.20	0.07	0.00	0.03	0.05	0.02
Bacteria	Chloroflexi	TK17				0.06	0.18	0.00	0.00	0.08	0.04
Bacteria	Chloroflexi	TK17	mle1-48			0.60	0.01	0.00	0.00	0.00	0.02
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.00	0.03	0.00	0.24	0.00	0.22
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			0.83	0.15	0.46	1.22	0.19	1.76
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.00	0.00	5.89	0.28	0.02	0.78
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Cyanobacteria	ML635J-21				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.03	0.05	0.00	0.04	0.89	0.00
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia				0.00	0.04	0.01	0.00	0.00	0.06
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			1.08	0.19	1.04	0.28	0.49	0.46
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.19	0.04	0.07	0.03	0.48	0.03
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.26	0.06	0.03	0.03	0.14	0.37
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.00	0.21	0.00	0.03	0.00	0.06
Bacteria	Elusimicrobia	Endomicrobia				0.46	0.48	0.26	0.23	0.08	0.34
Bacteria	FBP					0.00	0.09	0.00	0.00	0.60	0.01
Bacteria	FCPU426					0.01	0.00	0.00	0.00	0.00	0.00

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Fibrobacteres					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.00	0.00	0.00	0.00	0.00	0.26
Bacteria	Firmicutes	Bacilli	Bacillales			0.03	0.00	0.03	0.00	0.00	0.19
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.02	0.00	0.01	0.00	0.00	0.11
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.02	0.00	0.07	0.02	0.09	0.18
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.24	0.02	0.00	0.00	0.06	0.10
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.00	0.00	0.00	0.03	0.04	0.01
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.00	0.00	0.00	0.05
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.00	0.03	0.03	0.00	0.02	0.05
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.00	0.04	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.07	0.72	0.07	0.01	0.49	1.07
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.09	0.00	0.00	0.00	0.00	0.01
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.00	0.00	0.01	0.01	0.00	0.01
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	0.12	0.07	0.05	0.01	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.01	0.21	0.00	0.00	0.00	0.04
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.00	0.02	0.01	0.00	0.00	0.03
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.30	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.01	0.03	0.01	0.02	0.02	0.64
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	OPB54			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	3BR-5F				0.10	0.01	0.12	0.01	0.21	0.00
Bacteria	GN02	BB34				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	GN02	GKS2-174				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	GN02	GN07				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN04					0.00	0.00	0.05	0.00	0.00	0.04
Bacteria	GN04	GN15				0.00	0.04	0.10	0.02	0.00	0.11
Bacteria	GN04	MSB-5A5				0.09	0.02	0.00	0.00	0.00	0.02
Bacteria	Gemmatimonadetes	Gemm-1				0.51	0.78	0.17	0.02	0.22	0.28
Bacteria	Gemmatimonadetes	Gemm-2				0.08	0.24	0.03	0.00	0.01	0.03
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.19	0.00	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.00	0.13	0.03	0.00	0.06	0.14
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.00	0.00	0.00	0.00	0.00	0.29
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.00	0.15	0.04	0.01	0.00	0.05
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.00	0.05	0.00	0.00	0.00	0.17
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.00	0.00	0.03	0.00	0.00	0.00

Table A2 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Bacteria	MVS-104					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	NC10	24-Dec	JH-WHS47			0.33	0.65	0.27	0.25	0.23	0.12
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	1.08	0.65	0.33	0.02	0.45	0.00
Bacteria	NC10	wb1-A12				0.22	0.00	0.00	0.03	0.00	0.05
Bacteria	NKB19					0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.04	0.02	0.00	0.36	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		5.24	1.17	0.83	1.85	1.61	1.80
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.00	0.19	11.95	0.59	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.00	0.00	0.23	0.03	0.00	0.01
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.19	0.02	0.01	0.14	1.31	0.62
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	2.17	1.12	0.03	0.01	0.17	0.01
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.72	0.80	1.15	0.64	0.21	3.67
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		0.09	0.04	0.00	0.43	0.04	0.25
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.00	0.00	0.03	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.00	0.00	1.88	0.04	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.00	0.00	1.80	0.12	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.00	0.00	0.02	0.00	0.00	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OC31					0.00	0.00	0.02	0.00	0.00	0.02
Bacteria	OD1					0.01	0.04	1.24	0.06	0.03	0.01
Bacteria	OD1	ABY1				0.03	0.13	1.36	0.23	0.31	0.24
Bacteria	OD1	Mb-NB09				0.05	0.35	0.01	0.10	0.00	0.01
Bacteria	OD1	SM2F11				0.00	0.01	0.05	0.00	0.00	0.00
Bacteria	OD1	ZB2				0.00	0.38	1.88	0.25	0.23	0.06
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.02	0.10	0.03	0.00	0.13	0.00
Bacteria	OP11	OP11-4				0.00	0.00	0.37	0.01	0.00	0.00
Bacteria	OP3					0.00	0.00	0.74	0.01	0.00	0.00
Bacteria	OP3	BD4-9				0.00	0.02	3.73	0.13	0.04	0.00
Bacteria	OP3	PBS-25				4.19	1.39	6.47	6.01	1.19	6.63
Bacteria	OP3	koll11				5.13	2.17	5.52	9.92	4.04	9.00
Bacteria	OP3	koll11	GIF10			0.00	0.00	1.16	0.17	0.00	0.00
Bacteria	OP3	koll11	GIF10	kpj58rc		0.01	0.19	0.18	0.06	0.04	0.13
Bacteria	PAUC34f					0.06	0.81	0.04	0.00	1.05	0.18
Bacteria	Planctomycetes					0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Planctomycetes	BD7-11				0.25	0.05	0.10	0.02	0.10	0.24
Bacteria	Planctomycetes	C6	MVS-107			0.00	0.17	0.06	0.00	0.03	0.24
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190				0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Planctomycetes	OM190	CL500-15			0.00	0.03	0.00	0.03	0.00	0.03
Bacteria	Planctomycetes	OM190	agg27			0.00	0.08	0.05	0.01	0.00	0.20

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.18	0.03	0.62	0.18	0.03	0.22
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Planctomycetes	Pla4				0.05	0.02	0.00	0.04	0.15	0.31
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.67	0.07	0.01	0.12	0.10	0.12
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.00	0.02	0.00	0.25	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.00	0.03	0.00	0.06	0.11	0.31
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.03	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.00	0.00	0.02	0.02	0.00	0.01
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.00	0.10	0.04	0.04	0.00	0.21
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.00	0.01	0.17	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.00	0.05	1.04	0.04	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria					0.00	0.18	5.70	0.28	0.01	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.18	0.03	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.01	0.33	0.05	0.00	0.00	0.23
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.00	0.00	0.00	0.34	0.03	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.00	0.00	0.00	0.00	0.06	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.01	0.01	0.00	0.07	0.02	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.01	0.10	0.01	2.09	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.23	0.11	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.41	0.34	0.12	0.00	0.00	0.52
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.09	0.10	0.01	0.38	0.02	0.29
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.01	0.00	0.06	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.00	0.08	0.01	0.00	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.06	0.01	0.00	0.00	0.01	0.07
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.00	0.36	0.17	0.04	0.00	0.24
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.02	0.09	0.02	0.00	0.01	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.06	0.41	0.24	0.02	0.07	0.25
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.03	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.00	0.02	0.00	0.07	0.93	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.09	0.00	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.11	0.00	0.00	0.00	0.02	0.02

Table A2 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.05	0.00	0.01	0.01	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.00	0.00	0.01	0.00	0.00	0.28
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.08	0.02	0.15	0.00	0.00	0.32
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.33	0.00	0.10	0.22	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.00	0.00	0.33	0.04	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		0.53	2.45	0.59	0.43	0.15	1.33
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	3.55	0.49	0.00	0.00	0.00	0.28
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			0.00	0.28	0.12	0.04	0.08	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.00	0.01	0.06	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.00	0.00	0.07	0.62	0.00	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.00	0.00	0.00	0.26	0.00	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.17	0.02	0.00	0.00	0.16	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.00	0.06	0.01	0.00	0.11	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.00	0.03	0.02	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.05	0.05	0.02	0.33	0.20	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.22	0.05	0.02	0.02	0.03	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.20	0.00	0.00	0.03	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.00	0.15	0.79	0.07	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria				4.56	2.86	1.29	0.32	2.53	1.60
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.51	0.05	0.06	1.16	0.05	0.18
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		1.22	0.10	0.18	0.87	0.27	0.28
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.01	0.00	0.21	0.00	0.00	0.05
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.08	0.01	0.03	0.46	0.00	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.02	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.04	0.01	0.00	0.00	0.01	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.58	0.07	0.01	0.00	0.28	0.06
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.28	0.05	0.04	0.00	0.11	0.06
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.03	0.02	0.00	0.00	0.02	0.06

Table A2 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.00	0.00	0.00	0.00	0.05	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.00	0.00	0.17	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	0.00	0.12	0.44	0.20	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.38	0.20	0.05	0.00	0.08	0.21
Bacteria	Proteobacteria	Betaproteobacteria	MND1			2.33	3.42	0.59	0.03	1.45	1.21
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.02	0.02	0.03	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.47	0.19	0.28	0.04	0.44	0.29
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.01	0.01	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			1.01	0.00	0.00	0.00	0.07	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.01	0.00	0.03	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.00	0.00	0.00	0.02	0.00	0.09
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	0.00	0.01	0.01	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		0.00	0.19	0.13	0.00	0.09	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.00	0.01	0.00	0.00	0.00	0.07
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.00	0.00	0.09	0.08	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.00	0.14	0.16	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.00	0.01	0.01	0.00	0.00	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			0.00	0.02	0.18	0.07	0.00	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.00	0.06	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria				0.90	0.47	0.70	1.20	1.16	0.56
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.00	0.00	0.03	0.01	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.05	0.32	0.03	0.00	0.00	0.12
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.02	0.15	0.00	0.00	0.00	0.19
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.00	0.00	0.13	0.02	0.00	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.00	0.01	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.00	0.11	0.10	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.00	0.56	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.00	1.03	0.05	0.00	0.00	0.05
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		0.00	0.00	0.76	0.03	0.08	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.00	0.07	0.03	0.08	0.00	0.09

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.06	0.13	0.18	0.00	0.04	0.08
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.49	0.54	0.34	0.16	1.44	1.45
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.00	0.05	0.01	0.03	0.00	0.16
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.00	0.00	0.05	0.03	0.00	0.19
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.00	0.01	0.02	0.00	0.00	0.10
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.00	0.00	0.00	0.00	0.25	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.00	0.03	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.05	0.02	0.00	0.00	0.09	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.00	0.00	0.00	0.00	0.00	0.43
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.12	0.15	0.08	0.39	0.32	0.39
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.00	0.29	0.00	0.00	0.00	0.24
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.00	1.42	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.00	0.00	0.09	0.13	0.00	0.13
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		2.54	2.05	1.20	1.92	0.47	1.55
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.00	0.00	0.16	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		0.35	3.12	0.04	0.06	0.54	0.86
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria				0.00	0.00	0.00	1.61	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.19	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.00	0.02	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.01	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			0.00	5.34	0.03	0.25	0.09	0.35
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.02	0.01	0.00	0.04	0.05	0.02

Table A2 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 8	KM 9	KM 10	KM 11	KM 12	KM 13
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.00	0.00	0.00	0.00	0.10	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.00	0.06	0.04	0.00	0.28	0.12
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		0.07	1.11	0.33	0.20	0.25	1.33
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	0.15	0.22	0.15	0.09	0.02	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.45	0.86	0.05	0.01	0.06	0.59
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.05	0.12	0.06	0.01	0.06	0.35
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.00	0.04	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.00	0.00	0.41	0.06	0.00	0.12
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	1.53	0.09	0.01	0.27	0.40	0.33
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.05	0.01	0.01	0.00	0.03	0.21
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.99	0.01	0.13	0.01	0.20	7.02
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.00	0.06	0.03	0.02	0.07	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.00	0.05	0.05	0.00	0.00	0.25
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.00	0.00	0.00	0.00	0.00	0.18
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00	0.06	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.00	0.00	0.00	0.16	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.03	0.01	0.00	0.02	0.01	0.33
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	SBR1093					0.38	0.00	0.00	0.00	0.00	0.00
Bacteria	SR1					0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.00	0.00	0.00	0.11	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4	Other	Other	Other	0.00	0.03	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.26	0.03	0.00	0.04	0.22	0.14
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		0.00	0.09	0.10	0.03	0.00	0.62

Table A2 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 8**	**KM 9**	**KM 10**	**KM 11**	**KM 12**	**KM 13**
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.24	1.48	0.11	0.06	0.26	0.38
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.00	0.00	0.01	0.00	0.00	0.03
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.32	0.04	0.10	0.19	0.02	0.39
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.00	0.05	0.00	0.00	0.00	0.06
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.26	2.13	0.26	0.07	0.35	1.24
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.06	0.41	0.02	0.00	0.00	0.02
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.02	0.31	0.01	0.00	0.11	0.06
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.00	0.00	0.00	0.00	0.00	0.10
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.00	0.19	0.00	0.00	0.02	0.05
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.21	0.12	0.45	0.03	0.06	0.21
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.00	0.00	0.02	0.00	0.00	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	WS3	PRR-12				0.23	0.02	0.02	0.00	0.01	0.07
Bacteria	WS3	PRR-12	Sediment-1			0.21	0.24	0.02	0.00	0.01	0.17
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.49	0.25	0.12	0.16	0.03	0.27

Table A3 Taxonomic QIIME results at the genus level by sample (KM14-KM20).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Unassigned	Other	Other	Other	Other	Other	14.18	0.15	7.76	3.56	8.72	3.74
Archaea	Crenarchaeota	MBGA				0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Crenarchaeota	MBGA	NRP-J			0.00	0.00	0.00	0.01	0.23	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.01	0.00	0.00	0.01	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.01	0.00	0.00	0.02	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.31	0.00	1.99	0.08	0.06	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	0.49	0.00	5.75	0.54	4.98	0.08
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		0.20	0.00	0.02	0.02	3.80	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.00	0.00	0.01	0.00	0.00	0.00
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.01	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.00	0.00	0.00	0.00	0.07
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.02	0.00	0.00	0.00	0.17
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.01	0.00	0.00	0.00	0.01	0.00
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			0.16	0.00	0.06	0.01	0.02	0.00
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.31	0.00	0.10	0.02	0.07	0.00
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			0.72	0.00	0.46	0.21	0.54	0.11
Bacteria						0.00	0.00	0.00	0.00	0.00	0.09
Bacteria	AC1					0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	AC1	HDBW-WB69				0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Acidobacteria					0.09	0.00	0.02	0.03	0.36	0.01
Bacteria	Acidobacteria	Acidobacteria-5				0.25	0.00	0.01	0.04	0.29	0.00
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.06	0.00	0.00	0.01	0.06	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			1.49	0.01	0.13	0.26	8.61	0.01
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.12	0.03	0.09	0.14	0.50	0.01
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.03	0.02	0.04	0.05	0.05	0.00
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		0.03	0.00	0.01	0.00	0.34	0.00
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.00	0.00	0.00	0.00	0.07	0.00
Bacteria	Acidobacteria	BPC102				0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	BPC102	MVS-40			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.23	0.00	0.00	0.00	0.00	0.00

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Acidobacteria	DA052	Ellin6513			0.30	0.00	0.02	0.00	0.21	0.00
Bacteria	Acidobacteria	EC1113				0.15	0.00	0.00	0.00	0.06	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.12	0.01	0.07	0.05	1.59	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.00	0.28	0.00	2.12	0.04	0.13
Bacteria	Acidobacteria	RB25				0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.05	0.00	0.00	0.00	0.13	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.08	0.00	0.00	0.00	0.16
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.00	0.00	0.00	0.00	0.04	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.00	0.00	0.00	0.01	0.03	0.07
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	1.60	0.01	0.80	0.00	0.04
Bacteria	Acidobacteria	TM1				1.04	0.00	0.00	0.00	0.05	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.00	0.00	0.00	0.01	0.01	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.00	0.00	0.07	0.06	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.02	0.00	0.00	0.01	0.09	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.01	0.01	0.40	0.01	0.11	0.00
Bacteria	Acidobacteria	iii1-8	32-20			0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.01	0.00	0.02	0.01	0.11	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.00	0.08	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.00	0.02	0.00	0.00	0.01
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.00	0.00	0.00	0.16	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.01	0.08	0.00	0.00	0.00	0.09
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.00	0.00	0.01	0.04	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.02	0.00	0.03	0.01	0.04	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.06	0.07	0.02	0.15	0.39	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.03	0.03	0.03	0.04	0.10	0.07
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.00	0.00	0.00	0.15	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.00	0.00	0.00	0.04	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.01	0.07	0.01	0.66	0.02	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.01	0.01	0.04	0.02	0.12	0.04
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.00	0.00	0.00	0.00	0.50
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.01	0.00	0.00	0.03	0.00	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.00	0.00	0.00	0.19
Bacteria	Actinobacteria	Thermoleophilia				0.00	6.47	0.00	0.00	0.00	1.42
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.00	0.00	0.00	0.00	0.00	0.00

Table A3 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 14	KM 15	KM 16	KM 17	KM 19	KM 20
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		0.03	0.01	0.08	0.02	0.08	0.00
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.01	0.11	0.04	0.02	0.10	0.00
Bacteria	AncK6					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Armatimonadetes	0319-6E2				0.02	0.00	0.08	0.00	0.01	0.00
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	BHI80-139					0.02	0.00	0.00	0.01	0.02	0.02
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.35	1.86	0.01	0.01	0.00	1.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.11	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.19	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.02	0.01	0.00	0.00	0.00	0.06
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.02	0.07	0.00	0.01	0.54	0.02
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.01	0.01	0.04	0.74	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.01	0.00	0.00	0.14	0.06	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.00	0.51	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.62	0.18	0.01	0.32	0.06	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.96	0.01	0.03	2.70	0.23	0.12
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	1.82	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			1.27	0.11	0.03	1.57	1.68	0.43
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.07	0.02	0.04	0.09	0.07	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.12	0.07	0.10	2.97	0.38	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.12	0.19	0.06	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.10	0.07	0.01	1.49	0.35	0.15
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.08	0.04	0.02	0.01	0.00	0.14
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.00	0.00	0.08	0.00	0.00	0.00
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.00	0.00	0.00	0.00	0.86
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			2.37	0.00	0.20	0.00	2.06	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.01	0.00	0.00	0.00	0.32	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.07	0.00	0.20	0.00	0.32	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.02	0.00	0.06	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.94	0.01	10.69	0.00	0.71	0.04
Bacteria	Chlorobi	BSV26				0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Chlorobi	BSV26	A89			0.38	0.18	0.00	0.01	0.06	0.30
Bacteria	Chlorobi	BSV26	C20			0.06	0.00	0.00	0.01	1.37	0.00
Bacteria	Chlorobi	BSV26	PK329			0.00	0.20	0.00	0.05	0.00	0.46
Bacteria	Chlorobi	BSV26	VC38			0.01	0.17	0.00	0.00	0.34	0.04
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.00	0.10	0.00	0.00	0.00	0.12

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.00	0.83	0.00	0.00	0.00	0.15
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.00	0.02	0.00	0.00	0.00	0.29
Bacteria	Chlorobi	OPB56				0.04	0.07	0.00	0.03	0.39	0.00
Bacteria	Chlorobi	SJA-28				0.01	0.25	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Other	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31			0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.00	0.00	0.00	0.24	0.04	0.00
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.10	2.25	0.06	0.02	0.14	0.54
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.02	1.09	0.00	0.00	0.03	0.57
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.00	0.00	0.00	0.44	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.00	0.00	0.00	0.00	1.44	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.00	0.01	0.01	0.00	0.05	0.01
Bacteria	Chloroflexi	Ellin6529				0.02	0.01	0.01	0.01	0.38	0.01
Bacteria	Chloroflexi	Gitt-GS-136				0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.00	0.00	0.03	0.00
Bacteria	Chloroflexi	P2-11E				0.02	0.00	0.01	0.00	0.00	0.00
Bacteria	Chloroflexi	S085				0.05	0.01	0.01	0.01	0.09	0.00
Bacteria	Chloroflexi	SAR202				0.11	0.00	0.02	0.73	0.06	0.04
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.04	0.00	0.00	0.00	0.02	0.00
Bacteria	Chloroflexi	TK17				0.01	0.00	0.00	0.00	0.02	0.00
Bacteria	Chloroflexi	TK17	mle1-48			0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.10	0.82	0.04	0.04	0.00	0.90
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.30	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			0.34	0.00	2.87	0.07	0.02	0.00
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			0.00	0.00	0.00	0.00	0.04	0.00
Bacteria	Cyanobacteria	ML635J-21				0.00	0.63	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.02	0.00	0.01	0.00	0.00	0.00
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Elusimicrobia	Elusimicrobia				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			0.73	0.04	0.38	0.07	0.28	0.92
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.30	0.00	0.06	0.01	0.37	0.00
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.29	0.00	0.02	0.01	0.02	0.00
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.25	0.00	0.00	0.01	0.01	0.00
Bacteria	Elusimicrobia	Endomicrobia				0.49	0.00	0.04	0.01	0.42	0.00
Bacteria	FBP					0.09	0.00	0.00	0.00	0.08	0.00
Bacteria	FCPU426					0.06	0.00	0.00	0.00	0.10	0.00

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Fibrobacteres					0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.39	0.00	0.00	0.01	0.08	0.00
Bacteria	Firmicutes	Bacilli	Bacillales			0.01	0.01	0.10	0.00	0.02	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.08	0.05	0.02	0.00	0.03	0.05
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.01	0.08	0.29	0.00	0.04	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.05	0.01	0.03	0.22	0.03	0.11
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.00	0.11	0.00	0.00	0.00	0.01
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.27	0.00	0.00	0.05
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.34	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	7.61	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.23	0.00	0.01	0.22	0.02	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.12	0.00	0.02	0.02	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.12	0.26	0.04	6.64	0.03	0.07
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	1.53	0.00	0.00	0.00	0.02
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.14	0.47	0.02	0.01	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.08	0.00	0.33	0.23	0.01	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	1.26	0.00	0.61	2.08	0.01	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.45	0.01	0.43	0.45	0.01	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.04	0.00	0.09	0.41	0.01	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.12	0.00	0.00	1.76	0.01	0.04
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.04	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.00	0.00	0.06	0.00	0.00
Bacteria	Firmicutes	Clostridia	OPB54			1.36	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.34	0.00	0.00	0.00	0.00	0.10
Bacteria	GN02	3BR-5F				0.04	0.00	0.05	0.00	0.00	0.00
Bacteria	GN02	BB34				0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	GN02	GKS2-174				0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	GN07				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN04					0.01	0.01	0.00	0.00	0.00	0.00
Bacteria	GN04	GN15				0.03	0.30	0.00	0.01	0.00	0.12
Bacteria	GN04	MSB-5A5				0.04	0.00	0.00	0.01	0.00	0.00
Bacteria	Gemmatimonadetes	Gemm-1				0.32	0.00	0.10	0.02	0.54	0.00
Bacteria	Gemmatimonadetes	Gemm-2				0.02	0.00	0.01	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.00	0.00	0.00	0.01	0.12	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.02	0.00	0.00	0.01	0.66	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.04	0.00	0.00	0.01	0.56	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.32	0.00	0.01	0.03	0.00	0.00

Table A3 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 14	KM 15	KM 16	KM 17	KM 19	KM 20
Bacteria	MVS-104					0.00	0.12	0.00	0.00	0.00	0.11
Bacteria	NC10	24-Dec	JH-WHS47			0.06	0.00	0.02	0.05	0.13	0.00
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	0.05	0.00	0.02	0.00	0.10	0.00
Bacteria	NC10	wb1-A12				0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	NKB19					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.04	0.00	0.00	0.04	0.18	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		0.55	0.00	0.11	0.22	0.92	0.24
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.05	0.00	0.25	0.55	0.07	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.01	0.11	0.00	0.00	0.07	0.12
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.05	0.00	0.01	0.02	0.06	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	0.77	0.00	0.06	0.13	5.08	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.23	1.64	0.30	1.47	1.01	0.17
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		0.25	0.00	0.00	0.05	0.03	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.16	0.14	0.01	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.00	0.04	0.01	0.00	0.08	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.01	15.36	0.00	0.01	0.00	0.61
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.02	1.07	0.00	0.00	0.00	0.68
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OC31					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OD1					0.20	0.00	0.06	0.01	0.19	0.88
Bacteria	OD1	ABY1				0.38	0.28	0.25	0.02	0.06	0.02
Bacteria	OD1	Mb-NB09				0.05	0.00	0.04	0.00	0.00	0.00
Bacteria	OD1	SM2F11				0.10	0.00	0.02	0.00	0.13	0.32
Bacteria	OD1	ZB2				0.69	0.00	0.25	0.02	0.27	0.03
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.00	0.00	0.00	0.00	0.07	0.00
Bacteria	OP11	OP11-4				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OP3					0.00	0.03	0.19	0.07	0.02	0.26
Bacteria	OP3	BD4-9				0.06	0.00	0.81	0.05	1.02	0.94
Bacteria	OP3	PBS-25				4.55	0.00	1.46	0.38	0.95	0.26
Bacteria	OP3	koll11				9.39	0.00	4.12	1.17	2.02	0.01
Bacteria	OP3	koll11	GIF10			0.14	0.06	0.72	0.06	3.42	4.58
Bacteria	OP3	koll11	GIF10	kpj58rc		0.14	0.00	0.05	0.01	0.09	0.00
Bacteria	PAUC34f					0.52	0.01	0.02	0.04	0.58	5.57
Bacteria	Planctomycetes					0.02	0.00	0.09	0.00	0.11	0.15
Bacteria	Planctomycetes	BD7-11				0.20	0.00	0.00	0.02	0.02	0.00
Bacteria	Planctomycetes	C6	MVS-107			0.15	0.00	0.01	0.46	0.19	0.00
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.32	0.00
Bacteria	Planctomycetes	OM190				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190	CL500-15			0.01	0.00	0.03	0.01	0.00	0.23
Bacteria	Planctomycetes	OM190	agg27			0.01	0.00	0.22	0.07	0.05	0.00

Table A3 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 14	KM 15	KM 16	KM 17	KM 19	KM 20
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.04	1.25	0.11	0.03	0.00	0.54
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.00	0.00	0.00	0.00	0.16
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.00	0.02	0.32	0.00	0.00	0.32
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Pla4				0.03	0.00	0.00	0.01	0.03	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.04	0.03	0.01	0.25	0.18	0.09
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.00	0.00	0.00	0.01	0.01	0.43
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.03	0.00	0.00	0.05	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.00	0.00	0.00	0.04	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.01	0.02	0.01	0.01	0.02	0.00
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.03	0.00	6.89	0.05	0.22	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.12	0.00	0.03	0.01	0.04	0.39
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.25	4.22	0.35	0.08	0.10	0.03
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.00	0.00	0.00	0.03	0.00	0.04
Bacteria	Proteobacteria					0.08	0.01	0.28	0.15	0.32	0.64
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.13	0.00	0.07	0.07	0.29	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.04	0.00	0.29	0.07	0.01	0.19
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.00	0.01	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.04	0.25	0.03	0.11	0.04	0.07
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.06	0.01	0.00	0.02	0.03	0.15
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.01	0.00	0.00	0.00	0.24	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.22	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.06	0.23	0.31	0.17	0.24	0.20
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.01	0.11	0.00	0.01	0.05	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.00	0.17	0.00	0.08	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.01	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.04	0.00	0.02	0.03	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.11	0.07	0.02	0.14	0.02	0.07
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.48	0.36	0.34	0.03	0.20	0.16
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.00	0.00	0.00	0.01	0.29	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.21	0.46	0.12	0.04	0.50	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.00	0.01	0.00	0.01	0.05	0.32
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.00	0.04	0.01	0.00	0.00	0.23
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.06	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.00	0.04	0.00	0.01	0.04	0.00

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.00	0.01	0.00	0.10	0.01	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.01	0.00	0.00	0.02	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.01	0.00	0.00	0.22	0.03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.05	0.00	0.00	0.67	0.11	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.03	0.02	0.02	0.04	0.04	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.01	0.14	0.01	3.33	0.19	0.17
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		1.20	0.34	2.45	0.57	1.29	0.36
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.01	0.00	0.01	11.61	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.12	0.00	0.00	0.51	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	0.02	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			1.11	0.03	5.02	0.05	0.10	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.12	0.00	0.01	0.01	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.03	0.99	0.01	0.00	0.00	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.46
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.02	0.01	0.02	0.00	0.01	0.13
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.02	0.15	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.02	0.06	0.00	0.01	0.01	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.01	0.12	0.00	0.01	0.11	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.01	0.02	0.01	0.00	0.09	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.00	0.03	0.00	0.39	0.16	0.18
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.12	0.04	0.05	0.04	0.08	0.13
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.01	0.08	0.00	0.07	0.02	0.14
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.33	0.09	0.00	0.02	0.40	0.12
Bacteria	Proteobacteria	Betaproteobacteria				1.52	0.52	0.17	0.10	1.91	0.55
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.14	0.18	0.04	1.04	0.18	0.53
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		1.05	0.66	0.08	13.25	0.62	2.30
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.00	0.00	0.00	0.09	0.01	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.06	0.01	0.00	0.33	0.03	0.09
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.08	0.11	0.00	0.04	0.28	0.33
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.01	0.00	0.00	0.11	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.00	0.00	0.01	0.49	0.05	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.54	0.00	0.01	0.05	0.13	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.76	0.41	0.04	1.19	0.33	0.07
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.08	0.14	0.01	1.28	0.01	0.00

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.01	0.00	0.00	0.58
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.01	0.00	0.00	0.00	0.01	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.08
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	0.03	4.66	0.02	0.02	0.07	4.06
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.07	0.00	0.00	0.07	0.17
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.30	0.00	0.02	0.02	0.06	0.00
Bacteria	Proteobacteria	Betaproteobacteria	MND1			5.50	0.10	0.03	0.23	1.33	0.14
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.24	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.66	0.11	0.00	0.01	0.02	0.35
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.19	1.12	0.22	0.06	1.22	0.29
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.00	0.14	0.02	0.00	0.05	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.03	0.01	0.00	0.01	0.01	0.07
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.00	0.12	0.00	0.08	0.16	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.08	0.00	0.00	0.00	0.01	0.04
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	1.70	0.61	0.02	1.05	0.04	2.77
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		1.38	5.66	0.01	0.31	0.50	1.26
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.24	0.00	0.01	3.30	0.20	0.05
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.10	1.59	0.01	0.02	0.00	0.14
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.44	0.06	0.00	0.21	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.04	0.02	0.00	0.01	0.01	0.03
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.02	0.16	0.00	0.03	0.11	0.16
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			0.04	0.83	0.01	0.00	0.00	4.00
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.00	0.02	0.00	0.00	0.01	2.37
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria				1.17	1.28	0.17	0.08	0.13	0.15
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.00	0.01	0.00	0.00	0.00	0.07
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.26	0.00	0.03	0.21	0.03	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.07	0.04	0.01	0.68	0.06	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.56	0.25	0.38	0.02	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.02	0.22	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.00	0.09	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.72	1.90	0.00	0.02	0.00	15.95
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.02	0.01	0.00	0.00	0.00	0.09
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.04	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.19	0.21	0.00	0.00	0.01	1.76
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		0.13	0.00	0.11	0.06	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.15	0.00	0.01	0.02	0.06	0.00

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.01	0.70	0.00	0.00	0.00	0.36
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.39	0.00	0.01	0.02	0.26	0.07
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.88	0.10	0.10	0.38	1.17	11.24
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.19	0.00	0.39	0.02	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.02	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.16	0.01	0.07	0.02	0.06	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.04	0.00	0.00	0.00	0.00	0.53
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.00	0.00	10.09	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.00	0.00	0.00	0.16	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.18	0.00	0.04	0.01	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.26	0.00	0.00	0.01	0.55	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.04	0.00	0.00	0.00	0.65	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.00	0.00	0.00	0.00	1.26	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.11	0.04	0.01	0.01	0.17	0.27
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.04	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.00	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		0.63	0.73	0.49	0.27	1.14	0.24
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.01	0.03	0.00	0.00	0.00	0.36
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		0.04	0.00	0.00	0.08	0.08	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.08	0.00	0.00	0.00	0.00	1.64
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.20	0.05	0.00	0.13	0.00	0.25
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.01	0.72	0.00
Bacteria	Proteobacteria	Gammaproteobacteria				0.00	0.36	0.00	0.22	0.00	2.06
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.14	0.00	0.01	0.12	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.02	0.00	0.01	0.84	0.29	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.49	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.47	0.13	0.01	1.00	0.02	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.08	0.00	0.06	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			3.30	0.00	0.00	0.07	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.00	0.00	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.28	1.04	0.04	0.12	0.02	0.06

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.01	13.18	0.00	0.00	0.00	0.16
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.88	0.00	0.40	0.40	1.31	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		2.09	0.00	1.17	0.04	0.86	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	1.68	0.00	1.08	0.02	0.13	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.10	0.00	0.21	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.81	0.04	0.21	0.01	0.58	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.62	0.01	1.80	0.00	0.17	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.15	0.00	0.18	0.02	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.00	3.10	0.06	0.01	0.00	2.91
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.00	0.00	0.00	0.00	1.10
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.00	0.24	0.00	5.33	0.53	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	0.02	0.02	0.76	0.09	0.15	1.14
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.02	0.00	0.00	0.05	0.10	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	1.13	0.67	0.04	3.40	1.39	0.16
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.24	0.00	1.94	0.02	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.05	0.01	0.02	0.02	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.01	0.00	0.00	0.34	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.01	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.68	0.02	0.01	0.00	0.36	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.35	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.00	0.11	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.00	0.01	0.01	0.00	0.05	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.00	0.00	0.17	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	SBR1093					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	SR1					0.05	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.18	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.01	0.00	0.00	0.01	0.00	0.09
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4	Other	Other	Other	0.23	0.00	0.12	0.00	0.01	0.02
Bacteria	TM6	SJA-4				0.10	0.00	0.17	0.01	0.00	0.00
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.07	0.00	0.01	0.00	0.01	0.00
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		1.04	0.12	0.24	0.16	0.40	0.93

Table A3 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 14**	**KM 15**	**KM 16**	**KM 17**	**KM 19**	**KM 20**
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	1.07	0.05	0.03	0.15	2.21	1.14
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.07	0.04	0.00
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.00	0.10	0.04	0.23	0.01	0.26
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.10	0.00	0.07	0.03	0.05	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.02	0.00	0.00	0.00	0.04	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.44	0.18	0.34	0.17	5.15	0.04
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.03	0.00	0.00	0.00	0.04	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.10	0.00	0.03	0.57	0.68	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.05	0.10	16.34	0.22	0.03	0.17
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.00	0.00	0.01	0.00	0.03	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.04	0.09	0.00	0.05	0.39	0.07
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.00	0.00	0.09	0.01	0.15	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.43	0.00	0.04
Bacteria	WS3	PRR-12				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	WS3	PRR-12	Sediment-1			0.01	0.00	0.00	0.00	0.03	0.00
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.10	0.00	0.00	0.03	0.09	0.01

Table A4 Taxonomic QIIME results at the genus level by sample (KM21-KM26).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Unassigned	Other	Other	Other	Other	Other	26.17	18.37	15.57	25.31	9.51	13.99
Archaea	Crenarchaeota	MBGA				0.00	0.01	0.00	0.03	0.01	0.00
Archaea	Crenarchaeota	MBGA	NRP-J			0.02	0.00	0.00	0.40	0.46	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.10	0.00	0.00	0.18	0.02	0.02
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.71	0.19	0.00	0.28	0.10	0.10
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	0.50	1.29	0.00	1.20	0.12	0.36
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		1.04	0.04	0.00	4.27	7.42	0.02
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.04	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.01	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.00	3.03	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.01	0.37	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.08	0.12	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2			0.00	0.00	0.00	0.02	0.01	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.11	0.00	0.00	0.08	0.02	0.01
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			0.01	0.01	0.00	0.03	0.00	0.07
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.13	0.28	0.00	0.67	0.16	0.13
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			4.66	2.70	1.17	1.88	1.49	0.75
Bacteria						0.00	0.03	0.00	0.00	0.00	0.00
Bacteria	AC1					0.09	0.00	0.00	0.00	0.11	0.16
Bacteria	AC1	HDBW-WB69				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria					0.23	2.41	0.00	0.20	0.25	0.15
Bacteria	Acidobacteria	Acidobacteria-5				0.34	0.46	0.00	0.83	1.45	0.03
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.06	0.11	0.00	0.02	0.15	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			2.32	2.25	0.00	5.00	2.15	0.32
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.00	0.11	0.00	0.02	0.07	0.01
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.01	0.03	0.00	0.06	0.00	0.00
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		0.04	0.11	0.00	0.67	1.83	0.01
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.00	0.00	0.00	0.03	0.00	0.00
Bacteria	Acidobacteria	BPC102				0.01	0.05	0.00	0.04	0.01	0.00
Bacteria	Acidobacteria	BPC102	MVS-40			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.02	0.05	0.00	0.10	0.00	0.00

Table A4 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 21	KM 22	KM 23	KM 24	KM 25	KM 26
Bacteria	Acidobacteria	DA052	Ellin6513			0.31	0.24	0.00	1.06	0.27	0.04
Bacteria	Acidobacteria	EC1113				0.18	1.25	0.00	0.46	0.65	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.09	0.31	0.00	0.73	0.87	0.27
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.01	0.00	0.16	0.00	0.25	0.00
Bacteria	Acidobacteria	RB25				0.01	0.05	0.00	0.16	0.03	0.00
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.01	0.11	0.00	0.26	0.33	0.04
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.00	0.07	0.00	0.07	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.04	0.00	0.00	0.06	0.01	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.00	0.00	0.07	0.01	0.00	0.00
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	TM1				0.04	0.06	0.00	0.69	0.43	0.08
Bacteria	Acidobacteria	[Chloracidobacteria]				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.01	0.00	0.00	0.00	0.05	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.01	0.03	0.00	0.00	0.19	0.02
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.00	0.03	0.00	0.58	0.06	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.02	0.01	0.04	0.01	0.02	0.00
Bacteria	Acidobacteria	iii1-8	32-20			0.01	0.00	0.00	0.02	0.01	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.06	0.02	0.00	0.01	0.07	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.00	0.00	0.15	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.01	0.21	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.01	0.00	0.00	0.08	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.00	0.00	0.00	0.00	0.03	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.01	0.01	0.00	0.00	0.01	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.04	0.00	0.27	0.00	0.00	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.00	0.02	0.00	0.00	0.31	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.00	0.00	0.00	0.00	0.01	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.00	0.00	0.00	0.00	0.01	0.10
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.00	0.01	0.00	0.02	0.02	0.04
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.00	0.00	0.03	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.02	3.16	0.00	0.00	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.84	0.00	0.00	0.25	0.34	0.02
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia				0.00	0.00	7.36	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.02	0.00	0.00	0.00	0.00	0.00

Table A4 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 21	KM 22	KM 23	KM 24	KM 25	KM 26
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		0.40	0.06	0.00	0.05	0.02	0.01
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.04	0.06	0.38	0.01	0.04	0.01
Bacteria	AncK6					0.00	0.01	0.00	0.02	0.15	0.00
Bacteria	Armatimonadetes	0319-6E2				0.00	0.00	0.09	0.01	0.00	0.00
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.01	0.00	0.00	0.08	0.00	0.00
Bacteria	BHI80-139					0.00	0.01	0.00	0.00	0.02	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.15	0.12	0.61	0.02	0.04	0.14
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.00	0.00	0.86	0.01	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.05	0.09	0.00	0.40	0.01	0.01
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.00	0.00	0.00	0.00	0.03	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.00	0.01	0.00	0.02	0.02	0.10
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.00	0.00	0.03	0.08	0.60	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			0.13	0.20	0.00	0.34	0.73	0.31
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.00	0.00	0.00	0.03	0.03	0.03
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.04	0.00	0.00	0.00	0.04	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.06	0.04	0.07	0.27	0.14	0.02
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.00	0.00	0.06	0.00	0.42	0.13
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.04	0.04	0.00	0.00	0.00	0.00
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			0.09	0.05	0.00	0.55	0.11	0.04
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.01	0.01	0.00	0.00	0.02	0.01
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.00	0.00	0.00	0.01	0.10	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.14	0.09	0.00	0.42	0.11	0.01
Bacteria	Chlorobi	BSV26				0.10	0.01	0.00	0.00	0.03	0.00
Bacteria	Chlorobi	BSV26	A89			0.17	0.07	0.09	0.57	0.13	0.21
Bacteria	Chlorobi	BSV26	C20			0.11	0.20	0.00	0.44	0.23	0.12
Bacteria	Chlorobi	BSV26	PK329			0.04	0.01	0.49	0.00	0.00	0.00
Bacteria	Chlorobi	BSV26	VC38			0.00	0.13	0.00	0.10	0.35	0.02
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.00	0.00	1.25	0.00	0.00	0.00

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.00	0.02	1.41	0.00	0.01	0.00
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.00	0.00	0.54	0.00	0.01	0.00
Bacteria	Chlorobi	OPB56				0.00	0.00	0.00	0.00	0.34	0.00
Bacteria	Chlorobi	SJA-28				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Other	Other	Other	Other	0.05	0.01	0.00	0.03	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31			0.00	0.18	0.26	0.00	0.01	0.03
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.03	0.02	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.12	0.44	0.00	0.29	0.40	0.18
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.43	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.00	0.17	1.92	0.04	0.25	0.04
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.00	0.19	0.00	0.00	0.01	0.03
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.00	0.27	0.00	0.00	0.00	0.02
Bacteria	Chloroflexi	Ellin6529				0.11	0.09	0.37	0.08	0.20	0.00
Bacteria	Chloroflexi	Gitt-GS-136				0.02	0.01	0.00	0.01	0.01	0.00
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.00	0.00	0.08	0.00
Bacteria	Chloroflexi	P2-11E				0.03	0.01	0.00	0.03	0.05	0.00
Bacteria	Chloroflexi	S085				0.07	0.11	0.00	0.10	0.06	0.01
Bacteria	Chloroflexi	SAR202				7.33	0.80	0.00	2.20	0.18	0.10
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.10	0.17	0.00	0.45	0.21	0.00
Bacteria	Chloroflexi	TK17				0.11	0.06	0.00	0.33	0.02	0.00
Bacteria	Chloroflexi	TK17	mle1-48			0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.07	0.00	0.38	0.00	0.37	0.02
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			2.24	0.02	0.00	0.90	0.13	0.11
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	ML635J-21				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.00	0.13	0.09	0.00	0.10	0.00
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia				0.02	0.00	0.00	0.02	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			0.12	0.25	0.25	0.25	0.36	0.30
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.29	0.02	0.00	0.20	0.11	0.02
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.16	0.00	0.00	0.25	0.07	0.03
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.03	0.00	0.00	0.00	0.03	0.04
Bacteria	Elusimicrobia	Endomicrobia				0.25	0.09	0.00	0.30	0.08	0.18
Bacteria	FBP					0.01	0.00	0.00	0.14	0.03	0.00
Bacteria	FCPU426					0.00	0.01	0.00	0.01	0.05	0.00

Table A4 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 21	KM 22	KM 23	KM 24	KM 25	KM 26
Bacteria	Fibrobacteres					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.01	0.06	0.00	0.24	0.01	0.05
Bacteria	Firmicutes	Bacilli	Bacillales			0.00	0.00	0.15	0.02	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.00	0.01	0.00	0.10	0.02	0.02
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.00	0.00	0.00	0.02	0.02	0.02
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.00	0.00	0.21	0.04	0.02	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.00	0.01	0.00	0.00	0.05	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.00	0.00	0.00	0.00	0.76	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.00	0.02	0.25	0.00	4.63	0.03
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.00	0.00	0.00	0.00	0.02	0.02
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	0.00	0.02	0.00	0.22	0.18	0.04
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.00	0.01	0.00	0.06	0.72	0.11
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.00	0.01	0.00	0.00	0.24	0.01
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.00	0.02	0.00	0.01	1.61	0.05
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.00	0.01	0.00	0.00	0.38	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.00	0.00	0.00	0.09	0.00
Bacteria	Firmicutes	Clostridia	OPB54			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	3BR-5F				0.08	0.00	0.00	0.00	0.00	0.21
Bacteria	GN02	BB34				0.01	0.13	0.00	0.00	0.00	0.02
Bacteria	GN02	GKS2-174				0.00	0.00	0.00	0.02	0.01	0.00
Bacteria	GN02	GN07				0.16	0.00	0.00	0.00	0.00	0.04
Bacteria	GN04					0.01	0.00	1.08	0.00	0.00	0.00
Bacteria	GN04	GN15				0.08	0.04	0.73	0.02	0.00	0.01
Bacteria	GN04	MSB-5A5				0.05	0.01	0.00	0.09	0.02	0.01
Bacteria	Gemmatimonadetes	Gemm-1				0.61	0.12	0.04	0.29	0.78	0.04
Bacteria	Gemmatimonadetes	Gemm-2				0.05	0.41	0.00	0.05	0.03	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.00	0.00	0.00	0.00	0.34	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.01	0.05	0.00	0.13	0.26	0.03
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.01	0.05	0.00	0.06	0.19	0.02
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.17	0.13	0.00	0.05	0.00	0.01
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.00	0.02	0.00	0.00	0.00	0.13

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	MVS-104					0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	NC10	24-Dec	JH-WHS47			0.57	0.18	0.00	0.45	0.43	0.11
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	0.07	0.83	0.00	0.79	0.61	0.02
Bacteria	NC10	wb1-A12				0.16	0.00	0.00	0.09	0.00	0.03
Bacteria	NKB19					0.01	0.18	0.00	0.02	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.02	0.01	0.00	0.03	0.02	0.01
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		2.87	0.83	0.00	3.11	1.95	0.28
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.11	0.07	0.10	0.00	0.25	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.00	0.00	0.24	0.00	0.00	0.04
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.56	0.04	0.00	0.25	0.10	0.05
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	0.13	1.00	0.00	3.93	1.48	0.09
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.86	0.35	0.07	0.67	2.01	0.10
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		0.61	0.08	0.00	0.13	0.18	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.00	0.02	0.13	0.00	0.01	0.68
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.00	1.08	0.93	0.00	0.02	0.04
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.01	0.13	1.66	0.00	0.00	0.06
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.00	0.04	1.69	0.00	0.00	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.88	0.00	0.00	0.00
Bacteria	OC31					0.00	0.01	0.00	0.01	0.00	0.01
Bacteria	OD1					0.07	0.11	12.48	0.14	0.09	0.07
Bacteria	OD1	ABY1				0.09	0.13	0.05	0.12	0.14	0.35
Bacteria	OD1	Mb-NB09				0.03	0.01	0.00	0.04	0.03	0.02
Bacteria	OD1	SM2F11				0.00	0.01	0.18	0.00	0.01	0.00
Bacteria	OD1	ZB2				0.13	0.98	0.26	0.17	0.09	0.35
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.00	0.00	0.00	0.00	0.04	0.00
Bacteria	OP11	OP11-4				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OP3					0.07	1.27	0.01	0.00	0.03	0.01
Bacteria	OP3	BD4-9				0.10	5.20	1.02	0.00	0.08	0.78
Bacteria	OP3	PBS-25				6.58	2.35	0.00	2.34	0.73	1.26
Bacteria	OP3	koll11				13.78	2.61	0.00	5.22	4.27	2.68
Bacteria	OP3	koll11	GIF10			0.09	5.00	5.27	0.00	0.42	0.31
Bacteria	OP3	koll11	GIF10	kpj58rc		0.41	0.04	0.01	0.13	0.12	0.06
Bacteria	PAUC34f					0.10	0.23	0.00	0.60	0.88	0.13
Bacteria	Planctomycetes					0.01	0.00	0.00	0.04	0.00	0.00
Bacteria	Planctomycetes	BD7-11				0.17	0.09	0.00	0.17	0.11	0.02
Bacteria	Planctomycetes	C6	MVS-107			0.02	0.21	0.00	0.23	0.43	0.04
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190				0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190	CL500-15			0.00	0.04	0.01	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190	agg27			0.02	0.12	0.00	0.04	0.01	0.02

Table A4 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 21	KM 22	KM 23	KM 24	KM 25	KM 26
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.18	0.09	0.00	0.19	0.41	0.05
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.00	0.01	0.00	0.01	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Pla4				0.62	0.00	0.00	0.08	0.04	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.04	0.01	0.00	0.05	0.12	0.02
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.20	0.00	0.00	0.15	0.01	0.01
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.00	0.00	0.00	0.15	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.00	0.01	0.00	0.00	0.37	0.00
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.02	0.03	0.00	0.01	0.11	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.00	0.46	0.00	0.00	0.02	0.38
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.06	0.62	0.00	0.00	0.04	1.36
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.00	0.01	0.02	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.01	0.05	0.00	0.00	0.03	0.01
Bacteria	Proteobacteria					0.19	0.28	0.28	0.19	0.43	0.23
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.01	0.00	0.00	0.04	0.06	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.03	0.12	0.00	0.04	0.46	1.65
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.00	0.00	0.00	0.15	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.00	0.00	0.33	0.02	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.01	0.00	0.00	0.05	0.07	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.05	0.06	0.33	0.10	0.39	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.00	0.01	0.05	0.01	0.08	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.01	0.06	0.00	0.02	0.01	0.93
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.01	0.00	0.00	0.01	0.07	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.09	0.08	0.85	0.06	0.08	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.03	0.04	0.11	0.02	0.10	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.02	0.14	0.00	0.10	0.17	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.00	0.05	0.00	0.04	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.06	0.16	1.31	0.07	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.00	0.00	4.72	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.02	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.00	0.01	0.00	0.01	0.04	0.01

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.00	0.00	0.00	0.00	0.01	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.00	0.01	0.00	0.00	0.02	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.00	0.02	0.04	0.00	0.05	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.00	0.00	0.00	0.00	0.27	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		0.98	0.84	0.24	1.24	1.47	4.19
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.01	0.01	0.00	0.03	0.04	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.00	0.04	0.00	0.03	0.17	3.95
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.00	0.00	0.00	3.81
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	0.35	0.45	0.00	0.89	0.15	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			0.14	0.07	0.00	0.19	0.08	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.00	0.01	0.12	0.02	0.07	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.05	0.01	0.00	0.01	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.00	0.00	0.18	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.00	0.01	0.21	0.00	0.02	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.02	0.09	0.00	0.03	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.10	0.12	0.12	0.13	0.06	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.02	0.08	0.05	0.17	0.08	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.04	7.64	0.00	0.02	0.10	0.10
Bacteria	Proteobacteria	Betaproteobacteria				1.19	7.61	0.01	2.55	3.37	2.29
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.04	0.07	0.05	0.06	0.58	0.23
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		0.11	0.08	0.61	0.09	4.81	0.61
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.00	0.00	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.00	0.02	0.02	0.02	0.04	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.00	0.00	0.00	0.00	0.01	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.01	0.00	0.00	0.01	0.01	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.09	0.07	0.00	0.15	1.63	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.12	0.18	0.02	0.15	3.13	0.18
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.00	0.02	0.00	0.02	0.26	0.00

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.00	0.22	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	0.00	7.75	2.14	0.10	0.01	1.45
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.04	0.19	0.00	0.07	0.00
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.17	0.30	0.00	0.68	0.08	0.26
Bacteria	Proteobacteria	Betaproteobacteria	MND1			1.11	1.45	0.01	1.55	1.32	0.22
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.00	0.02	0.00	0.00	0.00	0.29
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.00	0.02	0.00	0.00	0.02	1.74
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.33	0.05	0.14	0.09	0.41	0.18
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.01	0.00	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			0.11	0.00	0.00	0.13	0.01	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.00	0.07	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.00	0.01	0.00	0.00	0.05	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.01	0.00	0.00	0.02	0.00	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	0.00	0.03	0.08	0.20	0.16	1.09
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		0.10	0.14	1.08	0.34	0.27	11.17
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.00	0.03	0.00	0.00	0.83	0.08
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.00	0.00	0.00	0.00	0.18	0.32
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.00	0.00	0.00	0.00	0.00	0.38
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.00	0.08	0.00	0.00	0.09	0.46
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.00	0.00	0.06	0.02	0.02	0.24
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			0.00	0.85	0.16	0.02	0.01	22.70
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.00	0.00	0.22	0.00	0.03	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.05	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria				2.28	0.66	0.78	0.90	0.55	0.75
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.00	0.02	0.15	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.06	0.04	0.00	0.16	0.00	0.32
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.00	0.00	0.00	0.03	0.39	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.02	0.05	0.00	0.00	0.00	0.89
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.00	0.01	0.00	0.00	0.00	0.05
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.00	0.02	11.44	0.00	0.00	1.63
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.00	0.00	0.35	0.00	0.11	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.00	0.00	0.00	0.00	0.00	0.13
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.01	0.05	0.19	0.00	0.01	0.29
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		0.00	0.70	0.00	0.00	0.00	0.62
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.05	0.01	0.00	0.00	0.00	0.01

Table A4 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 21	KM 22	KM 23	KM 24	KM 25	KM 26
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.00	0.03	0.55	0.00	0.00	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.20	0.03	0.00	0.25	0.08	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.63	0.09	0.00	1.12	0.30	0.31
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.23	0.05	0.00	0.09	0.00	0.54
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.03	0.02	0.00	0.07	0.06	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.00	0.00	0.03	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.00	0.01	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.00	0.01	0.00	0.04	0.05	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.05	0.00	0.00	0.07	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.36	0.09	0.04	0.07	0.02	0.17
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.16	0.01	0.00	0.02	0.08	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.10	0.18	0.00	0.15	0.01	0.04
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.00	0.03	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.32	0.24	1.09	0.00	0.00	0.09
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.00	0.15	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		4.23	3.47	0.00	2.53	1.81	0.23
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	0.00	0.00	1.66
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.00	0.95	0.00	0.00	0.02	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		1.12	0.72	0.00	0.56	0.57	0.05
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.04	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria				0.00	0.00	0.16	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.00	0.00	0.00	0.01	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.00	0.02	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.10	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.01	0.00	0.00	0.07	0.05	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.01	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.00	0.00	0.00	0.01	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			0.69	0.08	0.00	0.26	0.59	0.12
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.08	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.00	0.01	0.44	0.02	0.00	0.00

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.04	0.09	0.00	0.12	0.47	0.50
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		0.19	0.19	0.00	0.61	0.17	0.36
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	0.16	0.06	0.00	0.08	0.01	0.09
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.17	0.02	0.00	0.07	0.29	0.04
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.06	0.03	0.00	0.02	0.04	0.09
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.04	0.17	0.25	0.00	0.01	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.00	1.12	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.06	0.00	0.00	0.00	1.94	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.00	0.79	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	0.08	0.26	0.70	2.12	0.46	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.01	0.07	0.00	0.03	0.04	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.06	0.05	0.14	0.31	1.18	0.08
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.00	0.02	0.00	0.00	0.26	0.05
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.44	0.12	0.00	0.08	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.00	0.09	0.00	0.01	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00	0.03	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.00	0.01	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	SBR1093					0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	SR1					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.00	0.00	0.00	0.00	0.00	0.32
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.57
Bacteria	TM6	SJA-4	Other	Other	Other	0.00	0.00	0.00	0.06	0.00	0.00
Bacteria	TM6	SJA-4				0.01	0.00	0.00	0.04	0.00	0.00
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.05	0.01	0.00	0.06	0.03	0.02
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		0.02	0.10	0.00	0.20	0.14	0.13

Table A4 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 21**	**KM 22**	**KM 23**	**KM 24**	**KM 25**	**KM 26**
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.06	0.29	0.00	0.67	0.64	0.39
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.00	0.09	0.00
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.00	0.00	0.00	0.00	0.02	0.00
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.02	0.30	0.00	0.13	0.04	0.07
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.01	0.02	0.00	0.03	0.03	0.01
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.44	0.17	0.02	1.75	1.50	0.11
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.00	0.01	0.00	0.07	0.01	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.01	0.01	0.00	0.10	0.65	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.00	0.00	0.00	0.27	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.01	0.00	0.00	0.04	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.01	0.02	0.07	0.19	1.20	0.13
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	WS3	PRR-12				0.02	0.00	0.00	0.02	0.04	0.00
Bacteria	WS3	PRR-12	Sediment-1			0.15	0.01	0.00	0.07	0.28	0.05
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.12	0.08	0.00	0.97	0.08	0.03

Table A5 Taxonomic QIIME results at the genus level by sample (KM27-KM32).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Unassigned	Other	Other	Other	Other	Other	31.66	28.74	28.87	4.84	4.91	9.71
Archaea	Crenarchaeota	MBGA				0.00	0.02	0.01	0.00	0.00	0.00
Archaea	Crenarchaeota	MBGA	NRP-J			0.01	0.23	0.30	0.00	0.03	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.01	0.01	0.00	0.00	0.03	0.00
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.03	0.12	0.05	0.00	0.02	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.37	2.53	0.03	0.00	0.29	0.05
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	0.67	0.06	0.26	0.14	0.36	0.01
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		0.89	0.47	1.71	0.00	0.21	0.00
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.00	0.00	0.00	0.04	0.00	0.07
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.00	0.00	0.00	0.00	0.09
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.00	0.00	0.29	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.00	0.00	0.04	0.00	0.92
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.02
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.00	0.00	0.25	0.00	0.01
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.00	0.00	0.02	0.00	0.07
Archaea	Euryarchaeota	Thermoplasmata	E2			0.02	0.00	0.01	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.01	0.00	0.38
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.05	0.00	0.13	0.00	0.03	0.00
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			0.20	0.04	0.00	0.00	0.00	0.00
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.23	0.11	0.15	0.00	0.10	0.20
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			3.89	3.23	2.13	0.01	1.10	0.00
Bacteria						0.00	0.00	0.00	0.00	0.00	0.39
Bacteria	AC1					0.00	0.31	0.00	0.00	0.01	0.00
Bacteria	AC1	HDBW-WB69				0.01	0.21	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria					0.25	0.18	0.04	0.00	0.04	0.00
Bacteria	Acidobacteria	Acidobacteria-5				0.25	0.24	6.81	0.00	0.04	0.00
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.03	0.03	0.01	0.01	0.02	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			1.44	2.35	4.56	0.80	0.60	0.17
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.00	0.04	0.04	0.03	0.00	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.07	0.09	0.01	0.00	0.25	0.21
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		0.04	0.04	0.23	0.00	0.01	0.00
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Acidobacteria	BPC102				0.04	0.13	0.04	0.00	0.00	0.00
Bacteria	Acidobacteria	BPC102	MVS-40			0.01	0.03	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.04	0.14	0.00	0.00	0.01	0.00

Table A5 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 27	KM 28	KM 29	KM 30	KM 31	KM 32
Bacteria	Acidobacteria	DA052	Ellin6513			0.21	0.35	0.48	0.01	0.07	0.00
Bacteria	Acidobacteria	EC1113				0.03	0.23	1.53	0.01	0.10	0.00
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.08	0.06	0.01	0.01	0.02	0.02
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.01	0.00	0.00	0.01	1.75	0.79
Bacteria	Acidobacteria	RB25				0.00	0.00	0.02	0.00	0.13	0.00
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.02	0.04	0.49	0.00	0.02	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.01	0.00	0.06	0.00	0.01	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.00	0.00	0.00	0.01	0.01	0.00
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	TM1				0.02	0.79	0.04	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.02	0.00	0.03	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.02	0.01	0.00	0.01	0.11	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.03	0.06	0.08	0.00	0.00	0.00
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.06	0.00	0.00	0.00	0.04	0.08
Bacteria	Acidobacteria	iii1-8	32-20			0.01	0.11	0.02	0.00	0.03	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.01	0.00	0.00	0.01	0.01	0.01
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.00	0.00	0.01	0.01	0.03
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.00	0.00	0.00	0.00	0.04	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.01	0.00	0.01	0.01	0.08	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.01	0.00	0.00	0.01	0.11	0.04
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.03	0.01	0.00	0.02	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.01	0.00	0.00	0.03	0.22	0.02
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.05	0.13	0.00	0.02	0.58	0.03
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.00	0.00	0.00	0.00	0.04	0.11
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.00	0.00	0.01	0.06	0.00	0.38
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.77	7.70	1.02	0.00	0.38	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia				0.00	0.00	0.00	0.02	0.00	0.01
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.00	0.00	0.00	0.00	0.00	0.00

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		0.32	0.41	0.03	0.03	0.07	0.01
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.04	0.04	0.04	0.00	0.04	0.26
Bacteria	AncK6					0.00	0.00	0.04	0.00	0.00	0.00
Bacteria	Armatimonadetes	0319-6E2				0.01	0.00	0.00	0.00	0.04	0.22
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.03	0.00	0.00	0.00	0.00	0.00
Bacteria	BHI80-139					0.00	0.01	0.02	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.15	0.00	0.03	0.08	0.08	0.11
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.00	0.00	0.00	0.28	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.00	0.00	0.00	19.86	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.05	0.02	0.03	0.26	0.31	2.77
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.00	0.00	0.00	0.00	0.17	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.00	0.00	0.00	0.00	0.65	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.01	0.05	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.18	0.00	0.13	0.10	4.25	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.02	0.00	0.00	0.87	1.54	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			0.18	0.54	0.14	1.04	1.79	1.49
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.01	0.00	0.00	0.00	0.27	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.00	0.00	0.00	0.85	2.47	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.00	0.03	0.07	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.01	0.00	0.43	0.00	0.00	0.00
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.07	0.02	0.05	0.19	1.13	0.32
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.07	0.00	0.00	0.00	0.11	0.14
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.01	0.02	0.01	0.01	1.21	0.00
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			0.46	0.14	0.06	0.01	0.01	0.05
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.01	0.00	0.00	0.00	0.00	0.90
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.06	0.02	0.44	0.03	0.00	0.32
Bacteria	Chlorobi	BSV26				0.04	0.01	0.01	0.00	0.01	0.00
Bacteria	Chlorobi	BSV26	A89			0.15	0.17	0.51	0.00	0.22	0.03
Bacteria	Chlorobi	BSV26	C20			0.09	0.08	0.01	0.01	0.02	0.00
Bacteria	Chlorobi	BSV26	PK329			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlorobi	BSV26	VC38			0.03	0.08	0.02	0.12	0.00	0.07
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.00	0.00	0.00	0.21	0.00	0.19
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlorobi	OPB56				0.00	0.00	0.00	0.00	0.12	0.26
Bacteria	Chlorobi	SJA-28				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Chloroflexi	Other	Other	Other	Other	0.01	0.03	0.13	0.00	0.04	0.00
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.23
Bacteria	Chloroflexi	Anaerolineae	A31			0.00	0.04	0.01	0.00	0.00	0.45
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.01	0.00	0.00	0.20	0.21	0.00
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.13	0.29	0.15	0.02	0.03	0.00
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.00	0.00	0.00	0.05	0.07	0.81
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.00	0.02	0.00	0.03	0.00	0.00
Bacteria	Chloroflexi	Ellin6529				0.06	0.08	0.10	0.09	0.03	0.00
Bacteria	Chloroflexi	Gitt-GS-136				0.03	0.02	0.05	0.00	0.00	0.00
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Chloroflexi	P2-11E				0.06	0.10	0.06	0.00	0.01	0.00
Bacteria	Chloroflexi	S085				0.12	0.16	0.16	0.28	0.03	0.00
Bacteria	Chloroflexi	SAR202				0.74	4.02	0.64	0.00	5.82	0.00
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.05	0.06	0.44	0.00	0.01	0.00
Bacteria	Chloroflexi	TK17				0.04	0.10	0.14	0.00	0.06	0.00
Bacteria	Chloroflexi	TK17	mle1-48			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.07	0.01	0.23	0.14	0.25	12.68
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			2.29	0.09	1.24	0.00	0.03	0.00
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Cyanobacteria	ML635J-21				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.00	0.00	0.02	0.04	0.00	0.07
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.05	0.00	0.28
Bacteria	Elusimicrobia	Elusimicrobia				0.05	0.02	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			0.14	0.28	0.35	0.39	0.13	0.12
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.35	0.01	0.12	0.00	0.02	0.00
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.60	0.03	0.02	0.00	0.01	0.00
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.03	0.02	0.07	0.00	0.01	0.00
Bacteria	Elusimicrobia	Endomicrobia				0.33	0.23	0.17	0.00	0.03	0.00
Bacteria	FBP					0.05	0.04	0.03	0.00	0.00	0.00
Bacteria	FCPU426					0.00	0.01	0.05	0.00	0.00	0.00

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Fibrobacteres					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.02	0.00	0.02	0.00	0.01	0.00
Bacteria	Firmicutes	Bacilli	Bacillales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.01	0.00	0.00	0.00	0.03	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.53	0.11	0.02	0.01	0.02	0.04
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.06	0.00	0.07	0.04	0.02	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.01	0.00	0.01	0.00	0.07	0.02
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.00	0.00	0.01	0.15	0.30	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.00	0.00	0.06	0.01	0.21	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.01	0.00	0.01	1.10	2.65	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.01	0.00	0.05	0.00	0.60	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.00	0.00	0.00	0.01	0.38	0.01
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	0.01	0.00	0.00	0.01	0.07	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.02	0.00	0.01	0.01	0.86	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.00	0.00	0.00	0.04	0.41	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.01	0.00	0.01	0.38	0.45	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.00	0.00	0.00	0.00	0.10	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.00	0.00	0.00	0.23	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Firmicutes	Clostridia	OPB54			0.02	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.00	0.00	0.00	2.49	0.00	0.00
Bacteria	GN02	3BR-5F				0.22	0.03	0.00	0.00	0.01	0.00
Bacteria	GN02	BB34				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	GKS2-174				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	GN07				0.03	0.05	0.00	0.00	0.00	0.00
Bacteria	GN04					0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	GN04	GN15				0.08	0.02	0.04	0.07	0.06	0.19
Bacteria	GN04	MSB-5A5				0.08	0.14	0.04	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemm-1				0.19	0.72	0.12	0.12	0.07	0.39
Bacteria	Gemmatimonadetes	Gemm-2				0.03	0.10	0.02	0.00	0.04	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.01	0.01	0.01	0.00	0.01	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.05	0.00	0.00	0.01	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.02	0.03	0.04	0.00	0.08	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.03	0.13	0.00	0.00	0.00	0.00
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.00	0.00	0.00	0.01	0.00	0.00

Table A5 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 27	KM 28	KM 29	KM 30	KM 31	KM 32
Bacteria	MVS-104					0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	NC10	24-Dec	JH-WHS47			0.34	1.00	0.31	0.01	0.04	0.00
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	0.02	1.04	0.50	0.00	0.03	0.00
Bacteria	NC10	wb1-A12				0.06	0.01	0.00	0.00	0.07	0.00
Bacteria	NKB19					0.00	0.00	0.00	0.00	0.05	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.03	0.01	0.06	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		2.22	3.10	2.73	0.01	0.80	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.06	0.00	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.00	0.00	0.00	0.91	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.90	0.24	0.28	0.00	0.22	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	0.08	0.65	0.15	0.00	0.06	0.01
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.99	0.42	0.41	8.27	2.23	0.37
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		0.82	0.15	0.06	0.00	0.07	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.00	0.50	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.00	0.01	0.00	0.04	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.01	0.00	0.00	0.20	0.00	0.09
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.00	0.00	0.00	1.30	0.00	0.46
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OC31					0.00	0.00	0.00	0.05	0.00	0.00
Bacteria	OD1					0.16	0.28	0.05	0.11	0.01	0.77
Bacteria	OD1	ABY1				0.52	0.32	1.82	0.01	0.01	0.00
Bacteria	OD1	Mb-NB09				0.20	0.09	0.04	0.00	0.03	0.00
Bacteria	OD1	SM2F11				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	OD1	ZB2				0.36	0.56	0.30	0.02	0.11	0.00
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.00	0.00	0.14	0.00	0.00	0.00
Bacteria	OP11	OP11-4				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OP3					0.09	0.00	0.00	0.19	0.00	1.07
Bacteria	OP3	BD4-9				0.19	0.23	0.00	2.04	0.00	1.85
Bacteria	OP3	PBS-25				7.67	1.99	2.40	0.09	0.96	0.00
Bacteria	OP3	koll11				14.97	6.84	7.60	0.18	3.15	0.00
Bacteria	OP3	koll11	GIF10			0.05	0.41	0.00	0.53	0.00	6.37
Bacteria	OP3	koll11	GIF10	kpj58rc		0.21	0.19	0.02	0.00	0.08	0.00
Bacteria	PAUC34f					0.15	0.39	0.23	0.07	0.00	0.00
Bacteria	Planctomycetes					0.00	0.00	0.00	0.01	0.01	0.00
Bacteria	Planctomycetes	BD7-11				0.16	0.08	0.17	0.00	0.02	0.00
Bacteria	Planctomycetes	C6	MVS-107			0.03	0.05	0.05	0.05	0.19	0.00
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190				0.23	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190	CL500-15			0.02	0.05	0.00	0.05	0.07	0.00
Bacteria	Planctomycetes	OM190	agg27			0.00	0.02	0.00	0.00	0.14	0.05

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.14	0.09	0.01	0.31	0.05	0.00
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.00	0.00	0.14	0.00	2.53
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.02	0.00	0.00	0.04	0.03	0.00
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.00	0.00	0.23
Bacteria	Planctomycetes	Pla4				0.06	0.03	0.16	0.00	0.02	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.02	0.03	0.62	0.06	0.01	0.01
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.22	0.05	0.01	0.00	0.05	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.01	0.00	0.00	0.00	0.01	0.02
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.05	0.02	0.03	0.01	0.09	0.10
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.03	0.04	0.00	0.16	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.10	0.91	0.00	0.01	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.04	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria					0.02	0.17	0.00	0.12	0.03	0.21
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.00	0.00	0.05	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.01	0.01	0.08	0.16	0.01	0.53
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.01	0.00	0.00	0.00	0.04	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.00	0.00	0.04	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.02	0.01	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.02	0.02	0.00	0.00	0.07	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.01	0.00	0.00	0.00	0.08	0.28
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.01	0.00	0.01	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.06	0.02	0.06	0.53	0.41	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.01	0.01	0.00	0.01	0.20	0.33
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.01	0.00	0.00	0.00	0.11	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.00	0.00	0.00	0.04	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.00	0.00	0.01	0.01	0.08	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.00	0.00	0.02	0.10	0.20	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.03	0.03	0.03	0.08	0.04	0.68
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.01	0.02	0.02	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.02	0.08	0.35	0.02	0.18	0.33
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.04	0.01	0.03	0.00	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.00	0.01	0.00	0.15	0.00	1.65
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.00	0.45	0.00	0.13
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.00	0.00	0.01	0.01	0.08	0.01

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.01	0.00	0.00	0.00	0.12	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.00	0.01	0.00	0.00	0.04	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.00	0.01	0.00	0.00	0.23	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.02	0.03	0.00	0.00	0.08	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.02	0.00	0.02	0.04	0.25	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.01	0.00	0.03	0.00	0.16	0.07
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.08	0.00	0.01	0.36	0.82	0.37
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.00	0.06	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		0.25	0.48	0.16	0.29	1.18	0.14
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.02	0.00	0.00	0.44	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.01	0.00	0.00	0.06	5.98	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	0.05	0.01	0.33	0.00	0.04	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			0.15	0.03	0.16	0.00	0.99	0.14
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.00	0.00	0.06	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.01	0.00	0.00	0.01	0.01	0.73
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.01	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.01	0.01	0.00	0.00	0.03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.05	0.00	0.00	0.02	0.01	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.01	0.00	0.00	0.01	0.01	1.66
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.03	0.00	0.07	0.02	0.09	1.44
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.07	0.01	0.06	0.01	0.19	0.56
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.00	0.00	0.00	0.00	0.20	0.19
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.01	0.01	0.03	0.10	0.06	0.04
Bacteria	Proteobacteria	Betaproteobacteria				0.83	3.30	0.55	0.46	0.25	0.04
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.79	0.02	0.04	0.03	0.67	0.06
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		0.24	0.03	0.17	2.16	8.67	0.31
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.00	0.00	0.00	0.01	0.01	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.02	0.00	0.00	0.00	0.04	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.00	0.01	0.01	0.01	0.66	0.33
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.00	0.00	0.00	0.03	0.17	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.05	0.00	0.01	0.02	2.44	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.39	0.03	0.22	0.26	6.62	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.05	0.00	0.01	0.12	1.02	0.00

Table A5 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 27	KM 28	KM 29	KM 30	KM 31	KM 32
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.01	0.00	0.00	0.08	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	0.00	0.00	0.00	0.64	0.09	0.90
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.02	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.23	0.10	0.03	0.00	0.08	0.00
Bacteria	Proteobacteria	Betaproteobacteria	MND1			0.65	1.11	0.58	0.39	0.24	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.00	0.00	0.00	0.10	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.17	0.03	0.47	2.06	0.11	12.23
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.01	0.01	0.02	1.32	0.00	0.07
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			0.06	0.00	0.11	0.00	0.02	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.04	0.00	0.00	0.01	0.31	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.03	0.00	0.00	0.00	0.00	0.08
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	0.03	0.00	0.00	0.15	1.64	0.74
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		0.07	0.04	0.10	1.25	0.08	4.56
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.12	0.00	0.00	0.00	1.64	0.05
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.03	0.00	0.00	2.27	0.01	0.49
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.05	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.02	0.01	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.01	0.01	0.00	0.10	0.00	0.08
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			0.00	0.01	0.00	0.25	0.01	2.16
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.00	0.01	0.00	0.92	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.00	0.02	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria				2.51	3.28	1.23	0.18	0.17	0.20
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.06	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.00	0.00	0.00	0.10	0.00	0.50
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.02	0.04	0.00	0.43	0.03	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.09	0.00	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.01	1.00	0.00	0.03	0.00	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.00	0.00	0.00	0.64	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.00	0.00	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.01	0.00	0.00	0.58	0.05	0.09
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.00	0.00	0.00	0.21	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.01	0.00	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.01	0.16	0.00	0.05	1.38	1.18
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		0.02	0.26	0.00	0.18	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.48	0.00	0.00	0.00	0.01	0.00

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.00	0.00	0.00	0.12	0.00	0.07
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.13	0.00	0.08	0.01	0.02	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.85	0.13	0.37	0.08	0.38	0.03
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.32	0.28	0.18	0.00	0.01	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.05	0.01	0.07	0.04	0.14	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.00	0.00	0.00	0.01	0.31	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.02	0.01	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.27	0.06	0.05	0.00	0.01	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.11	0.00	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.02	0.01	0.01	0.00	0.03	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.00	0.04	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.16	0.02	0.00	0.20	0.00	0.19
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.00	0.00	0.42	0.00	0.08
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.00	0.00	0.25	0.00	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.01	0.00	0.18
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		2.31	4.36	5.48	0.16	0.68	0.05
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	1.20	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.02	0.00	0.00	0.07	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		1.11	3.08	3.55	0.00	0.52	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.00	0.00	0.00	0.34	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.18	0.11	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Gammaproteobacteria				0.00	0.00	0.00	0.00	0.00	0.98
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.03	0.00	0.00	0.01	0.15	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.00	0.00	0.00	0.03	0.12	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.16	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.00	0.00	0.00	0.07	1.47	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.00	0.00	0.04	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.00	0.14	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			0.24	0.93	0.04	0.04	0.07	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.01	0.01	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.00	0.00	0.00	0.00	0.03	0.00

Table A5 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 27	KM 28	KM 29	KM 30	KM 31	KM 32
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.14	0.01	0.07	0.00	0.07	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		0.59	0.21	0.82	0.81	0.05	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	0.22	0.09	0.40	0.00	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.07	0.18	0.08	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.12	0.00	0.04	0.14	0.11	0.08
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.03	0.00	0.03	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.01	0.11	0.00	18.43	0.02	10.44
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	3.05	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	1.70	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.00	0.00	0.00	0.00	0.32
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.00	0.00	0.00	0.84
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.10	0.00	0.00	0.07	0.04	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.00	0.75	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	0.73	0.03	0.33	0.01	0.14	0.54
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.00	0.04	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.10	0.14	0.31	0.03	0.01	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.08	0.05	0.05	1.53	3.80	0.07
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.00	0.01	0.01	0.01	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.39	0.04	0.00	0.02	0.06	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.09	0.00	0.00	0.00	0.93	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.00	0.00	0.01	0.07	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.01	0.00	0.00	0.00	0.00	0.84
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.01	0.00	0.03	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.00	0.00	0.00	0.05	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	SBR1093					0.01	0.02	0.00	0.00	0.00	0.00
Bacteria	SR1					0.00	0.00	0.16	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.00	0.01	0.00	0.01	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4				0.02	0.00	0.01	0.00	0.00	0.00
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.11	0.06	0.55	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		0.02	0.10	0.25	0.11	0.67	0.03

Table A5 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 27**	**KM 28**	**KM 29**	**KM 30**	**KM 31**	**KM 32**
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.38	0.45	2.87	0.31	0.85	0.10
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.00	0.00	0.00	0.00	0.60	0.19
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.07	0.11	2.27	0.00	0.01	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.06	0.01	0.02	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.40	0.82	1.52	0.04	0.26	0.35
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.03	0.01	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.01	0.02	0.33	0.04	0.31	0.01
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.01	0.00	0.05	0.00	0.00	0.12
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.04	0.41	0.00	0.00	0.01	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.07	0.00	0.09	0.75	0.06	0.04
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.00	0.12	0.00
Bacteria	WS3	PRR-12				0.07	0.00	0.04	0.00	0.00	0.00
Bacteria	WS3	PRR-12	Sediment-1			0.05	0.04	0.06	0.00	0.06	0.00
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.25	0.23	0.15	0.02	0.07	0.00

Table A6 Taxonomic QIIME results at the genus level by sample (KM33-KM38).

						Relative abundance (%)					
Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 33**	**KM 34**	**KM 35**	**KM 36**	**KM 37**	**KM 38**
Unassigned	Other	Other	Other	Other	Other	14.78	7.88	11.42	20.75	1.36	15.56
Archaea	Crenarchaeota	MBGA				0.03	0.00	0.01	0.00	0.00	0.01
Archaea	Crenarchaeota	MBGA	NRP-J			0.09	0.00	0.04	0.03	0.00	0.12
Archaea	Crenarchaeota	Thaumarchaeota	Other	Other	Other	0.00	0.00	0.09	0.01	0.00	0.15
Archaea	Crenarchaeota	Thaumarchaeota	AK31			0.06	0.00	0.07	0.11	0.00	0.16
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae		0.22	0.00	0.34	0.50	0.36	0.92
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	Nitrosopumilus	0.45	1.38	0.68	0.84	1.94	0.33
Archaea	Crenarchaeota	Thaumarchaeota	Cenarchaeales	SAGMA-X		0.78	0.00	0.67	1.04	0.00	0.48
Archaea	Crenarchaeota	Thaumarchaeota	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.01	0.00	0.01	0.00	0.00	0.00
Archaea	Euryarchaeota	DSEG	ArcA07			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	MSBL1	SAGMEG-1	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanomicrobiales	Methanoregulaceae	Candidatus Methanoregula	0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME-2D		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2			0.00	0.00	0.01	0.00	0.00	0.04
Archaea	Euryarchaeota	Thermoplasmata	E2	DHVEG-1		0.00	0.00	0.00	0.00	0.00	0.00
Archaea	Euryarchaeota	Thermoplasmata	E2	[Methanomassiliicoccaceae]		0.04	0.00	0.03	0.15	0.00	0.02
Archaea	[Parvarchaeota]	[Micrarchaea]	[Micrarchaeles]			0.01	0.00	0.00	0.06	0.00	0.04
Archaea	[Parvarchaeota]	[Parvarchaea]	WCHD3-30			0.03	0.16	0.07	0.24	0.00	0.26
Archaea	[Parvarchaeota]	[Parvarchaea]	YLA114			2.20	0.00	2.46	1.52	0.00	3.45
Bacteria						0.00	0.00	0.00	0.00	0.01	0.01
Bacteria	AC1					0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	AC1	HDBW-WB69				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Acidobacteria					0.28	0.28	0.15	0.81	0.04	0.28
Bacteria	Acidobacteria	Acidobacteria-5				1.19	0.00	1.32	1.27	0.00	0.20
Bacteria	Acidobacteria	Acidobacteria-6	CCU21			0.02	0.00	0.02	0.05	0.01	0.00
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15			3.11	0.73	9.47	2.95	0.01	1.87
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	RB40		0.06	0.00	0.08	0.00	0.00	0.03
Bacteria	Acidobacteria	Acidobacteria-6	iii1-15	mb2424		0.02	0.00	0.07	0.17	0.00	0.03
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae		0.29	0.00	0.01	0.05	0.00	0.04
Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter	0.04	0.00	0.00	0.02	0.00	0.00
Bacteria	Acidobacteria	BPC102				0.00	0.00	0.01	0.01	0.00	0.00
Bacteria	Acidobacteria	BPC102	MVS-40			0.14	0.00	0.00	0.02	0.00	0.00
Bacteria	Acidobacteria	DA052	E29			0.06	0.00	0.06	0.17	0.00	0.06

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Acidobacteria	DA052	Ellin6513			0.34	0.15	0.45	0.36	0.00	0.23
Bacteria	Acidobacteria	EC1113				2.17	0.00	0.20	0.21	0.00	0.17
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae		0.14	0.00	0.00	0.00	0.00	0.02
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix	0.01	0.00	0.00	0.00	0.00	0.18
Bacteria	Acidobacteria	RB25				0.02	0.00	0.00	0.06	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	JH-WHS99			0.18	0.00	0.03	0.07	0.00	0.03
Bacteria	Acidobacteria	Solibacteres	Solibacterales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	PAUC26f		0.02	0.00	0.24	0.04	0.00	0.00
Bacteria	Acidobacteria	Solibacteres	Solibacterales	[Bryobacteraceae]		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Acidobacteria	Sva0725	Sva0725			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Acidobacteria	TM1				0.49	0.00	0.01	0.05	0.00	0.04
Bacteria	Acidobacteria	[Chloracidobacteria]				0.00	0.00	0.07	0.01	0.00	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	24-Nov			0.05	0.00	0.00	0.00	0.00	0.05
Bacteria	Acidobacteria	[Chloracidobacteria]	PK29			0.03	0.00	0.18	0.00	0.00	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41			0.02	0.00	0.00	0.03	0.00	0.01
Bacteria	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075		0.00	0.00	0.05	0.00	0.01	0.00
Bacteria	Acidobacteria	iii1-8	32-20			0.00	0.00	0.03	0.07	0.00	0.00
Bacteria	Acidobacteria	iii1-8	DS-18			0.01	0.00	0.47	0.04	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Acidimicrobiia	Acidimicrobiales	EB1017		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1		0.00	0.00	0.00	0.00	0.00	0.16
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	0.00	0.00	0.00	0.00	0.36	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	0.00	0.00	0.00	0.00	0.18	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	0.00	0.61	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	0.00	0.35	0.00	0.00	0.01	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Salinibacterium	0.01	0.04	0.00	0.00	0.68	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae		0.01	0.00	0.00	0.00	0.59	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	0.00	0.01	0.01	0.01	0.13	0.01
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Nocardia	0.00	0.00	0.66	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	0.00	0.28	0.03	0.04	0.25	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella	0.02	0.00	0.02	0.02	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Actinobacteria	WCHB1-81	At425_EubF1		0.00	0.86	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	OPB41				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae		0.39	0.00	0.68	0.12	0.00	0.02
Bacteria	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia				0.00	0.41	0.00	0.00	0.00	0.00
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales			0.00	0.00	0.01	0.00	0.00	0.00

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae		0.08	0.00	0.28	0.37	0.00	0.02
Bacteria	Actinobacteria	Thermoleophilia	Solirubrobacterales			0.01	0.00	0.02	0.00	0.00	0.00
Bacteria	AncK6					0.07	0.00	0.00	0.00	0.00	0.00
Bacteria	Armatimonadetes	0319-6E2				0.02	0.00	0.37	0.01	0.00	0.00
Bacteria	Armatimonadetes	[Fimbriimonadia]	[Fimbriimonadales]	[Fimbriimonadaceae]		0.01	0.00	0.00	0.02	0.00	0.00
Bacteria	BHI80-139					0.03	0.00	0.01	0.02	0.00	0.15
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			0.00	0.72	0.06	0.01	0.00	0.02
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Paludibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae		0.13	0.00	0.04	0.01	0.01	1.44
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter	0.00	0.41	0.01	0.00	0.78	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Emticicia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Flectobacillus	0.00	0.00	0.00	0.00	2.45	0.00
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Leadbetterella	0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola	0.00	0.00	16.49	0.06	0.00	0.05
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.01	0.16	0.09	0.04	0.00	2.20
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	[Weeksellaceae]	Chryseobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales			0.30	0.68	0.04	0.20	0.90	1.20
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae		0.00	0.30	0.53	0.01	0.57	5.08
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.00	0.00	0.56	0.00	0.00	0.04
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Bacteroidetes	VC2_1_Bac22				0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae		0.15	0.02	0.12	0.07	0.25	0.21
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	Sediminibacterium	0.03	0.15	0.00	0.00	1.58	2.17
Bacteria	Bacteroidetes	[Saprospirae]	[Saprospirales]	Saprospiraceae		0.00	0.00	0.00	0.07	0.00	0.00
Bacteria	Caldithrix	Caldithrixae	Caldithrixales	Caldithrixaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales			0.02	0.00	0.12	0.05	0.00	0.06
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chlamydiae	Chlamydiia	Chlamydiales	Rhabdochlamydiaceae	Candidatus Rhabdochlamydia	0.26	0.00	0.01	0.02	0.00	0.05
Bacteria	Chlorobi	BSV26				0.21	0.00	0.20	0.09	0.00	0.01
Bacteria	Chlorobi	BSV26	A89			0.32	0.00	0.23	0.28	0.00	0.11
Bacteria	Chlorobi	BSV26	C20			0.11	0.00	0.08	0.27	0.00	0.05
Bacteria	Chlorobi	BSV26	PK329			0.00	0.00	0.07	0.06	0.00	0.00
Bacteria	Chlorobi	BSV26	VC38			0.02	0.86	0.00	0.16	0.00	0.02
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00

Table A6 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 33**	**KM 34**	**KM 35**	**KM 36**	**KM 37**	**KM 38**
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae		0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	[Melioribacteraceae]		0.00	0.61	0.00	0.00	0.03	0.02
Bacteria	Chlorobi	OPB56				0.00	0.00	0.23	0.00	0.01	0.02
Bacteria	Chlorobi	SJA-28				0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Other	Other	Other	Other	0.00	0.00	0.00	0.12	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	A31			0.00	0.00	0.01	0.00	0.00	0.01
Bacteria	Chloroflexi	Anaerolineae	A31	S47		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.00	0.00	0.00	0.03	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	GCA004			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	H39			0.25	2.03	0.08	0.27	0.00	0.21
Bacteria	Chloroflexi	Anaerolineae	WCHB1-50			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Anaerolineae	envOPS12			0.02	1.98	0.01	0.03	0.00	0.21
Bacteria	Chloroflexi	Chloroflexi	[Roseiflexales]	[Kouleothrixaceae]		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales			0.00	0.00	0.00	0.02	0.00	0.00
Bacteria	Chloroflexi	Dehalococcoidetes	Dehalococcoidales	Dehalococcoidaceae		0.00	1.00	0.00	0.02	0.00	0.00
Bacteria	Chloroflexi	Ellin6529				0.21	0.01	0.06	0.12	0.00	0.05
Bacteria	Chloroflexi	Gitt-GS-136				0.02	0.00	0.03	0.06	0.00	0.02
Bacteria	Chloroflexi	Ktedonobacteria	TK10			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Chloroflexi	P2-11E				0.02	0.00	0.05	0.02	0.00	0.06
Bacteria	Chloroflexi	S085				0.94	1.01	0.25	0.16	0.00	0.06
Bacteria	Chloroflexi	SAR202				3.63	0.21	8.46	1.58	0.39	0.37
Bacteria	Chloroflexi	TK10	AKYG885	5B-12		0.28	0.00	0.06	0.25	0.00	0.05
Bacteria	Chloroflexi	TK17				0.26	0.00	0.52	0.35	0.00	0.03
Bacteria	Chloroflexi	TK17	mle1-48			0.01	0.00	0.02	0.02	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	MLE1-12			0.21	0.00	0.01	0.37	0.00	0.13
Bacteria	Cyanobacteria	4C0d-2	SM1D11			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Cyanobacteria	4C0d-2	SM2F09			0.49	0.00	0.65	2.64	0.00	0.36
Bacteria	Cyanobacteria	Chloroplast	Stramenopiles			0.00	0.19	0.20	0.02	0.59	0.01
Bacteria	Cyanobacteria	Chloroplast	Streptophyta			4.43	0.28	0.17	0.21	10.62	0.10
Bacteria	Cyanobacteria	ML635J-21				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia					0.08	0.00	0.00	0.00	0.00	0.03
Bacteria	Elusimicrobia	29-Apr				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Elusimicrobia	Elusimicrobia				0.04	0.00	0.00	0.00	0.00	0.02
Bacteria	Elusimicrobia	Elusimicrobia	Elusimicrobiales			0.12	0.07	0.13	0.21	1.03	0.19
Bacteria	Elusimicrobia	Elusimicrobia	FAC88			0.09	0.00	0.00	0.19	0.00	0.16
Bacteria	Elusimicrobia	Elusimicrobia	IIb			0.05	0.00	0.01	0.65	0.00	0.11
Bacteria	Elusimicrobia	Elusimicrobia	MVP-88			0.02	0.00	0.08	0.04	0.00	0.01
Bacteria	Elusimicrobia	Endomicrobia				0.05	0.00	0.11	0.35	0.00	0.37
Bacteria	FBP					0.03	0.00	0.01	0.02	0.00	0.00
Bacteria	FCPU426					0.00	0.00	0.06	0.00	0.00	0.00

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Fibrobacteres					0.00	0.00	0.00	0.00	0.00	0.41
Bacteria	Fibrobacteres	Fibrobacteria	258ds10			0.00	0.00	0.10	0.01	0.00	0.03
Bacteria	Firmicutes	Bacilli	Bacillales			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.01	0.83	0.01	0.00	3.86	0.04
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.00	0.22	0.01	0.01	1.56	0.00
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	0.03	0.27	0.00	0.04	1.17	0.01
Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Caloramator	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	0.00	0.00	0.00	0.01	0.00	0.03
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Acetobacterium	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfosporosinus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Pelosinus	0.00	0.00	0.00	0.00	0.00	0.05
Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Sporomusa	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Acidaminobacteraceae]	Fusibacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Firmicutes	Clostridia	OPB54			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	3BR-5F				0.00	0.00	0.01	0.09	0.00	0.17
Bacteria	GN02	BB34				0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	GN02	GKS2-174				0.00	0.01	0.00	0.00	0.00	0.00
Bacteria	GN02	GN07				0.00	0.00	0.02	0.01	0.00	0.01
Bacteria	GN04					0.00	0.39	0.01	0.00	0.00	0.00
Bacteria	GN04	GN15				0.01	0.42	0.05	0.14	0.00	0.03
Bacteria	GN04	MSB-5A5				0.02	0.00	0.18	0.07	0.00	0.02
Bacteria	Gemmatimonadetes	Gemm-1				0.44	0.00	0.32	0.62	0.02	0.28
Bacteria	Gemmatimonadetes	Gemm-2				0.02	0.00	0.07	0.15	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes				0.00	0.01	0.00	0.00	0.00	0.02
Bacteria	Gemmatimonadetes	Gemmatimonadetes	C114			0.04	0.00	0.08	0.05	0.00	0.00
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.00	0.00	0.00	0.00	0.00	0.08
Bacteria	Gemmatimonadetes	Gemmatimonadetes	KD8-87			0.02	0.00	0.01	0.00	0.00	0.02
Bacteria	Lentisphaerae	[Lentisphaeria]	Lentisphaerales	Arctic95B-10		0.00	0.00	0.07	0.03	0.00	0.01
Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae		0.00	0.00	0.00	0.00	0.00	0.06

Table A6 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 33**	**KM 34**	**KM 35**	**KM 36**	**KM 37**	**KM 38**
Bacteria	MVS-104					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	NC10	24-Dec	JH-WHS47			0.72	0.00	0.39	0.94	0.23	1.02
Bacteria	NC10	24-Dec	Methylomirabiliales	Methylomirabiliaceae	Candidatus Methylomirabilis	0.27	0.00	0.07	0.02	0.00	0.14
Bacteria	NC10	wb1-A12				0.01	0.00	0.16	0.22	0.00	0.04
Bacteria	NKB19					0.35	0.00	0.04	0.01	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales			0.18	0.00	0.07	0.02	0.00	0.03
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	0319-6A21		4.06	0.26	2.97	3.60	0.05	3.24
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	29-Apr		0.02	0.00	0.00	0.00	0.00	0.07
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	FW	29-Apr	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae		0.21	0.00	0.32	0.69	0.00	0.09
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	JG37-AG-70	0.61	0.00	0.02	0.00	0.04	0.12
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.71	5.36	0.37	1.00	0.31	1.55
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Leptospirillaceae]		3.00	0.00	0.27	0.81	0.00	0.31
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	Other	0.00	0.00	0.00	0.00	0.00	0.04
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]		0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	BD2-6	0.00	0.52	0.00	0.00	0.00	0.07
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	GOUTA19	0.00	2.26	0.00	0.01	0.00	0.00
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	[Thermodesulfovibrionaceae]	LCP-6	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OC31					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	OD1					0.06	0.41	0.10	0.22	0.00	0.78
Bacteria	OD1	ABY1				0.08	0.00	0.07	0.13	0.00	0.32
Bacteria	OD1	Mb-NB09				0.13	0.00	0.08	0.10	0.00	0.13
Bacteria	OD1	SM2F11				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	OD1	ZB2				0.06	0.35	0.54	0.04	0.00	0.63
Bacteria	OP1	[Acetothermia]	[Acetothermales]			0.09	0.00	0.00	0.00	0.00	0.04
Bacteria	OP11	OP11-4				0.00	0.11	0.00	0.00	0.00	0.00
Bacteria	OP3					0.02	0.00	0.00	0.00	0.02	0.24
Bacteria	OP3	BD4-9				0.02	0.00	0.00	0.00	0.05	0.56
Bacteria	OP3	PBS-25				4.09	0.66	2.34	7.48	0.19	2.91
Bacteria	OP3	koll11				8.05	0.00	6.93	14.22	0.23	5.63
Bacteria	OP3	koll11	GIF10			0.05	0.00	0.00	0.00	1.36	1.10
Bacteria	OP3	koll11	GIF10	kpj58rc		0.02	0.00	0.12	0.05	0.00	0.21
Bacteria	PAUC34f					0.47	0.00	0.01	0.39	0.00	0.06
Bacteria	Planctomycetes					0.00	1.00	0.00	0.07	0.00	0.00
Bacteria	Planctomycetes	BD7-11				0.35	0.00	0.10	0.29	0.00	0.25
Bacteria	Planctomycetes	C6	MVS-107			0.49	1.02	0.13	0.18	0.00	0.04
Bacteria	Planctomycetes	ODP123	T8-B82			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	OM190				0.06	0.00	0.06	0.13	0.00	0.04
Bacteria	Planctomycetes	OM190	CL500-15			0.00	0.32	0.03	0.29	0.00	0.07
Bacteria	Planctomycetes	OM190	agg27			0.07	0.00	0.13	0.19	0.54	0.03

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Planctomycetes	Phycisphaerae	CCM11a			0.09	6.03	0.13	0.29	0.00	0.24
Bacteria	Planctomycetes	Phycisphaerae	MSBL9			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales			0.00	0.00	0.00	0.00	0.00	0.23
Bacteria	Planctomycetes	Phycisphaerae	mle1-8			0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	Planctomycetes	Pla4				0.07	0.00	0.08	0.25	0.00	0.08
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae		0.02	0.00	0.01	0.02	0.00	0.03
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae	Gemmata	0.01	0.00	0.00	0.00	0.00	0.01
Bacteria	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae		0.05	0.00	0.25	0.39	0.00	0.16
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	A17	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomyces	0.03	0.01	0.03	0.03	0.01	0.04
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Other	0.01	3.77	0.01	0.00	0.00	0.02
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Brocadia	0.01	0.87	0.00	0.32	0.38	0.65
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	Brocadiaceae	Candidatus Scalindua	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Planctomycetes	[Brocadiae]	Brocadiales	W4		0.01	0.00	0.00	0.00	0.87	0.20
Bacteria	Proteobacteria					0.18	0.00	0.02	0.00	0.00	0.34
Bacteria	Proteobacteria	Alphaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria				0.01	0.00	0.04	0.05	0.00	0.26
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.00	0.04	0.10	0.01	0.53	0.13
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.00	0.34	0.00	0.10	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.00	0.61	0.00	0.02	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	0.02	0.18	0.58	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.04	0.11	0.10	0.00	0.53	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Ellin329			0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.02	0.00	0.08	0.06	0.11	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Other	0.02	0.00	0.01	0.02	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae		0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.00	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.01	0.00	0.06	0.00	0.04	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.00	0.48	0.00	0.01	0.00	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.02	0.00	0.00	0.03	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	0.12	0.61	0.10	0.03	0.14	0.12
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		0.01	0.83	0.03	0.00	0.74	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	0.09	0.94	0.08	0.27	6.19	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		0.01	0.00	0.00	0.01	0.00	0.01

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	0.00	0.00	0.02	0.01	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Other	0.01	0.35	0.02	0.00	2.99	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.00	0.00	0.04	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	0.00	0.00	0.07	0.02	0.00	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae		0.01	0.00	0.06	0.03	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	0.03	0.00	0.62	0.00	0.01	4.15
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae		1.10	1.34	1.01	0.55	0.48	0.50
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum	0.01	0.49	0.00	0.00	0.00	1.66
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Magnetospirillum	0.00	0.31	0.00	0.00	0.00	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Novispirillum	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Phaeospirillum	0.06	0.00	0.55	0.23	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales			0.00	0.00	0.02	0.03	0.00	1.24
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae		0.02	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	mitochondria	Other	0.67	2.43	0.02	0.18	1.07	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Other	Other	0.04	0.01	0.00	0.00	0.17	0.62
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae		0.00	0.00	0.00	0.00	0.00	0.08
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.02	0.00	0.37	0.02	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Kaistobacter	0.01	0.00	0.03	0.02	0.01	0.01
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.01	0.21	0.00	0.02	0.95	0.07
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.02	0.00	0.00	0.04	0.72	0.06
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.04	0.59	0.43	0.03	2.05	0.08
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.00	0.00	0.08	0.02	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Zymomonas	0.00	0.00	0.00	0.00	0.78	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Other	Other	Other	0.04	0.31	0.02	0.00	0.00	0.04
Bacteria	Proteobacteria	Betaproteobacteria				1.21	1.48	1.03	1.81	0.40	0.46
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae		0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Other	0.11	0.01	0.91	1.14	0.23	0.66
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		0.74	0.62	1.33	0.53	1.64	3.59
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	0.00	0.00	0.01	0.00	0.04	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	0.01	0.00	0.11	0.00	0.00	1.45
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.04	0.00	0.05	0.10	2.41	1.01
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.01	0.00	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	0.02	0.04	0.00	0.00	0.25	0.11
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Other	0.49	0.00	0.03	0.31	0.00	0.02
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae		0.26	0.00	0.11	0.10	0.00	0.41
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium	0.04	0.00	0.07	0.01	0.00	0.12

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Polynucleobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Ralstonia	0.00	0.22	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Other	0.01	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	Gallionella	0.01	10.84	0.00	0.01	0.24	0.57
Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	IS-44			0.56	0.00	0.26	0.26	0.00	0.04
Bacteria	Proteobacteria	Betaproteobacteria	MND1			5.03	1.35	1.51	1.80	0.01	0.20
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			0.00	0.00	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		0.11	0.00	0.05	0.28	19.90	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	0.00	0.00	0.01	0.01	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae		0.00	0.00	0.00	0.00	0.57	0.41
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales			0.00	0.00	0.19	0.05	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae		0.00	2.10	0.07	0.00	0.00	0.11
Bacteria	Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae		0.00	0.00	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Other	0.00	0.23	0.00	0.00	0.00	1.11
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		0.23	0.00	0.05	0.10	0.47	1.97
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	0.04	0.01	0.00	0.00	0.00	0.21
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dok59	0.00	0.00	0.00	0.01	0.00	0.62
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio	0.00	0.00	0.00	0.00	0.00	0.50
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sterolibacterium	0.00	0.00	0.00	0.00	0.00	0.06
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Sulfuritalea	0.00	0.00	0.00	0.00	0.00	0.07
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Zoogloea	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Betaproteobacteria	SBla14			0.01	0.19	0.00	0.00	0.02	0.14
Bacteria	Proteobacteria	Betaproteobacteria	Thiobacterales			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Other	Other	Other	0.07	0.00	0.00	0.05	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria				1.17	0.36	0.97	1.77	0.02	0.87
Bacteria	Proteobacteria	Deltaproteobacteria	AF420338			0.00	0.00	0.00	0.00	0.00	0.27
Bacteria	Proteobacteria	Deltaproteobacteria	BPC076			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae		0.19	0.00	0.07	0.05	0.00	0.13
Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.00	0.00	0.01	0.00	0.00	0.14
Bacteria	Proteobacteria	Deltaproteobacteria	DTB120			0.05	8.01	0.01	0.07	0.00	0.18
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae		0.00	1.33	0.00	0.00	0.01	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	0.02	0.10	0.00	0.00	0.00	0.07
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae		0.00	1.86	0.00	0.00	0.11	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	FAC87			0.00	0.00	0.00	0.14	0.00	0.00

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Proteobacteria	Deltaproteobacteria	MBNT15			0.03	0.94	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46			0.04	0.00	0.01	0.13	0.08	0.17
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			0.72	0.81	0.50	0.76	0.09	0.38
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	0319-6G20		0.01	0.00	0.00	0.00	0.00	0.04
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae		0.00	0.00	0.17	0.09	0.00	0.10
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.11	0.00	0.02	0.03	0.00	0.01
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Anaeromyxobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	OM27		0.01	0.00	0.00	0.00	0.00	0.12
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Other	0.03	0.00	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j			0.01	0.00	0.03	0.07	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NB1-j	MND4		0.03	0.00	0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	NKB15			0.11	0.00	0.13	0.11	0.00	0.08
Bacteria	Proteobacteria	Deltaproteobacteria	PB19			0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Spirobacillales			0.01	0.00	0.01	0.10	0.00	0.23
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	JTB36		0.31	0.00	0.03	0.03	0.00	0.02
Bacteria	Proteobacteria	Deltaproteobacteria	Sva0853	SAR324		0.01	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae		0.00	0.10	0.03	0.17	0.00	0.10
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfobacca	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Syntrophus	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae		12.53	0.53	1.99	4.83	0.86	2.05
Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	Syntrophobacter	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]			0.00	0.44	0.00	0.01	0.00	0.04
Bacteria	Proteobacteria	Deltaproteobacteria	[Entotheonellales]	[Entotheonellaceae]		2.54	0.00	0.30	1.00	0.00	0.24
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	0.00	0.00	0.00	0.00	0.00	0.68
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfuricurvum	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	Sulfurimonas	0.00	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria				0.02	0.00	0.00	0.00	0.00	0.42
Bacteria	Proteobacteria	Gammaproteobacteria	34P16			0.05	0.00	0.01	0.00	0.00	0.31
Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae		0.00	0.13	0.00	0.00	0.00	0.62
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Other	Other	0.00	0.00	0.00	0.07	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	125ds10		0.10	0.00	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	211ds20		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Cellvibrio	0.07	0.00	0.00	0.00	0.00	0.17
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Microbulbifer	0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	OM60		0.00	0.00	0.00	0.00	0.01	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales			0.55	0.00	0.92	0.36	0.00	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae		0.10	0.00	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.02	0.18	0.02	0.01	2.48	0.37

Table A6 continued

Kingdom	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**KM 33**	**KM 34**	**KM 35**	**KM 36**	**KM 37**	**KM 38**
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Trabulsiella	0.00	0.00	0.00	0.01	0.81	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales			0.02	0.00	0.03	0.04	0.01	0.09
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae		0.34	0.00	0.13	0.53	0.78	0.16
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella	0.01	0.07	0.01	0.26	0.01	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.04	2.55	0.00	0.09	0.37	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.00	0.00	0.01	0.02	0.36	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Tatlockia	0.00	0.00	0.03	0.00	0.56	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Crenotrichaceae	Crenothrix	0.03	0.01	0.02	0.00	0.00	0.14
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		0.00	0.00	0.00	0.00	0.00	0.09
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	PYR10d3			0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other	0.00	0.00	0.19	0.00	0.00	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	0.29	1.66	0.19	0.29	7.52	0.24
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	0.00	0.00	0.00	0.00	0.78	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca	0.00	0.00	0.00	0.00	0.00	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae		0.05	0.03	0.98	0.13	0.07	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.49	1.97	1.83	0.33	1.87	0.65
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae		0.02	0.00	0.01	0.01	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae		0.00	0.00	0.19	0.44	0.01	0.05
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.01	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	0.00	0.25	0.02	0.01	1.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	0.00	0.33	0.00	0.09	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	0.00	0.00	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.02	0.21	0.00	0.03	1.97	0.01
Bacteria	SBR1093					0.00	0.00	0.00	0.01	0.00	0.00
Bacteria	SR1					0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Spirochaeta	0.00	0.00	0.00	0.00	0.00	0.20
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Leptospiraceae	Turneriella	0.00	0.00	0.00	0.00	0.09	0.00
Bacteria	Spirochaetes	[Leptospirae]	[Leptospirales]	Sediment-4	SJA-88	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4	Other	Other	Other	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	TM6	SJA-4				0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	Entomoplasma	0.00	0.00	0.00	0.00	0.00	1.42
Bacteria	Verrucomicrobia	Other	Other	Other	Other	0.05	0.00	0.03	0.00	0.00	0.03
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae		0.05	0.27	0.01	0.83	0.02	0.18

Table A6 continued

Kingdom	Phylum	Class	Order	Family	Genus	KM 33	KM 34	KM 35	KM 36	KM 37	KM 38
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.34	0.40	0.19	0.65	0.11	0.19
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter	0.00	0.00	0.00	0.00	0.00	0.01
Bacteria	Verrucomicrobia	[Methylacidiphilae]	S-BQ2-57			0.03	0.00	0.04	0.04	0.00	0.13
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Other	Other	0.02	0.00	0.09	0.07	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]			0.68	0.56	0.94	1.57	0.00	0.19
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin515		0.08	0.00	0.01	0.02	0.00	0.01
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	Ellin517		0.20	0.00	0.28	0.03	0.00	0.02
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	R4-41B		0.00	0.00	0.68	0.41	0.00	0.47
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	[Pedosphaeraceae]	Other	0.33	0.00	0.42	0.05	0.00	0.00
Bacteria	Verrucomicrobia	[Pedosphaerae]	[Pedosphaerales]	auto67_4W		0.19	0.00	0.00	0.22	0.01	0.09
Bacteria	Verrucomicrobia	[Spartobacteria]	[Chthoniobacterales]	[Chthoniobacteraceae]	Chthoniobacter	0.00	0.39	0.00	0.01	0.30	0.00
Bacteria	WPS-2					0.00	0.00	0.00	0.00	0.00	0.05
Bacteria	WS3	PRR-12				0.00	0.00	0.00	0.03	0.00	0.00
Bacteria	WS3	PRR-12	Sediment-1			0.05	0.00	0.08	0.10	0.00	0.04
Bacteria	WS3	PRR-12	Sediment-1	PRR-10		0.15	0.30	0.28	0.27	0.00	0.03