

**Bacterial Colonization of Point-of-Use (PoU) Drinking Water Filters,  
Selection of Opportunistic Pathogens and  
Presence of Antibiotic Resistance Genes**

**by**

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## Abstract

Commercial activated carbon block (ACB) point-of-use (PoU) drinking water filters are widely used to remove chemicals of concern from tap water. ACB PoU filters, however, are an incubator of bacteria because they remove disinfectant residual and adsorb organic compounds that can serve as bacterial substrates. The chemicals adsorbed on the ACB, such as disinfection byproducts (DBPs), may interact with colonizing bacteria. Bacterial growth in ACB PoU filters raises questions about whether waterborne bacteria that pose health risks can be enriched, such as enteric-related bacteria, opportunistic pathogens, and antibiotic resistant gene (ARG)-carrying bacteria. The goal of this dissertation is to understand how ACB PoU filters change the microbial ecology of drinking water using culture-based and culture-independent methods. A lab-scale ACB PoU filter system experiment was conducted to study the bacterial composition shifts across the filters with and without the addition of pentachlorophenol (PCP), a surrogate chlorinated phenolic disinfection byproduct. The results show that the PoU filter has a primary effect on altering the bacterial composition and increasing the abundance of *Mycobacterium*, while the influence of PCP was subtle. A field study was conducted to evaluate the prevalence of ARGs across the ACB PoU filters installed at different households in Flint, Michigan. The study indicates that ACB PoU filters raised the occurrence and abundance of some ARGs in the tap water. The increase in ARGs across filters was also detected in a lab-scale system in Ann Arbor. Lastly, the mechanism of bacterial migration through the ACB PoU filters was studied by spiking inert bacterial-sized particles (1  $\mu\text{m}$ ) and fluorescent-tagged *Escherichia coli* and

*Pseudomonas aeruginosa* into the system. We found that preferential flow pathways existed in the ACB, allowing bacteria to pass through rapidly. Differences in growth, biofilm formation, and physical properties of the spiked species determine their migration and survival through the ACB PoU filters.

# Chapter 1

## Introduction

### 1.1 Background

Point-of-use (PoU) drinking water treatment devices are used to treat tap water for drinking and cooking purpose. Many people use PoU treatment devices to improve the aesthetics of tap water, such as taste and odor, and remove chemicals of concern. Disinfectants, such as chlorine and chloramine, have been used to maintain residual levels throughout drinking water distribution networks; however, chemical disinfectants can impart undesirable flavor, which is one of the major complaints against tap water (Puget et al., 2010). Despite consumer concerns about the aesthetic quality and health of tap water, most American's are served by drinking water systems that are in compliance with state and federal standards (Allaire et al., 2018). Nevertheless, emerging contaminants are increasingly being detected in tap water and reported on. For example, studies have reported that antibiotics are present in drinking water treatment plant source waters and are not fully removed during treatment (Glassmeyer et al., 2017; Ye et al., 2007). Many unregulated disinfection byproducts (DBPs) are generated during disinfection processes and are present at trace level in drinking water (Richardson, 2003; Richardson et al., 2007). Given the public's interest in reducing their exposure to chemicals of concern and to improve the aesthetic quality of water, more consumers are turning to point-of-use (PoU) treatment at home (Cullen, 2017).

Faucet-mounted activated carbon block (ACB) PoU filters are among the most popular devices used in home-based drinking water treatment. ACB, first introduced in the early 1970's, is composed of powdered activated carbon that is bound by polymers and shaped into a cylinder with an annular channel. Manufacturer's typically wrap the cylindrical block with a fabric to keep the ACB from breaking apart during manufacturing and use. This design provides a large surface area for chemical adsorption and low pore sizes for particle filtration, which is ideally

suited to achieve both aesthetic improvements and chemical removal from tap water (Silverstein, 2006).

Commercial ACB PoU filters are certified through NSF/ANSI Standard 42 and 53 for reducing particles (including protozoan cysts), and inorganic and organic chemicals that are of aesthetic and health importance (NSF International/ANSI, 2015a, 2015b). However, these filters are not certified to achieve bacterial removal and, instead, provide a suitable environment for bacterial growth. This growth is most likely supported by organic compounds from the tap water that become reversibly adsorbed onto the ACB and can serve as growth substrates (Wallis et al., 1974) as well as the lack of disinfectant residual, which is destroyed through reactions with the activated carbon (Bauer and Snoeyink, 1973; Suidan et al., 1977). Consequently, the literature provided by device manufacturer's clearly states that they do not recommend use of ACB PoU filters in waters that are inadequately disinfected or are "microbiologically unsafe."

ACB PoU filters are known to change the number and types of bacteria present in filtered tap water, as determined both by traditional culture-based methods (Chaidez and Gerba, 2004; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981) and DNA-based biomolecular methods (Wu et al., 2017). Multiple studies have shown that heterotrophic bacterial counts (measured as a heterotrophic plate count, HPC) in the effluent of ACB PoU filters increase with time and exceed the levels in the tap water influent, even within the manufacturers' recommended usage period (Chaidez and Gerba, 2004; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981). One previous study using culture-based methods detected changes in the diversity of bacterial composition across the ACB PoU filters that were fed with chlorinated tap water (Su et al., 2009a). These culture-based studies showed that ACB PoU filters alter the abundance and type of bacteria present in filtered water relative to the influent tap water. However, culture-based studies are vulnerable to the limitations of culturing methods, since they only detect a small fraction of the drinking water bacterial population (Allen et al., 2004). A goal of this research was to use culture-independent approaches coupled with culture-based methods to evaluate how the microbial ecology of tap water is changed by the PoU ACB filters.

The fact that bacterial growth occurs in ACB PoU filters raises the question of whether filter use increases microbially-mediated risks in drinking water. The conventional approach to microbial monitoring involves testing for enteric bacterial pathogens such as *Escherichia coli*, which can

cause gastrointestinal illness. Increasingly, opportunistic pathogens such as *Pseudomonas aeruginosa*, nontuberculous mycobacteria (NTM) and *Legionella spp.* are of interest in drinking water and can cause upper respiratory illness and, in some cases, skin rashes. Newly recognized biological hazards such as antibiotic resistant bacteria (ARB) and antibiotic resistant genes (ARGs) have gained more attention since they have been observed in engineered systems with increasing frequency over the past several decades (Vaz-Moreira et al., 2014). Given that the bacterial composition of drinking water can be reshaped by ACB PoU filters, it is reasonable to ask whether the filter environment can also influence the fate of these bacterial species of concern as well as the quality of filtered water. This dissertation attempts to address this question.

Opportunistic pathogens, enteric-related species, and bacteria carrying ARGs are the three types of bacterial agents of concern focused on in this dissertation. Opportunistic pathogens including *P. aeruginosa* and species belonging to the non-tuberculosis Mycobacteria (NTM) (a group of Mycobacteria that includes some species that present a risk to public health) were found in the effluent of ACB PoU filters (Chaidez and Gerba, 2004) and hospital filters (Falkinham, 2010) that processed tap water. Although the dose of opportunistic pathogens required to make healthy people sick are much greater than for enteric pathogens (Leclerc, 2003), *Pseudomonas aeruginosa* and NTM are responsible for the majority of hospital-acquired infections (Gargano et al., 2017). The enteric pathogens are believed to be less of a concern because some species of enteric related pathogens are suppressed by the growth of heterotrophic bacteria on granular activated carbon (Camper et al., 1985). However, we cannot ignore that these enteric pathogens can reside in drinking water biofilms in a viable but non-culturable state (Wingender and Flemming, 2011), making them unable to be detected by culture-based methods. Given that the ACB PoU filters may harbor pathogenic bacteria, some of which exhibit resistance to disinfectants that also correspond with the presence of antibiotic resistance mechanisms (Jia et al., 2015), the ACB PoU filters may support the presence of antibiotic resistant bacteria. Complicating this further, chemicals that can be adsorbed on the ACB PoU filters may affect the antibiotic resistance of the colonizing bacteria through horizontal gene transfer that can occur in biofilms (Molin and Tolker-Nielsen, 2003). Evaluating if ACB PoU filters can enrich the number of opportunistic pathogens, enteric-related species and ARGs is crucial, especially for immune-compromised populations that are vulnerable to infection.



This dissertation is focused on improving our understanding of the microbial ecology of ACB PoU drinking water filters. Chapter 2 provides a literature background on what is known. Specifically, it focuses on studies that assessed bacteria growth in ACB PoU drinking water filters based on traditional culture dependent approaches, the current findings on bacterial abundance and community composition in drinking water, and the prevalence of ARGs and ARBs that were found in drinking water. Chapter 3 identifies the effect of ACB PoU filters on the drinking water bacterial community structure with and without exposure to pentachlorinated phenol, a surrogate non-regulated disinfection byproduct. Chapter 4 reports on whether ACB PoU filters change the type and abundance of ARGs in a chlorinated and chloraminated drinking water system. Chapter 5 further presents information on how bacteria and bacterial-sized particles move through ACB PoU filters using fluorescently-tagged bacteria: *P. aeruginosa* and *E. coli* and fluorescent microspheres. This dissertation lays out the foundation for microbial ecology studies in filtration systems that use ACB as the filter media, including faucet-mounted ACB PoU filters, under-the-sink treatment devices, refrigerator water filters, and water foundation filtration systems also known as hydration stations.

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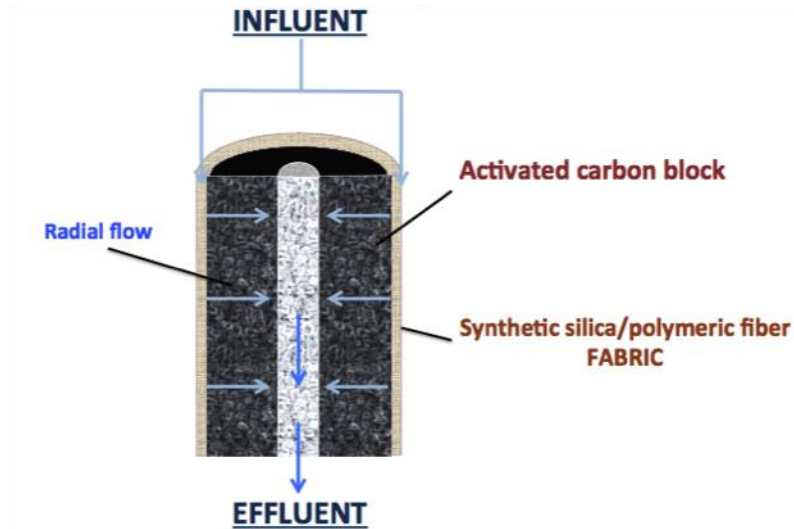
## Chapter 2

### Literature Review

#### 2.1 Activated carbon block PoU filters as an incubator of bacteria

Communities increasingly rely upon PoU filters at the tap for an additional barrier of protection from waterborne contaminants, especially in recent water contamination events. During the Flint water crisis, the faucet mounted ACB PoU filters were recommended as one of the options for the residences to remove elevated levels of lead and disinfection byproducts (DBPs) from tap water in homes. The PoU filtration technologies have been evaluated to be effective in treating chemical contaminants (Brown et al., 2017). However, the PoU filters can support the growth of bacteria and may increase the risk of enhancing pathogen levels in poorly disinfected waters (Sobsey, 2002). The microbiological changes across the ACB PoU filters have yet to be fully characterized.

The faucet-mounted ACB PoU filter is a type of commercially available pressure filter that relies on physical adsorption and mechanical filtration to remove inorganic and organic chemicals of concern. The filter media, ACB, is composed of fine activated carbon powder that is held together by a polymer binder and molded into a solid cylinder block. A synthetic silica fabric mesh is wrapped around the ACB to protect the carbon surface against the outer plastic housing. The ACB PoU filter must be operated typically with a minimum line pressure of 138 kPa (20 psig) to achieve flow through the device (LLC, 2017). During operation, the influent water flows radially from the outside surface through the carbon block pore network, and then exits the filter from the center effluent channel of the ACB (Fig. 2-1). The filters are certified through National Sanitation Foundation/American National Standards Institutes Standard 42 and 53 for reducing particulate matter with diameters between 0.5 to  $< 1 \mu\text{m}$ , taste and odor from chlorine or chloramines, iron, manganese, hydrogen sulfide, heavy metals, fluoride, nitrate, nitrite and volatile organic chemicals (NSF /ANSI, 2015a, 2015b). The design process volumes of the devices are 100 gallons.



**Fig. 2-1 Cross sectional structure of ACB PoU filters**

The ACB-based filters are effective in controlling aesthetic and health-related chemical contaminants from the water, but are not intended to remove bacteria. A few studies evaluated the bacterial quality of faucet-mounted ACB PoU filters and found elevated heterotrophic bacteria counts in the effluent relative to filter influent concentrations (Chaidez and Gerba, 2004; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981). ACB PoU filters can also increase the abundance of certain groups or species in the tap water. Chaidez et al. (2004) found that the water treated by ACB PoU filters had higher levels of *Aeromonas hydrophila*, acid-fast organisms, *Pseudomonas aeruginosa* and total coliform than the influent tap water (Chaidez and Gerba, 2004). Total coliform, an indicator of enteric pathogens, can either persist in the carbon filter for several days after transient contamination occurred in the influent water (Tobin et al., 1981), or pass through the filters directly without growth or accumulation (Fiore and Babineau, 1977). The elevated abundance of heterotrophic bacteria in ACB PoU filters may reduce the sensitivity of total coliform culture assays. It was found, for example, that total coliform enumeration became unreliable when the heterotrophic plate counts exceeded 500-100 CFU/mL (Geldreich, 1978). Therefore, the total coliform abundance reported in these past studies may be underestimated.

The ACB PoU filters are suited for bacteria to grow because of several reasons. The filters remove chlorine or chloramine residual from the tap water and enrich organic carbons on the surface of the carbon. Granular activated carbon is capable of adsorbing various organic compounds, some of which can be substrates and nutrients for bacterial growth (Weber, Jr. et al., 1978). Wallis et al. found that the charcoals of the PoU filters that processed 600 gallons of drinking water can support the growth of drinking water indigenous bacteria (Wallis et al., 1974). Both heterotrophic and coliform bacteria can attach or colonize in cracks and crevices of carbon particles from granular activated carbon filters in drinking water treatment plants (Camper et al., 1986; LeChevallier et al., 1984).

Overnight and static water conditions may promote bacterial growth in the ACB PoU filters. The effluent of ACB PoU filters that were stagnated for eight hours produced one to two orders of magnitude higher heterotrophic bacterial effluent concentrations than those that were operated hourly (Tobin et al., 1981). Stagnation periods up to days can result in a much more significant increase of heterotrophic bacterial counts in the effluent of ACB PoU filters. Geldreich et al. 1985 discovered the heterotrophic bacterial counts from the first draw of filtered water increased  $10\text{-}10^4$  folds relative to the influent after a six-week no-flow period (Geldreich et al., 1985). Su et al. examined the effect of temperature on effluent quality of ACB PoU filters and found that higher temperature resulted in higher heterotrophic bacterial concentrations in the effluent (Su et al., 2009). Since after a long period of stagnation, the water temperature increases to room ambient temperature, this could be an important factor promoting for bacterial growth in ACB PoU filters.

Research has shown that ACB PoU filters can change the bacterial community composition of the influent tap water. Geldreich et al. (1985) spiked several opportunistic pathogens in one single dose with dechlorinated tap water to the ACB PoU filters and found certain species passed through the filters directly, including *Enterobacter cloacae*, *Escherichia coli* and *Salmonella typhimurium*. Species including *Citrobacteri freundii*, *E. aerogenes*, *Serratia marcescens*, and *Pseudomonas aeruginosa* colonized the filters and were detected in the effluent up to five months after their introduction (Geldreich et al., 1985). Su et al. (2009) evaluated the indigenous bacterial community differences between the influent and effluent of ACB PoU filters by feeding only tap water. Of seven species that were found in influent tap water, only *Acinetobacter lwoffii*,

*Brevundimonas vesicularis* and *Stenotrophomonas maltophilia* were detected in the effluent (Su et al., 2009). The reasons that some species were not present in the effluent are unclear. It is possible that some species are incapable of competing for nutrients and organic substrates with indigenous bacteria that colonized on the activated carbon (Rollinger and Dott, 1987).

Most of the past studies are constrained by their reliance on culture dependent methods, which can only detect a small fraction of the drinking water bacterial population (Allen et al., 2004). These studies may underestimate the total abundance of bacteria that can be increased by ACB PoU filters and thus overlook the overall shifts in bacterial composition altered by the ACB PoU filters. Future studies should apply both culture-based and culture-independent approaches to examine how the microbial ecology of tap water is changed by the PoU ACB filters.

## **2.2 Bacterial abundance and composition in drinking water**

The growth conditions for in ACB PoU filters can be similar with the drinking water condition. Reported total concentrations drinking water bacteria range from  $10^3$  to  $10^6$  cell/mL (Berry et al., 2006; Hammes et al., 2008; Hoefel et al., 2003). The most ubiquitous bacteria genera in treated drinking water include *Acidovorax*, *Curvibacter*, *Sphingomonas*, *Aeromonas*, *Acinetobacter*, *Pseudomonas*, *Legionella*, *Rhodococcus*, *Gordonia*, *Mycobacterium*, *Flavobacterium*, *Bacillus* and *Clostridium* (Vaz-Moreira et al., 2014). These drinking water bacteria may have a few of the following attributes to counteract the stresses caused by oligotrophic drinking water conditions: the ability of alternating living states between planktonic and surface-attached stages, the ability of utilizing organic carbon or other limiting compounds, and the ability to grow in the starvation-survival lifestyle.

The physiological states of bacteria change in response to the stress in the environment. Firstly, the size of bacterial cells may become smaller. It has been found that the sessile and planktonic bacterial cells are able to reduce to a size of 0.3  $\mu\text{m}$  (Bartram et al., 2003). Smaller sized bacteria have a larger surface/volume ratio and thus achieve a more efficient uptake of nutrients and carbon substrates under oligotrophic conditions. Secondly, some bacteria may enter into a viable but non-culturable (VBNC) state. In this state, the bacteria are metabolically active, while being incapable of undergoing the sustained cellular division required for growth in or on a medium normally supporting growth of that cell.

Biofilm formation enhances the ability of drinking water bacteria to adapt to changing environmental conditions and resistance to disinfectants. Biofilms provide protection for bacteria from predation by bacteriophage, amoeba, and free-living protozoa (Donlan, 2002). Bacteria in the biofilm live in close proximity and thus are capable of perceiving and responding to the presence of neighboring microbial populations, which is recognized as quorum sensing (Donlan, 2002). Organic matter in drinking water is mostly polymeric and high-molecular-weight substances (Escobar et al., 2001) that are hard to utilize by a single organism. The metabolically diverse consortia in biofilms can utilize different components of drinking water NOM, and metabolites produced by one organism may become useful substrates for other organisms (Bartram et al., 2003). In addition, the extracellular polymeric substances (EPS) in biofilms have different reactivity towards monochloramine (Xue et al., 2014) and chlorine (Xue et al., 2012); in both cases, however, EPS reduces the concentration of disinfectants within biofilms. Therefore, bacteria residing in biofilms can be protected from disinfectants, including members of *Pseudomonas*, *Acinetobacter*, *Flavobacteria*, *Legionella*, *Mycobacterium*, and *Sphingomonas* (Chiao et al., 2014; Santos et al., 2016; Wolfe et al., 1985).

Most drinking water bacteria have limited public health significance; however, pathogenic bacteria can be present in drinking water and are known sources of waterborne disease (Beer et al., 2015). Nowadays, waterborne disease in the US is largely due to opportunistic pathogens as the exposure likelihood to waterborne enteric pathogen has declined (Gargano et al., 2017). Due to the compliance of drinking water treatment regulation, the mortality of gastrointestinal infections from enteric pathogens decreases throughout the years (Beer et al., 2015; Craun et al., 2010). Gargano et al. compared the mortality rates from diseases that can be transmitted by water in 2003-2009 periods in the USA and found that the most deaths were due to the infections caused by opportunistic pathogens (Gargano et al., 2017). A total of 6939 annual total deaths that were associated with 13 infections from waterborne pathogens were documented. Among them, only 7% were associated with enteric pathogens (493 deaths) including *Campylobacter*, *E. coli*, *Salmonella*, and *Shigella*, as well as enteric parasitic and virus (Gargano et al., 2017). Infections associated with the opportunistic pathogens including *Pseudomonas* (4855 deaths, 70%), nontuberculous mycobacteria (NTM) (1216 deaths, 18%), and *Legionella* (Legionnaires' disease, 250 deaths, 4%) caused 91% of deaths in the study. Below we discussed the risk of *P. aeruginosa*, NTM, and enteric-related pathogens that are common in drinking water.



*P. aeruginosa* can cause infections in the lungs, urinary tract, and surgical wound. The infective dose for *P. aeruginosa* is quite high for healthy individuals. In one study, no disease symptoms were evident in healthy subjects even after exposure to oral doses up to  $2.0 \times 10^8$  CFU (Buck and Cooke, 1969). However, immunocompromised patients are at high risk of developing *P. aeruginosa* infections, including pneumonia, bacteremia, and urosepsis (Victorica and Galván, 2001). *P. aeruginosa* was isolated from the burns and scabs of 50-60% of hospitalized patients, as opposed to 1.2-6% of healthy individuals (Botzenhart and Döring, 1993). Therefore, waterborne *P. aeruginosa* is viewed as a significant source of infections in healthcare settings.

Nontuberculous mycobacteria (NTM) are common heterotrophic bacteria that can be found in various terrestrial and aquatic environments (Tortoli, 2003). Among NTM, some species such as *M. avium* pose potentially pathogenic effects to humans or animals; whereas some are non-pathogenic or only exceptionally pathogenic. These mycobacterium species are named as "nontuberculous" to be differentiated from other obligate pathogenic mycobacteria that are generally not found in the environment, such as *Mycobacterium tuberculosis* or *M. leprae* (Tortoli, 2003).

The majority of NTM infections are caused by *Mycobacterium avium* complex (MAC), which is comprised of *M. avium* and *M. intracellulare* (Falkinham et al., 2001). MAC can cause infections in lungs, gastrointestinal tract, skin and soft tissues particularly in immunocompromised patients. (Jones et al., 1995; Prince et al., 1989; Rosenzweig and Schlueter, 1981). Information about the infectious dose of MAC was developed from mice models, showing that multiple oral doses of  $10^4$  -  $10^8$  CFU of *M. avium* increased the mortality and infection rate of mice (Bermudez et al., 1992). The precise mode of transmission of MAC from contaminated drinking water could be ingestion and inhalation. However, the relationship of the exposure pathways to MAC did not link well with the infection rate, thus the risk of exposure to MAC from drinking water systems is still unclear and needs further study (National Research Council, 2006).

The waterborne enteric bacteria that have been detected in US drinking water in recent ten years include *Campylobacter*, *E. coli*, *Salmonella*, and *Shigella* (Gargano et al., 2017). Enteric bacteria are able to colonize the human intestinal and gastrointestinal tract. The infectious dose of *Salmonella* for healthy individuals is in the range of  $10^7$ - $10^8$  cells, while some hundred cells only

are required to cause clinical illness with *E. coli* O157:H7, *Campylobacter* and *Shigella*. There are enteric-related opportunistic pathogens that pose potential health effects to human, including *Klebsiella pneumoniae*, *Enterobacter aerogenes*, *Enterobacter cloacae*, and *Citrobacterium freundii* (National Research Council, 2006). The enteric-related pathogens are expected to be removed during drinking water treatment process, as regulated by the Federal regulation under the Safe Drinking Water Act. Violations tend to be infrequent but cannot be neglected. There were 95,754 violations that pose immediate health concerns in the period of 1982-2015 (Allaire et al., 2018). Total coliform and *E. coli* violations occurred most frequently, representing 37% and 2 % of all health-based violations. Presence of coliforms in the drinking water distribution system is usually interpreted to indicate an external contamination event occurs. Aging distribution network may have fractures, corruptions, leaky joints, and main breaks, and thus no longer provide a barrier against external contamination. Localized neighborhoods suffering from disrepair within the drinking water distribution system, therefore, have a higher probability of contamination by enteric-related bacteria.

Little is known about the fate and survival of either opportunistic pathogens or enteric bacteria in PoU filters. The bacterial growth in the ACB PoU filters raises the question that if the use of ACB PoU filters increases the risk of exposing bacterial health hazards from drinking water. Since the bacterial composition in drinking water could be reshaped by the ACB PoU filters, it is highly possible that the PoU filter environment will also influence the fate of these bacterial species of concern within the PoU filters, as well as the filter effluent. To determine if the enteric-related pathogens and the opportunistic pathogens can be enriched and enter to the filter effluent, the mechanisms of bacterial migration through the filters should be evaluated.

### **2.3. Potential dissemination of antibiotic resistance genes in ACB PoU filters**

Bacteria that evolve resistance mechanisms to a group or multiple groups of antibiotics are antibiotic resistant bacteria (ARB). These bacteria derive resistance to antibiotics due to chromosomal gene mutations and inductive expression of the antibiotic resistance genes (ARGs) (Neu, 1992). The ARGs can be originally within chromosomal DNA or are taken up from other bacterial species by horizontal gene transfer. Infections caused by antibiotic resistant pathogens are more difficult to treat than those caused by non-resistant pathogens. During the past decades,

the overuse of antibiotics has led to an increased discharge of antibiotics into the environment, especially from the waste streams and agricultural runoff (Baquero et al., 2008). The released antibiotics select for and increase naturally occurring ARB in aquatic environment. Therefore, the spread of antibiotic resistance has led to higher medical costs, prolonged hospital stays and increased mortality, thus becoming one of the major challenges in 21<sup>st</sup> century (Cosgrove, 2006; Li and Webster, 2018).

Bacteria can disseminate antibiotic resistance between species by horizontal gene transfer or vertical transfer. The mechanisms of horizontal gene transfer among bacteria are transformation, a bacterium takes up extracellular DNA donated from the other bacterial cell; and conjugation, a bacterium takes up the plasmid from the other bacterial cell through direct contact. Conjugation with plasmid transfer of DNA is particularly common in the *Enterobacteriaceae* family and *Pseudomonas* (Neu, 1992). The bacteria that have intrinsic antibiotic resistance can disseminate the ARGs by vertical transfer. Such intrinsic antibiotic resistance is often regulated by multiple genes, and is unlikely to be shared with other species through horizontal gene transfer. Intrinsic resistance genes thus can only be passed to the offspring cells by the original bacterial host. An important example of an intrinsic resistance mechanism that is common in drinking water is the multidrug efflux pump system (Ma et al., 2017).

Biofilm formation in ACB PoU filters may facilitate horizontal gene transfer and enrichment of the ARGs. Horizontal gene transfer of ARGs can occur in drinking water biofilms because of the density of proximate and competent bacteria (Hausner and Wuertz, 1999; Madsen et al., 2012; Ohlsen et al., 2003). In biofilms of a drinking water treatment plant, mobile genetic elements that are capable of acquiring ARGs, class 1 integrons gene cassettes (*intI1*, *qac*, and *sul* genes), were found and may facilitate genes exchange among drinking water bacteria (Farkas et al., 2013). In addition, diffusion of disinfectants into EPS and other biofilm components can expose bacteria to sub-inhibitory concentrations of disinfectants, albeit briefly due to the reactivity of disinfectants with the biofilm (Xue et al., 2014, 2012). Sub-inhibitory concentrations of disinfectants such as chlorine, chloramine, H<sub>2</sub>O<sub>2</sub>, or certain disinfection byproducts (chlorite and iodoacetic acid) can induce the SOS stress response in bacteria and thus enhance a higher frequency of conjugative gene transfer in biofilms (Li et al., 2016; Zhang et al., 2017).

The ACB PoU filters may change the distribution of antibiotic resistance genes by altering the bacterial community structure of the tap water. At the influent side of ACB PoU filters, bacteria may form biofilms that are intermittently exposed to disinfectant residuals from the influent during filter use, then remain stagnant when the filter is not in use (Fig. 2-1). Jia et al. proposed the shifts of bacterial community structures due to chlorination simultaneously alter the distribution of antibiotic resistances in the drinking water (Jia et al., 2015). The chlorination disinfection process is likely to be the major selection factor for certain ARB in drinking water. Khan et al. recovered chlorine-resistant bacteria from the drinking water and found they are resistant to multiple antibiotics, including tetracycline, sulfamethoxazole and amoxicillin (Khan et al., 2016). Common genera that are resistant to disinfectants (Chiao et al., 2014; Wolfe et al., 1985) in treated drinking water, such as *Sphingobium*, *Sphingomonas*, *Pseudomonas* and *Acinetobacter*, have intrinsic ARGs on their chromosomal genomes (Vaz-Moreira et al., 2014) and may be selected for in ACB PoU filters.

Chemicals, such as DBPs, can be adsorbed on ACB PoU filters and may affect the antibiotic resistance of colonizing bacteria. Chlorinated phenols are a group of DBPs that form as intermediate disinfection byproducts (DBPs) when phenolic moieties react with chlorine to ultimately yield regulated DBPs (Pomes et al., 2000). Our research group found that chlorinated phenols can upregulate the multidrug efflux pump in *Pseudomonas aeruginosa* (Ghosh et al., 2011). This response causes *P. aeruginosa* to efflux several antibiotics, including fluoroquinolones,  $\beta$ -lactams, tetracyclines, chloramphenicol, and sulfonamide (Ghosh et al., 2011). In drinking water, halogenated phenols seldom exceed 100 ng/L in different drinking water utilities (Sithole and Williams, 1986). While chlorinated phenols in drinking water are low, they would be concentrated at the surface of the activated carbon filter media. Bacteria that colonize within the filter can be exposed to higher chlorinated phenol and may develop antibiotic resistance.

## 2.4 References

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## Chapter 3

### **The microbial colonization of activated carbon block point-of-use (PoU) filters with and without chlorinated phenol disinfection byproducts**

#### **3.1 Introduction**

Point of use (PoU) drinking water filtration devices are increasingly deployed by consumers as a stopgap approach to deal with tap water quality concerns, including inorganic and organic chemicals as well as taste and odor issues. Only limited research has been undertaken, however, to determine the effect these all-in-one treatment devices have on bacteria from the distribution system that pass into filters when the faucet is turned on. Given that the structure and abundance of bacterial communities in drinking water distribution systems, including opportunistic pathogens, are known to shift in response to the concentration of disinfectants, halogenated and non-halogenated organic compounds, metals, and nutrients (Gillespie et al., 2014; Stanish et al., 2016; Wang et al., 2014), it is reasonable to expect that PoU filter performance will also influence the fate of bacteria within filters and, consequently, in filtered drinking water. Given that 2 and 19% annual market growth in PoU devices is expected over the next decade until 2030 in developed countries and developing countries with fast growing economies (Freedonia, 2013), respectively, more research is needed to examine the microbial ecology of these devices under the conditions they are used so that risks that come from employing PoU filters can be understood.

Commercial PoU filters in the United States most commonly employ activated carbon as the primary filter and adsorbing material, although materials and designs in other countries are more varied. Faucet-mounted PoU filters, the type considered in our study, consist of a fabric pre-filter and a low-porosity activated carbon block (ACB). Their carbon block design requires line pressures of at least 210 kPa (30 psi) for water throughput as a result of their very low porosity, and thus these filters are unlikely to allow influent microorganisms to traverse the entire filter media depth as long as the ACB is not cracked or otherwise compromised during use. ACB PoU filters are certified for water quality through NSF/ANSI Standards 53 and 42, which target

removal of health-based (heavy metals, fluoride, nitrate, and a range of volatile organic chemicals) and aesthetic (chlorine for taste-and-odor concerns, chloramine, iron, manganese, hydrogen sulfide, zinc) contaminants (NSF International/ANSI, 2015a, 2015b). Notably, the certification does not include removal of bacteria. Indeed, the World Health Organization has long held that any PoU filter with an activated carbon base is inappropriate to use in poorly disinfected waters because it will support the excessive growth of bacteria and increase the risk of enhancing pathogen levels (Sobsey, 2002).

Only a few published studies have evaluated changes in microbial community abundance or composition across ACB PoU filters. These studies used culture-based methods and consistently showed that bacterial counts are elevated in filtered water relative to the influent tap water (Chaidez and Gerba, 2004; Geldreich et al., 1985; Molloy et al., 2008; Reasoner et al., 1987; Su et al., 2009b; Tobin et al., 1981; Wallis et al., 1974). In addition, when changes in microbial diversity were tracked across PoU filters in one study, diversity decreased even as total cell counts increased (Su et al., 2009b). Culture-based studies have implicated the enrichment of opportunistic pathogens like *Pseudomonas aeruginosa* (Chaidez and Gerba, 2004) and *Stenotrophomonas maltophilia* (Su et al., 2009b) across the filter. Given that PoU filters are user-maintained, wide variations in usage patterns that may impact bacterial colonization and filtered water microbial quality are possible. These studies indicate that ACB PoU filters change the microbial community counts and composition that consumers are exposed to relative to tap water; however, the impact of this shift on public health is not well characterized. Importantly, past studies are constrained by the use of culture-based methods; culture-independent techniques coupled with culture-based methods can provide a more comprehensive understanding of how PoU filters influence drinking water microbial ecology.

Since PoU filters are designed to remove halogenated DBPs, it is logical to ask whether DBP accumulation within filters has a significant impact on the microbial communities that colonize them. We are particularly interested in chlorophenol-based DBPs, which are unregulated DBPs that are formed from phenolic moiety precursors in natural organic matter at low levels in response to both chlorine and monochloramine (Heasley et al., 2004; Rebenne et al., 1996). Our past work showed that chlorinated phenols upregulate the MexAB-OprM multi-drug resistance

efflux pump in *P. aeruginosa* (Ghosh et al., 2011), which may make bacteria with this or similar efflux pumps vulnerable to enhanced biofilm formation because quorum sensing molecules are also released by these systems (Martinez et al., 2009; Maseda et al., 2004). We hypothesize that chlorophenol-based DBPs may enhance microbial colonization of PoU filter surfaces. Indeed, our preliminary data suggest that chlorophenols induce biofilm formation by *P. aeruginosa* (data in Section A.1 in Appendix A).

In this study, we evaluated how bacteria colonized PoU filters with and without a supplemental chlorophenol-based DBP. We selected pentachlorophenol (PCP) as our model DBP, which has the strongest effect among the chlorophenols we have studied on the MexAB-OprM system (Ghosh et al., 2011), and applied it at 100 ng/L and below to mimic concentrations of chlorinated phenols detected in the few drinking water studies where these chemicals have been monitored (Michałowicz, 2005; Sithole and Williams, 1986; Zhao et al., 2012). By conducting experiments with and without PCP, we were able to evaluate the relative impact of PoU filter architecture versus the role of trace DBP concentrations on microbial ecology.

### **3.2 Materials and Methods**

#### **Bench-scale PoU manifold system**

A manifold system (Fig. S3-1) with three pairs of commercial PoU filters (faucet-mounted type) was fed with municipal tap water (Ann Arbor, Michigan) and the influent to each pair was spiked with 0, 50, or 100 ng/L of PCP (Fig 3-1). Each PoU filter consisted of an annular activated carbon block (ACB) surrounded by a synthetic fabric mesh, which serves as an ACB prefilter. The ACB is held together with a proprietary, low melting point polymer binder. Surface areas, average pore size, and porosities of the carbon block material were determined for three unused filters with a pressure sorption analyzer (Micromeritics, ASAP 2050) (Table S3-2). The fabric mesh was separated based on visually apparent layers, and consists of at least three distinct layers of synthetic silica or polymer-coated silicic fibers, as determined by scanning electron microscopy and X-ray microanalysis (Fig. S3-2). Water radially flowed from the fabric face, through the ACB, and exited through the inner channel of the filter directly into an effluent reservoir (without connection tubing). Effluent reservoirs were autoclaved on days when samples were collected to perform microbiological analysis. Sterile foil was applied loosely over the PoU

filter – effluent reservoir opening to protect the effluent reservoir from contamination not associated with the PoU filter flow.

Influent reservoirs were filled at the beginning of each daily cycle with tap water, which was spiked with a known amount of base-solubilized PCP stock solution to meet the influent target concentrations. Before filling influent containers, the tap water was allowed to run at least 15 minutes until a steady-state water temperature was achieved to purge stagnant water from the plumbing. The source of Ann Arbor municipal water supply is primarily Huron River water that is treated using lime softening and coagulation, settling, ozonation, filtration, and chloramination.

To simulate the daily on-off flow and stagnation periods of normal household use, influent water was pumped (Brass Rotary Vane Pump, Procon) intermittently from covered influent reservoirs to the three manifold systems. The pump program was set to run once hourly for 16 hr, followed by a night time stagnation period of 8 hr. A design daily process volume of about 8 L was targeted and the filters were operated for 67 days. Due to decreases in hydraulic permeability in the filters over the course of the experiment, filter cycles were gradually lengthened in an attempt to maintain a constant daily process volume; however, the daily process volume gradually decreased toward the end of the run to around 7 L/day. Exact process volumes were determined by weighing the effluent reservoir. The total processed volume for each filter averaged 137% of the manufacturer's rated design process volume for the filter cartridge (100 gallons, or 379 L) (Table S3-3).

At the end of the run period, each PoU filter was cut open and photographed (Fig. S3-3). The fabric mesh surrounding the PoU filter media were removed using aseptic technique from the carbon block, photographed (Fig. S3-4) and stored at either -20 °C for exocellular polymeric substance (EPS) analysis or -80 °C for nucleic acid-based analyses; methods for both are given below.

#### Water quality analyses

Samples were collected for water quality analysis from the influent and effluent according to the schedule in Table S3-4. The frequency (daily, weekly or bi-weekly) and type (grab or two-week composite) of samples collected varied for different sample locations and water quality parameters are also described in Table S3-4. All analyses were in accordance with Standard

Methods (APHA et al., 2005). Briefly, total alkalinity was analysed using the titration method according to Standard Method 2320. The free chlorine and total chlorine were measured by the N, N-diethyl-p-phenylenediamine (DPD) colorimetric method (Standard Method 4500-Cl G) with a pocket colorimeter (Hach, Loveland, CO). Heterotrophic plate counts (HPCs) were performed by the R2A spread plate method (Standard Method 9215C) or membrane filter method for counts  $\leq 10^2$  CFU/mL (Standard Method 9215D). Dissolved (DOC) and total organic carbon (TOC) were determined using a Shimadzu ASI-V TOC analyzer equipped with an infrared detector (Standard Method 5310B). Specific UV absorbance was determined by Standard Method 5910 B, and analysis of chlorophenols (di-, tri- and pentachlorophenol) is described in Section 6 of Electronic Supplemental Information. Finally, pH was monitored using an Orion 3-Star Benchtop pH meter (Thermo Fisher Scientific, Beverly, MA). The probe calibration was confirmed at least once daily when in use.

#### Total protein and extracellular polymeric substance (EPS) measurements of the fabric biomass

Biomass from each of the six PoU filter fabric samples was extracted at the end of the experiment and the concentrations of total protein, EPS protein, and EPS carbohydrate were determined. Fabric samples were cut into 1.5 x 1.5 cm<sup>2</sup> sections, which were then cut into small pieces and placed in glass vials with 8 mL of deionized water. EPS was isolated from the fabric via sonication. The samples were sonicated in an ice bath for 30 s at 25% amplitude (150 J/mL) with a ¼” diameter microtip sonicator (Model VCX500, 750 watts, Cole Parmer, Vernon Hills, IL). The sonication setting was optimized to yield maximum carbohydrate and protein while limiting cell lysis (Pellicer-Nàcher et al., 2013). Following sonication, the liquid phase was filtered through a 0.2 µm PVDF syringe filter to remove cells and fabric debris from solution. Carbohydrate was measured by the phenol-sulfuric acid method (Masuko et al., 2005). EPS protein was measured from the filtered liquid phase using the micro-bicinchoninic acid (microBCA) method (Smith et al., 1985). To measure total protein, cell lysis of fabric samples was accomplished by heating at 95°C in a 0.1 M sodium hydroxide solution for one hour. The cooled solution was sonicated using the same settings as were used for EPS extraction to reduce biomolecule clumping. The liquid phase was filtered through a 0.2 µm PVDF syringe filter and analyzed using the microBCA method. We confirmed that clean fabric from an unused PoU filter

did not interfere with the total protein method. Cellular protein was calculated as the difference between total protein and EPS protein.

#### DNA extraction from fabric and water samples

DNA was extracted from influent and effluent water samples on two to four dates for each treatment over the last three weeks of operation. Two liter water samples were filtered through sterile 0.22  $\mu\text{m}$  polycarbonate membrane filters (Millipore GTTP04700, Billerica, MA). DNA was also extracted from the six PoU fabric pieces that had been handled in a sterile manner and stored at  $-80^{\circ}\text{C}$ . Each PoU fabric was cut into four equal strips with an area of  $2.25\text{ cm}^2$  serving as sample replicates. Both polycarbonate membrane filters and fabrics were cut further into small pieces for DNA extraction. A three-step bead beating method with lysis buffer was evaluated and chosen (based on DNA recovery) as the best method to extract DNA. Polycarbonate membrane filter and PoU fabric pieces were added to  $300\ \mu\text{L}$  lysis buffer provided with the DNA IQ™ Reference Sample Kit for MaxWell® 16 (Promega, Madison, WI, USA) with  $0.5\text{ g}$  zirconium beads (previously baked at  $400\ ^{\circ}\text{C}$  for 4 hours) and beaten for 2 minutes using a Bead Beater (BioSpec, Bartlesville, OK, USA). After centrifuging at  $12,500\times g$  for 10 min to pellet the beads and particulate matter, the aqueous phase was collected. The process was repeated two more times as described except that only  $150\ \mu\text{L}$  lysis buffer was added at the start. The aqueous phase was collected after each process and composited into a single vial for DNA purification. Sixty microliters of Proteinase K ( $20\text{ mg/mL}$ ) was added to the cumulative liquid phase volume and incubated at  $56^{\circ}\text{C}$  for 20 minutes to remove nucleases. DNA was purified with a Maxwell 16 automated DNA extraction instrument (Promega, Madison, WI, USA) and eluted in  $50\ \mu\text{L}$  elution buffer provided in DNA IQ™ Reference Sample Kit for MaxWell® 16 (Promega, Madison, WI, USA). The amount of DNA extracted was quantified using PicoGreen reagent (Invitrogen, Carlsbad, CA, USA) and ranged from  $0.16$  to  $64\text{ ng}/\mu\text{L}$ . Using the same extraction and DNA quantification protocol, a blank extraction conducted with nuclease-free water yielded a DNA concentration of  $0.01\text{ ng}/\mu\text{L}$ . The final concentrations (based on amount extracted) of DNA in water samples or on fabric mesh are given in Table S3-5.

#### 16S rRNA gene PCR and sequence analysis

DNA extracts were submitted for 16S rRNA gene amplicon sequencing at the University of Michigan Medical School using the protocol outlined by Kozich *et al* (Kozich et al., 2013). This protocol uses dual index-labeled primers that target the V4 region of bacterial and archaeal 16S rRNA genes (515F/806R) (Caporaso et al., 2012). Pooled and purified libraries were sequenced on an Illumina MiSeq sequencer, using v2 chemistry 2x250 (500 cycles) paired-end reads. A total of 1,862,282 sequences were obtained from the 54 samples sequenced for this study to compare the similarity of bacterial community composition and structure between treatments. The raw data are available at the NCBI Sequence Read Archive database under access No. SRP072518. All data processing was conducted using Mothur (v 1.32.1)(Schloss et al., 2009) based on the MiSeq standard operating protocol accessed on April 2013 using SILVA Release 102 April 2012 for alignment. After data quality filtering (including chimera removal), a total of 1,521,189 sequences were retained in the final data library (Table S3-6). The sequences were assigned a taxonomy using naïve Bayesian Classifier(Wang et al., 2007) with a confidence threshold of 80%. The sequences were clustered using the average neighbor approach to form operational taxonomic units (OTUs) with a sequence similarity cutoff of 97% (3% sequence divergence). Consensus taxonomy for each OTU was determined using classify.otu with a consensus taxonomy cutoff = 51%.

### Statistical analysis

Nonparametric Shannon diversity(Chao and Shen, 2003) and Shannon evenness indices (Hill et al., 2003) were estimated in Mothur (v 1.35.0) (Schloss et al., 2009). The nonparametric Shannon index ranges between 0 and unbounded values, with higher values indicating both higher richness and evenness. Shannon evenness ranges between 0 and 1, with 0 indicating not even and 1 indicating completely even composition. Sequences were subsampled to the depth of the sample with lowest sequence count (8,906 sequences). A neighbor-joining tree of the sequences constructed with Clearcut (Evans et al., 2006) was analysed by unweighted and weighted UniFrac metrics as implemented by Mothur (Lozupone and Knight, 2005). The significance of UniFrac reported dissimilarities between samples (i.e. *p* values) were determined by conducting 1000 random permutation tests. The unweighted Unifrac accounts for the presence and absence of observed taxa between samples to estimate the dissimilarity between them, while weighted Unifrac incorporates the differences in relative abundance of observed taxa



between samples to estimate dissimilarity (Lozupone et al., 2007). Jaccard and abundance-based Jaccard (Chao et al., 2005) are OTU-based dissimilarity indices that are used to assess the overlap between different sample locations or PCP treatments. Distance indices between location or PCP treatment groups were compared by nonparametric Kruskal-Wallis rank sum test. The UniFrac-based distance matrices were imported into R (<http://www.r-project.org>) for permutational multivariate analysis of variance (PERMANOVA) using the "vegan" package. Two-dimensional Principle Coordinate Analysis (PCoA) plots were generated to visualize the similarity between bacterial communities based on the UniFrac distance metrics. Permutational univariate analysis of variances (PERANOVA) were performed to compare the Unifrac distances within each replicate to the average of pooled samples, thus further confirming whether the two dimensional clustering patterns seen in the PCoA plots were statistically supported by differences in the distance matrices (Schloss, 2008). We used corr.axis to determine the OTUs driving the clustering pattern as observed using the distance matrices constructed from UniFrac metrics (Pearson correlation,  $p < 0.05$ ). The Kruskal-Wallis test was conducted to compare the diversity indices and relative abundance of OTUs between sample types or PCP treatments.

### qPCR

Selected influent and effluent DNA samples from different collection dates, and fabric DNA samples from different extraction replicates were composited to determine total bacterial 16S rRNA gene by quantitative PCR (qPCR). qPCR was performed on an eppendorf® Mastercycler (Eppendorf, Germany). The PCR mixture (10  $\mu$ L) consisted of Fast-Plus EvaGreen Master Mix (Biotium, CA, USA), primer sets (0.5  $\mu$ M each, Eub338: 5'-ACT-CCT-ACG-GGA-GGC-AGC-AG-3', Eub518: 5'-ATT-ACC-GCG-GCT-GCT-GG-3') (Fierer et al., 2005), 0.625 mg/mL BSA, and 1  $\mu$ L template DNA. Nuclease free water and genomic DNA of *P. aeruginosa* were included in all qPCR assays as negative and positive controls, respectively. All analyses were performed in triplicate. A standard curve was generated by amplifying 8-fold serially diluted PCR amplicons with a known amount of gene copies for each targeted gene. The thermal cycling program was set at 95°C for 2 min, followed by 35 cycles of 5 s at 95°C, 5 s at 58°C, and 25 s at 72°C. A melting curve was used to ensure specificity of amplification.

### **3.3 Results**

Effluent heterotrophic bacteria concentrations exceed influent levels.

Influent and effluent HPC profiles are presented in Fig. 3-2 over the 67-day operating period of the PoU manifold system. Influent HPC concentrations were relatively stable across all treatments (with and without PCP) and ranged between  $10^1$  and  $10^3$  CFU/mL with a mean concentration of  $1.6 \times 10^2 \pm 2.5 \times 10^2$  CFU/mL. In contrast, effluent HPC values increased for all treatments over the first 30 days of operation when counts increased rapidly (some counts could not be recorded because dilutions were insufficient to allow reliable counts). Effluent samples eventually stabilized at an average of  $2.3 \times 10^4 \pm 1.0 \times 10^4$  CFU/mL after 40 days or when the filters were at approximately 85% of the manufacturer's recommended maximum throughput volume. The average DNA concentrations extracted from the influent and effluent samples were  $10 \pm 4$  and  $390 \pm 320$  ng/L, respectively (Table S3-5), and corroborate the large increase in cell abundance in the effluent. Culture-based methods are vulnerable to underestimation due to an inability to cultivate a wide range of bacteria on a single growth medium and due to a cell's entry into a "viable but not culturable" growth state (Trevors, 2011), and extracted DNA from environmental samples is vulnerable to overestimation due to extracellular DNA or DNA associated with non-viable cells (Frostegård et al., 1999); nevertheless, considered together, these data indicate a substantial and statistically significant increase in bacterial cell abundance between influent and effluent.

PCP exposure impacted the fabric biofilm in a way that is only partly explained by biofilm biochemical composition.

The fabric surrounding the influent side of the ACB serves as a "pre-filter" and we expected it would develop a significant biofilm. After opening the filters at the end of the experiment (Fig S3-3), we observed distinct fabric coloration differences between the control and PCP-fed filters (Fig. S3-4). The control fabrics were dark grey (Fig. S3-4 (b)) while the fabrics from all filters exposed to PCP were medium (50 ng/L, Fig S3-4(c)) to light tan (100 ng/L, Fig S3-4 (d)); in contrast, unused fabric mesh was bright white. To determine if color variations between treatments were due to differences in either biomass amounts or extracellular polymer (EPS) composition across PCP treatments, protein and carbohydrate analyses were conducted on the biofilm. As demonstrated in Fig. 3-3, averages of total protein were  $40 \pm 9.0$ ,  $41 \pm 5.2$ , and  $36 \pm 2.1$   $\mu\text{g BSA}/\text{cm}^2$  for 0, 50, and 100 ng/L PCP treatment, respectively. Cell protein averages were  $21 \pm 10$ ,  $21 \pm 8.6$ , and  $25 \pm 2.9$   $\mu\text{g BSA}/\text{cm}^2$  for 0, 50, and 100 ng/L PCP treatment, respectively.

There was no significant impact of PCP treatment on either total biomass (via total protein,  $p=0.45$ ) or cellular protein (total protein – EPS protein,  $p=0.71$ ), indicating that exposure to 100 ng/L PCP over the lifetime of a PoU filter did not influence the extent of overall biofilm growth and that differences in total cell mass do not explain the shift in biofilm color across PCP treatments. EPS carbohydrate concentrations averaged  $7.9 \pm 2.7$ ,  $6.9 \pm 2.2$ , and  $7.7 \pm 1.1$  mg glucose/cm<sup>2</sup> for 0, 50, and 100 ng/L PCP treatment, respectively, and was also not significantly different across treatments ( $p=0.83$ ). The EPS protein for the 100 ng/L PCP treatment ( $11 \pm 1.5$  µg BSA/cm<sup>2</sup>) was significantly lower than the control ( $19 \pm 2.4$  µg BSA/cm<sup>2</sup>) and 50 ng/L PCP treatments ( $18 \pm 1.6$  µg BSA/cm<sup>2</sup>) based on Tukey's pairwise analysis ( $p=0.49$  for 0 vs. 50 ng/L,  $p=0.002$  for 0 vs. 100 ng/L, and  $p=0.001$  for 50 vs. 100 ng/L PCP treatment). In turn, averages of the EPS carbohydrate:protein ratio were  $0.4 \pm 0.5$ ,  $0.3 \pm 0.4$ , and  $0.6 \pm 0.2$  for 0, 50, and 100 ng/L PCP treatment, respectively; the ratio for the 100 ng/L PCP treatment was significantly higher than the 50 ng/L PCP treatment ( $p<0.05$ ) based on Tukey's pairwise analysis ( $p=0.79$  for 0 vs. 50 ng/L,  $p=0.13$  for 0 vs. 100 ng/L, and  $p=0.03$  for 50 vs. 100 ng/L PCP treatment). These results indicate that the extent of cell formation on the PoU filter fabric was similar across all three treatments. This result, however, does not exclude the possibility that changes in microbial community composition and function could have caused the color shade change in the biofilms.

#### Bacterial community structure is influenced primarily by PoU filter configuration.

The community diversity in the control (0 ng/L PCP) influent, fabric, and effluent samples changed significantly across the PoU filters. The number of dominant OTUs (defined here as taxa having a relative abundance equal to or greater than 1%) in influent, fabric and effluent samples were 34, 22 and 15, and represented 75, 87 and 94 % of the total characterized communities, respectively. A nonparametric Shannon index and Shannon evenness index were computed for influent ( $4.17 \pm 0.24$  and  $0.66 \pm 0.02$ ), fabric ( $3.15 \pm 0.03$  and  $0.54 \pm 0.01$ ), and effluent ( $2.40 \pm 0.04$  and  $0.49 \pm 0.04$ ) communities, respectively; both indexes are statistically different between the three sample locations based on Kruskal-Wallis test ( $p < 0.05$ ). This suggests that influent communities had the highest diversity and a slightly more even structure because influent samples had more minor taxa with a relative abundance smaller than 1% compared to other sample types. Conversely, effluent communities were dominated by only a handful of OTUs, were the least diverse, and the least even among the three sample locations.

A relative abundance analysis exemplified these community differences across sample locations (Table A in Appendix D). The most “highly dominant” (defined as  $\geq 5\%$  relative abundance) OTUs are mostly distinct (Table 1) and show informative patterns. Influent samples were dominated by *Hydrogenophaga sp.*, which was also the second most abundant in effluent communities but of modest abundance in fabric communities. Three other OTUs (two Unclassified *Bacteroidetes* and *Brevundimonas*) were “highly dominant” in the influent and present in decreasing relative abundance along the water flow path, suggesting the filter imposed a selective pressure against these taxa in contrast to others that became more abundant. These four OTUs plus other lower abundance OTUs that became less abundant across the flow path are designated as “filtered OTUs” (blue shaded bars) in Fig. 3-4. “Highly dominant” fabric OTUs (including *Sphingopyxis sp.*, *Mycobacterium sp.*, *Aquabacterium sp.*, *Acidovorax sp.* and an unclassified *Sphingomonadaceae*) are classified as “attached OTUs” (red shaded bars) in Fig. 3-4. Finally, the most “highly dominant” OTUs found in the effluent (an unclassified *Proteobacteria*, an unclassified *Betaproteobacteria*, an unclassified *Bacteria*, and *Nitrospira*) were of low relative abundance in the influent and are classified as “unfiltered OTUs” (green shaded bars) in Fig. 3-4. Indeed, even across all treatments, the most dominant OTUs in the effluent community were significantly different from the influent (Table S3-7,  $p < 0.001$ ). The filter location had a more significant influence on microbial composition than PCP treatment (Table S3-8). Across all locations, these results show that the PoU filter significantly impacted where and to what degree different OTUs proliferated across the control PoU filters. In conclusion, the most highly dominant taxa across the three locations are generally different, implying selective pressures influencing community structure changes across the filter flow path.

Trace PCP has a subtle but significant effect on community structure in the filter fabric and effluent. Influent, effluent, and fabric communities were significantly different independent of treatment when the dominant OTUs are considered ( $p < 0.001$ , UniFrac analysis), as shown in Fig 5. The influent community structure does not vary with the presence of PCP ( $p > 0.05$ , UniFrac analysis, data not shown), despite the variation among samples with time (See section A.10 in Appendix A). In contrast, fabric and effluent communities were affected by PCP (Table S3-9). For fabric samples, PCP concentration was relevant (Fig. 3-6,  $p < 0.001$  from PERANOVA) as demonstrated by eight dominant OTUs that changed with PCP concentration (Fig. S3-5). For effluent samples, only three OTUs showed a significant shift in relative abundance in the

presence of PCP (Fig. S3-6), but PCP concentration was not relevant (Fig. 3-7,  $p > 0.017$  from PERANOVA with Bonferroni correction). Four OTUs proliferated considerably in either the fabric or effluent community with PCP treatment. Among them are two "attached OTUs" (shaded red in Fig. 3-4), *Mycobacterium* (OTU 3) and *Sphingomonas* (OTU 6), which had significantly higher relative abundance in PCP-exposed fabric samples. Furthermore, *Mycobacterium* (OTU 3) and *Sphingopyxis* (OTU 1) are "attached OTUs" that had significantly higher relative abundance in the effluent of PCP-exposed filters ( $p < 0.05$ , Kruskal-Wallis test). Interestingly, *Mycobacterium* (OTU 3) was the only OTU that showed an increase in relative abundance with PCP treatment in both fabric and effluent ( $p < 0.05$ , Kruskal-Wallis test). The majority of "unfiltered OTUs" (shaded green in Fig. 3-4) and *Hydrogenphaga* (OTU 4) (shaded yellow in Fig. 3-4) in the effluent all had similar relative abundances between PCP treatments. Note that the relative abundance of one "filtered OTU", *Pseudomonas* (OTU 24), decreased significantly in fabric samples exposed to PCP ( $p < 0.05$ , Kruskal-Wallis test). Collectively, these results show that attached OTUs on the fabric were more responsive to PCP treatments than when they were in the effluent, and few of them carried this effect to the downstream side of the filter.

The water chemistry differed between the filter influent and effluent. Influent and effluent microbial communities were exposed to distinctly different water chemistry due to concentration changes in PCP, total chlorine residual, pH (Fig. S3-7) and total organic carbon (Fig. S3-8) across the filter (Tables S3-7 and S3-8). No PCP was detected in the PoU filter effluent over the course of the experiment, and calculations show that PCP only penetrated  $\leq 25 \mu\text{m}$  into the ACB due to sorption (see Section A. 13.4 in Appendix A). Influent total chlorine residuals averaged  $2.5 \pm 0.46 \text{ mg/L}$  as  $\text{Cl}_2$  and effluent concentrations were below the detection limit of the test kit ( $0.2 \text{ mg/L}$  as  $\text{Cl}_2$ ) until day 49 when the PCP-fed system effluents had concentrations around the detection limit. Monochloramine, the form of chloramine expected at the influent pH 8.9, is known to be converted by reactions with activated carbon to chloride, ammonia and  $\text{N}_2$  (Komorita and Snoeyink, 1985). The likely presence of ammonia (which was, unfortunately, not measured) would be available to support bacterial growth on the filter and should be compared to the performance of PoU filters in free chlorine-treated systems where ammonia would, presumably, be much less. The increase in *Nitrospira* relative abundance across all effluent samples also suggests the presence of sufficient ammonia to support the strain's growth.

There was no significant difference between average TOC and DOC concentrations in the influent samples ( $p = 0.45$ ), indicating that the measurable organic carbon introduced to the filters was dissolved (Table S3-9). Influent TOC concentrations ranged between 1.8 and 3.7 mg/L with a mean concentration of 2.4 mg/L (with and without PCP). Effluent TOC values ranged between less than 1.0 and 6.0 mg/L with a mean concentration of 2.1 mg/L (with and without PCP) (Table S3-10). Occasional sloughing of cell biomass or periodic generation of soluble microbial products may account for the effluent TOC variability. TOC removals were not statistically different between treatments (Fig S3-8). The net average organic carbon mass removed by the PoU filters was  $343 \pm 208$  mg; whereas the total average mass of organic carbon fed to the filters was  $1,136 \pm 99$  mg for the duration of the experiment. TOC was detected in all effluent samples analysed, starting approximately two weeks into the experiment, suggesting rapid breakthrough and would have been available to support bacterial growth in the effluent.

Changes in chemical species across the filter, coupled with the correlation between dominant taxa in the fabric and effluent communities, led us to estimate the absolute abundances of highly dominant OTUs across filter location between PCP treatments by multiplying total 16S rRNA gene copies by relative abundance. Although this method is just an estimate, it allows us to observe trends in how highly dominant OTUs change between the influent and effluent of the PoU systems. Among the highly dominant fabric OTUs (Table 3-1), *Sphingopyxis* (OTU1), *Aquabacterium* (OTU5), *Acidovorax* (OTU2), and *Nitrospira* (OTU20) had higher absolute abundance in the effluent than the influent for all PCP treatments (Table 3-2). *Brevundimonas* (OTU30), *Mycobacterium* (OTU3), and an unclassified betaproteobacteria (OTU10) had higher absolute abundance in the effluent relative to the influent of systems treated with 50 and 100 ng/L PCP. Among genera that are known to contain opportunistic pathogens found in drinking water, the most significant among the dominant taxa found in this study is *Mycobacterium* (OTU 3); however, the sequencing amplicon size does not allow us to identify if pathogenic forms were present. Of equal importance is the absence of taxa linked to opportunistic pathogens in our study but that have historically been observed in drinking water. Four *Legionella* OTUs were detected, but at trace abundance (total no. of reads  $\leq 36$ ) and there was no consistent pattern of change in abundance across the PoU filters. Likewise, three *Pseudomonas* sp. were detected in very low abundance (total no. of reads  $\leq 39$ ). Only one *Pseudomonas* taxa (OTU24) was higher than 1% in influent samples, and decreased across the filter (Fig. 3-4). The partial 16S rRNA

sequence (253 bp) of all *Pseudomonas* OTUs were evaluated via a BLAST search and none included *P. aeruginosa* as an associated taxon. The *Mycobacterium* data show that PoU filters may be able to increase the abundance of selected opportunistic pathogens across the flow path of activated carbon block PoU filters.

### **3.4 Discussion**

#### **PoU filters supported biofilm growth upstream of the activated carbon block**

Calculations show that most of the biofilm found on the fabric was due to growth that occurred during the two month PoU study. We calculated the protein mass that would exist on the fabric if all cells from the influent over the course of the study were retained, assuming our plate counts only captured 10% of the total bacterial population (Section A.14 in Appendix A), and estimated that fabrics would have 4  $\mu\text{g}$  cell protein/ $\text{cm}^2$ . We also calculated the amount of biomass that would grow on the total mass of PCP applied to the PCP-supplemented filter systems, assuming at least one bacterial strain was present that could mineralize all the PCP applied (Section A.15 in Appendix A). For this scenario, we calculated that the 100 ng/L PCP fed-fabric would support growth of  $2.5 \times 10^{-2}$   $\mu\text{g}$  cell protein/ $\text{cm}^2$ . Both estimates are six to 2000 times smaller than the average fabric cell protein measured, which was 23  $\mu\text{g}/\text{cm}^2$ . Therefore, we conclude that substantial cell growth occurred on the fabric over the course of the study, presumably on sorbed TOC, soluble TOC and microbial decay products; however, PCP did not significantly support growth.

#### **PoU filtration alters bacterial abundance and community composition in filtered drinking water.**

Our results show that ACB PoU filters increase the abundance of bacteria in filtered drinking water relative to what is present in the premise plumbing that supplies the PoU filter, and is consistent with past PoU filter studies that used culture-based methods (Chaidez and Gerba, 2004; Geldreich et al., 1985; Molloy et al., 2008; Reasoner et al., 1987; Su et al., 2009b; Tobin et al., 1981; Wallis et al., 1974). Despite this increase, there is a decrease in bacterial community diversity (richness and evenness) across the filters, which could be linked to changes in BDOC (biodegradable organic carbon) across the filter. The historical average BDOC concentration in

the source water was 1.3 - 1.6 mg/L (Lee and Deininger, 2003), which is 60% of the TOC measured during our study, suggesting that most of the TOC was available to support microbial growth. This growth would be focused in the biofilm, upstream of the activated carbon block within range of the carbon surface where the TOC would adsorb. Although we did not measure the composition of TOC in effluent versus influent samples, we expect that the nature of effluent organic carbon was different and could have been more recalcitrant in the effluent as is often seen during conventional drinking water treatment that invokes biologically active GAC (Volk and Lechevallier, 2002). A reduction in BDOC across filters could explain the dominance of the community by only a handful of OTUs with an ability to grow well on the few biodegradable organic constituents present, thus resulting in decreased microbial richness in the effluent.

It is noteworthy that the influent bacteria are likely to be predominantly planktonic (Gillespie et al., 2014; Hammes et al., 2008) while the fabric bacteria survive by growing in biofilms; therefore, planktonic bacteria that can transition to biofilm growth are likely favoured for growth on the fabric wrap of ACB PoU filters. Other studies of community structure in drinking water distribution systems have shown that the planktonic bacteria present in bulk water are different from sessile bacteria that grow in biofilms on the walls and scale of the same pipe systems (Liu et al., 2014), suggesting that the predominant planktonic bacteria do not favour biofilm growth but are not necessarily precluded from it. The fate of planktonic bacteria derived from the distribution system and applied to an activated carbon block PoU filter, like that used in our study, is unclear. It is possible that bacteria that grow preferentially in a planktonic state are caught by the biofilm through sieving and either transition to a biofilm growth state or eventually succumb to death and lysis, which provides nutrients that support the growth of biofilm-thriving strains.

We hypothesize that community composition differences observed in the fabric biofilm is a complex outcome of the mode of operation and the structure of the filter. The PoU filter fabric is wrapped around and in close contact with the surface of the activated carbon block; bacteria can grow on the activated carbon block surface (not measured by us in this study) and also on the fabric wrap (measured during this study), and constitute upstream biomass. These microorganisms would be exposed to hourly (< 1 min) pulses of residual chloramine disinfectant as it flows to the block from the influent for 16 hours, then no new flow for an 8 hour stagnation



period where substantial growth could occur. The pulsed growth environment in the filter housing is, admittedly, quite different from what is common in distribution systems. The biofilm bacteria would also be exposed to BDOC that sorbed to the activated carbon block and is in equilibrium with the liquid zone immediately adjacent to the ACB surface. Furthermore, the ACB and fabric biofilms would have also been exposed to equilibrium concentrations of PCP and disinfection byproducts that also sorbed to the ACB surface, and could have resulted in the selection of taxa that are able to resist the stress effects of these chemicals and grow on them. Indeed, the fabric-abundant OTUs including *Sphingopyxis*, *Sphingomonas*, *Mycobacterium*, and *Acidovorax* are of genera known to include species capable of degrading chlorinated compounds (Godoy et al., 2003; Häggblom et al., 1988; Monferra et al., 2005; Yang et al., 2006). Our study did not evaluate growth kinetic differences among different OTUs found on the filters; however, it appears that these multiple factors affected growth in a way that reduced the community diversity across the flow path.

The increase in effluent HPC with time and structurally distinct composition of effluent bacterial communities suggest that bacteria colonized and grew inside the filter annular space in a way that inoculated the effluent water flow. Theoretically, bacteria should not pass through an intact activated carbon block since its average pore size (22 Å measured during this study) is much smaller than a bacterial cell. The observed passage of bacteria through the filter, however, indicates the likely presence of a few preferential flow paths of larger than average diameter. Another possible source of inoculum for the effluent community is residual bacteria from the manufacturing process itself. More study of the transport pathway in ACB filters is needed to test these two hypotheses and is currently underway in our laboratory. Although the inoculum source(s) for the effluent channel remain(s) unknown, the significant increase in effluent cell counts relative to the influent suggests that bacteria colonized and grew on the activated carbon face of the effluent chamber or passed through the block from the fabric biofilm and influent. Since our effluent samples were composited over 24 hours, it is possible that the discharge of bacteria via the effluent was sporadic and occurred when biofilm detachment or sloughing events occurred.

It is interesting that *Nitrospira* became abundant in the effluent relative to levels in the influent across all filters, although we have not confirmed which species were present. The likely

presence of ammonia as a product of the reaction of chloramine with the ACB may have supported growth of the nitrifier and should be compared to the performance of PoU filters in free chlorine-treated systems where ammonia concentrations would, presumably, be much less. Pinto et al. (Pinto et al., 2015) found comammox in Ann Arbor's distribution system, a metabolism performed by some *Nitrospira*, which suggests complete nitrification to nitrate is possible. Perhaps more importantly, these results imply that there is a path for bacteria from the distribution system through the filter to the effluent. In this way, *Nitrospira* is serving as a non-pathogenic bacterial tracer that is unlikely to have been inoculated by the manufacturing process.

### **Trace concentrations of PCP shifted bacterial community structure and abundance in the fabric and effluent.**

As hypothesized, PCP influenced the composition of bacterial biofilm in PoU filters, though shifts were subtle. The total biomass amount did not change with PCP exposure, however. Three dominant OTUs in the fabric and effluent shifted with PCP exposure: *Mycobacterium* in fabric and effluent, *Sphingomonas* in fabric, and *Sphingopyxis* in effluent. *Pseudomonas aeruginosa*, the strain we based our hypothesis on, was not present at a detectable abundance during this study. Although none of the affected taxa contain the resistance-nodulation-division (RND) MexAB-OprM multidrug efflux pump associated with our initial hypothesis, Mycobacteria contain an RND homolog called Mycobacterial membrane protein large transporters (MmpLs) that is associated with exporting multiple antibiotics and may play a role in detoxification-mediated efflux of other chemicals (Chalut, 2016; Pasca et al., 2005). Furthermore, *Sphingopyxis* and *Sphingomonas* also have RND homologs (Shintani et al., 2007; Universal Protein Resource, n.d.) and belong to the family of Sphingomonadaceae that are known to be chlorine-resistant (Furuhata et al., 2007; Khan et al., 2016). Some strains of *Sphingomonas* found in drinking water systems have also demonstrated antibiotic resistance (Khan et al., 2016; Vaz-Moreira et al., 2011). The mechanisms that lead to the selection of these taxa in the presence of PCP are unclear. The impact on the biofilm communities was apparent phenotypically as well, as biofilm color changed in response to PCP. We cannot determine whether this was due to the subtle shifts in composition or physiological changes in response to PCP. The bacterial communities in the effluent of filters where PCP was added to the influent were different from those in the non-PCP control effluent, even though we did not detect PCP in any effluent sample (detection limit, 10

ng/L). It is not clear what factors affected the effluent communities. Collectively, and although mechanisms have not been elucidated, these data show that chemicals present at trace (ng/L) concentrations were able to influence the community structure in a PoU filter. This suggests that disinfection byproducts and, indeed, the kind of disinfectant used will influence the microbial community found in PoU filters.

### **The abundance of *Mycobacteria* is affected by the activated carbon block PoU filter**

The *Mycobacterium* genus was among the five dominant OTUs that were enriched on all fabric samples under all treatment conditions, and *Mycobacterium* was also enriched in the effluent relative to the influent treated with PCP. Numerous species of nontuberculosis *Mycobacteria* (NTM) have been found in drinking water (Hilborn et al., 2006; Vaerewijck et al., 2005; Wang et al., 2012), including in Ann Arbor drinking water (Chiao et al., 2014). Genetic and epidemiological methods have been employed to show that NTM may cause infection to immuno-compromised humans (Falkinham, 2011; Falkinham et al., 2008). Due to their hydrophobic cell wall component, *Mycobacteria* have strong resistance to disinfectants, especially chloramine (Baron et al., 2014), and easily adhere to form biofilms in drinking water systems (Gomez-Smith et al., 2015; Mullis and Falkinham, 2013; Revetta et al., 2013; Williams et al., 2009). Adding to their tolerance of disinfectants is their ability to co-associate with amoeba in drinking water distribution systems, which provides protection against disinfectants (Delafont et al., 2014). Amoeba would be readily retained by the PoU filters given their size, consistent with testing done during certification of the filters (NSF International/ANSI, 2015b). In summary, the selection of *Mycobacterium* across the activated carbon block PoU filters in this study show that filters may increase one's exposure to opportunistic pathogens that are otherwise present at lower numbers in distributed drinking water.

Deployment of faucet-mounted, activated carbon block PoU filters is on the rise, especially in the wake of very public incidents of public drinking water contamination. These filters are primarily and justifiably used to remove non-biological contaminants that the filters are certified to remove. An unintended consequence of using ACB PoU filters, however, is that they change the structure and abundance of the microbial community that consumers are exposed to. This community shift is influenced by both the physical design of the filter and, to a lesser degree,

trace chemicals present in the water. Indeed, the World Health Organization has warned against use of activated carbon block filters as a sole point-of-use treatment method for over two decades (Sobsey, 2002). The microbiological changes experienced across these filters may be particularly problematic for immune-compromised individuals who are vulnerable to infection, and justifies considering use of an additional protective barrier to provide disinfection; however, further study is needed to determine whether and under what conditions this is needed. Our results provide an initial assessment of the consequence of deploying point-of-use treatment on distributed drinking water systems and suggest a need to better understand the public health consequences of this choice.

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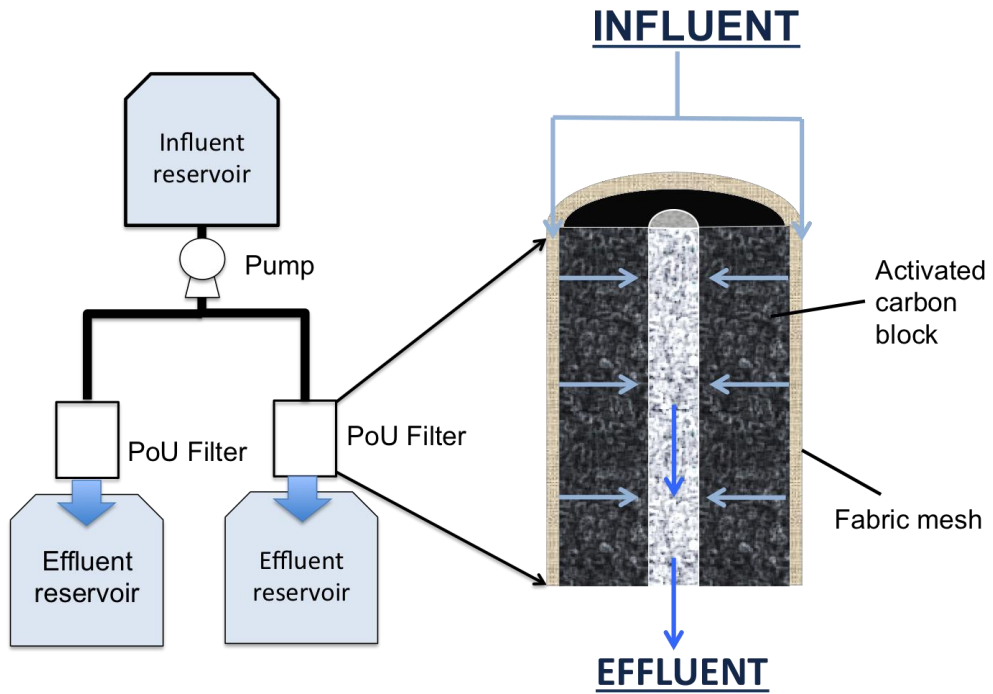
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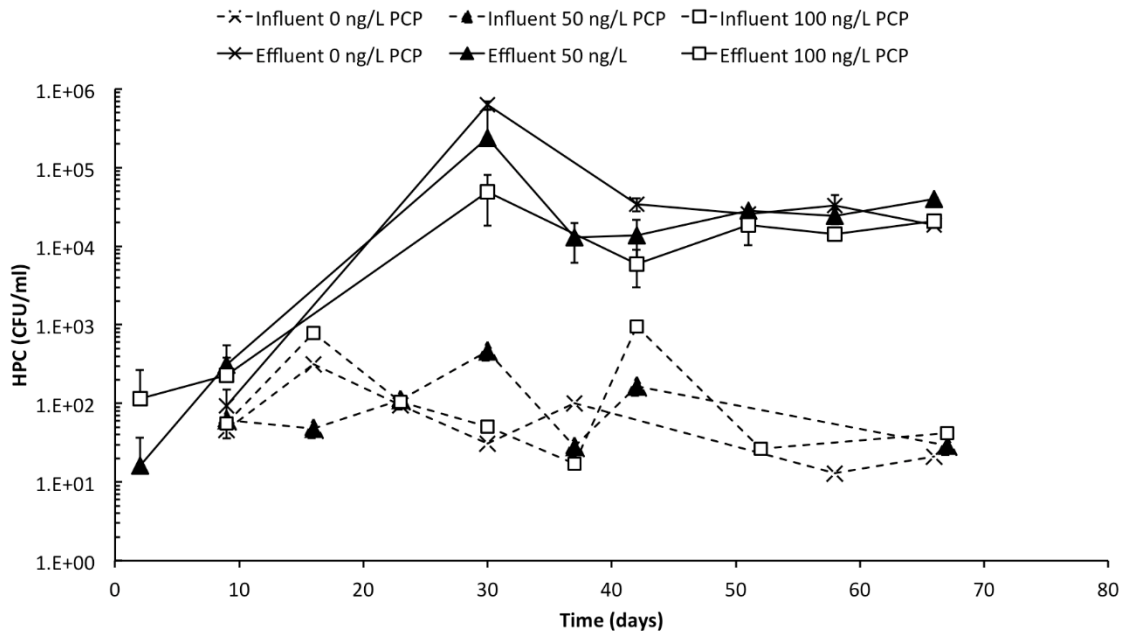


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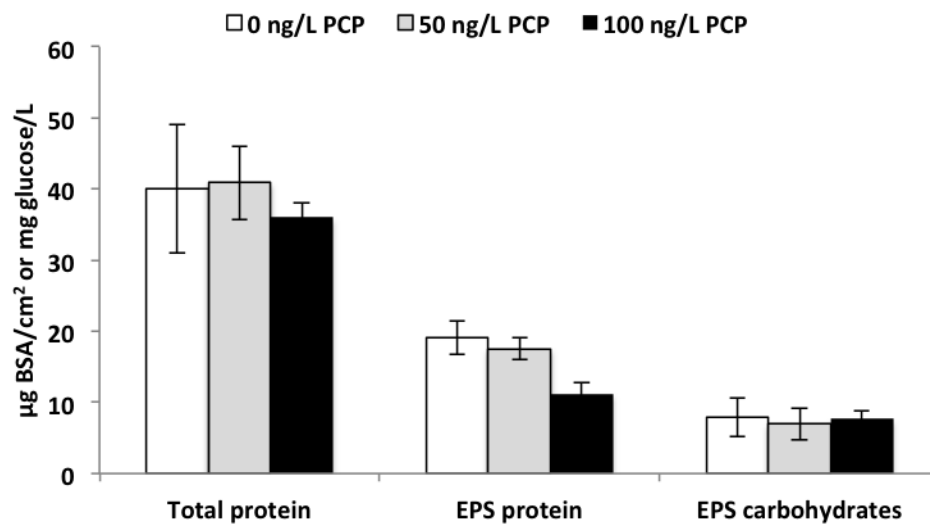
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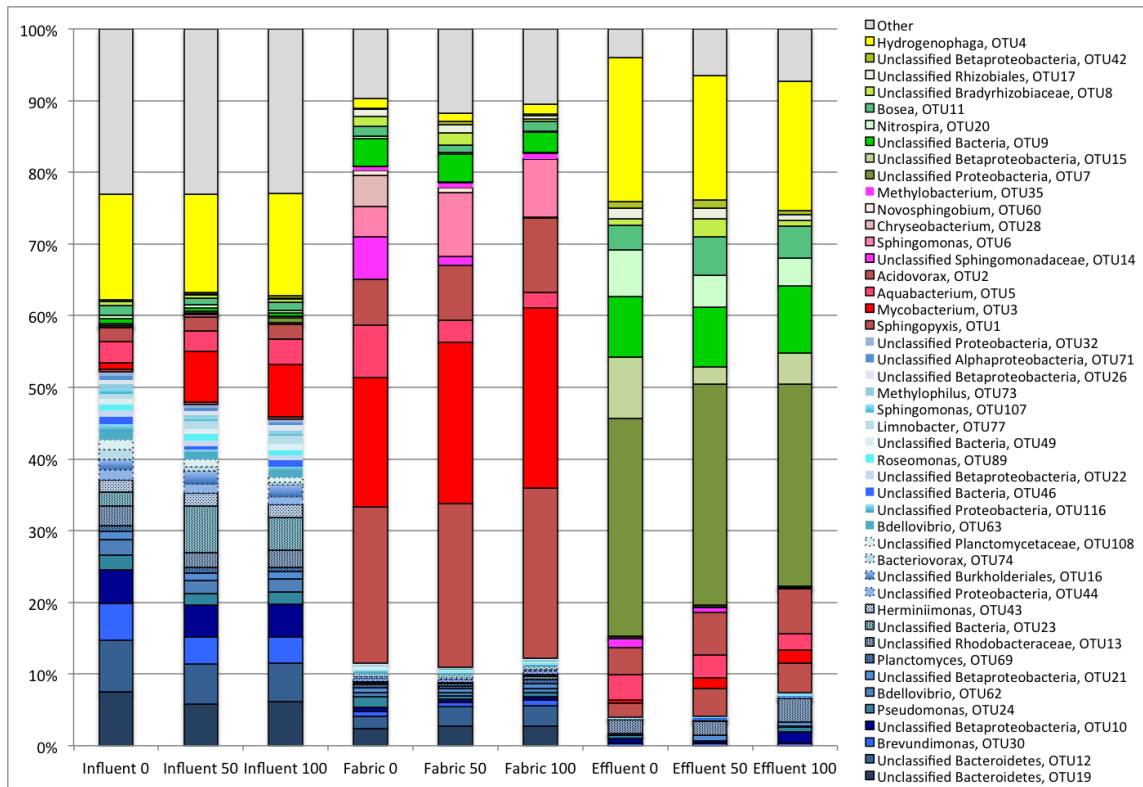
**Fig. 3-1 Schematic of PoU manifold system (left) and the cross sectional profile of filter construction (right). Influent flow is indicated by blue arrows.**



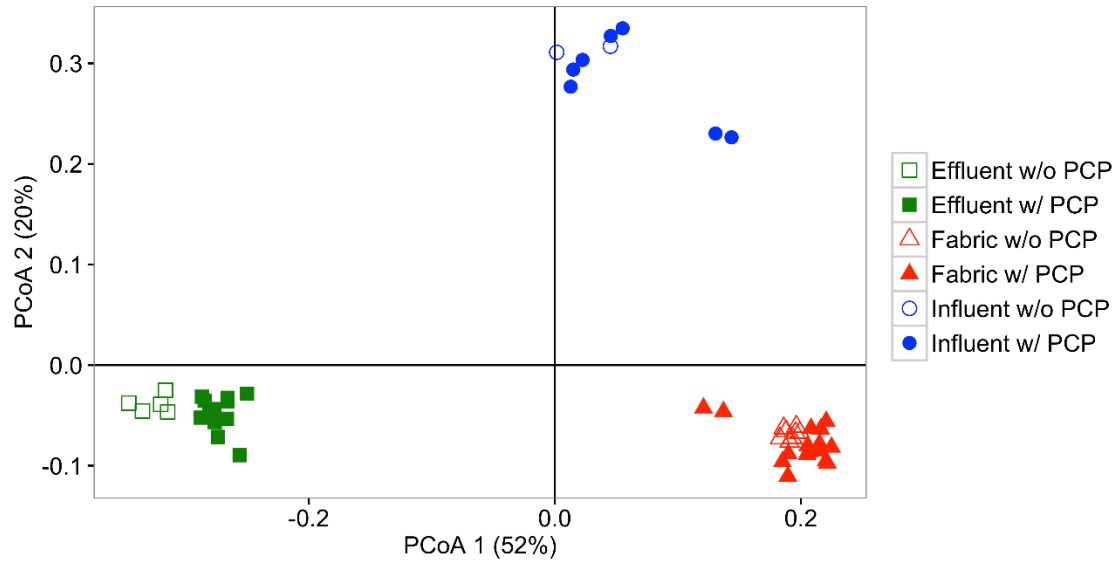
**Fig. 3-2 Concentrations of heterotrophic plate counts in influent (dashed line) and effluent (solid line) during operation. The PoU filters were fed with 0 ng PCP/L (cross), 50 ng PCP/L (triangle), or 100 ng PCP/L (square). Standard deviations of effluent samples are indicated by the error bars.**



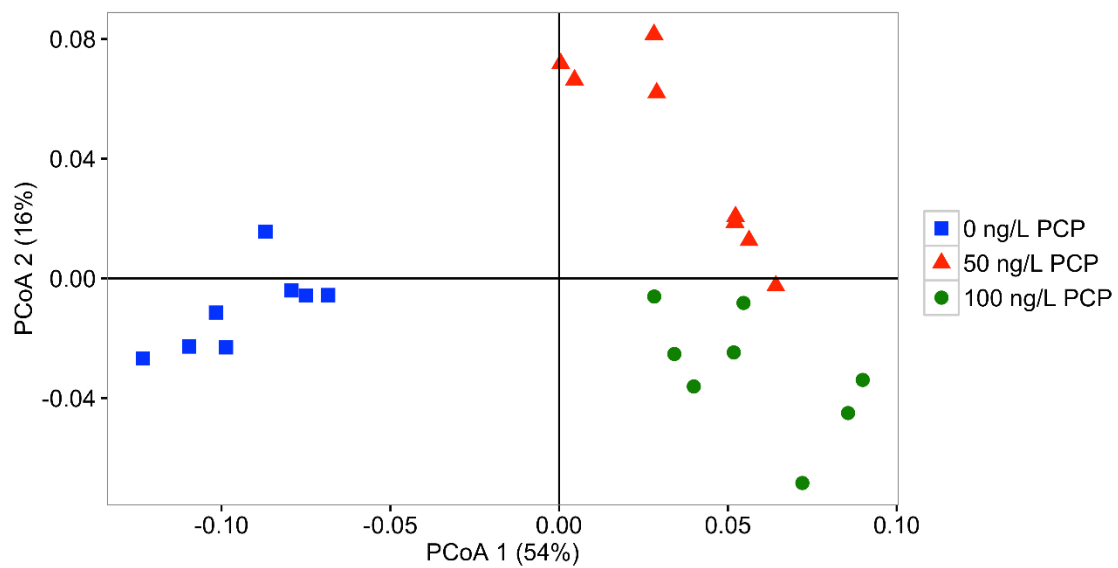
**Fig. 3-3 Biofilm compositions on fabrics treated with 0, 50, 100 ng/L PCP treatments.**



**Fig. 3-4 Relative abundance of dominant taxa across all sample types. The number beside sample name indicates the level of PCP treatment. Taxa names are labeled at the right. Taxa in blue colors are “filtered OTUs” that mainly present in influent and fabric. Taxa in red colors are “attached OTUs” that flourish at fabrics samples. Taxa in green colors are “unfiltered” OTUs that have relative abundance greater in effluent than influent. Taxa in yellow color have similar abundance in the influent and effluent. Noted that not all OTUs mentioned above was included, this figure only shows dominant OTUs with relative abundance > 1% and correlated with PCP treatment.**

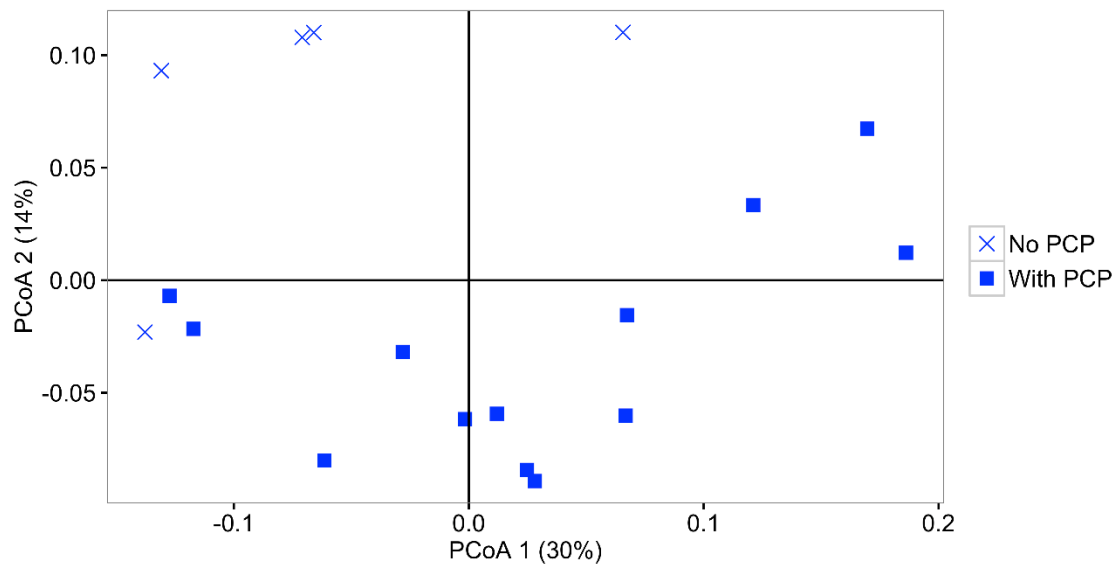


**Fig. 3-5 PCoA plot based on Weighted UniFrac comparing bacterial community structure of fabric (collected at the end of operation, triangle), influent (circle) and effluent (square) from different time points without (blank) and with (solid) PCP treatment.**



**Fig. 3-6 PCoA plot based on Weighted UniFrac comparing fabric bacterial community structure fed with 0 ng PCP/L (square), 50 ng PCP/L (triangle), or 100 ng PCP/L (circle).**





**Fig. 3-7 PCoA plot based on Weighted UniFrac comparing effluent bacterial community structure fed without PCP (cross) and with PCP (square). PCP exposed samples are combined because there was no significant difference between 50 and 100 ng/L treatments.**

**Table 3-1 Highly dominant OTU (>5%) in PoU filter influent, fabric, and effluent samples in the absence of PCP\***

Highly Dominant Taxa (OTU#)	Influent	Fabric	Effluent
<i>Hydrogenophaga</i> (4)	<b>14.8%</b>	1.4%	<b>20.1%</b>
Unclassified Bacteroidetes (19)	<b>7.5%</b>	2.4%	0.0%
Unclassified Bacteroidetes (12)	<b>7.2%</b>	1.7%	0.0%
<i>Brevundimonas</i> (30)	<b>5.2%</b>	0.7%	0.3%
<i>Sphingopyxis</i> (1)	0.4%	<b>21.9%</b>	2.0%
<i>Mycobacterium</i> (3)	1.0%	<b>18.0%</b>	0.4%
<i>Aquabacterium</i> (5)	2.9%	<b>7.2%</b>	3.6%
<i>Acidovorax</i> (2)	1.9%	<b>6.5%</b>	3.8%
Unclassified Sphingomonadaceae (14)	0.1%	<b>5.9%</b>	1.3%
Unclassified Proteobacteria (7)	0.1%	0.0%	<b>30.4%</b>
Unclassified Betaproteobacteria (15)	0.2%	0.0%	<b>8.6%</b>
Unclassified Bacteria (9)	0.7%	3.8%	<b>8.4%</b>
<i>Nitrospira</i> (20)	0.5%	0.3%	<b>6.6%</b>

\*Values shown in bold are the highly dominant OTUs present in each environment.

**Table 3-2 Estimated absolute abundances of highly dominant OTU in PoU filter influent, fabric and effluent samples across all PCP treatments\***

Highly Dominant Taxa (OTU#)	0 ng/L PCP		50 ng/L PCP		100 ng/L PCP	
	Influent	Effluent	Influent	Effluent	Influent	Effluent
<i>Hydrogenophaga</i> (4)	6E+04	<b>1E+05</b>	5E+02	<b>2E+05</b>	1E+03	<b>2E+05</b>
Unclassified Bacteroidetes (19)	3E+04	0E+00	2E+02	0E+00	6E+02	2E+01
Unclassified Bacteroidetes (12)	3E+04	1E+02	2E+02	1E+02	5E+02	1E+02
<i>Brevundimonas</i> (30)	2E+04	2E+03	1E+02	<b>4E+03</b>	4E+02	<b>3E+03</b>
Unclassified Betaproteobacteria (10)	2E+04	5E+03	2E+02	<b>3E+03</b>	5E+02	<b>1E+04</b>
<i>Sphingopyxis</i> (1)	2E+03	<b>1E+04</b>	1E+01	<b>4E+04</b>	4E+01	<b>4E+04</b>
<i>Mycobacterium</i> (3)	4E+03	2E+03	3E+02	<b>2E+04</b>	7E+02	<b>2E+04</b>
<i>Aquabacterium</i> (5)	1E+04	2E+04	1E+02	<b>4E+04</b>	4E+02	<b>2E+04</b>
<i>Acidovorax</i> (2)	8E+03	<b>3E+04</b>	8E+01	<b>6E+04</b>	2E+02	<b>6E+04</b>
Unclassified Sphingomonadaceae (14)	6E+02	8E+03	0E+00	<b>8E+03</b>	6E+00	<b>5E+02</b>
Unclassified Proteobacteria (7)	3E+02	<b>2E+05</b>	2E+00	<b>3E+05</b>	1E+01	<b>3E+05</b>
Unclassified Betaproteobacteria (15)	7E+02	<b>6E+04</b>	7E+00	<b>3E+04</b>	2E+01	<b>4E+04</b>
Unclassified Bacteria (9)	3E+03	<b>6E+04</b>	2E+01	<b>9E+04</b>	5E+01	<b>9E+04</b>
<i>Nitrospira</i> (20)	2E+03	<b>4E+04</b>	2E+01	<b>5E+04</b>	3E+01	<b>4E+04</b>

\*Estimated absolute abundance = Relative abundance (%) × total 16S rRNA gene (copy no./L)/4.2 copies/genome. Average copy no. of 16S rRNA gene is 4.2 copy no. per cell (Vetrovsky et al. 2013). The total number of 16S rRNA genes were [Influent]:  $2 \times 10^6$  in 0 ng/L,  $2 \times 10^4$  in 50 ng/L;  $4 \times 10^4$  in 100 ng/L PCP treatment; [effluent]:  $3 \times 10^6$  in 0 ng/L,  $5 \times 10^6$  in 50 ng/L;  $4 \times 10^6$  in 100 ng/L PCP treatment. Values in bold are the OTUs that have higher estimated abundance in effluent than in influent.

## Chapter 4

### Prevalence of antibiotic resistance genes in two drinking water sources treated by activated carbon block point-of-use (PoU) filters

#### 4.1 Introduction

The dissemination of antibiotic resistance has become one of the major challenges in the 21<sup>st</sup> century since it has resulted in higher medical costs, prolonged hospital stays and increased mortality (Cosgrove, 2006; Li and Webster, 2018). The overuse of antibiotics has caused an increased discharge of antibiotics into the environment, especially from domestic wastewater streams and agricultural runoff (Baquero et al., 2008). There is concern that antibiotics released into natural environments can select for and increase antibiotic resistance among indigenous bacteria in aquatic environments. However, the presence of antibiotic resistant bacteria (ARB) and antibiotic resistance genes (ARGs) is not always linked to detection of antibiotics. For example, several studies of finished drinking water that have low or non-detected levels of antibiotics still contain various ARB and ARGs (Garner et al., 2018; Jia et al., 2015; Ma et al., 2017; Shi et al., 2013; Xi et al., 2009; Xu et al., 2016). Researchers have proposed that bacteria exposed to disinfectants and stress reactions to that exposure, as well as the exchange of genetic elements across bacterial species, i.e. horizontal gene transfer, are two primary mechanisms that enrich for ARB in drinking water (Garner et al., 2018; Jia et al., 2015; Ma et al., 2017; Shi et al., 2013). Jia et al. (2015) found that the predominant types of ARGs are related to chlorine-resistant species, such as *Pseudomonas spp.* In drinking water biofilms, horizontal gene transfer is believed to occur frequently as a way to cope with oxidative stresses imposed by the drinking water environment (Molin and Tolker-Nielsen, 2003). Altogether, past studies strongly suggest that drinking water processes and environments within drinking water systems can select for and spread ARB and ARGs.

Activated carbon block (ACB) PoU filters, which have been used widely to remove chemicals of concern from distributed drinking water, are significant harbors for bacterial growth and biofilms

(Chaidez and Gerba, 2004; Geldreich et al., 1985; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981; Wallis et al., 1974; Wu et al., 2017) but have not been uniformly studied to understand their role in enhancing ARB and ARG levels in filtered water. Bacterial biofilms that grow on the ACB surface and fabric wrap on the upstream side of ACB PoU filters are intermittently exposed to disinfectant residuals from the influent during filter use, then remain stagnant when the filter is not in use. During the stagnant period, nutrients and dissolved organic matter that sorb and exist in equilibrium with surrounding moisture in the ACB become available to these biofilms. We conjecture that those bacteria that are most resistant to the periodic disinfectant pulses during filter use are among those that can grow preferentially in the filter. In this way, disinfectant tolerant bacteria may be selected for across PoU filters. For example, our previous study (Chapter 3; Wu et al., 2017) found that a chlorinated phenolic disinfection byproduct can enrich for the *Mycobacteria* genera inside ACB PoU filters, and increase the absolute abundance in the effluent relative to the influent. Some *Mycobacterium* species found in drinking water contain intrinsic antibiotic resistance (Garner et al., 2018; Gomez-Alvarez et al., 2016). Therefore, we hypothesized that it is possible for the increase in *Mycobacteria* abundance across ACB PoU filters to also increase ARGs.

The goal of this study was to identify AGRs associated with bacterial taxa that show a propensity to increase in abundance across ACB PoU filters, and to measure exemplar ARGs directly to determine if, in fact, such an increase occurs. To do this, we evaluated ACB PoU filters that received tap water from two distinct drinking water distribution systems. One set of filters were connected for 2 months to a lab-scale PoU filter manifold located in a large building that received chloraminated softened tap water from Ann Arbor, MI with and without a low (ng/L) concentration of spiked PCP (Wu et al., 2017). The second set of filters were of variable age and use patterns from a field campaign of 16 houses in Flint, MI when the city was served by chlorinated, unsoftened Lake Huron water. We use a statistical analysis to report on the most likely pattern of ARG change across ACB PoU filters in both cases, and discuss the relevance of the outcome.

## **4.2 Materials and Methods**

### *Sample Collection and DNA extraction*

Drinking water samples from Ann Arbor were collected as batch samples from a lab-scale PoU filter rig described previously (Wu et al., 2017). Briefly, the influent sample came from a reservoir stored for 24 hours and replenished daily. The water source was a faucet in a large University building, served by the Ann Arbor drinking water treatment system which uses mostly surface (river) and some groundwater as a source, and treats with lime softening, ozone pre-disinfection, sand and activated carbon rapid filtration, and chloramination. The city of Ann Arbor has a relatively well maintained distribution system. Drinking water samples from Flint, Michigan were collected from residential homes in compliance with Wayne State University IRB #105015B3X (Love et al., in preparation). Influent samples were 2 L grab samples taken after an extended (overnight) period of no use and after an initial 1 L sample was collected. PoU filter effluent samples were 2 L first flush grab samples. All samples were filtered through 0.22  $\mu\text{m}$  polycarbonate membrane filters (Millipore GTTP04700, Billerica, MA).

DNA extraction was performed using the same method as in Chapter 3 (Wu et al., 2017). Because the DNA was used to support multiple experiments, beyond those reported in this dissertation, the amount of DNA was limited for some samples.

#### *Selection of DNA samples for shotgun metagenomic sequencing*

A subset of DNA samples that contained enough DNA to obtain a high resolution sequenced product were selected for shotgun metagenomic sequencing. (Table S4-1). A total of one influent, two effluent and two fabric samples were chosen from controls and DBP-treated samples from the Ann Arbor study (Wu et al., 2017). In addition, a total of seven samples were chosen from the Flint, MI study (Love et al., in preparation) and included: the influent to PoU filters in House samples 5a, 12a, 13a and 14a, and the first flush effluent samples from PoU filters in Houses 9b, 11b and 14a. Note that only one sample set reflects the influent and effluent from the same house (14a). Based on the number of *Enterobacteriaceae* detected, three samples (effluent of House 9b, 11b, and 14a) with the higher mean gene copy per 250 mL of drinking water ( $6808 \pm 1807$  gene copies/250mL) are classified as "highly abundant *Enterobacteriaceae*". The rest of the samples with an average of  $114 \pm 91$  *Enterobacteriaceae* gene copies per 250 mL are classified as "low abundance *Enterobacteriaceae*."

#### *Metagenomic sequencing*

DNA samples were prepared for shotgun metagenomic sequencing at the University of Michigan DNA Sequencing Core. DNA was fragmented using standard Covaris sonication (Covaris, Woburn, MA). Fragmented DNA was then prepared as a standard Illumina library using Kapa reagents (Kapa Biosystems, Wilmington MA) on an Apollo instrument (WafterGen Bio-systems, Fremont, CA), where the fragments were end-repaired, A-tailed, and adapter-ligated. The total insert size is 550 bp. The samples were then PCR amplified and pooled. Final libraries were checked for quality and quantity by TapeStation (Agilent, Santa Clara, CA) and qPCR using Kapa's library quantification kit for Illumina Sequencing platforms (catalog #KK4835) (Kapa Biosystems). They were clustered on the cBot (Illumina) and sequenced on a 100-cycle paired end run on a HiSeq 4000 in High Output mode using version 3 reagents according to manufacturer's protocols (Illumina).

#### Metagenomic sequence analysis

Sequences from the raw sequencing outputs were dereplicated to reduce the size of the file. The sequences that are 100% identical over 100% lengths are clustered together. Then, the sequences are trimmed using Sickle (Modolo and Lerat, 2015) to remove the adapters. The trimmed sequences were assembled using the IDBA algorithm (version 1.1.1) (Peng et al., 2012) with the k-mer sizes of 21-101 and a step increase of 20 (Oh et al., 2018). The assembled contigs were searched against the Comprehensive Antibiotic Resistance Database (CARD, version 1.0.6) (Mcarthur et al., 2013). The sequences were annotated as ARGs according to the best BLAST result for each with an E-value of  $10^{-5}$  and a sequence similarity of above 80% over an alignment of at least 25 amino acids, as shown in past studies (Garner et al., 2018; Shi et al., 2013).

#### Primers and qPCR conditions

The DNA samples from previous studies (Love et al., 2018, Wu et al., 2017) were analyzed by qPCR to determine the abundance of selected ARGs across the ACB PoU filters and the biofilm samples from fabric, surface of the ACB, and surface of the inner core channel. Four ARGs were selected as exemplars of dominant taxa within each sample location (Wu et al., 2017; Love et al., in preparation) for further quantification by qPCR. *AIM-1* (*Pseudomonas aeruginosa*) and *oqxB* (*Enterobacteriaceae*) were selected for analysis in the Flint samples; *arr-1* and *rbpA* (both Mycobacteria) were selected for analysis in the Ann Arbor samples. All analyses were performed in triplicate. A standard curve was generated by amplifying 8-fold serially diluted PCR

amplicons with a known amount of gene copies for each targeted gene. All qPCR experiments were carried out on an Eppendorf® Mastercycler (Eppendorf, Germany). The PCR mixture (10  $\mu$ L) consisted of Fast-Plus EvaGreen Master Mix (Biotium, CA, US), primer sets (0.5  $\mu$ M each, Table 4-1), 0.625 mg/mL BSA, and 1  $\mu$ L template DNA. The reaction conditions were: 95°C for 2 min, followed by 40 cycles for 95 °C for 5 s, annealing for 5 s at defined temperature (shown in Table 4-1) and 72 °C for 25 s. The qPCR efficiency of the two genes was 90-94%, and R<sup>2</sup> values were 0.99 for the standard curves. A melting curve was used to confirm the qPCR amplified fragments specificity.

**Table 4-1 The primers of two fluorescent genes used in this study.**

Gene		Primer (5'-3')	Fragment size (bp)	Annealing Temp (°C)
<i>AIM-1</i>	Forward	AATGCCCTGAAGGTGTACG	98	55
	Reverse	CATCGACCAGGATATGGCCC		
<i>oqxB</i>	Forward	AAAGTGATTGCCGAGACCGT	270	58
	Reverse	GGAGAACAGATGCACCACCA		
<i>arr-1</i>	Forward	GTTCGGGTCGTCCTCGATCT	154	55
	Reverse	TGCGTCGAACTACGAAGAGG		
<i>rbpA</i>	Forward	ATAACGGCGAGGAGTTCGAC	158	55
	Reverse	CTCCAACAGCATGTCCCAGT		

### Statistical analysis

To determine the relationship of the occurrence and the abundance of the selected ARGs with water sample type (influent vs. effluent) and water quality characteristics, generalized linear regression models (Bolker et al., 2008) were conducted using the R package “lme4” (Bates et al., 2015). Specifically, a mixed effects logistic regression model was used to model the association of sample type with the occurrence (presence / absence) of ARGs. A mixed effects gamma regression was used to compare the association of the abundance of ARGs with water sample type and other continuous parameters, including water quality (temperature, pH, chlorine



residual), cartridge age, the total number of 23S rRNA gene targeting *Enterobacteriaceae* and 16S rRNA gene targeting all bacteria. When we conducted the gamma regression, we added a small constant (0.01) to the amount of ARGs that was below detection limit, to adjust the zero measurements because gamma regression cannot analyze dependent variables with a value of zero. For all analyses, the house was considered to be a random effect to account for the variation among houses. A backward selection was performed by sequentially dropping the variable with the largest P-value to determine the optimal model.

### 4.3 Results and Discussion

#### ARGs were found in tap water and ACB PoU filtered water

We used metagenomic sequence analysis to screen for ARGs in samples from the two selected drinking water sources. As an initial attempt, we selected a sequence similarity of at least 80% in defining ARGs as our goal was to target genes associated with the taxa of interest from each location (*Enterobacteriaceae* and *Pseudomonas aeruginosa* from Flint samples; *Mycobacterium* from Ann Arbor samples). A total of 15 and 11 antibiotic resistance types were detected in Flint and Ann Arbor samples, respectively (Table S4-2). The top ten ARGs that were detected in both systems are *mexF*, *mexK*, *mexW*, *mexB*, *cpxR*, *ceoB*, *adeG*, *mtrA* encoding RND multidrug efflux pumps, *RpoB2* conferring rifampin resistance, and *TriC* conferring triclosan resistance. Two of the top ARGs, *mexF* and *ceoB*, were detected in another drinking water distribution system (Ma et al., 2017). Another of the common ARGs, *adeG*, was found in surface water, wastewater and treated wastewater (Ng et al., 2017). These ten common ARGs are intrinsic resistance genes that can be carried by *P. aeruginosa* (*mexF*, *mexK*, *mexW*, *mexB*, *cpxR*) (Poole, 2001), *Burkholderia* spp. (*ceoB*) (Poole, 2001), *Acinetobacter baumannii* (*adeG*) (Cortez-cordova and Kumar, 2011), and *Mycobacterium* spp. (*mtrA*) (Nguyen et al., 2010). The intrinsic antibiotic resistance is often regulated by multiple genes, and is unlikely to be disseminated with other species through horizontal gene transfer. It is likely that the prevalence of these ARGs is associated with their occurrence in hosts that are common in drinking water.

## The Ann Arbor Case

### *The abundance of Mycobacteria-associated ARGs changed across PoU filters*

Among all the genes that were present in Ann Arbor-derived samples, we used qPCR to compare the absolute abundance of two ARGs, *arr-1* and *rbpA*, across the PoU filters. These genes were selected because they were associated with the intrinsic antibiotic resistance of NTM species and had been found previously in drinking water (Garner et al., 2018; Gomez-Alvarez et al., 2016). The *arr-1* gene encodes for ADP-ribosyltransferases that are responsible for drug inactivation of rifampin in the genome of *Mycobacterium smegmatis* (Baysarowich et al., 2008). The *rbpA* gene encodes for RNA-polymerase binding protein in *Mycobacteria*, which can interact with RNA polymerase and reduce its susceptibility to rifampin (Dey et al., 2011). The abundance of *arr-1* and *rbpA* in the effluent of PCP-treated, PoU filtered water was one to two orders of magnitude larger than influent water (Table 4-2). The prevalence of these mycobacteria-associated ARGs is consistent with our previous findings in Chapter 3, which show that absolute abundance of *Mycobacteria* increased between the influent and effluent of ACB PoU filters when PCP was present (Wu et al., 2017). Both ARGs were detected in the fabric biofilms, which were enriched with *Mycobacterium spp* (Wu et al., 2017).

The enrichment of *arr-1* in the fabric may be related the oxidative stress generated by chloramine. The enzyme ADP-ribosyltransferase is produced through *arr-1* in response to double stranded DNA breaks in *M. smegmatis* caused by oxidative stress (Stallings et al., 2011). In the Ann Arbor PoU filters, bacteria in the fabric biofilm were exposed intermittently to residual chloramine when the filter was operated; then during stagnation periods when growth occurred, we hypothesize that those bacteria that are less vulnerable to the effects of chloramine would thrive. In the fabric biofilm, chloramine can diffuse into the biofilm and enter bacterial cell walls to generate oxidative stressors that react with the nucleic acids or DNA (Dodd, 2012; Dukan and Monod, 1996; Shih and Lederberg, 1976). Therefore, bacteria carrying *arr-1* may be selected for among the fabric populations to counteract chloramine exposure.

**Table 4-2 Abundance of selected ARGs in the Ann Arbor ACB PoU filter system. The sample size of each sample type is indicated in the parenthesis.**

Average gene copies (copy/100 mL)	PCP treatment		
	0 ng/L	50 ng/L	100 ng/L
<i>arr-1</i>			
Influent (N=1)	4×10 <sup>3</sup>	2×10 <sup>2</sup>	3×10 <sup>2</sup>
Effluent (N=2)	7×10 <sup>2</sup>	1×10 <sup>4</sup>	4×10 <sup>3</sup>
Fabric (N=2)	2×10 <sup>5</sup>	9×10 <sup>4</sup>	1×10 <sup>5</sup>
<i>rbpA</i>			
Influent (N=1)	2×10 <sup>2</sup>	2×10 <sup>1</sup>	3×10 <sup>1</sup>
Effluent (N=2)	1×10 <sup>3</sup>	1×10 <sup>3</sup>	5×10 <sup>2</sup>
Fabric (N=2)	4×10 <sup>2</sup>	9×10 <sup>1</sup>	1×10 <sup>2</sup>

## The Flint Case

### *The abundance of Enterobacteriaceae associated with the diversity and type of ARG*

In the samples from Flint, samples highly abundant in *Enterobacteriaceae* had more types of ARGs (144 ARG determinants) than the samples with low *Enterobacteriaceae* abundance (93 ARG determinants) (Table S4-2). The highly abundant *Enterobacteriaceae* samples contained ARGs that had previously been found in the genomes of enteric-related organisms, including *AcrF* in *E. coli* and *Shigella sonnei* (Lau and Zgurskaya, 2005), *emrE* in *E. coli* (Schuldiner, 2009), and *mdtK* in *Salmonella enterica* (Nishino et al., 2006). Some ARGs found in samples highly abundant in *Enterobacteriaceae* were also found in soil and wastewater environments (Ng et al., 2017), including genes encoding for EfrAB which is produced by *Enterococcus faecalis* genomes (Lee et al., 2003), and EmrAB-TolC efflux pumps which are produced by *E. coli* (Lomovskaya et al., 1995).

### *The occurrence and abundance of selected ARGs increased across ACB PoU filters*

Among all the ARGs that were present in the Flint samples, we selected two genes (*AIM-1* and *oqxB*) that were relevant to abundant bacterial taxa of interest in Flint (Love et al., in preparation): *P. aeruginosa* and *Enterobacteriaceae*. Both taxa met the following criteria: 1) they are prevalent in other drinking water systems as well as our study system, 2) they are often

detected in biofilms, 3) they contain functional genes relevant to biofilm formation, and 4) they have the capability to horizontally transfer genes.

*AIM-1* was selected because it is a transferable ARG that was previously discovered on the genome of a clinical *P. aeruginosa* isolate. The *AIM-1* gene encodes an Ambler class B beta-lactamase. It is among a new class of metallo beta lactamases (MBLs) that were recovered from a male aboriginal immunocompromised Australian patient having a *P. aeruginosa* infection (Yong et al., 2012). This encoding enzyme degrades beta-lactam antibiotics, including carbapenems, piperacillin, cephalothin, cefoxitin, cefotaxime, cefuroxime, and ceftazidime. Unlike most other transferable ARGs that are part of a class 1 integron, the *AIM-1* gene found in *P. aeruginosa* from Australia was found associated with a class of insertion sequence elements, ISCR. In our study, the *AIM-1* gene was detected in water from both the high and low abundance *Enterobacteriaceae* samples.

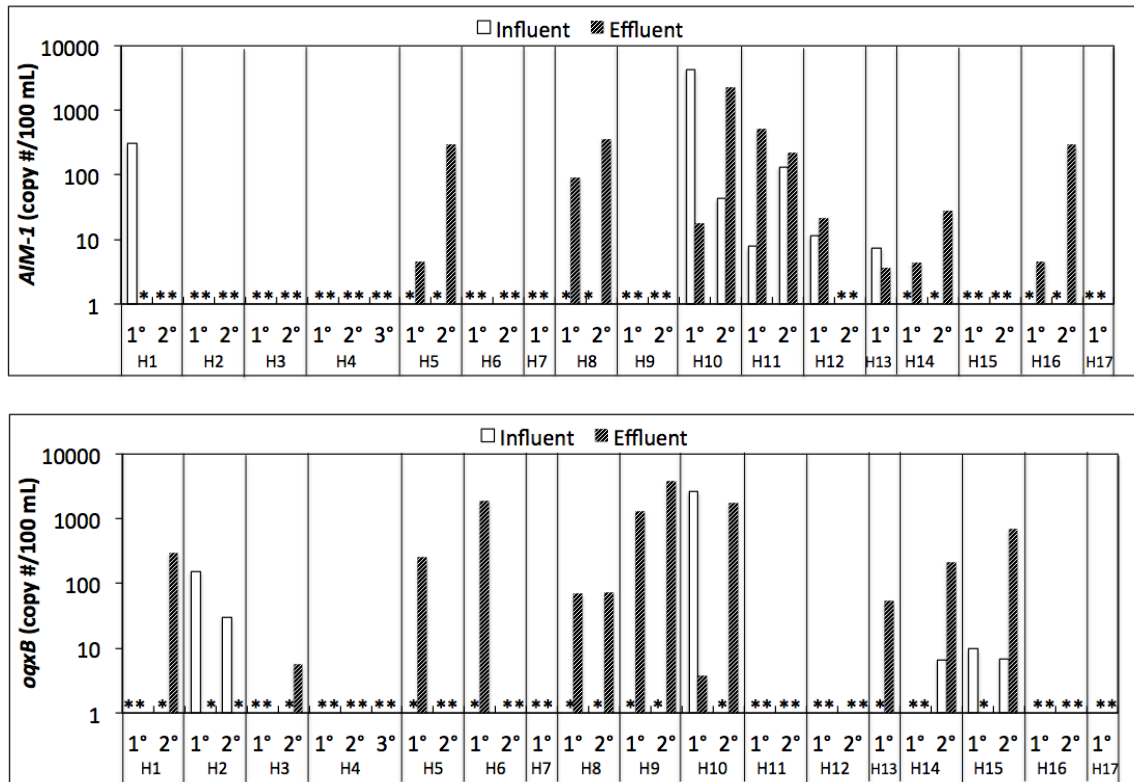
The gene *oqxB* is a plasmid-mediated efflux pump (OqxAB) that has a wide substrate specificity that confers resistance to fluoroquinolones, nalidixic acid, chloramphenicol, trimethoprim, and benzalkonium chloride. The *oqxB* gene was found in the genomes and plasmids of several coliform bacteria, including *E. coli*, *Salmonella* and *Klebsiella pneumoniae*, and in a human *Enterobacteriaceae* clinical isolate (Kim et al., 2009). It was also found in wastewater and soil samples (Li et al., 2012). In our study, this gene was detected in water from both the high and low abundance *Enterobacteriaceae* samples.

Fig. 4-1 shows the absolute abundance (gene copies/100 mL of drinking water) of *AIM-1* and *oqxB* in the influent or effluent of the ACB PoU filters. *AIM-1* and *oqxB* were below detection in more than half of the influent and effluent samples. However, they were detected in PoU filter effluents (43% for *AIM-1*, 40% for *oqxB*) more often than filter influents (22% for *AIM-1*, 18% for *oqxB*) across all households.

To understand if the selected ARGs were likely to be enriched in the filters and thus resulted in high levels in the filter effluent, we compared the occurrence and abundance of the selected ARGs in either influent or effluent by the logistic regression model. The drinking water bacterial communities were significantly different between sampled houses (Love et al., in preparation) and may affect the distribution of antibiotic resistance genes in and out of the associated PoU filters. Therefore, we used the mix effect logistic regression to group the households as a nested

factor that would affect the presence and abundance of the selected ARGs. In this analysis, we found that the probability of occurrence of the *AIM-1* in the effluent was significantly higher than the influent within the same house ( $p < 0.05$ ). In contrast, *oqxB* genes were present in both influent and effluent samples and were almost significant ( $p = 0.05$ ) (Table 4-3). If we only account for the household samplers with low *Enterobacteriaceae* abundance (gene copies  $< 75\%$  quintile), the probability of *AIM-1* and *oqxB* occurrence was not significantly different between the influent and effluent of the ACB PoU filters ( $p = 0.24$  for *AIM-1* and  $0.31$  for *oqxB*).

The association of ARG abundance and water sample type (influent vs. effluent), water temperature, pH, chlorine residual, cartridge age, and the total number of 23S rRNA genes targeting *Enterobacteriaceae* and 16S rRNA genes targeting all bacteria were evaluated (Table 4-4). We found that *AIM-1* and *oqxB* abundances were positively associated with water types. This indicates that the ACB PoU filter effluent contained a significantly higher concentration of the two genes than the influent. *AIM-1* abundance was also associated with the chlorine residual, which is known to be confounded by the water type since chlorine residual in the influent tap was removed from the effluent by the ACB PoU filters. The abundance of *oqxB* was positively associated with pH, the absolute abundance of *Enterobacteriaceae*, and the total 16S rRNA gene. The association of *oqxB* with the abundance of *Enterobacteriaceae* may be explained by the observation that *oqxB* was found on the genomes of enteric-related organisms. Cartridge age was not significantly associated with either of the two ARGs.



**Fig. 4-1 The Abundance of *AIM-1* (top) and *oqxB* (bottom) across ACB PoU filters. The non-detected values are marked with an asterisk.**

**Table 4-3 The odds ratio of the occurrence of selected ARGs in filter effluent vs. influent.**

Gene	Nested by all households		Within low <i>Enterobacteriaceae</i> households	
	Odds ratio	<i>P</i> value	Odds ratio	<i>P</i> value
<i>AIM1</i>	10.43	<0.05	3.13	0.24
<i>oqxB</i>	3.46	0.05	2.11	0.31

Log (p/(1-p)) =  $\alpha \times$  (Presence of the selected ARG) +  $\beta$ , where p is the probability of the occurrence of selected ARG,  $\alpha$  is the odds in influent,  $\beta$  is the odds in the effluent.

**Table 4-4 Water parameters significantly associated with the abundance of selected ARGs.**

Parameters	Estimate slope	P value
<i>AIM1</i>		
Water types	0.72	0.030
Chlorine residual	-0.89	0.028
<i>oqxB</i>		
Water types	4.12	<0.001
pH	3.53	<0.001
<i>Enterobacteriaceae</i>	1.51	<0.001
Total 16S rRNA gene	1.05	0.0044

\*Model output of generalized mixed model (selected ARGs abundance - water parameters with household grouped as random effect).

#### ***ARGs accumulated in biofilms inside the PoU filters***

For effluents where *AIM-1* or *oqxB* were detected, their corresponding influent samples did not necessarily have detectable ARGs. This response may have occurred if bacteria that carry the ARGs proliferated in the carbon cartridge and were flushed out to the effluent during filtration. We evaluated the distribution of *AIM-1* and *oqxB* on the biofilms of the ACB surface, fabric, and inner core from those PoU filters that had detectable ARGs in the influent or effluent. We detected *AIM-1* on 86% of the PoU filters in any of the biofilm locations. Most accumulated on the surface of the ACB effluent channel (71%), followed by the fabric biofilm (43%), and the influent side of the ACB surface (29%). In contrast, *oqxB* was detected in only 57% of the PoU filters and was most frequently detected on the influent side of the ACB filter (38%) followed by the effluent ACB channel surface (29%), and fabric (19%). The results indicate that the filters may provide a reservoir for the growth of bacteria carrying the *oqxB* and *AIM-1* genes. *AIM-1* was more frequently detected in biofilm samples of the ACB effluent channel compared to *oqxB*, suggesting that the hosts of *AIM-1* may traverse the whole depth of the ACB more easily than the hosts of *oqxB*.

This study demonstrates that ACB PoU filters can increase the occurrence probability and abundance of selected ARGs across ACB PoU filters in two drinking water systems that were studied. The ARGs that can be exchanged among bacterial species by horizontal gene transfer

(*AIM-1* and *oqxB*) or are intrinsic on genomes of *Mycobacteria* spp. (*arr-1* and *rbpA*) were both enriched across ACB PoU filters and, thus, increased in concentration across the filters. We also found more types of ARGs in the Flint water system than the Ann Arbor system. Comprehensive immunological studies of ARBs in drinking water and associated infections and diseases have not, to our understanding, been conducted. We believe that this study shows the importance of examining the risk that ACB PoU filters impose to possible exposure to ARB and their genes when using such devices to treat tap water at the point of use.



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## Chapter 5

### Transmission and colonization of bacteria in activated carbon block (ACB) point-of-use (PoU) filters

#### 5.1 Introduction

Commercial Point-of-Use (PoU) drinking water filters are widely implemented in households to remove chemicals of concern, taste and odor, and disinfectant residuals in tap water. These ACB PoU filters are certified through NSF/ANSI Standard 42 and 53 for removing particles (including protozoan cysts), and inorganic and organic chemicals that are of aesthetic and health importance (NSF International/ANSI, 2015a, 2015b). Halogenated DBPs (Stalter et al., 2016) and metals such as lead and copper (Deshommes et al., 2010) can be effectively removed by the ACB PoU filters by the tap water. In a 2017 U.S. market survey, it is estimated that 72% of consumers own at least one filtration product; among these, faucet-mounted water filters are the third most commonly owned device (Cullen, 2017). Faucet-mounted filters utilize a solid block of compressed and polymer fused carbon, or the activated carbon block (ACB), as the filter media. The ACB contains massive surface area for physical adsorption and low porosity for mechanical filtration (Silverstein, 2006) to remove chemical contaminants.

The ACB-based filters are effective in controlling aesthetic and health-related chemical contaminants from the water, but they are not designed to remove bacteria. Multiple studies have used culture-based methods to show that heterotrophic bacterial counts increase with time in the effluent of ACB PoU filters to levels that exceed those in the tap water influent, even when used within the manufacturers' recommended usage period (Chaidez and Gerba, 2004; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981). Other culture-based studies found that the composition of bacteria in the filter effluent was different from the tap water (Chaidez and Gerba, 2004; Su et al., 2009; Wu et al., 2017). Chaidez et al. (2004) found that indigenous *Aeromonas hydrophila*, *Pseudomonas aeruginosa* and total coliforms were more abundant in the effluent

than in the influent using culture-based techniques (Chaidez and Gerba, 2004). Although culture-based studies can only detect a small fraction of the drinking water bacterial population (Allen et al., 2004), we similarly showed that ACB PoU filters alter the bacterial composition in filter effluents using culture-independent techniques (Wu et al., 2017, Chapter 3).

Despite evidence that some bacteria can pass through or grow in ACB PoU filters, it is unclear how bacteria move through them. The porosity of the ACB is expected to be very low, for example line pressures of at least 210 kPa (30 psi) are required for water to pass through. In an earlier study, we estimated that the average pore size of the activated carbon in one brand of ACB PoU filters is 22 Å (Wu et al., 2017), which is much smaller than the size of average (1 µm) or starved oligotrophic (0.1 µm) bacteria in drinking water (Silbaq, 2009). Influent microorganisms are unlikely to traverse the entire filter media depth, therefore, unless there are pore networks with diameters that are much larger than the mean pore size. Even if preferential flow channels of bacterial size are present in the ACB, previously observed differences between the bacterial community structure of influent and effluent samples suggests that only a fraction of bacterial species are able to remain viable and migrate through an ACB (Chaidez and Gerba, 2004; Su et al., 2009; Wu et al., 2017). Beyond the question of transport mechanism, survival- and selection- related factors must also control the changes in bacterial community structure within the ACB PoU filter.

The goal of this study is to assess the transmission and growth of two bacteria species with different physiological characteristics and public health significance in commonly used commercial faucet-mounted ACB filters. To learn more about the particle physical transport pathways in the filters, separate breakthrough studies were conducted with bacteria-sized microspheres. Negatively charged, low density fluorescent microspheres were selected to simulate “abiotic” bacteria in these studies. Bacterial breakthrough experiments were conducted by simultaneously spiking fluorescent protein-tagged forms of *Escherichia coli* and *Pseudomonas aeruginosa* into tap water containing monochloramine as the residual disinfectant. An important distinction in the approach relative to other literature studies were the steps taken to ensure that the spiked strains were acclimated to the oligotrophic conditions of tap water by first exposing them to limited nutrient and carbon sources at concentrations typical of tap water. *E. coli* was selected because it is a pathogenic indicator bacteria for fecal contamination but is

known to be readily outcompeted by indigenous bacteria in low-nutrient environments (Lehtola et al., 2007). *P. aeruginosa* is an opportunistic pathogen that can form biofilms in drinking water and survive for long periods (Moritz et al., 2010). Exposure to *P. aeruginosa* and *E. coli* from contaminated water occurs by various routes. The exposure routes that pose the greatest health risk for *P. aeruginosa* are via skin (direct contact) and lung (inhalation) (Mena and Gerba, 2009), while for pathogenic *E. coli* strains the route with the greatest risk is through oral exposure (consumption). Studying the intra-filter migration of two species with different properties and exposure routes offers a better understanding of the bacterial exposure risks posed by ACB PoU filters.

## **5.2 Materials and Methods**

### **5.2.1 Filter manifold system**

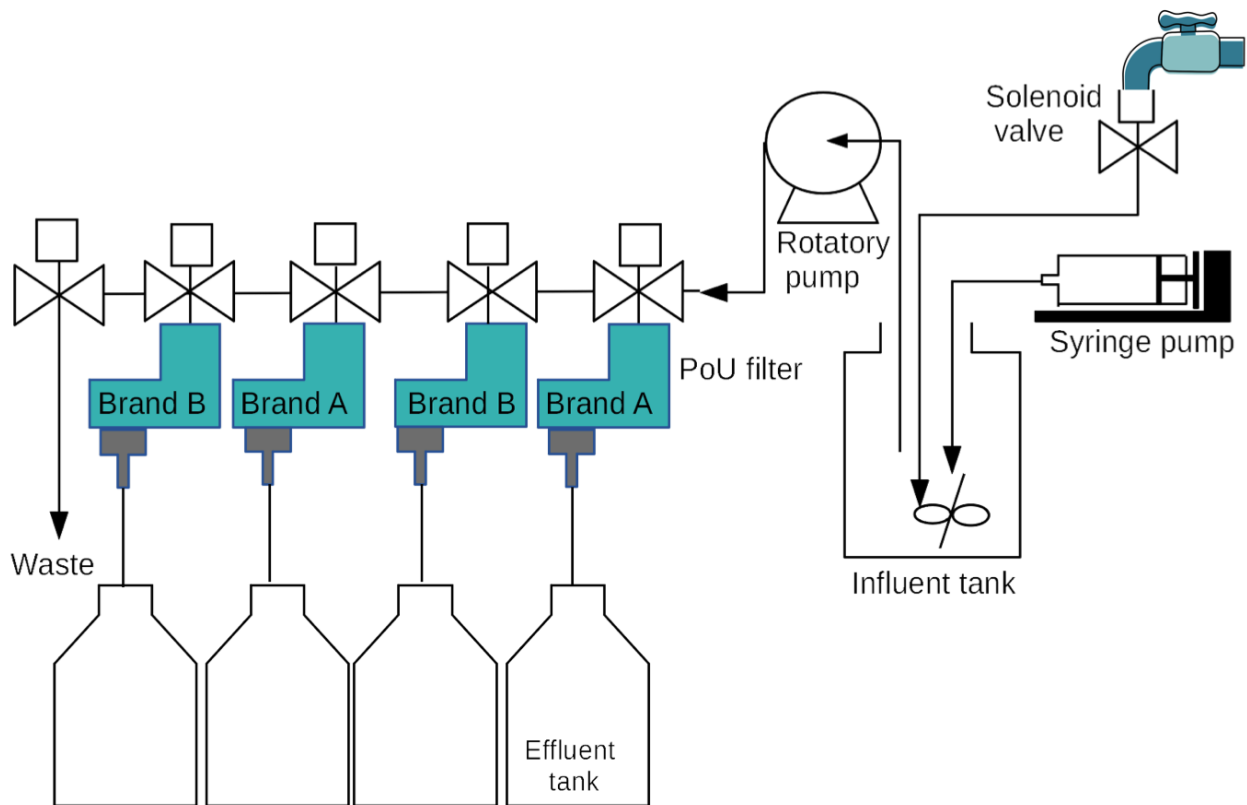
A lab-scale manifold system with two brands of ACB PoU filters was constructed for the spiking test of fluorescent bacteria (Fig. 5-1). Both brands of ACB PoU filters contain a synthetic fabric mesh that is wrapped around the ACB to protect its surface against the outer plastic housing. During operation, the influent water flows radially from the outside surface through the carbon block pore network, and then exits the filter from the center effluent channel of the ACB. Chloraminated tap water (Ann Arbor, MI) mixed with known amounts of mCherry-tagged *E. coli* and green fluorescent protein (GFP)-tagged *P. aeruginosa* was intermittently fed to the PoU filters under control by a LabVIEW program designed to simulate household use. Duplicate filters of each brand (Brand A and B) were tested and connected in parallel with one brand next to the other (A– B – A – B). Half a liter of influent water was pumped (Brass Rotary Vane Pump, Procon) from the influent reservoir to each filter hourly for 11 hr and followed by an overnight stagnation period of 13 hr. Influent pumping took from 5 to 7 sec, depending upon the life stage of the filter (pumping intervals increased slightly as the filters aged and headloss increased). The order of filtration was rotated every day so that each filter received the first flush of influent every fourth day. The system was operated for a total of 29 days, comprising an application phase (23 days, when fluorescent bacteria were mixed with the tap water influent) and a washout phase (6 days with no supplemental fluorescent bacteria).

The influent was automatically prepared every hour during operation. The manifold pipes were washed by 2 L of tap water to flush out the stagnant water. Influent tank was then filled with 2.3



L tap water and mixed with 2 mL stock solutions of mCherry-tagged *E. coli* and GFP-tagged *P. aeruginosa* ( $3\text{-}5 \times 10^5$  cell/mL) for 2 min to obtain a final concentration of  $5 \times 10^2$  cell/mL. The stock solutions were stored in two 60 mL syringes and injected to the influent tank by the syringe pump (Chemyx, Stafford, TX). At the end of the cycle, the rest of the influent was drained into a waste container.

Filter breakthrough tests with abiotic fluorescent microspheres were conducted with the same manifold system with a few modifications: each filter received influent hourly for 16 hr followed by an 8 hr overnight stagnation. The influent was made by mixing 1.8 L of deionized water with a 3 mL fluorescent microsphere suspension ( $3 \times 10^8$  particle/mL, pH 8.3, described in section 5.2.2) to obtain the a final concentration of  $5 \times 10^5$  particle/mL.



**Fig. 5-1 Schematic of PoU filter manifold system.**

## 5.2.2 Cultures and reagents used

### Fluorescently-tagged bacterial cultures

Two chromosomally-tagged fluorescent bacteria, GFP-tagged *Pseudomonas aeruginosa* PAO1 (University of Notre Dame, IN) (Choi et al., 2005) and mCherry-tagged *E. coli* MG1655 (Rensseler Polytechnic Institute, NY) (Englaender et al., 2017), were used in this study. The gene encoding fluorescent reporter protein was incorporated directly into the chromosome of the species where the constructed DNA can be stably maintained without the need for antibiotic selection. Each species was constructed to have a single copy of the fluorescent gene next to a housekeeping gene. The GFP gene was inserted downstream of the *glmS* gene encoding glucosamine synthetase (Choi et al., 2005). The mCherry gene was integrated into the intergenic region of *atpI* encoding ATP synthase protein I and *gidB* encoding methyltransferase (Englaender et al., 2017). The genes that are adjacent to fluorescent genes are responsible for essential metabolic pathways to ensure the stability of the engineered phenotype in water environment (Eberl et al., 1997). Expression of mCherry was induced by addition of 100  $\mu$ M isopropyl  $\beta$ -D-1-thiogalactopyranoside (IPTG) to the syringe stock.

To ensure both species remained active under oligotrophic conditions in drinking water for 24 hours, the two species were grown in 1X, 10X, 50X, and 250X serially diluted R2A medium, each for 24 hours. Then 5 mL of 250X-diluted R2A bacterial solution was transferred to 45 mL dechloraminated/0.22  $\mu$ m filtered tap water for 24 hours prior to using as a syringe stock. The tap water for acclimation was dechloraminated with sodium thiosulfate; however, the tap water used to dilute the culture stocks was not dechloraminated (Influent total chlorine over the period of operation was  $0.86 \pm 0.12$  mg/L as  $\text{Cl}_2$ ). The fluorescence of *E. coli* and *P. aeruginosa* was detectable by the flow cytometry after mixing with tap water for 2 min (the maximum retention time of the mixing reservoir that was pumped into the filters). The additional background total organic carbon (TOC) contributed from the R2A medium from the acclimated stock cultures to the filters was estimated to be 206  $\mu$ g TOC per filter throughout the application phase.

### Fluorescent microsphere suspensions

Carboxylate-modified yellow-green FluoSpheres beads (ThermoFisher, Waltham, MA) that have a negative surface charge of 0.1826 meq/g and diameter of  $0.99 \pm 0.022$  were used in this study. The stock concentration contained approximately  $3 \times 10^{10}$  particles/mL. To prevent agglomeration,

the stock was diluted to  $3 \times 10^8$  particles/mL by 100 mM borate-boric acid buffer solution (30 mM sodium tetraborate (Fisher Scientific, Hampton, NH) and 40 mM HCl (Sigma-Aldrich, St. Louis, MO) made in deionized water). The pH of the buffer was adjusted to be similar to Ann Arbor tap water (pH 8.3) by 1M sodium hydroxide (Fisher Scientific, Hampton, NH). The borate-boric acid buffer system was used because this system dissociates ions with an ionic strength of 35 mM.

### **5.2.3 Sampling protocols and parameters**

Sampling was slightly different between the biotic (fluorescent bacteria) and abiotic (microsphere) breakthrough tests. The following water sample types were collected for the breakthrough test of fluorescent bacteria: filter influent, 500 mL grab filter effluent, and 11-hr composite filter effluent samples. The effluent samples were collected every two days and measured for culturability and fluorescent bacteria concentration, and were collected twice a week for bacterial measurements on total and membrane-intact cell counts. Comparisons of the grab and composite samples enabled quality control evaluations of the stability of fluorescent and total bacteria concentrations in the effluent container. During the microsphere breakthrough test, the influent and 500 mL effluent grab samples from the 1st, 9th, and 15th cycles were collected every day for analysis.

### **5.2.4 Analytical methods**

#### Flow cytometry

Flow cytometry was used to determine the cell counts of fluorescently tagged bacteria, total bacteria, and fluorescent microspheres. Because of the nature of fluorescently-tagged cells, indigenous cells and microspheres, the methods were slightly different.

The flow cytometer used for fluorescently tagged bacteria and fluorescent microspheres was a ZE5 cell analyzer (Bio-Rad, CA). The instrument was set to agitate for 5 sec per sample to maintain cell suspension. All samples were injected into the flow cytometer with a flow rate of 1  $\mu\text{L/s}$ . The analysis of populations was carried out using the Everest Flow cytometry analysis software. To gate the fluorescent bacteria, the forward scatter of the two fluorescent bacteria was detected by the 405 nm forward scatter small particle detector set at a photomultiplier tube voltage of 347 V with linear gain. Green fluorescence emitted from *P. aeruginosa* was detected via the GFP detector set at the voltage of 491 V with logarithmic gain. The red fluorescence

emitted from *E. coli* was detected via the mCherry detector of 587 V with logarithmic gain. The acquisition of each sample stopped when a total of 1,000 events was acquired or the flow-through volume reached 300  $\mu$ L. The detection limit of the two fluorescent bacteria was tested by diluting the acclimated fluorescent bacterial suspensions with the buffer containing 3 mM potassium dihydrogen (Fisher Scientific, Pittsburgh, PA) and 4 mM magnesium chloride (Fisher Scientific, Pittsburgh, PA). The lowest diluted suspension that can be detected was 50 cell/mL, and was taken to be the detection limit of the instrument. The flow cytometry dot plots of detection limit, examples of the influent, and effluent samples are given in Figs. S1-S2.

The fluorescence of the microspheres was detected via a GFP detector at a voltage of 391 V. The forward and side scatter of the microspheres were collected by the 488 nm forward scatter detectors and 488 nm side scatter detectors in linear gain with the voltage of 365 V and 675 V. The acquisition of each sample stopped when 10,000 events or 40  $\mu$ L flow-through volume was reached. The flow cytometry dot plots of the examples of the influent and effluent samples are given in Fig. S3.

Total bacterial measurements were conducted using a BD Accuri C6 Plus flow cytometer (BD Accuri cytometers, Belgium). Bacterial cells were stained by adding 1  $\mu$ L of SYTO Green (1,000X) and 20  $\mu$ L of propidium iodide (PI, 1 mg/mL, 1.5 mM) into 979  $\mu$ L of water sample to obtain 1X SYTO Green and 0.03 mM PI in the final solution. SYTO® Green stains all bacterial cells irrespective of membrane damage. PI stains the membrane-compromised cells. After the addition of the dyes, samples were vortexed and incubated in a dark environment at room temperature for 15 mins. A total of 40  $\mu$ L of each sample was measured at a flow rate of 14  $\mu$ L/min using fluorescent detectors 1 (FL1: 533  $\pm$  30 nm) and 3 (FL3: > 670). SYTO® Green allows discrimination between fluorescent cells and non-fluorescent debris in the FL1 detector. PI was detected in the FL3 detector (emission filter > 670 nm). A threshold value of 800 was applied on the FL1 channel. All data were analyzed by BD Accuri C6 software.

#### Culturing viable fluorescently-tagged bacteria

To evaluate the presence of culturable bacteria, 50 mL of water samples that were diluted 1, 10X, and 100X and were filtered through a 0.22  $\mu$ m membrane (Millipore, Billerica, MA), and the membrane filters were placed onto *Pseudomonas* isolation agar (Fisher Scientific, Hampton, NH) or M Endo LES agar (Fisher Scientific, Hampton, NH)(APHA et al., 2005) and incubated 35<sup>o</sup> C

for 24-48 hours, respectively (APHA et al., 2005; Brown and Lowbury, 1965). The presence of *P. aeruginosa* was indicated by green colonies; coliform colonies presented with a pink to dark-red color and metallic surface sheen. To validate the presence of *E. coli*, the dark-red and gold colonies cultured from M Endo LES agar were transferred to nutrient agar with 4-methylumbelliferyl- $\beta$ -D-glucuronide (MUG). *E. coli* are the colonies that produce the enzyme  $\beta$ -glucuronidase and hydrolyzes the MUG substrate to produce a blue fluorescence around the periphery of the colony under long-wave UV light at 365 nm.

### Quantitative PCR (qPCR)

The extracted DNA of the effluent water samples, biofilm of the filter inner channel and ACB fabric was analyzed by qPCR targeting GFP and mCherry genes. All analyses were performed in triplicate. A standard curve was generated by amplifying 7-fold serially diluted GFP-tagged *P. aeruginosa* or mCherry-tagged *E. coli* with a known amount of gene copies for each targeted gene. All qPCR experiments were carried out on an Eppendorf® Mastercycler (Eppendorf, Germany). The PCR mixture (10  $\mu$ L) consisted of Fast-Plus EvaGreen Master Mix (Biotium, CA, US), primer sets (0.5  $\mu$ M each, Table 5-1), 0.625 mg/mL BSA, and 1  $\mu$ L template DNA. The reaction conditions were estimated based on primer sequences and features of the polymerase used. The following conditions were ultimately used: 95°C for 2 min, followed by 35 cycles for 95°C for 5 sec, annealing for 5 sec at defined temperature (shown in Table 5-1) and 72°C for 25 sec. The qPCR efficiency of the two genes was 90-94%, and R<sup>2</sup> values were 0.99 for the standard curves. A melting curve was used to confirm the specificity of qPCR amplified fragments.

**Table 5-1 qPCR primers for two fluorescent chromosomal genes used in this study.**

Gene		Primer (5'-3')	Fragment size (bp)	Annealing Temperature (°C)	Reference
GFP	Forward	TGCCATGTG TAATCCCAG CA	97	55	This study
	Reverse	CTGTCCACACAATCTGCCC T			
mCherry	Forward	GGCGAAGAAGACAACATG GC	231	54	(Englaender et al., 2017).
	Reverse	CGGATGCTTAACGTACGCT TTCG			

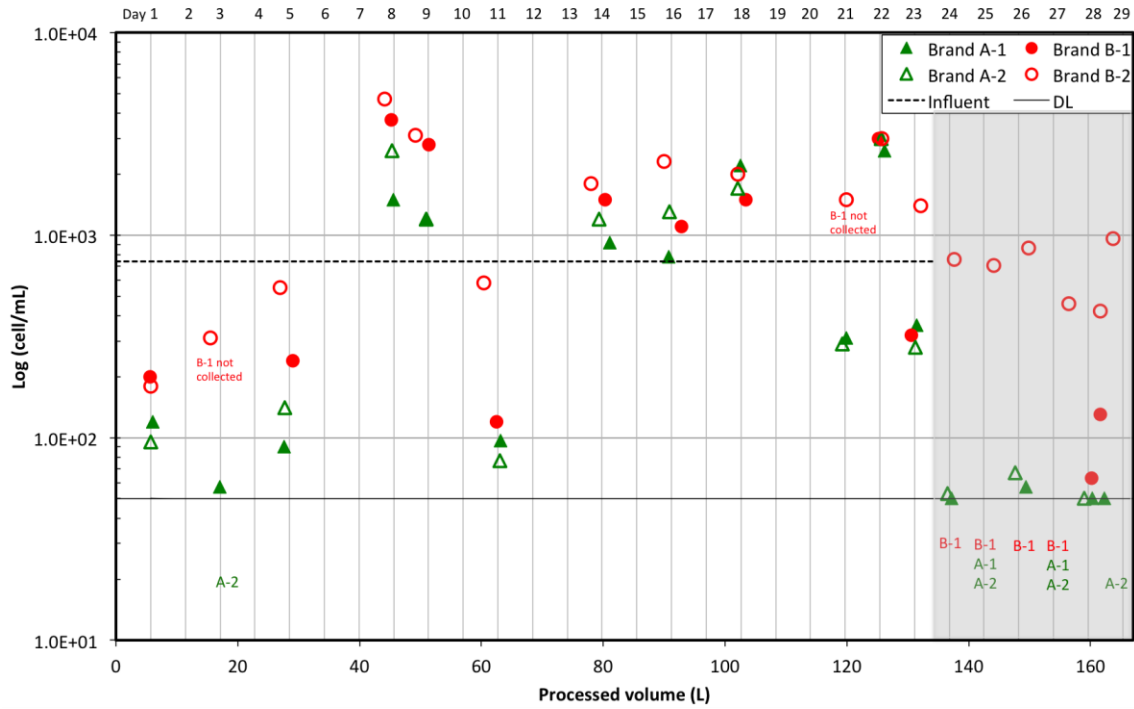
### 5.3 Results and Discussion:

#### 5.3.1 Breakthrough of fluorescent bacteria and 1 $\mu\text{m}$ microspheres provides evidence of preferential pathways

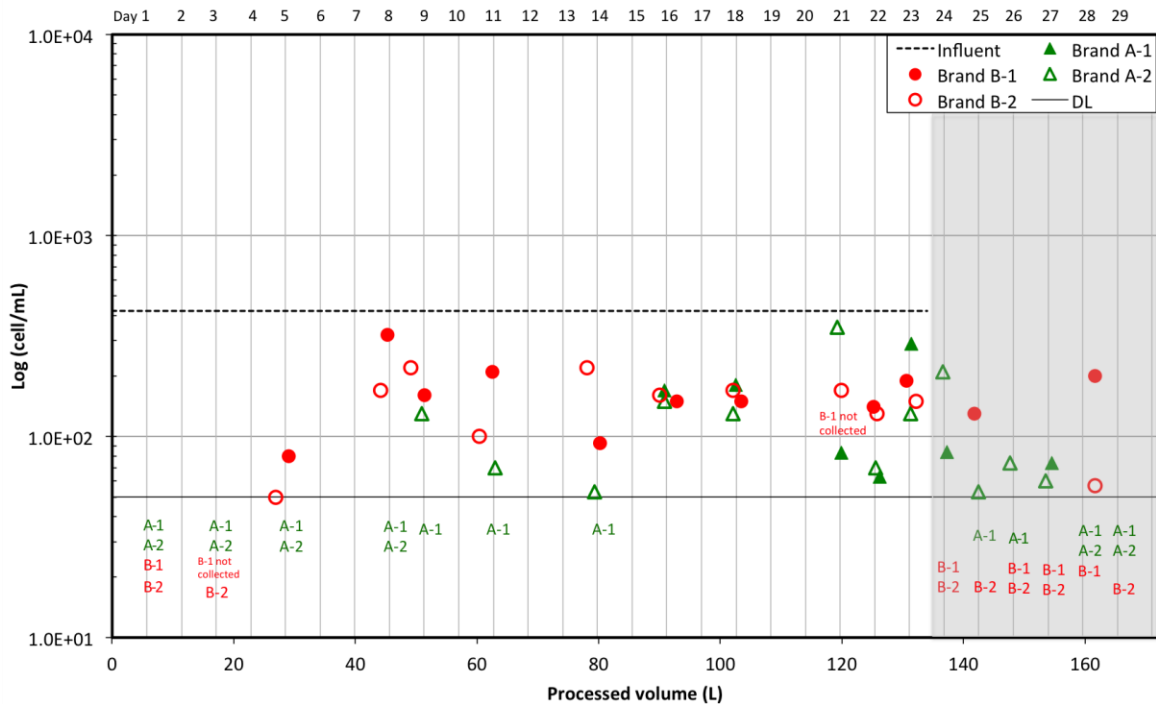
Breakthrough profiles of two fluorescent bacteria, which were spiked into the tap water influent of two ACB PoU filters brands, are presented in Fig. 5-2. The concentrations in Fig. 5-2 were measured from the composite samples. We found that the concentrations of fluorescent bacteria from the grab samples of the 1st, 5th, and 11th cycle of the day were similar to the composite samples ( $p > 0.05$ , one-sided t test). Therefore, the composite samples can be used to represent the average of hourly effluent samples because the fluorescent bacteria did not proliferate or die in the effluent jar. Both species, *P. aeruginosa* and *E. coli*, were detected in the effluents of Brand A and Brand B filters, and in the case of *P. aeruginosa* within the first day, indicating that there must be flow pathways of sufficient size to allow bacteria to pass from the influent to the effluent of the ACB.

The existence of such preferential flow pathways is also supported by breakthrough experiments with bacterial-sized inert fluorescent microspheres (1  $\mu\text{m}$  diameter). The microsphere suspension was buffered to achieve a pH of 8.3 in order to ensure that the carboxylate surface groups were maximally negatively charged. The suspension pH was also similar to Ann Arbor tap water so that protonation conditions of the ACB surface were simulated. We calculated that the resulting solution ionic strength in the influent solution was 0.06 mM. The conditions of significant negative surface charge and modest ionic strength were sufficient to minimize particle aggregation. We did not, for example, observe any aggregation from the flow cytometry dot plots for the microsphere measurements. As shown in Fig. 3, the microspheres were detected in the effluent of both filter brands immediately after the first half-liter of influent was applied. The breakthrough of microspheres, which are not subject to growth and decay, demonstrates the capability of negatively charged micron-sized particles to migrate from the influent to the effluent at process volumes that represent 0.1% of the filter's design process volume (100 gal or 379 L). We believe this is the first time that breakthrough of abiotic bacterial-sized particles has been demonstrated in these filters.

(A)

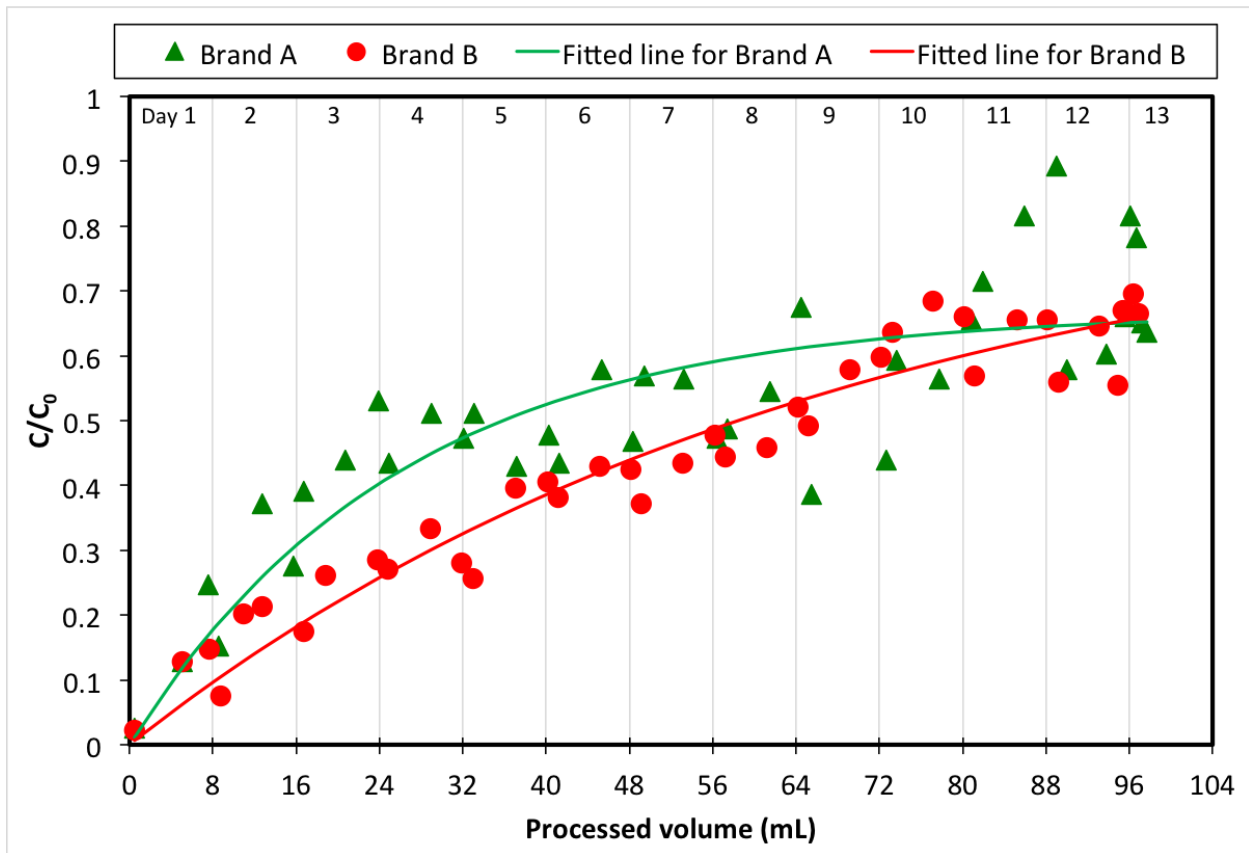


(B)



**Fig. 5-2 Breakthrough of (A) GFP-tagged *P. aeruginosa* and (B) mCherry-tagged *E. coli* through duplicate ACB PoU filters of Brand A (green) and Brand B (red). Addition of fluorescent bacteria stopped after Day 23 (after 131 L). Washout (shaded region) continued through Day 29. The detection limit of flow cytometry is 50 cell/mL. The written symbols**

under the detection limit (DL) line are of non-detect measurements. The average influent is  $7.4 \times 10^2$  cell/mL for *P. aeruginosa* and  $4.2 \times 10^2$  cell/mL for *E. coli* (N=12 for both species). Noted that at day 8 (44 L), *P. aeruginosa* was overloaded to the ACB PoU filters and the influent concentration ( $3.6 \times 10^3$  cell/mL) was five times of the average influent. Effluent data points of Brand B-1 were missing on day 3 and 21.



**Fig. 5-3 Average of the normalized microsphere breakthrough in duplicates of Brand A and B filters. The fitted model was based on the average  $C/C_0$  of each brand.  $C$  and  $C_0$  are the effluent and influent concentration of microspheres, respectively. The average microsphere influent concentration is  $5.2 \times 10^5 \pm 1.3 \times 10^5$  particle/mL. The model fitted for Brand A is  $C/C_0 = 0.67 \times (1 - \exp(-0.039 \cdot \text{Vol}))$ , for Brand B is  $C/C_0 = 0.87 \times (1 - \exp(-0.015 \cdot \text{Vol}))$ .**



### 5.3.2 *P. aeruginosa* and *E. coli* exhibit different breakthrough and washout patterns

Comparisons of the breakthrough of both fluorescent bacteria reveals that *P. aeruginosa* was detected earlier and achieved greater levels of breakthrough than *E. coli* during the application phase (Fig. 5-2). The effluent *P. aeruginosa* concentration plateaued at levels up to 1.8 times greater than influent counts after 21% design water volume was filtered (around two weeks). On the contrary, effluent *E. coli* was under the detection limit (50 cell/mL) until day 5 for Brand B filters and day 9 for Brand A filters, then plateaued at 35% of the influent level. During the plateau period, we observed a wide variation in effluent concentration. The effluent *P. aeruginosa* concentrations varied between 30% and 4 times the influent level, and *E. coli* varied between 24% and 60% of the influent concentration (Fig. S5-4). These variations can be caused by clogging and a build up of hydraulic back pressure, followed by bacterial release as the pathways become unclogged. During the release or sloughing phases of these cycles, effluent concentrations of *P. aeruginosa* can dramatically exceed the influent level while *E. coli* approached the influent concentration. Note that the flow cytometry method used in this study only accounted for single cell counts and may underestimate the true sloughing concentrations, since it does not detect large clumps of fluorescent particles.

The later breakthrough of *E. coli* relative to *P. aeruginosa* suggest that *E. coli* was initially attached to the ACB and later was sloughed out from a population accumulating inside the ACB PoU filters. These findings were different from the Geldreich et al study, which introduced *P. aeruginosa*, *E. coli* and other organisms in a single spike into the dechlorinated tap as the influent to ACB PoU filters (Geldreich et al., 1985). Although there were differences in how bacteria were introduced between this study (continuous spike) and theirs (one-time spike), Geldreich et al. found that the spiked *E. coli* passed through the ACB PoU filter immediately but *P. aeruginosa* broke through later. The outcomes could be due to other differences in the preparation of spiked species and the use of different strains of the same species. The spiked *E. coli* used in Geldreich et al.'s study was prepared in a fresh rich medium that was then added to the dechlorinated tap without any acclimation. The nutritional state of microorganisms is known to impact the surface chemistry and charge of cells (Haznedaroglu et al., 2008), as well as their size (Morita, 1988). The *E. coli* species used in our study was different from that used in the Geldreich et al. study. Bolster et al. have shown that filtration rates of different *E. coli* strains have significantly different filtration rates in sand media under the same chemical conditions (C

H. Bolster et al., 2008). Many studies have demonstrated that the transport of bacteria through porous media is greatly affected by bacterial variables such as size, shape, hydrophobicity, and surface charge (See Zhong et al., 2017 as a review). The migration of bacteria through the flow pathways in the ACB PoU filters is likely to be affected by similar factors as well.

Washout tests were conducted after the effluent concentration had plateaued to examine if the fluorescent bacteria within the filter were able to continue to seed the effluent after they were no longer introduced to the influent. Tap water without inoculation was fed to the system during day 24-29. During this period, the effluent concentrations of *E. coli* and *P. aeruginosa* decreased to near the detection limit from all filters except for *P. aeruginosa* in the Brand B-2 filter (Fig. 5-2). The Brand B-2 filter had a stable *P. aeruginosa* level ( $7.0 \times 10^2 \pm 2.0 \times 10^2$  cell/mL) in the effluent throughout the washout phase. The fluorescent bacteria detected in the effluent should be sourced from the population that accumulated and survived inside the filters. It is not clear why only one of the filters established a steady-state level of *P. aeruginosa* during the washout phase; however, it may be related to hydraulic characteristic differences between the filters. The permeability of the Brand B-2 filter was the least among all tested filters (Table S5-1). In our previous work and other studies, the filter units of the same design model possessed variations in permeability, porosity, and surface area that were hypothesized to account for different microbiological outcomes (Geldreich et al., 1985; Wu et al., 2017). Given the lower hydraulic conductivity of the Brand B-2 filter, it was suspected that greater bacteria accumulation and biofilm shear conditions may have occurred in this filter, allowing the continued effluent seeding of *P. aeruginosa* to occur. It is noteworthy, however, that *E. coli* concentrations washed out rapidly, even in Brand B-2 filter, perhaps suggesting it was less able to compete with other microorganisms.

### **5.3.3 Evidence of growth of fluorescent bacteria in ACB PoU filters**

Mass balance evaluations were performed to test for evidence of fluorescent bacteria growth in the ACB filters. Cumulative cell counts of fluorescent bacteria detected in the filter influent and effluent over the application period are presented in Table S5-2. The average integrated *P. aeruginosa* counts leaving Brand A and Brand B filters were 1.1 times ( $1.2 \times 10^8$ ) and 2.1 times ( $2.0 \times 10^8$  cells), respectively, more than the average influent loading ( $9.7 \times 10^7$  cells). The cell

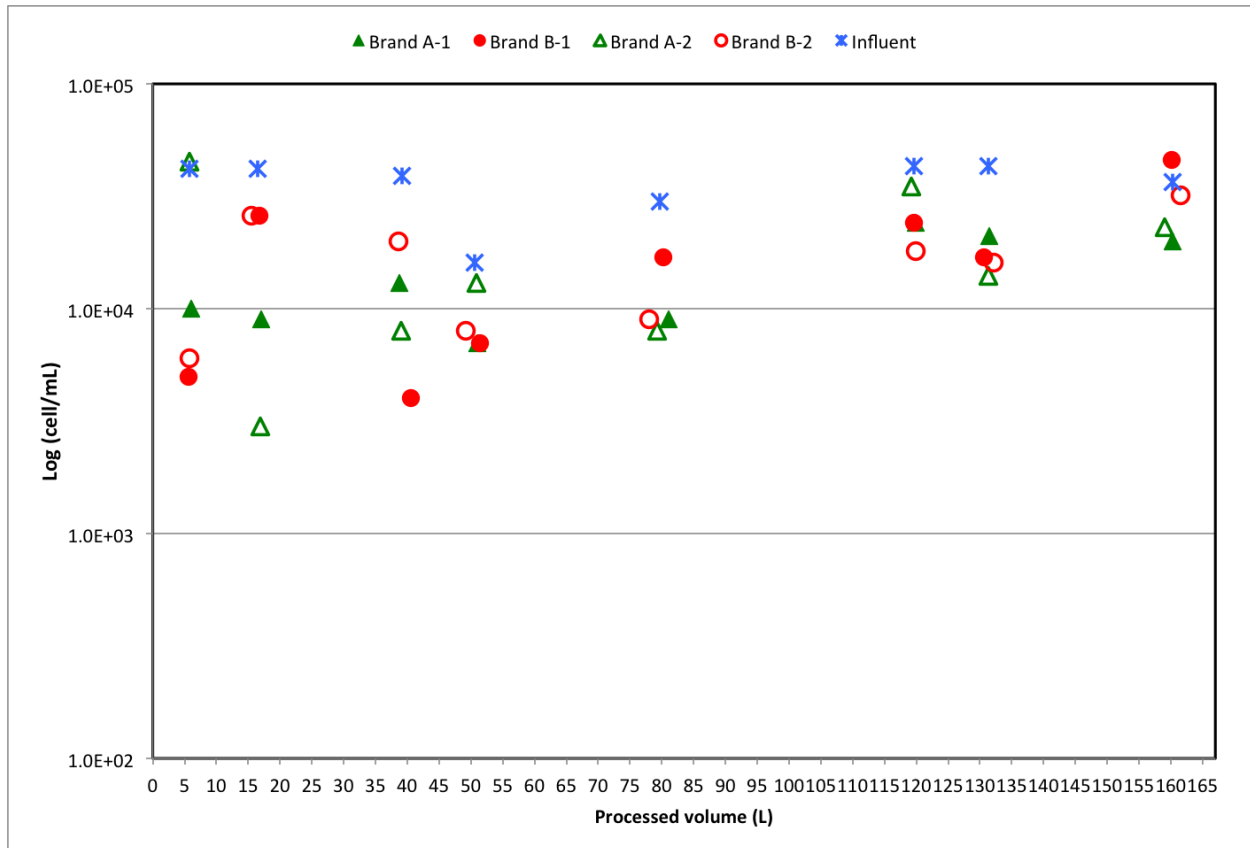
balance confirms that net *P. aeruginosa* growth must occur in the Brand B filters, allowing effluent concentrations to exceed influent concentrations. Since the cumulative influent and effluent cell counts of *P. aeruginosa* in the Brand A filters were nearly equal, more limited growth was possible in these filters. In contrast to *P. aeruginosa*, *E. coli* levels in the effluent were consistently lower than the influent in both Brand A and Brand B, and a cumulative total of 75% of *E. coli* was lost during the period that fluorescent-tagged bacteria were applied to the filters.

The growth evidence for *P. aeruginosa* suggests it may be more adapted to the ACB PoU filter environment than *E. coli*. *P. aeruginosa* is known to utilize various carbon sources so it can adapt to low-nutrient environment (Kooij et al., 1982a, 1982b). Past studies have shown that indigenous *P. aeruginosa* is frequently detected in ACB filter effluent when tap water is fed continuously, which suggests that the species' surface and growth characteristics enable it to pass through and colonize these filters (Chaidez and Gerba, 2004; Tobin et al., 1981). Conversely, some *E. coli* strains are known to have inferior kinetic properties for competing at low carbon concentrations with indigenous bacteria (Camper et al., 1991; Rollinger and Dott, 1987; Vital et al., 2012).

#### **5.3.4 The total membrane-intact cell counts in the effluent of ACB PoU filters did not exceed the influent level**

The fate of indigenous bacteria in the tap water was also monitored with flow cytometry by counting total membrane-intact cells. As shown in Fig. 5-4, the effluent total cell counts slowly approached the influent during the operation but did not exceed the influent level. Cell counts of approximately 40% of the influent level, however, were observed in the first sampling period after processing 5 L. The effluent bacterial counts ranged from  $8.8 \times 10^3$  to  $3.0 \times 10^4$  cell/mL, and increased over time to 83% of the influent level ( $3.6 \times 10^4 \pm 8.8 \times 10^3$ ). Multiple studies have shown that heterotrophic bacterial counts in the effluent of ACB PoU filters increase with time and exceed the levels in the tap water influent using culture-based methods (Chaidez and Gerba, 2004; Molloy et al., 2008; Reasoner et al., 1987; Tobin et al., 1981). However, the flow cytometry cell counts reported here are membrane-intact cells and account for both nonculturable and culturable cells, thus cytometry counts can be 1-2 log units greater than heterotrophic plate

counts (Hammes et al., 2008). Given the large difference in influent HPC (Wu et al., 2017) and membrane-intact cell concentrations (this study), most of the influent membrane-intact cells are probably not culturable, and therefore we would not expect the effluent total cell counts to exceed the influent.



**Fig. 5-4 Breakthrough of membrane-intact bacteria through ACB PoU filters of Brand A (green) and Brand B (red). Spiking of fluorescent bacteria stopped spiking after day 23 (after 131 L was processed).**

### 5.3.5 *P. aeruginosa* colonized entire ACB while *E. coli* was absent near filter exit port

We sought to determine whether the fluorescent bacteria could colonize surfaces across the entire depth of the ACB by evaluating their abundance at the entrance and exit surfaces of the PoU filters. Samples tested on the upstream side of the ACB included the pre-filter fabric mesh that wraps around the influent side ACB surface, and at the downstream side of the ACB, swabs of the activated carbon surface of the interior core of the effluent channel. In an earlier study, the fabric mesh in the Brand B filter was shown to consist of silicic fibers (Wu et al., 2017). We sacrificed the four filters after the washout test and collected biofilm samples from pieces of the fabric at three depths (top, middle, and bottom) and from swabs of the interior core effluent channel at the top, middle, and bottom. It is reasonable to assume that the amount of biomass in the fabric and effluent channel were smaller than during the application phase because they had

gone through washout. Some bacterial cells that were loosely attached to the surface at the application period may be more easily sloughed out to the effluent during washout. Therefore, the cells that can still be found on these locations after the washout phase can irreversibly attach to the fabric or the ACB.

The abundance patterns of the two types of fluorescent bacteria upstream and downstream biofilms of the ACB, as shown in Table 5-2, are consistent with greater mobility and survivability of *P. aeruginosa* relative to *E. coli* in ACB PoU filters. Bacterial abundance was characterized in terms of the number of fluorescent gene counts of both bacteria and the number of culturable *P. aeruginosa* cells. We were not able to enumerate culturable *E. coli* from the M Endo LES agar due to the competition from other non-coliform bacteria. The GFP genes and culturable *P. aeruginosa* cells were detected from both the fabric biofilm and the surface of the interior core channel. Therefore, it is likely that *P. aeruginosa* cells colonized the surface of flow pathways within the ACB.

Unlike *P. aeruginosa*, mCherry genes were detected from the fabric biofilm but not the effluent channel swabs. The number of mCherry genes was uniformly distributed at the top, center and bottom of the fabric. The estimated *E. coli* cell counts measured on the fabric ( $1.5 \times 10^5$  cell per total fabric area, Table S5-2) was 0.4% of the *E. coli* lost over the whole application period ( $4.2 \times 10^7$  cell counts, Table S5-2). Since there were no mCherry genes detected in swabs of the effluent channel surface, *E. coli* was either less able to colonize and survive in downstream locations of the filter or it was more effectively filtered at upstream locations within the ACB. Based on the washout phase of the experiment, low detectable levels of *E. coli* cells were still sloughed out to the effluent occasionally. The accumulation of *E. coli* within upstream regions of the filter could serve as a reservoir for *E. coli* to seed the filter effluent even when no inoculation was spiked in the influent.

**Table 5-2 Culturability and fluorescent gene counts of GFP-tagged *P. aeruginosa* and mCherry-tagged *E. coli* on the biofilm of ACB PoU filters\***

Biofilm location	Parameters	Brand A						Brand B					
		1			2			1			2		
		Top	Center	Bottom	Top	Center	Bottom	Top	Center	Bottom	Top	Center	Bottom
Fabric	<b>Culturability</b>												
	<i>P. aeruginosa</i>	+	+	+	+	+	+	++	+	++	++	++	+++
	<b>DNA (copy gene/cm<sup>2</sup>)</b>												
	<i>GFP</i> gene	3.3×10 <sup>2</sup>	5.2×10 <sup>2</sup>	5.5×10 <sup>2</sup>	3.1×10 <sup>2</sup>	2.9×10 <sup>2</sup>	1.9×10 <sup>2</sup>	1.7×10 <sup>2</sup>	9.6×10	3.1×10 <sup>2</sup>	8.1×10 <sup>2</sup>	6.4×10 <sup>2</sup>	6.7×10 <sup>2</sup>
	<i>mCherry</i> gene	5.4×10 <sup>2</sup>	5.5×10 <sup>2</sup>	4.0×10 <sup>2</sup>	8.3×10 <sup>2</sup>	7.7×10 <sup>2</sup>	4.5×10 <sup>2</sup>	6.0×10 <sup>3</sup>	2.0×10 <sup>3</sup>	2.0×10 <sup>3</sup>	2.1×10 <sup>3</sup>	2.2×10 <sup>3</sup>	1.4×10 <sup>3</sup>
Inner channel	<b>Culturability</b>												
	<i>P. aeruginosa</i>	+	+	+	+	+	+	++	+	++	+	+	+++
	<b>DNA (copy gene/cm<sup>2</sup>)</b>												
	<i>GFP</i> gene	ND	ND	4	ND	ND	2	3	ND	1.5×10	2.3×10 <sup>2</sup>	4.2×10	7.1×10 <sup>2</sup>
	<i>mCherry</i> gene	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

+: Detected 1-10 colonies

++: Detected 10-300 colonies

+++ : Detected >300 colonies

\**E. coli* could not be cultured because of competition with the indigenous bacteria from the background.

### 5.3.6 Two brands of ACB PoU filters exhibit different performance

In our study, we found that the bacterial migration patterns of fluorescent bacteria in Brand A and B filters differ in several respects. As was mentioned above, early breakthrough of *P. aeruginosa* was detected for both brands while *E. coli* was detected later in the Brand A filters relative to Brand B. Over the course of the application period, the integrated cell counts of *P. aeruginosa* from Brand B filter effluent were two times higher than Brand A, suggesting that Brand B filters allowed slightly greater net growth of *P. aeruginosa* than Brand A. (Table S5-2). In addition, the number of *P. aeruginosa* and *E. coli* cells on the Brand B fabric biofilm were three and four times higher than Brand A, respectively (Table S5-2). These differences suggest that certain design features of the Brand B filters favor greater colonization and accumulation of bacteria. It is possible that viable flow pathways in the Brand B filters offer greater surface area for biofilm growth.

Unlike bacterial breakthrough patterns, microsphere breakthrough patterns between the two PoU filter brands exhibit similar trends, as shown in Fig 5-3. The normalized breakthrough concentrations were described reasonably well with empirical exponential regression models as a function of processed water volume. The models suggest that slightly earlier breakthrough was observed with Brand A, but the ultimate predicted microsphere plateau concentration was slightly higher for Brand B. Given that models are based only on duplicates of each filter brand, more testing would be necessary to demonstrate whether these trends are statistically significant.

When the filters of both brands processed approximately 100 L of the microsphere suspension influent, the filters began to clog and we observed that the effluent concentrations of microspheres of both brands reached two to four times the influent level (Fig. S5-5). Given that all four of the filters were impacted simultaneously by clogging, aggregation of the microspheres in the influent reservoir may have been an issue and thus the data for process volumes greater than 100 L was not considered further.

The microsphere and bacterial breakthrough trends of the PoU filters differ from the general behavior of continuous flow filtration of colloidal particles in granular beds under strongly repulsive interaction conditions (Elimelech and O'Mella, 1990). For these filters, normalized effluent concentration attain in a near steady-state concentration after just a few pore volumes. In



our system, stagnation periods allow particle deposition due to diffusion. In addition, hydraulic pulses that likely cause shearing of deposited particles occur after each stagnation event. Thus the shape of the breakthrough curve reflect an increasingly repulsive interaction as particles or bacteria deposit on the pore walls and repel oncoming particles, leading to a more gradual increase in the normalized effluent concentration ( $C/C_0$ ) and an eventual plateau.

#### 5.4 Conclusions

This research study evaluated the breakthrough and transmission mechanisms of fluorescent-tagged *E. coli* and *P. aeruginosa*, as well as fluorescent 1  $\mu\text{m}$  diameter microspheres, in two commercial ACB PoU filter brands.

- The spiked *E. coli*, *P. aeruginosa*, and microspheres were detected in filter effluent despite the fact that the average pore size of the filter was much smaller than the bacteria or microspheres, indicating the ACB contain preferential flow pathways greater than 1  $\mu\text{m}$  in diameter for bacteria and particles to pass through.
- *P. aeruginosa* demonstrated greater mobility and potential for growth in the ACB PoU filters than *E. coli* under the oligotrophic conditions of the experiment. *P. aeruginosa* broke through the filters more quickly and plateaued in the effluent at levels two times the influent level, possibly due to its physiological properties and ability to colonize throughout the ACB.
- The effluent channel cultures and fluorescent gene abundance data support the finding that *P. aeruginosa* had greater biofilm colonization advantages compared to *E. coli*.
- Natural fluctuations in effluent concentration can occur due to clogging, followed by bacterial release as the pathways become unclogged. The variations can cause bacterial concentrations to significantly exceed or approach influent concentrations. This phenomenon likely depends on the microbial and particulate content of the influent water as well as stagnation patterns.

Manufacturer warnings on ACB filter products alert consumers that water supplies that are “microbiologically unsafe” or inadequately disinfected are not recommend for ACB PoU filter use. The findings in this study underscore the need to emphasize this limitation and alert users that the filters can increase the concentration of opportunistic pathogens relative to unfiltered water.

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## Chapter 6

### Main Findings and Future Research

In this dissertation, I evaluated the microbial ecology of ACB PoU filters by coupling culture dependent and independent methods. The objectives of this research align with a broader goal of producing data that can support efforts to better understand the health risks that waterborne opportunistic pathogens and ARGs pose to human beings. I first presented results about the effect of ACB PoU filters that processed water with and without a chlorophenol disinfection byproduct on a tap water bacterial community abundance and structure (Chapter 3). Second, I evaluated whether ACB PoU filters could enrich for bacteria that carry antibiotic resistance genes using samples from both lab and field studies (Chapter 4). The work presented in Chapter 5 was designed to better understand the mechanisms of bacterial migration through ACB PoU filters. The chapter specifically focused on evaluating how two bacterial species with different biofilm forming and infectious behaviors break through the most commonly deployed ACB faucet-mounted PoU filters. Through this dissertation, which applied both traditional culture-based and modern DNA- and metagenome-based methods to lab and field-scale samples, my work has advanced our understanding of microbial behavior and stability across ACB PoU filters that are being deployed at an increasing rate. The overall findings of this dissertation show that ACB PoU filters can significantly change the bacterial community structure and antibiotic resistance genome of tap water, and that common drinking water microbial analyses (coliforms and sometimes *E. coli*) are unlikely to detect changes in opportunistic pathogens that tend to proliferate in these filters.

In Chapter 3, I showed that PoU filters change the microbial community structure in filtered water relative to unfiltered tap water. To better understand the factors that contribute to this, I evaluated possible mechanisms in Chapter 5. The species used in the study, *E. coli* and *P. aeruginosa*, exhibited different breakthrough patterns and abilities for ACB colonization and, therefore, show different breakthrough and migration behaviors. Although the existence of

preferential flow channels of bacterial size in the ACB allowed influent bacteria to pass through the PoU filter, only a fraction of bacterial species from the influent were able to make the trip. It seems easier for bacteria that are known to form biofilms to end up at higher concentration in the effluent relative to the influent.

The study reported in Chapter 5 also shows that it is important to acclimate bacteria to the oligotrophic drinking water state, because the physiological properties of bacteria, such as surface charge, hydrophobicity, etc., can affect attachment and thus their transport patterns (Haznedaroglu et al., 2008). Therefore, additional research is needed to evaluate the characteristics or physiological properties that determine attachment, growth, and survival of bacteria that are adapted to drinking water in these filters. This information can further lead to the redesign of ACB PoU filters in ways that can reduce bacterial growth, or help determine which pretreatment or post-treatment steps should be applied to protect consumers from bacteria of concern in filtered water.

The work presented in Chapter 3 showed that chemicals present at trace levels were able to influence the microbial ecology in ACB PoU filters. Specifically, I found that a chlorinated phenolic DBP, pentachlorophenol (PCP), affected the bacterial community structure of ACB PoU filters (Wu et al., 2017), albeit to a minor (but significant) degree. As a result, other chemicals that can be adsorbed or deposited on the ACB over time, such as other hydrophobic DBPs, metals (Deshommes et al., 2010), and antibiotics (Michael et al., 2013), may also interact with the colonizing bacteria on the ACB. The interaction between adsorbed chemicals and colonizing bacteria may lead to unwanted effects, such as enrichment of antibiotic resistant bacteria (Michael et al., 2013; Poole, 2017). Indeed, this may have contributed to the observations in Chapter 4, which I believe is the first study that examines and quantifies changes in the abundance and type of antibiotic resistance genotypes across ACB PoU filters. Although I demonstrated that ACB PoU filters can change the types of ARGs and increase certain types of ARGs in the effluent relative to the influent, I did not determine if the detected ARGs are functional or a health risk. Bacteria can possess ARGs that cannot be expressed (Piddock, 2016). Therefore, future studies are needed to evaluate the antibiotic resistance phenotypes that proliferate across the ACB PoU filters, and under what conditions, to further ensure the public health risk, if any, associated with ARG proliferation across filters.

Understanding how ACB PoU filters enrich for ARGs is important if we are to evaluate possible strategies that would prevent ARG proliferation in these devices. However, the mechanisms of ARG enrichment in the ACB PoU filters are unknown. The hosts of ARGs may survive or colonize in the ACB, possibly in biofilms that can facilitate horizontal gene transfer of ARGs (Molin and Tolker-Nielsen, 2003), thus producing a higher abundance of ARGs in filtered water. I believe it is important to conduct future experiments to differentiate these two mechanisms.

The information in Chapters 3 and 5 reveal that ACB PoU filters can change the composition of and increase the concentration of opportunistic pathogens in filtered water over time (Wu et al., 2017). Therefore, consumers can be exposed to a higher concentration of these bacterial agents of concern relative to the tap water after using the ACB PoU filters for a period of time. The risk of adverse health effects for individuals who consume water from an ACB PoU filter depends on the number and type of bacteria exposed to and the general health condition of the individual. For example, sensitive populations, including elders and immunocompromised patients, are more likely to be infected by opportunistic pathogens (Leclerc, 2003). Future studies should assess the impact of bacterial community structure through ACB PoU filters as a function of time on the risk for the users who have marginalized health conditions.

This dissertation lays out a foundation for the microbial ecology of activated carbon block-based systems. Since ACB exists in other types of filtration systems, the results presented in this dissertation may also pertain to ACB-containing under-the-sink treatment devices, refrigerator water filters, and water foundation filtration systems (also called hydration stations). Since factors, such as the design of the filter cartridges including the capacity and porosity, the temperature of the device when in use, and the frequency of usage may affect how bacteria colonize these other common filter systems, it would be valuable to conduct similar research studies on these (increasingly) commonly used ACB filter systems.

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## **Appendices**

## **Appendix A.**

### **Supplementary Information for Chapter 3**

**The microbial colonization of activated carbon block point-of-use (PoU) filters with and without chlorinated phenol disinfection byproducts**

## **Contents:**

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16. Supplemental references

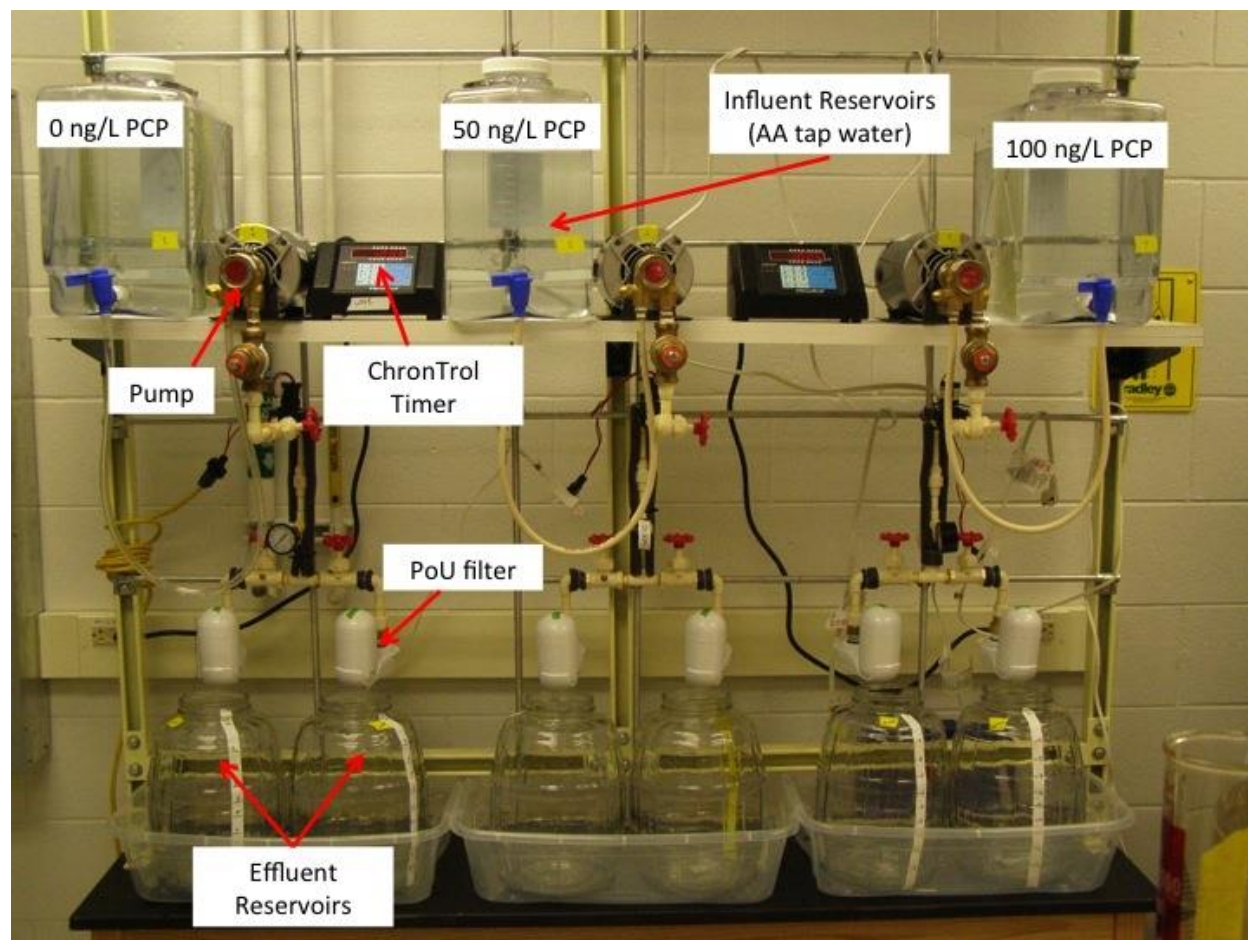
### A.1. Biofilm induction in *P. aeruginosa* strains with pentachlorophenol

Biofilm production by *P. aeruginosa* was quantified using a method described by O'Toole.(O'Toole, 2011) Overnight cultures of *P. aeruginosa* PAO1 and PA14 were diluted 1:100 in low salt LB medium and incubated with and w/o 100  $\mu$ M of pentachlorophenol in 96-well microtiter plates for 20 hours at 37°C. Following incubation, cells in liquid cultures were removed and cells attached to the microtiter plate wells were stained with crystal violet. Subsequently, crystal violet retained in each well was solubilized in 30% acetic acid and quantified at 550 nm. Both *P. aeruginosa* PAO1 and PA14 produced more biofilm in the presence of pentachlorophenol.

**Table S3-1. Biofilm quantity measured as optical density at OD550 nm.**

Strain name and condition	PAO1 w/o PCP	PAO1 with PCP	PA14 w/o PCP	PA14 with PCP
Optical density at OD550 nm	1.8 $\pm$ 0.2	3.1 $\pm$ 0.2	0.5 $\pm$ 0.1	0.9 $\pm$ 0.1

## A.2. PoU Manifold system setup and operation



**Fig. S3-1. Manifold system with influent reservoirs, duplicate PoU filters and effluent reservoirs.**

As shown in Fig. S1, the general apparatus for the experiment consisted of a 20 L polycarbonate carboy connected by tubing to a brass 3/8 inch Procon rotary vane pump rated at 100 gallons per hour (gph) with a maximum pressure of 250 psi and a maximum temperature of 150° F. The pump was powered by a ¼ horsepower Marathon Electric motor rated at 1725 rpm and 60/50 Hz. The rotary vane pump was directly connected to a ½ inch CASH ACME brass pressure regulator that allowed inlet pressure up to 400 psi and outlet pressure adjustable between 10 and 70 psi (maximum temperature 180 °F). This was set to approximately 42 psi on each rig to simulate household water pressure. Brass size adapters were in place to adjust between the 3/8 inch pump

and the ½ in pressure regulator. Following the pressure regulator, ½ inch CPVC manual flow regulator valve was in place to moderate the flow to the overall system. Half inch CPVC was then placed to connect to the ½ inch 120VAC pilot operated ALCON brand normally closed (NC) solenoid valves which controlled the flow. The solenoid valves could handle a maximum pressure of 150 psi and a maximum temperature of 120 °F. Half inch CPVC again followed the solenoid valve, at one point branching off to the pressure gauge as shown in Fig. S1. The flow was then split with a ½ inch CPVC T-connector and each branch contained a manual flow regulator valve because it was found that there was a great degree of hydraulic variation among the PoU filters. Finally a brass ½ inch CPVC to hose fitting was placed on the end and a number of faucet adapters were put into place to match one of four fittings that came with the faucet filter. Teflon tape and/or CPVC cement was used at each connection point as needed. Finally the PoU filter was attached to its proprietary fitting. The whole apparatus was affixed to the metal grid with zip ties for stability.

### A.3. Characteristics of commercial PoU filter

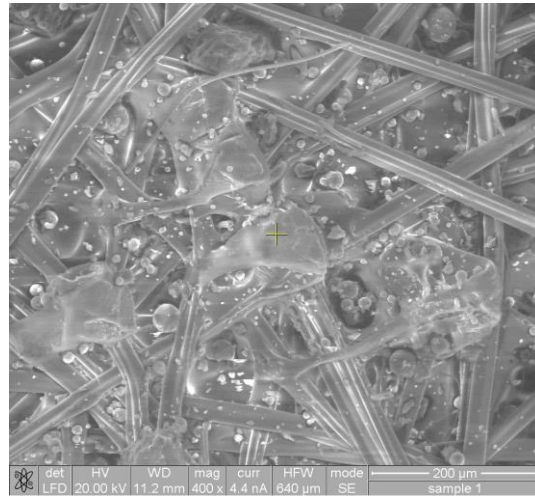
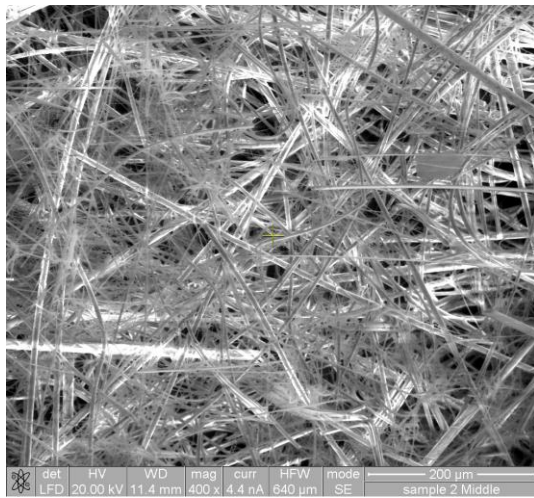
#### A.3.1 Physical characteristics of activated carbon block

**Table S3-2. Physical characteristics of commercial PoU activated carbon block\* :**

Filter No.	Brunauer-Emmett-Teller (BET) Surface Area, m <sup>2</sup> /g	Pore Size, Å	Porosity
1	578 (20)	22.1 (0.8)	0.0621 (0.0002)
2	661 (26)	21.8 (0.02)	0.0666 (0.0026)
3	548 (26)	22.1 (0.6)	0.0540 (0.0013)

\*Standard deviations are shown in the parenthesis

### A.3.2 SEM image of fabric membrane



(a)

(b)

**Fig. S3-2. SEM image of fabric membrane.**

Scanning electron micrographs of the two layers of the PoU filter fabric that make up the components extracted in biomass and community analyses. Both micrograph images are shown at the same magnification and the scale bar represents 200 μm. (a) Glass fiber filter layers that faced influent side. (b) Polymeric fiber filter layer that faced the activated carbon block.

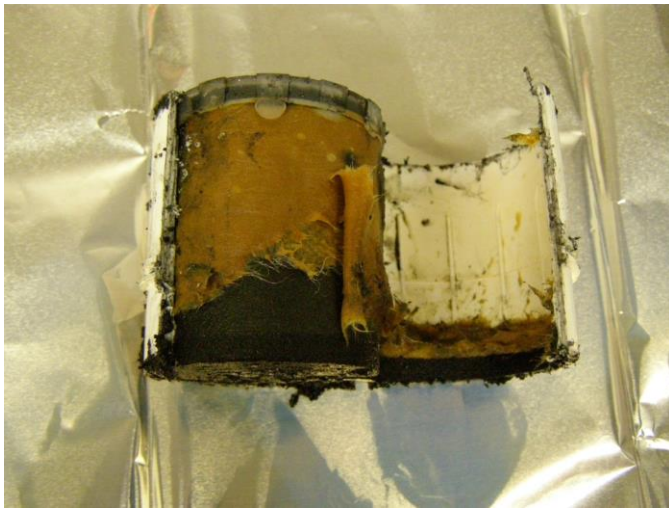


#### A.4. Table of the water volumes processed for PoU filters

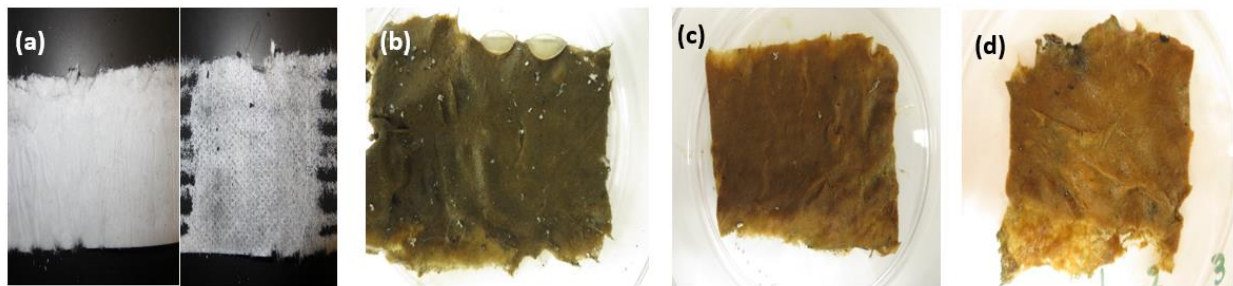
**Table S3-3. Total volumes of water processed for PoU filters.**

PCP treatment (ng/L)		Total volume of water processed (L)
0	Replicate 1	485
	Replicate 2	494
50	Replicate 1	505
	Replicate 2	562
100	Replicate 1	484
	Replicate 2	583
Average		519

#### A.5. Image of used fabric membranes



**Fig. S3. PoU filter disassembly.**



**Fig. S3-4. Representative images of fabric membranes. (a) Clean fabric that faced influent side (left) and activated carbon block (right); and used fabrics that were sacrificed after 67-day operation spiked with (b) 0 ng/L PCP; (c) 50 ng/L PCP; and (d) 100 ng/L PCP, respectively. The control fabric was dark grey while the fabrics of all filters exposed to PCP were medium to light tan.**

## A.6. Sample schedule and sample type

Water quality parameters including total alkalinity, total and dissolved organic carbon (TOC and DOC), specific UV absorbance (SUVA), pH, chlorophenols, free and total chlorine residual and heterotrophic plate count (HPC) were measured regularly in grab or composite samples as noted on the sample schedule in Table S3. For the two week composite sample, 150 mL aliquots were collected from each influent and effluent container daily, dechlorinated and acidified, and added to an amber composite glass jar for each sample location. Composited aliquots were collected daily for two weeks to create a composite sample for influent and effluent TOC and chlorophenol analysis.

**Table S3-4. Sample schedule and sample type of water analysis.**

Parameter	Frequency	Influent	Effluent	Sample type
Total alkalinity	Weekly	X		Grab
DOC	2 Weeks	X		Grab
SUVA	2 Weeks	X		Grab
pH	Weekly	X	X	Grab
Free and total Cl <sub>2</sub> residual	Weekly*	X	X	Grab
Chlorophenols	Daily	X	X	2-wk composite, acidified (pH 2)
TOC	Daily	X	X	2-wk composite, acidified (pH 2)
HPC	Weekly	X	X	Grab

\*Effluent samples were analyzed for total Cl<sub>2</sub> residual twice during the experiment (at 30 and 52 days).

## A.7. Chlorophenol analysis

Dichlorophenol, trichlorophenol, tetrachlorophenol, and pentachlorophenol were analyzed for and quantified using a solid phase extraction (SPE) and gas chromatography –electron capture detector (GC-ECD) method. The less chlorinated forms were analyzed in case they were formed as products of PCP degradation. The samples were concentrated by passing through a modified polystyrene divinyl benzene copolymer. The analytes were reverse-eluted with methanol and derivatized by acetic anhydride. The acetyl derivatives were extracted into hexane and then analyzed by GC-ECD.

One liter of water sample was spiked with 25  $\mu$ l of 1 mg/L dimethylnitrobenzene (DMNB), which functioned as a surrogate. The SPE cartridge was styrene/divinyl benzene porous polymer packing available as Supelclean ENVI-Chrom P (500 mg/6 ml) (Supelco, Bellefonte, PA). It was pre-conditioned with 3 mL methanol two times and activated by 3 mL acidified (pH2) Milli-Q water three times. The cartridges were kept wet during condition, and an additional 3 mL more Milli-Q water was added as the flow rate was adjusted to maintain the cartridge wet as the sample began to load.

The one liter water sample spiked with surrogate was loaded at the flow rate of 4-6 ml per minute (about 3-4 drops per second). After the sample had finished loading, 20 mL of acidified Milli-Q water was used to rinse the sample bottle two times and was passed through the cartridge. Finally, the cartridges were dried for 25-30 minutes on the manifold with the vacuum on to remove residual water.

Since chlorophenols are nonpolar, they were strongly retained by the sorbent. The SPE cartridge was turned upside down during the elution process. This reverse-elution helps to remove the chlorophenols on the sorbent surface and minimizes the volume of solvent, which achieves better recovery. Thus, 3 ml of methanol was used to reverse-elute analytes at a flow rate of 0.5 ml/minute (approximately 1 drop every 3-4 seconds). Before the first 3 mL methanol finished

passing through the cartridge, 2 mL more methanol was added for another elution. After the methanol passed through, the manifold port valves were fully opened to collect residual methanol. The eluent was stored below -10°C.

To improve the chromatographic detection of the analytes, the eluent was derivatized using acetic anhydride and extracted from methanol to hexane through the following steps. The methanol eluent was spiked with 2 ml of 5% potassium carbonate solution, 25 µL of 6 mg/L trichlorotoluene (TCT) as an internal standard, 2 mL hexane, and 400 µL of acetic anhydride in that order. The solution was vortexed for 40 s at 3000 rpm and let stand for 1 min. The top hexane phase was extracted into a 5 mL volumetric flask. Subsequently, another 1 mL hexane was added in the solution, and went through the same vortex step. The top hexane phase was collected and aggregated with the previous extract. The final volume was adjusted with hexane to 5 mL and stored in the GC vials. Since TCT was unaffected by the derivatization step, any variations in TCT area counts can be attributed to the extraction efficiency or instrument measurements.

The extracted samples were analyzed by HP 6890 series GC with ECD (Agilent, Palo Alto, USA). The column was an Agilent 19091H-433 GC-ECD capillary column (30 m × 0.25 mm i.d., 0.25-µm film thickness). The injector and detector temperatures were all set at 250°C. Nitrogen was used as the carrier gas at a flowrate of 0.9 mL/min. The GC oven temperature was started from initial temperature of 40°C, which was held for 30 s, followed by an increase at a rate of 10°C /min to 240°C, which was held for 2.5 min, and then increased at 10°C /min to 250°C, which was held for 3.5 min. The total run time was 27.5 min. A volume of 2.0 µL sample was injected into the GC.

The detection limit of pentachlorophenol was 10 ng/L. The detection limits of dichlorophenol, trichlorophenol, and tetrachlorophenol are 25 ng/L. During the operation of the PoU manifold system, no chlorophenols were detected in the influent control water samples.

## A.8. Total mass of DNA extracted

**Table S3-5. Total mass of DNA extracted<sup>1</sup>**

Sample type	PCP treatment (ng/L)	Operation days	DNA concentrations (ng/L water or ng/cm <sup>2</sup> fabric area)	
Influent	0	58	14	
		65	16	
		42	5	
	50	58	9	
		66	10	
		42	7	
	100	50	51	4
			58	15
			66	14
0		42	637	
		58	737	
		65	53	
Effluent	50	42	359	
		58	661	
		66	46	
	100	42	775	
		51	382	
		58	524	
Fabric <sup>3</sup>	0	67 (end)	1034 (389)	
	50	67 (end)	216 (83)	
	100	67 (end)	399 (145)	

<sup>1</sup> Standard deviations are shown in parenthesis.

<sup>2</sup> The averages are taken from the total sample number of two (duplicate PoU filter replicates of each treatment).

<sup>3</sup> Fabric DNA was extracted from four fabric pieces of each PoU filter replicate. The averages and standard deviations are taken from the total sample number of eight for each treatment.

## A.9. The number of quality-filtered sequences per sample

**Table S3-6 Number of quality-filtered sequences per sample**

Sample name (Sample code)	Number of quality filtered sequences
Influent at day 58 (12Infl1)	16969
Influent at day 65 (15Infl1)	18123
Influent spiked with 100 ng/L PCP at day 42 (11Infl3)	16730
Influent spiked with 100 ng/L PCP at day 51 (30Infl3)	21080
Influent spiked with 100 ng/L PCP at day 58 (12Infl3)	8906
Influent spiked with 100 ng/L PCP at day 66 (15Infl3)	33370
Influent spiked with 50 ng/L PCP at day 42 (11Infl2)	11826
Influent spiked with 50 ng/L PCP at day 58 (12Infl2)	15114
Influent spiked with 50 ng/L PCP at day 66 (15Infl2)	11140
Effluent from PoU filter replicate 1 at day 58 (12Effl1A)	31902
Effluent from PoU filter replicate 1 at day 65 (15Effl1A)	28817
Effluent from PoU filter replicate 2 at day 65 (15Effl1B)	21222
Effluent from PoU filter replicate 2 at day 42 (11Effl1B)	34660
Effluent from PoU filter replicate 2 at day 58 (12Effl1B)	32940
Effluent from PoU filter replicate 1 spiked with 50 ng/L PCP at day 42 (11Effl2A)	29800
Effluent from PoU filter replicate 1 spiked with 50 ng/L PCP at day 58 (12Effl2A)	24947
Effluent from PoU filter replicate 1 spiked with 50 ng/L PCP at day 66 (15Effl2A)	28433
Effluent from PoU filter replicate 2 spiked with 50 ng/L PCP at day 42 (11Effl2B)	35147
Effluent from PoU filter replicate 2 spiked with 50 ng/L PCP at day 58 (12Effl2B)	51757
Effluent from PoU filter replicate 2 spiked with 50 ng/L PCP at day 66 (15Effl2B)	34253
Effluent from PoU filter replicate 1 spiked with 100 ng/L PCP at day 51 (30Effl3A)	29097
Effluent from PoU filter replicate 1 spiked with 100 ng/L PCP at day 58 (12Effl3A)	39211
Effluent from PoU filter replicate 1 spiked with 100 ng/L PCP at day 66 (15Effl3A)	35273
Effluent from PoU filter replicate 2 spiked with 100 ng/L PCP at day 42 (11Effl3B)	29200
Effluent from PoU filter replicate 2 spiked with 100 ng/L PCP at day 51 (30Effl3B)	27007
Effluent from PoU filter replicate 2 spiked with 100 ng/L PCP at day 58 (12Effl3B)	45935
Effluent from PoU filter replicate 2 spiked with 100 ng/L PCP at day 66 (15Effl3B)	27316
Fabric from PoU filter replicate 1 (F1A1)	30653
Fabric from PoU filter replicate 1 (F1A2)	34762
Fabric from PoU filter replicate 1 (F1A3)	34063
Fabric from PoU filter replicate 1 (F1A4)	33036
Fabric from PoU filter replicate 2 (F1B1)	23241
Fabric from PoU filter replicate 2 (F1B2)	19724
Fabric from PoU filter replicate 2 (F1B3)	21551
Fabric from PoU filter replicate 2 (F1B4)	25802
Fabric from PoU filter replicate 1 with 50 ng/L PCP (F2A1)	30989
Fabric from PoU filter replicate 1 with 50 ng/L PCP (F2A2)	35717
Fabric from PoU filter replicate 1 with 50 ng/L PCP (F2A3)	39039

**Table S3-6 Number of quality-filtered sequences per sample (continue)**

Sample name (Sample code)	Number of quality filtered sequences
Fabric from PoU filter replicate 1 with 50 ng/L PCP (F2A4)	35982
Fabric from PoU filter replicate 2 with 50 ng/L PCP (F2B1)	24329
Fabric from PoU filter replicate 2 with 50 ng/L PCP (F2B2)	24866
Fabric from PoU filter replicate 2 with 50 ng/L PCP (F2B3)	25130
Fabric from PoU filter replicate 2 with 50 ng/L PCP (F2B4)	34280
Fabric from PoU filter replicate 1 with 100 ng/L PCP (F3A1)	31916
Fabric from PoU filter replicate 1 with 100 ng/L PCP (F3A2)	34024
Fabric from PoU filter replicate 1 with 100 ng/L PCP (F3A3)	35265
Fabric from PoU filter replicate 1 with 100 ng/L PCP (F3A4)	35306
Fabric from PoU filter replicate 2 with 100 ng/L PCP (F3B1)	26131
Fabric from PoU filter replicate 2 with 100 ng/L PCP (F3B2)	25446
Fabric from PoU filter replicate 2 with 100 ng/L PCP (F3B3)	33834
Fabric from PoU filter replicate 2 with 100 ng/L PCP (F3B4)	32299



**A.10. Relative abundance of dominant OTUs (>1%) in influent, effluent, and fabric samples.**

Influent community members were similar between PCP treatments ( $p>0.05$ , data not shown), despite the variation of the relative abundance among samples collected on different dates. Two OTUs (*Mycobacterium* and unclassified Bacteria OTU23) became “highly dominant” in the influent reservoirs that contained 50 and 100 ng/L PCP (Table 3-1). However, the relative abundances of these two OTUs were not significantly different between PCP treatments ( $p>0.05$ , Kruskal-Wallis test), not resulting in a significant influent community shift relative to the control.

**The data of relative abundance of all detected OTUs in Ann Arbor PoU filter manifold system are shown in Table A in Appendix D.**

## A.11. Statistical analysis of bacterial community structure

**Table S3-7. Bacterial composition dissimilarity across PoU filter and PCP treatments.**

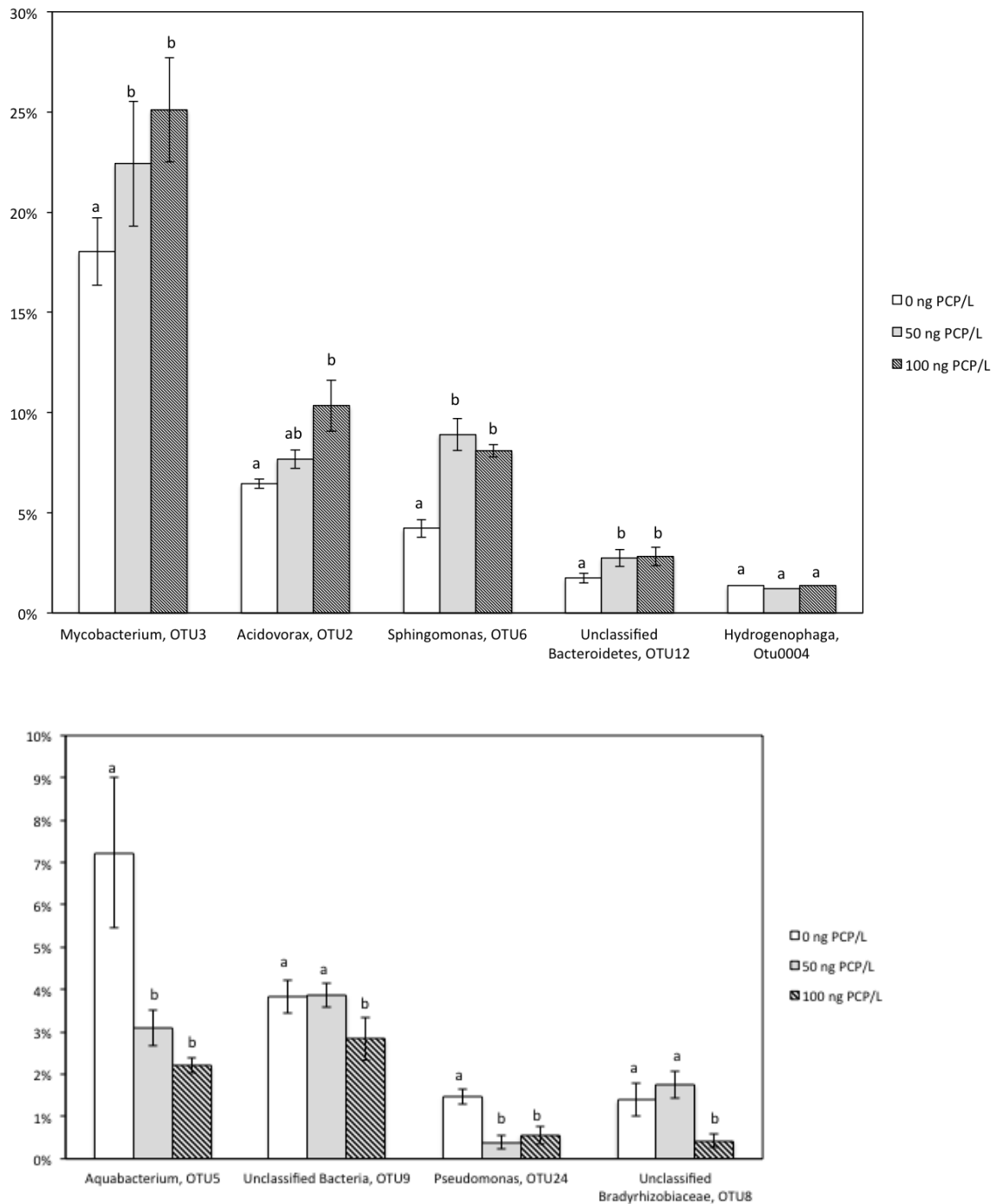
Mean $\pm$ standard deviation	Taxa-based dissimilarity index		Phylogeny-based dissimilarity index	
	Jaccard	Abundance-based Jaccard	Unweighted UniFrac	Weighted UniFrac
I. Within paired samples that received the same treatment				
Influent	0.57 $\pm$ 0.03 <sup>a</sup>	0.08 $\pm$ 0.02 <sup>a</sup>	0.54 $\pm$ 0.03 <sup>a</sup>	0.22 $\pm$ 0.03 <sup>a</sup>
Fabric	0.62 $\pm$ 0.05 <sup>b</sup>	0.03 $\pm$ 0.01 <sup>b</sup>	0.61 $\pm$ 0.05 <sup>b</sup>	0.06 $\pm$ 0.02 <sup>b</sup>
Effluent	0.64 $\pm$ 0.08 <sup>b</sup>	0.02 $\pm$ 0.01 <sup>c</sup>	0.65 $\pm$ 0.07 <sup>b</sup>	0.11 $\pm$ 0.03 <sup>c</sup>
Between influent and effluent	0.76 $\pm$ 0.07 <sup>c</sup>	0.30 $\pm$ 0.14 <sup>d</sup>	0.75 $\pm$ 0.07 <sup>c</sup>	0.46 $\pm$ 0.05 <sup>d</sup>
Between fabric and effluent	0.75 $\pm$ 0.06 <sup>c</sup>	0.12 $\pm$ 0.05 <sup>e</sup>	0.75 $\pm$ 0.05 <sup>c</sup>	0.49 $\pm$ 0.05 <sup>e</sup>
Between influent and fabric	0.66 $\pm$ 0.06 <sup>b</sup>	0.12 $\pm$ 0.05 <sup>e</sup>	0.64 $\pm$ 0.06 <sup>b</sup>	0.42 $\pm$ 0.05 <sup>f</sup>
II. Between PCP and control samples				
Influent	0.56 $\pm$ 0.04 <sup>a</sup>	0.07 $\pm$ 0.03 <sup>a</sup>	0.53 $\pm$ 0.04 <sup>a</sup>	0.20 $\pm$ 0.06 <sup>a</sup>
Fabric	0.64 $\pm$ 0.05 <sup>b</sup>	0.09 $\pm$ 0.02 <sup>f</sup>	0.63 $\pm$ 0.06 <sup>b</sup>	0.14 $\pm$ 0.02 <sup>g</sup>
Effluent	0.66 $\pm$ 0.08 <sup>b</sup>	0.02 $\pm$ 0.01 <sup>c</sup>	0.67 $\pm$ 0.07 <sup>b</sup>	0.14 $\pm$ 0.03 <sup>g</sup>

Letters indicate significant ( $P < 0.001$ ) differences based on Kruskal-Wallis test for each distance index. Groups with the same letters indicate they are not significantly different from each other.

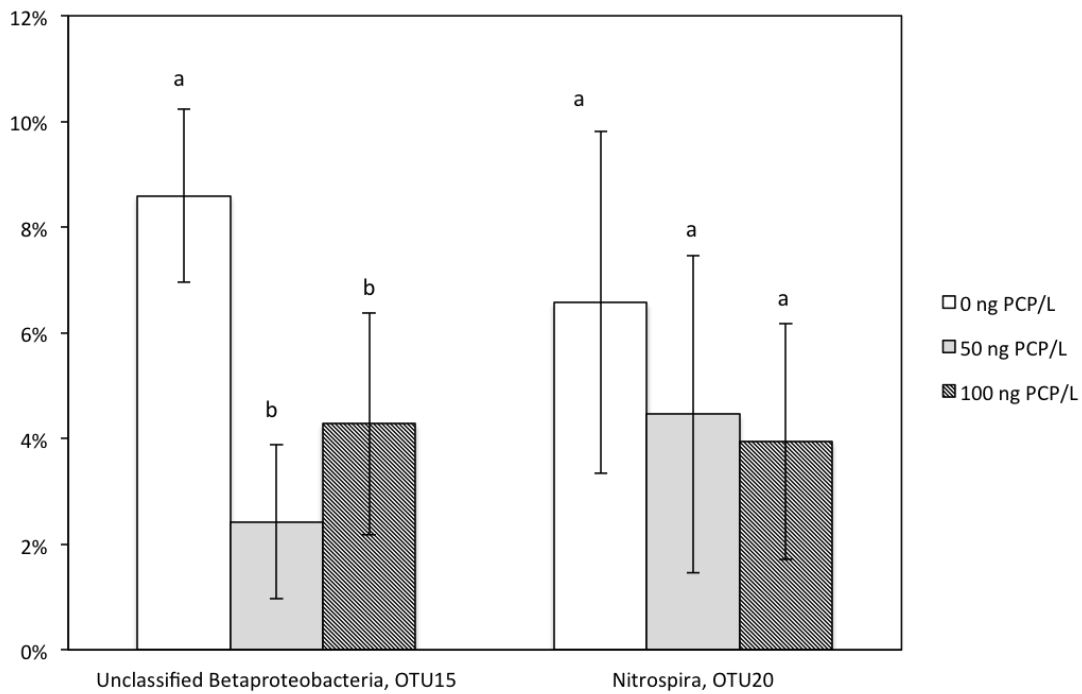
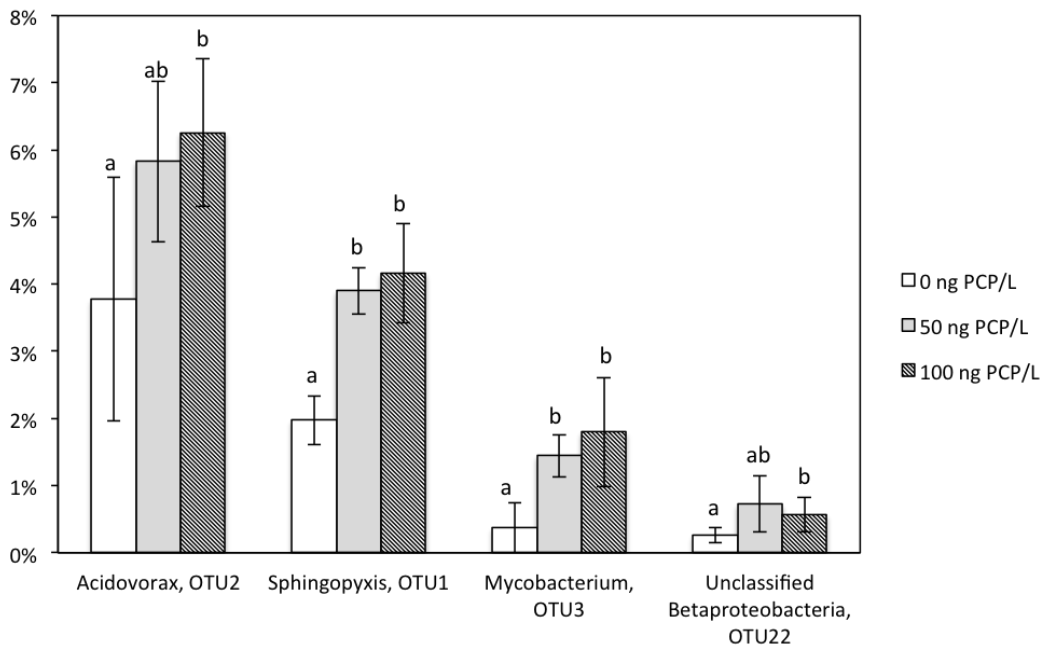
**Table S3-8. Multivariate permutational analysis (PERMANOVA) results comparing the bacterial composition between PoU filter location and PCP treatment.**

	Degrees of freedom	Sum of squares	Mean square	F.model	R <sup>2</sup>	Pr(>F)
Unweighted UniFrac distance						
PoU filter location	2	2.69	1.35	6.97	0.22	0.005
PCP treatment	2	0.56	0.28	1.46	0.046	0.045
Residuals	46	8.89	0.19		0.73	
Total	50	12.14			1.00	
Weighted UniFrac distance						
PoU filter location	2	3.34	1.67	221.49	0.88	0.005
PCP treatment	2	0.09	0.04	5.89	0.024	0.005
Residuals	46	0.35	0.008		0.092	
Total	50	3.77			1	

**A.12. OTUs correlated with Weighted Unifrac based PCoA plots of fabric and effluent samples.**



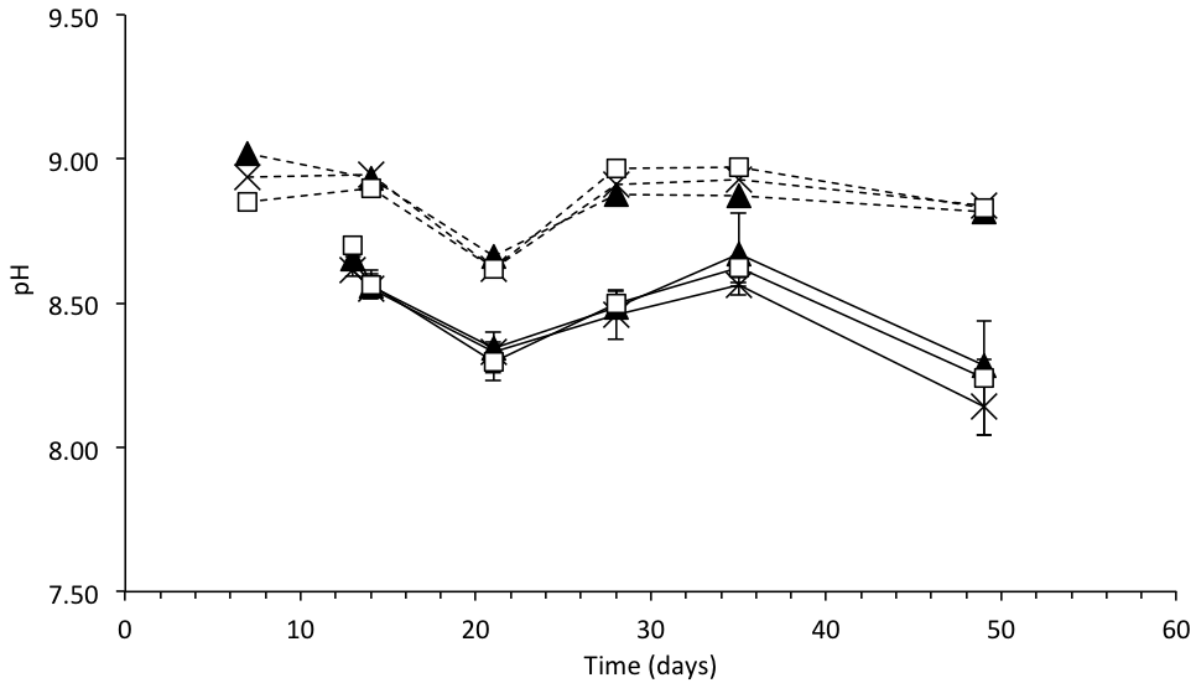
**Fig. S3-5. Relative abundance (y-axis) versus specified taxa (x-axis) for dominant OTUs (>1% relative abundance) of fabric samples that were correlated with Weighted Unifrac based PCoA plot (PCoA 1, 54%; PCoA 2, 16%). Letter Groups with the same letters indicate significant differences ( $p < 0.05$ ) between PCP treatments based on Tukey's pairwise analysis. They are not significantly different from each other.**



**Fig. S3-6. Dominant OTUs (>1%) of effluent samples that were correlated with Weighted Unifrac based PCoA plot (PCoA 1, 30%; PCoA 2, 14%). Letters indicate whether significant differences ( $p < 0.05$ ) occur between PCP treatments based on Tukey's pairwise analysis. Bars with the same letter are not significantly different from each other.**

## A.13. Water Chemistry of PoU filter

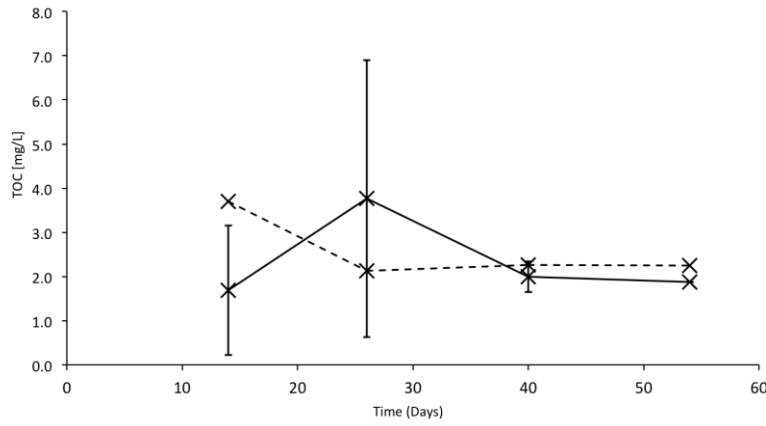
### A.13.1 Influent and effluent pH measurements



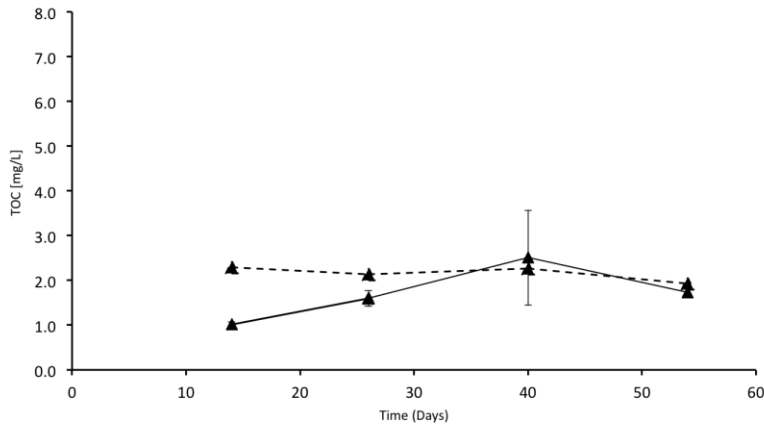
**Fig. S3-7. pH measurements in influent (dashed line) and effluent samples (solid line) of PoU filters during operation. The PoU filters were fed with 0 ng PCP/L (cross), 50 ng PCP/L (triangle), or 100 ng PCP/L (square). Standard deviations of effluent samples are indicated by the error bars.**

### A.13.2. TOC

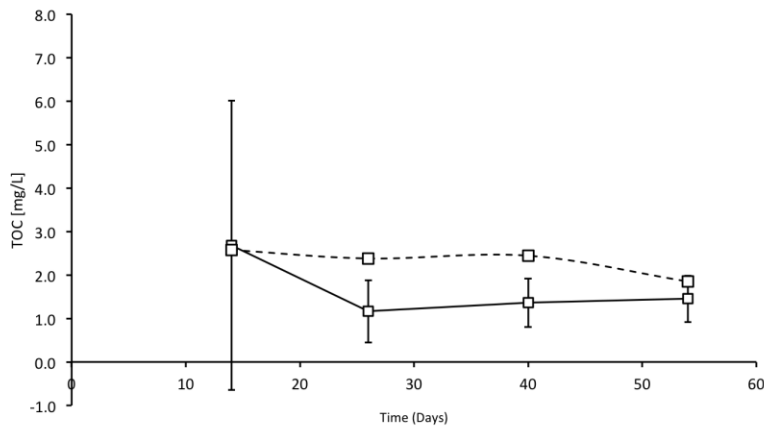
(a)



(b)



(c)



**Fig. S3-8. TOC concentrations in influent (dashed line) and effluent samples (solid line) during operation. (a) 0 ng PCP/L (cross); (b) 50 ng PCP/L (triangle); and (c) 100 ng PCP/L (square). Standard deviations of effluent samples are indicated by the error bars.**

### A.13.3. Average water quality of all treatments in influent and effluent

**Table S3-9. Average influent water quality of all treatments\*.**

Parameter	Avg. Conc.
pH	8.86 (0.12)
Total alkalinity (mg/L as CaCO <sub>3</sub> )	49.7 (9.5)
Total Cl <sub>2</sub> residual (mg/L as Cl <sub>2</sub> )	2.5 (0.5)
TOC (mg/L as C)	2.3 (0.4)
DOC (mg/L as C)	2.2 (0.2)
SUVA (L mg <sup>-1</sup> cm <sup>-1</sup> )	0.016 (0.003)
HPC (CFU/mL)	160 (250)

\*Standard deviations are shown in parentheses

**Table S3-10. Average effluent water quality of PoU Filters\*.**

Parameter	Treatment		
	0 ng/L PCP	50 ng/L PCP	100 ng/L PCP
pH	8.45 (0.17)	8.51 (0.16)	8.41 (0.39)
PCP (ng/L)	< 10 ng/L	< 10 ng/L	< 10 ng/L
Total Cl <sub>2</sub> residual (mg/L as Cl <sub>2</sub> )	< 0.2 mg/L	< 0.2 mg/L	< 0.2 mg/L
TOC (mg/L as C)	2. (1.66)	1.7 (0.7)	1.77 (1.55)
HPC (CFU/mL)	1.1×10 <sup>5</sup> (7.4×10 <sup>4</sup> )	4.5×10 <sup>4</sup> (3.1×10 <sup>5</sup> )	1.6×10 <sup>4</sup> (3.2×10 <sup>4</sup> )

\*Standard deviations are shown in the parenthesis



#### A.13.4. Estimation of the depth of penetration of PCP into activated carbon block

To determine the approximate penetration depth of PCP in the activated carbon block, the following assumptions were made. Biodegradation of PCP was neglected. Equilibrium adsorption of PCP by the activated carbon block was assumed to be modeled by a Freundlich isotherm. This is represented symbolically as follows:

$$\text{where } q_s(\text{mg/g GAC}) = K_F C_s^{1/n} \quad (\text{eq. S1})$$

$q_s$  is the PCP mass adsorbed on the solid phase,  $C_s$  is PCP concentration in aqueous phase,  $K_f$  and  $n$  are constants of the Freundlich isotherm model. Literature values of the constants  $K_f$  and  $n$  were reported by Dobb et al's (Dobbs and Cohen, 1980) for Filtrasorb 300 granular activated carbon, which typically has a surface area of 1000 m<sup>2</sup>/g GAC. (Hendricks, 2006) At the pH conditions of Ann Arbor tap water, pH 9,  $K_f = 100 \text{ mg}^{1+n} \text{g}^{-1} \text{L}^{-n}$  and  $n=0.41$ , were chosen in this approximation.

Perfect mass transfer was assumed, i.e., all of the sorbed PCP was contained within a layer that was equilibrated with influent concentrations of PCP. Therefore,  $C_s$  was the PCP influent concentration, 50 or 100 ng/L. With these values and eq. S1, the adsorbed concentrations on the solid phase ( $q_s$ ) were calculated as 1.72 and 2.29 mg PCP/g Filtrasorb carbon, or  $1.72 \times 10^{-7}$  and  $2.29 \times 10^{-7}$  mg/cm<sup>2</sup> carbon, exposed to 50 and 100 ng/L PCP treatments. Since the specific area of activated carbon block was measured as 600 m<sup>2</sup>/g, the masses of PCP adsorbed per mass of activated carbon block were estimated to be 1.03 and 1.37 mg PCP/g ACB carbon for the 50 and 100 ng/L PCP treatments.

The depth of the PCP saturated zone was then estimated for the ACB at the end of filter operation by assuming all of the PCP fed to the filter was held in the saturated zone (and the PCP mass in the solution phase (void volume) was negligible). The following equations were used:

$$\begin{aligned} &\text{Mass of PCP – saturated carbon zone (g carbon)} \\ &= \frac{\text{The total PCP mass adsorbed (mg PCP)}}{\text{The mass PCP adsorbed on the activated carbon block (mg PCP/g carbon)}} \end{aligned} \quad (\text{e.q. S2})$$

$$\begin{aligned} & \text{Volume of PCP – saturated carbon zone (cm}^3\text{)} \\ &= \frac{\text{Mass of saturated carbon zone (g carbon)}}{\text{The density of PCP of activated carbon block (g/cm}^3\text{)}} \end{aligned} \quad (\text{e.q. S3})$$

The depth of PCP penetration into the ACB, is the difference of the outer radius of the ACB,  $R_0$  and the radius,  $R_1$ , to the inner edge of the PCP-saturated ACB volume (see Fig. 1). The latter dimension can be estimated by calculating the annulus area of the saturated zone,  $A$  as follows:

$$\text{Annulus area of saturated zone, } A \text{ (cm}^2\text{)} = \frac{\text{Volume of PCP – saturated carbon zone (cm}^3\text{)}}{\text{The hHeight of activated carbon block (cm)}} \quad (\text{e.q. S4})$$

$A$  is related to  $R_0$  and  $R_1$  by,

$$A = \pi R_0^2 - \pi R_1^2 \quad (\text{e.q. S5})$$

Therefore, the approximate PCP penetration depth =  $R_0 - R_1$  can be determined from eqs. S4 and S5.

At the end of filter operation, the total mass of PCP fed was 0.027 and 0.054 mg at 50 and 100 ng/L PCP treatment. The ACB density was measured as 0.19 g/cm<sup>3</sup>. The height and the outer radius of the activated carbon block ( $R_0$ ) were 5.9 and 2.5 cm, respectively. With these values, the area of the PCP-saturated zone was estimated to be 0.023 cm<sup>2</sup> in 50 ng/L PCP treatment, and 0.035 cm<sup>2</sup> in 100 ng/L PCP treatment. The depth of penetration of PCP into activated carbon block was estimated to be about 15 μm for 50 ng/L PCP treatment, and 22 μm with 100 ng/L PCP treatment.

#### A.14. Estimation of cell protein obtained from the cell load in influents

If no cell growth occurred on the fabric, the bacterial cell mass that accumulated on the fabric would be equal to or less than (due to decay) the cell load from the influent of PoU filters over the period of operation. It was assumed that only 1% of cells are culturable using the HPC method.(Bartram et al., 2003)

$$\text{Cells applied to fabric} = \frac{\text{average influent conc (CFU/mL)} \times \text{volume of water processed (mL)}}{1\% \text{ (culturability of HPC test)}}$$

(e.q. S6)

Based on measured data, the average concentration of influent HPC was 160 CFU/mL (Table S3-9). The total volume of water processed was 519 L. Using these values and e.q. S6, the total number of cells applied to the fabric was estimated to be  $8.7 \times 10^9$  cells.

To convert the number of cells to protein from applied cells, it was assumed that all cells have the same dry weight as actively growing cell of *E.coli*,  $2.8 \times 10^{-13}$  g, where protein mass comprised 55% of total cell mass.(Neidhardt et al., 1996) In addition, 25% of cells that grew over the course of the study were assumed to remain at the end (i.e., an observed yield of 0.25 g cell theoretical oxygen demand per g of electron donor as theoretical oxygen demand); the rest would have been lysed and cytoplasmic matter would have been recycled as food to other growing cells. Therefore, the protein mass expected on the fabric at the end of the study is estimated to be  $3.3 \times 10^{-4}$  g. Since the fabric area was  $94.2 \text{ cm}^2$ , the protein from applied cells per fabric area would be  $3.6 \text{ }\mu\text{g/cm}^2$ . This compares to average measured cell protein on the fabric of  $23 \text{ }\mu\text{g/cm}^2$ . The difference implies that substantial cell growth occurred on the fabric.

## A.15. Estimation of cell protein formed from PCP utilization

### A.15.1. Theoretical yield of PCP

The theoretical yield of PCP is calculated based on the stoichiometry of the redox reaction. It was assumed that the starting material was completely consumed and no side or reverse reactions occur. The balanced organic half-reaction for PCP is given in equation S7.



The amount of energy that can be acquired from the redox reaction is the difference in the Gibb's formation potential for the reactants and products. Based on the free energies of formation ( $G_f^0$ ) shown in Table S3-11, the standard free energy change of the reaction ( $\Delta G^0$ ) at 1 atm pressure and 1M concentration is:

$$\Delta G^0 = \sum G_f^0 (\text{products}) - \sum G_f^0 (\text{reactants}) = 13.58 \text{ kJ/mole} = 13.58 \text{ kJ/e} - \text{eq}$$

The standard free energy change of the reaction at pH 7 ( $\Delta G^{0'}$ ) is calculated to be  $\Delta G^{0'} = \Delta G^0 + m\Delta G_f^0(\text{H}^+) = -35.91 \text{ kJ/e} - \text{eq}$ . The theoretical yield ( $f_s^0$ ) of PCP is estimated thermodynamically by the fraction of electron donor, A (eq. S8 and S9). It was assumed that ammonia is the nitrogen source and is available for cell synthesis. The efficiency of energy transfer,  $\epsilon$ , was assumed to be 0.6.  $n$  is +1 if  $\Delta G_p$  is positive, and vice versa.

$$A = -\frac{\frac{\Delta G_p}{\epsilon^n} + \frac{\Delta G_{\text{pyruvate}}}{\epsilon}}{\epsilon(\Delta G_a - \Delta G_d)} \quad (\text{eq. S8})$$

$$f_s^0 = \frac{1}{1+A} \quad (\text{eq. S9})$$

$\Delta G_p$  is the energy required to convert the cell carbon source to an intermediate stage. It is calculated by subtracting the amount of energy that can be formed from the PCP redox reaction ( $\Delta G^{0'}$ ) from the free energy of formation of pyruvate (Table S3-11) as follows:

$$\Delta G_p = 35.09 - \Delta G^{0'} = 72.49 \text{ kJ/e} - \text{eq}$$

$\Delta G_a$  and  $\Delta G_d$  are the free energies per electron equivalent for oxidation half reactions for the electron acceptor and electron donor, respectively. Oxygen is the electron acceptor because we

assumed the water is saturated throughout the PoU filter and the biofilm thickness during operating periods is not sufficient to cause anaerobic zones. As a minimum, this is a conservative estimate and will overestimate cell yield from PCP growth.  $\Delta G_d$  is equal to  $\Delta G^{\circ}$  since PCP is assumed to be the electron donor in this calculation. With the calculated  $\Delta G^{\circ}$ , the values shown in Table S3-11, eq. S8 and S9, the theoretical yield of PCP ( $f_s^{\circ}$ ) is calculated at 0.14.

#### **A.15.2. Theoretical oxygen demand of PCP on PCP-fed fabric membranes**

In order to determine the biomass that can be formed on the fabric due to growth on PCP, it was assumed that all of the PCP applied to the filter system adsorbed on the activated carbon block ( $2.8 \times 10^{-4}$  and  $5.7 \times 10^{-4}$  mg PCP/cm<sup>2</sup> in 50 and 100 ng/L PCP-fed filters, respectively) and was all utilized by the biomass (to obtain the most conservative estimate). Based on the theoretical oxygen demand (ThOD) of PCP, which is 0.54 mg ThOD/mg PCP, the PCP adsorbed on the activated carbon block contained  $1.5 \times 10^{-4}$  and  $3.1 \times 10^{-4}$  mg ThOD/cm<sup>2</sup> for 50 and 100 ng/L PCP fed-fabrics, respectively.

#### **A.15.3. Theoretical cell biomass and cell protein yielded from PCP utilization**

The biomass that can be yielded from the PCP is the product of the theoretical yield ( $f_s^{\circ}$ ) and the theoretical oxygen demand (ThOD) provided by the substrate. Thus, the amount of biomass that could grow on PCP was calculated to be  $2.2 \times 10^{-5}$  and  $4.3 \times 10^{-5}$  mg biomass as ThOD/cm<sup>2</sup> for 50 and 100 ng/L PCP fed-fabrics, respectively. Since cell protein comprises 55% of a prokaryotic cell by weight, (Neidhardt et al., 1996) the cell protein yields are thus  $1.2 \times 10^{-2}$  and  $2.5 \times 10^{-2}$   $\mu$ g cell protein/cm<sup>2</sup> for 50 and 100 ng/L PCP fed-fabrics, respectively. This is three orders of magnitude lower than the actual measured amount of biomass on the fabric, and indicates that under the conservative assumptions used in this estimate, PCP was not a major contributor to cell growth.

**Table S3-11. The free energies of formation ( $G_f^0$ ) for the compounds at 25 °C, 1 atm and 1M concentration.**

Compound	$G_f^0$
C <sub>6</sub> HCl <sub>5</sub> O (at pH 0)	-144.8 kJ/mol(Dolfing and Harrison, 1992)
H <sub>2</sub> O (at pH 0)	-237.17 kJ/mol(Madigan et al., 2010)
CO <sub>2</sub> (at pH 0)	-394.4 kJ/mol(Madigan et al., 2010)
H <sup>+</sup> (at pH 0)	0 kJ/mol(Madigan et al., 2010)
Cl <sup>-</sup> (at pH 0)	-131.4 kJ/mol(Oelkers et al., 1995)
H <sup>+</sup> (at pH 7)	-39.83 kJ/mol(Madigan et al., 2010)
Pyruvate (at pH 7)	35.09 kJ/e-eq(Grady Jr. et al., 2011)
O <sub>2</sub> (at pH 7)	-78.72 kJ/e-eq(Grady Jr. et al., 2011)

### A.15. Supplemental references

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## **Appendix B.**

### **Supplementary Information for Chapter 4**

**Prevalence of antibiotic resistance genes in two drinking water sources treated by activated carbon block point-of-use (PoU) filters**



**Table S4-1 Metagenomes datasets**

Sample name	<i>Enterobacteriaceae</i> , copy #/250 mL (Class*)	Size of metagenome, MB	Total no. of contigs assembled
Flint water system			
Influent of PoU05	60 (Low)	247.8	83183
Influent of PoU18	39 (Low)	363.8	167422
Influent of PoU19	242 (Low)	268.5	121363
Effluent of PoU23	6730 (High)	351.2	160042
Effluent of PoU25	4635 (High)	246.5	90372
Influent of POU21	Not detected (Low)	187.9	78323
Effluent of PoU21	9058 (High)	271.9	103097
Ann Arbor water system			
Fabric- 0PCP (A)	Not applied	240.33	105429
Fabric- 100PCP (B)	Not applied	196.7	94646
Influent - 0PCP	Not applied	146	51284
Effluent - 0PCP (A)	Not applied	145.4	50622
Effluent - 100PCP (A)	Not applied	172	65377

\*Low = low abundance *Enterobacteriaceae*; High = high abundance *Enterobacteriaceae*.

**Table S4-2 Types of ARGs in a chlorinated and a chloraminated system**

Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
ABC efflux pump		<i>vgaC</i>	
ABC multidrug efflux pump	<i>efrA</i> <i>msbA</i> <i>msrB</i> <i>msrC</i>	<i>msbA</i>	
		<i>patA</i>	
Aminocoumarin	<i>mdtB</i> <i>parY</i>	<i>mdtA</i> <i>mdtB</i>	<i>mdtB</i>
Aminoglycoside	<i>acrD</i> <i>baeR</i> <i>baeS</i> <i>AAC(2')-Ic</i>  <i>AAC(3)-IIIc</i> <i>AAC(6')-Ib8</i>  <i>aadA6</i> <i>ANT(3'')-IIa</i> <i>APH(3'')-Ib</i> <i>APH(3')-IIb</i> <i>APH(3')-IIc</i> <i>APH(6)-Id</i> <i>AAC(6')-Ib7</i>	<i>acrD</i>  <i>AAC(2')-Ic</i> <i>AAC(3)-Ic</i>  <i>AAC(6')-Ib8</i>  <i>AAC(6')-IIc</i>	<i>AAC(3)-IIIb</i>  <i>AAC(6')-Ib8</i> <i>AAC(6')-IIa</i> <i>AAC(6')-IIc</i>  <i>APH(3')-IIb</i>
Beta-lactam	<i>CGB-1</i>		<i>blaF</i> <i>CAU-1</i> <i>OXA-50</i> <i>OXA-60</i> <i>PDC-7</i> <i>PDC-9</i>

Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
Beta-lactam	<i>ACT-37</i> <i>ADC-18</i> <i>AIM-1</i> <i>CAU-1</i> <i>OmpK37</i> <i>L1</i> <i>OXA-114a</i> <i>OXA-133</i> <i>OXA-243</i> <i>OXA-3</i> <i>OXA-309</i> <i>OXA-334</i> <i>OXA-360</i> <i>OXA-50</i> <i>PDC-3</i> <i>PDC-5</i> <i>PDC-78</i>	<i>AIM-1</i> <i>CAU-1</i>         <i>OXA-50</i>         <i>PDC-93</i> <i>SHV-22</i>	
Bicyclomycin	<i>bcr-1</i>	<i>bcr-1</i>	<i>bcr-1</i>
Chloramphenicol	<i>floR</i>	<i>cmlA1</i> <i>cmlA6</i>	<i>floR</i>
Diaminopyrimidine antibiotic	<i>dfrB6</i>	<i>dfrE</i>	
Fluoroquinolone	<i>oqxA</i> <i>oqxB</i>  <i>mfpA</i>	<i>oqxB</i>   <i>mfpA</i>	<i>oqxB</i> <i>QepA</i>
Fosfomycin	<i>FosA</i>	<i>FosA</i>	<i>FosA</i>
Glycopeptide	<i>vanRG</i> <i>vanRM</i> <i>vanRO</i>		

Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
MATE-Multidrug efflux pump	<i>abeM</i> <i>MdtK</i> <i>PmpM</i>	<i>abeM</i>  <i>PmpM</i>	  <i>PmpM</i>
MFS-Multidrug efflux pump	<i>efpA</i> <i>emrB</i> <i>emrD</i> <i>emrR</i> <i>lrfA</i> <i>mdfA</i> <i>mdtG</i> <i>mdtH</i>	<i>efpA</i> <i>emrB</i> <i>emrD</i>  <i>lrfA</i>   <i>mdtH</i>	 <i>efpA</i>        
peptide antibiotics	<i>arnA</i> <i>bacA</i> <i>basS</i> <i>bcrA</i> <i>PmrE</i>   <i>YojI</i>	<i>arnA</i>  <i>basS</i>     <i>PmrF</i> <i>rosB</i>	<i>arnA</i>   <i>basS</i>     
Phenicol antibiotics	<i>cat</i> <i>catB7</i>   <i>cmx</i>	  <i>catB7</i>    	<i>cat</i> <i>catB7</i> <i>catB8</i>   
Rifampin	   <i>RbpA</i> <i>rpoB2</i>	   <i>RbpA</i> <i>rpoB2</i>	<i>arr-1</i> <i>arr-2</i> <i>arr-7</i> <i>RbpA</i> <i>rpoB2</i>
RND-Multidrug efflux pump	  <i>adeG</i> <i>adeH</i> <i>adeI</i>  <i>adeJ</i>	  <i>adeG</i> <i>adeH</i>  <i>adeJ</i>	     <i>adeB</i> <i>adeG</i>   

Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
RND-Multidrug efflux pump			
	<i>adeK</i>	<i>adeK</i>	
	<i>adeL</i>	<i>adeL</i>	
	<i>adeN</i>		
	<i>ArmR</i>		<i>ArmR</i>
	<i>cpxA</i>		
	<i>CpxR</i>	<i>CpxR</i>	<i>CpxR</i>
	<i>golS</i>		<i>golS</i>
	<i>mdsB</i>	<i>mdsB</i>	<i>mdsB</i>
	<i>mdtC</i>	<i>mdtC</i>	
	<i>MexA</i>		<i>MexA</i>
	<i>MexB</i>	<i>MexB</i>	<i>MexB</i>
	<i>MexC</i>		<i>MexC</i>
	<i>MexD</i>		<i>MexD</i>
	<i>MexE</i>		<i>MexE</i>
	<i>MexF</i>	<i>MexF</i>	<i>MexF</i>
	<i>MexH</i>		
	<i>MexI</i>	<i>MexI</i>	<i>MexI</i>
	<i>MexK</i>	<i>MexK</i>	<i>MexK</i>
	<i>MexL</i>		<i>MexL</i>
	<i>mexM</i>		<i>mexM</i>
	<i>mexP</i>		<i>mexP</i>
	<i>mexQ</i>		<i>mexQ</i>
	<i>MexV</i>		<i>MexV</i>
	<i>MexW</i>	<i>MexW</i>	<i>MexW</i>
	<i>mexX</i>		<i>mexX</i>
	<i>mexY</i>	<i>mexY</i>	<i>mexY</i>
	<i>mtrA</i>	<i>mtrA</i>	<i>mtrA</i>
	<i>MuxA</i>		<i>MuxA</i>
	<i>MuxB</i>	<i>MuxB</i>	<i>MuxB</i>
	<i>MuxC</i>		<i>MuxC</i>
	<i>OpmB</i>		<i>OpmB</i>
	<i>opmE</i>		<i>opmE</i>
	<i>OprJ</i>	<i>OprJ</i>	<i>OprJ</i>
	<i>OprM</i>	<i>OprM</i>	<i>OprM</i>
	<i>OprN</i>	<i>OprN</i>	<i>OprN</i>
	<i>smeB</i>		<i>smeB</i>
	<i>smeD</i>		<i>smeD</i>
	<i>smeE</i>	<i>smeE</i>	<i>smeE</i>
	<i>soxR</i>	<i>soxR</i>	<i>soxR</i>

Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
RND-Multidrug efflux pump		<i>TolC</i>	
	<i>mexN</i>	<i>mexN</i>	<i>mexN</i>
	<i>ceoB</i>	<i>ceoB</i>	<i>ceoB</i>
	<i>H-NS</i>		
	<i>ramA</i>		
	<i>acrA</i>		
	<i>acrB</i>		<i>acrB</i>
	<i>AcrF</i>		
	<i>adeB</i>		
		<i>amrB</i>	<i>amrB</i>
	<i>AxyX</i>		
	<i>AxyY</i>		
	<i>CRP</i>	<i>CRP</i>	
	<i>marA</i>		
			<i>mdsA</i>
	<i>MexG</i>	<i>MexG</i>	<i>MexG</i>
	<i>MexJ</i>		<i>MexJ</i>
	<i>OpmD</i>		<i>OpmD</i>
	<i>OprZ</i>		
		<i>smeA</i>	<i>smeA</i>
	<i>smeC</i>		<i>smeC</i>
			<i>smeF</i>
	<i>smeR</i>		<i>smeR</i>
		<i>smeS</i>	
SMR antibiotic efflux pump			
	<i>abeS</i>		
	<i>emrE</i>		
	<i>qacH</i>	<i>qacH</i>	
			<i>emrE</i>
Streptogramin			
	<i>vatE</i>		
Sulfonamide			
	<i>sul1</i>		
	<i>sul2</i>		
Tetracycline			
	<i>tet(42)</i>	<i>tet(42)</i>	<i>tet(42)</i>
		<i>tetA(48)</i>	
	<i>tetB(48)</i>		
	<i>tap</i>	<i>tap</i>	

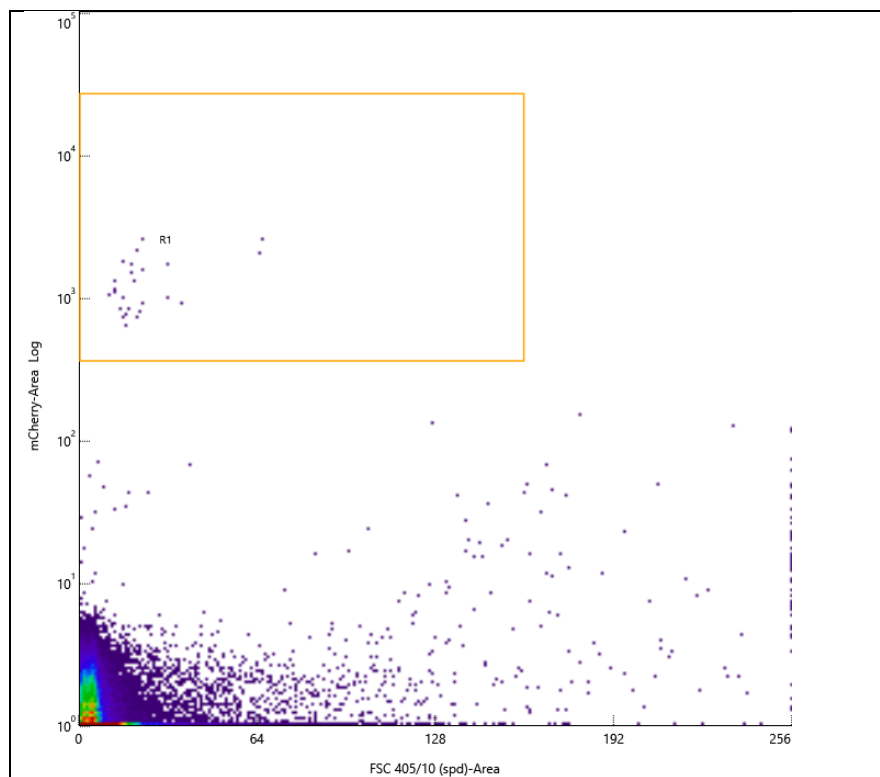
Type	Flint system		Ann Arbor system
	High <i>Enterobacteriaceae</i>	Low <i>Enterobacteriaceae</i>	
	<i>tet(C)</i>	<i>tet(C)</i>	
	<i>tet(G)</i>		
	<i>tet(V)</i>		
	<i>tetM</i>		
Triclosan	<i>TriA</i>		<i>TriA</i>
	<i>TriB</i>	<i>TriB</i>	<i>TriB</i>
	<i>TriC</i>	<i>TriC</i>	<i>TriC</i>
	<i>OpmH</i>	<i>OpmH</i>	<i>OpmH</i>

## **Appendix C.**

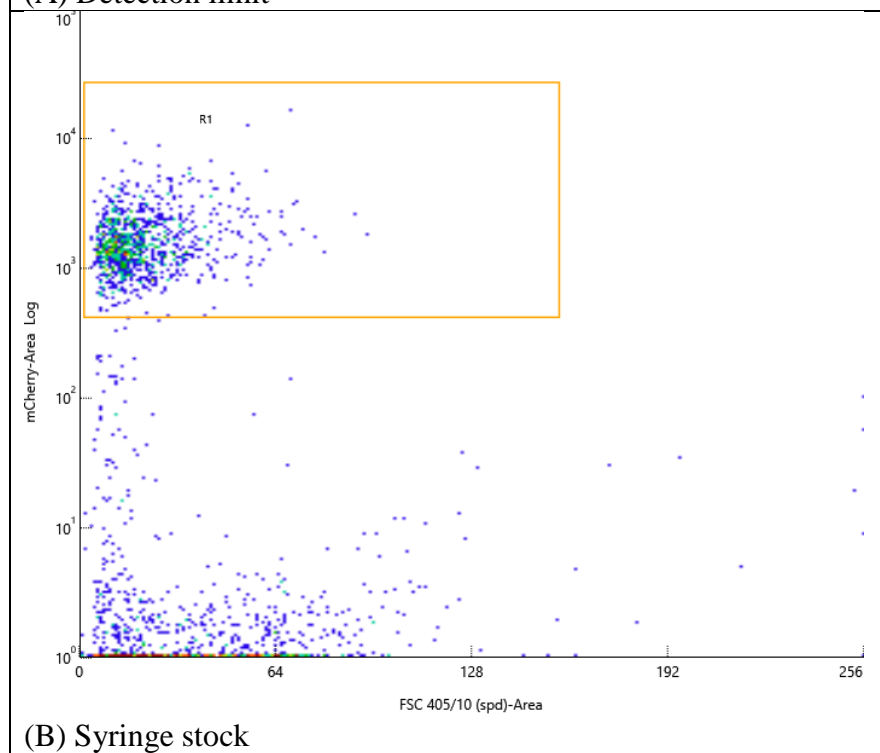
### **Supplementary Information for Chapter 5**

**Transmission and colonization of bacteria in activated carbon block (ACB) Point-of-use (PoU) filters**



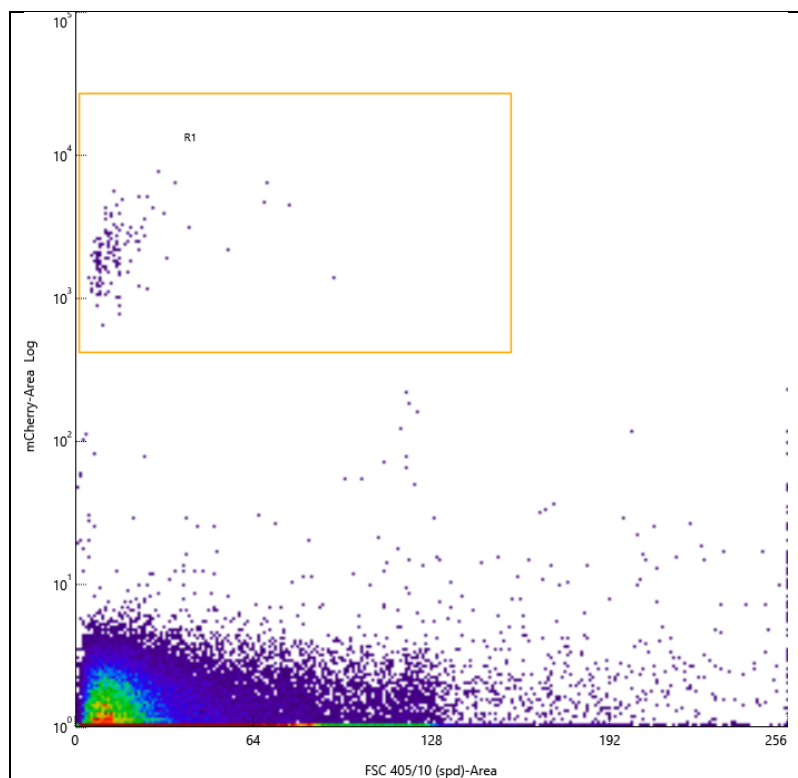


(A) Detection limit

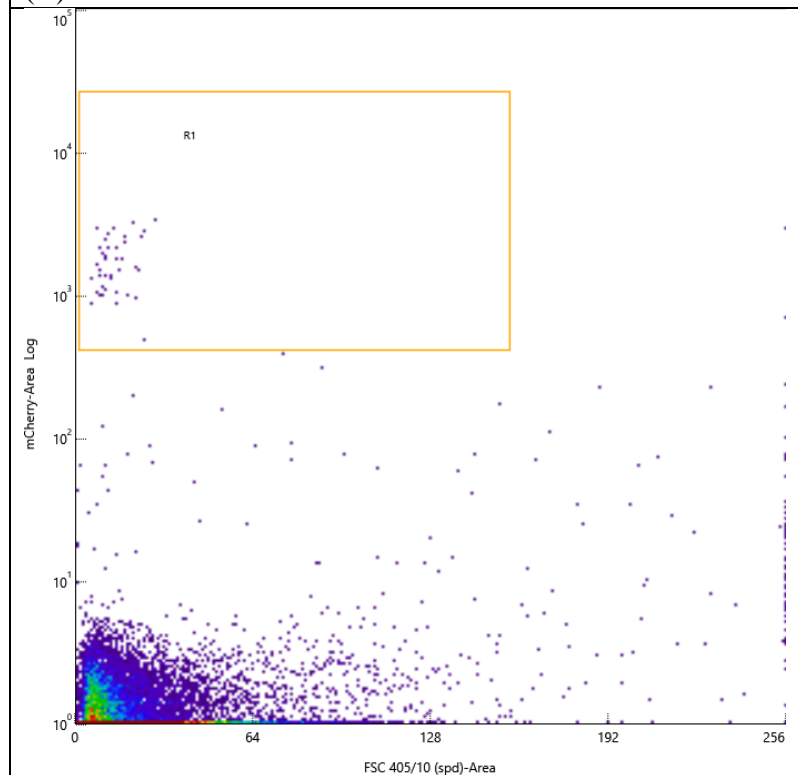


(B) Syringe stock

**Fig. S5-1** Flow cytometry dot plots of mCherry-tagged *E. coli*

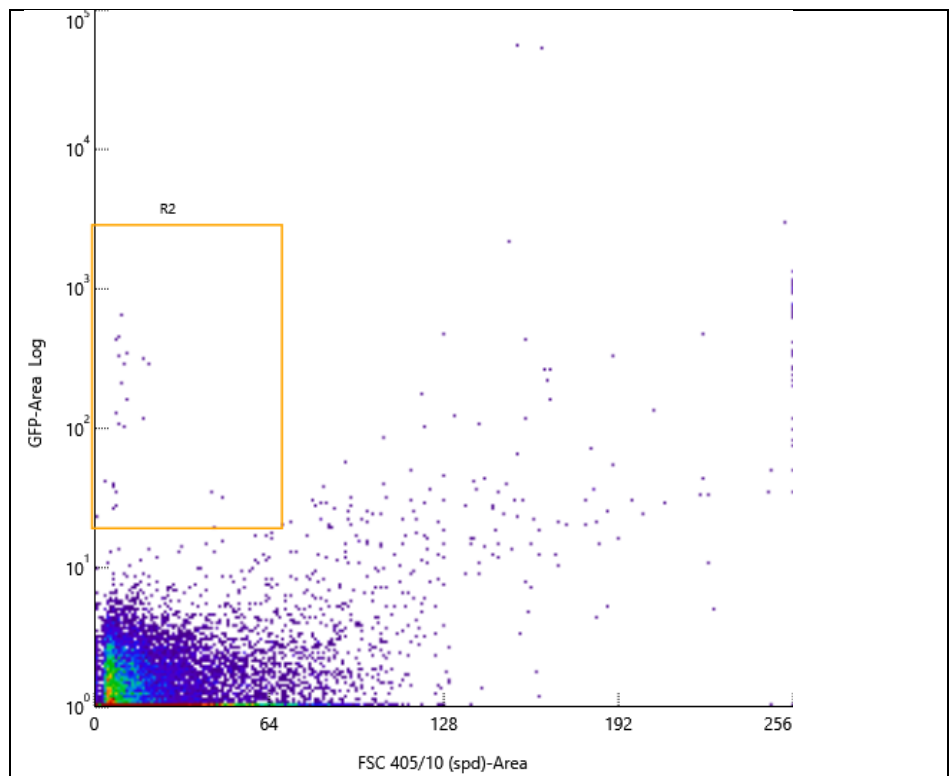


(C) Influent

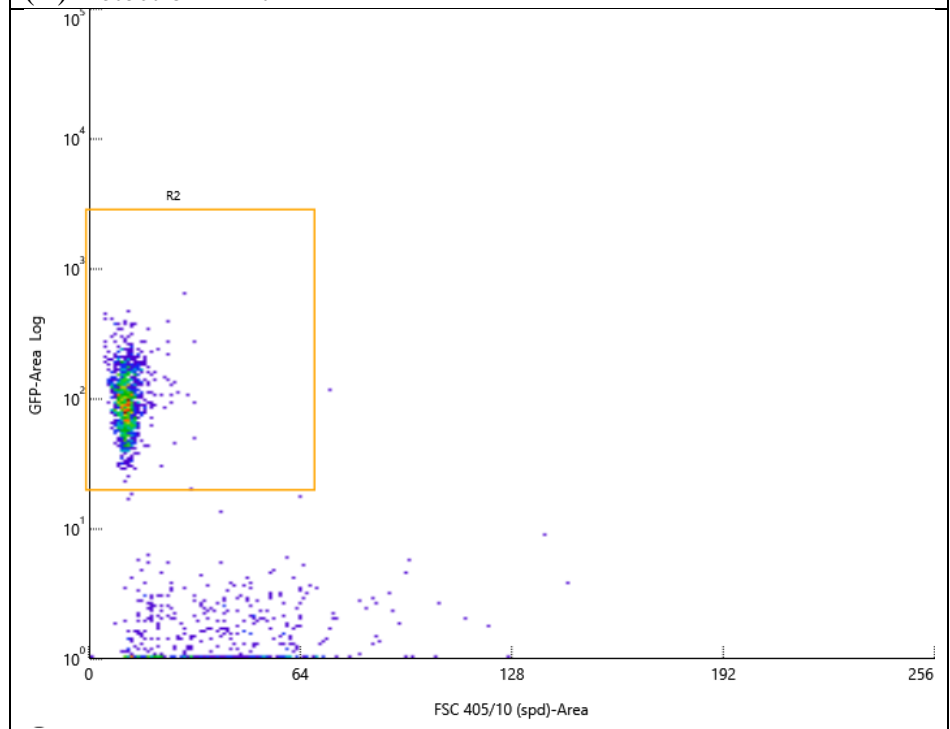


(D) Effluent

**Fig. S5-1 Flow cytometry dot plots of mCherry-tagged *E. coli* (continuous)**

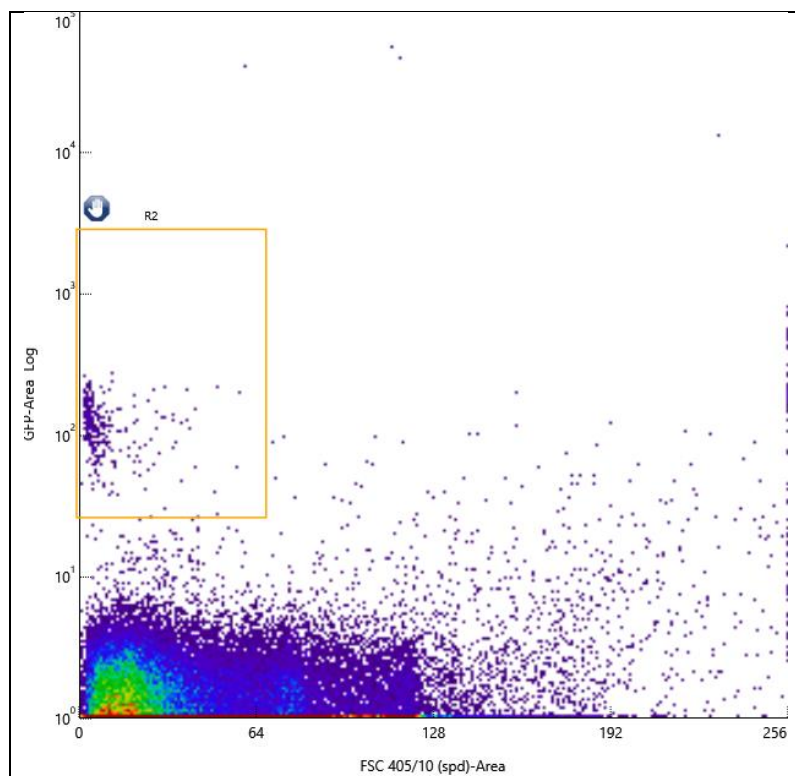


(A) Detection limit

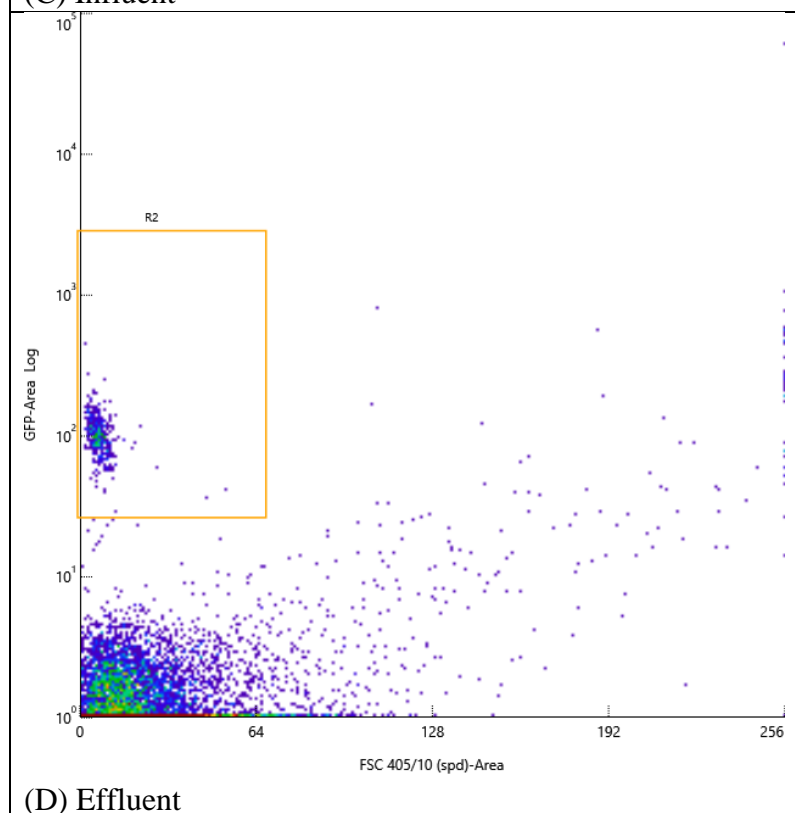


(B) Syringe stock

**Fig. S5-2** Flow cytometry dot plots of GFP-tagged *P. aeruginosa*

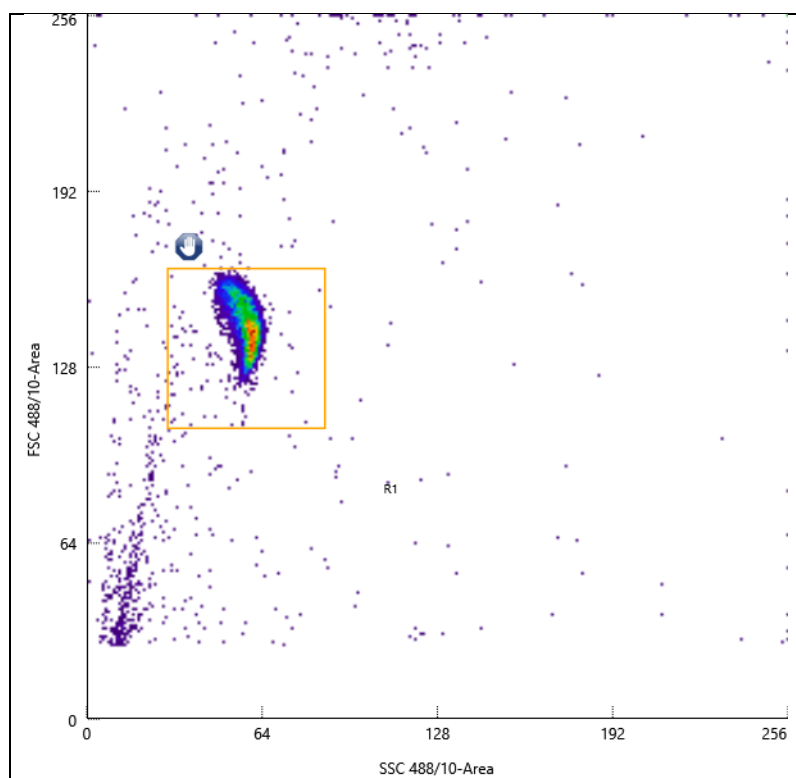


(C) Influent

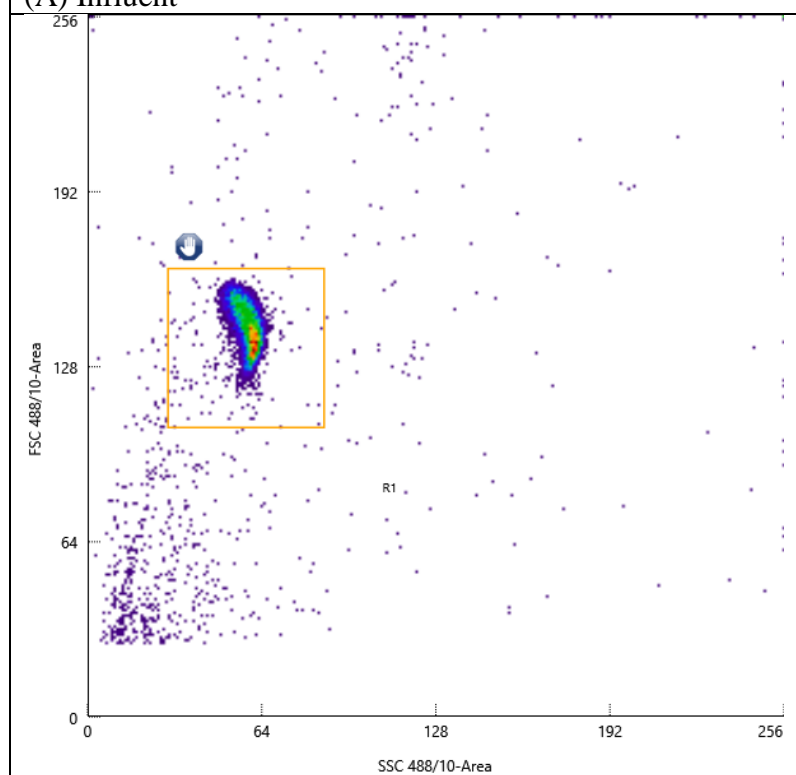


(D) Effluent

**Fig. S5-2** Flow cytometry dot plots of GFP-tagged *P. aeruginosa* (continuous)

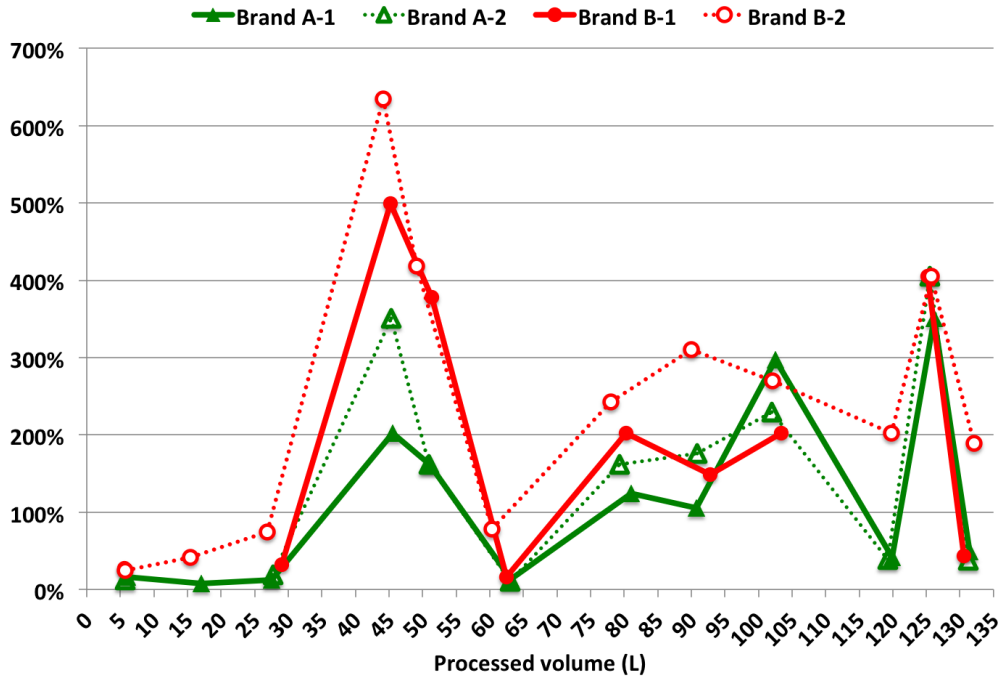


(A) Influent

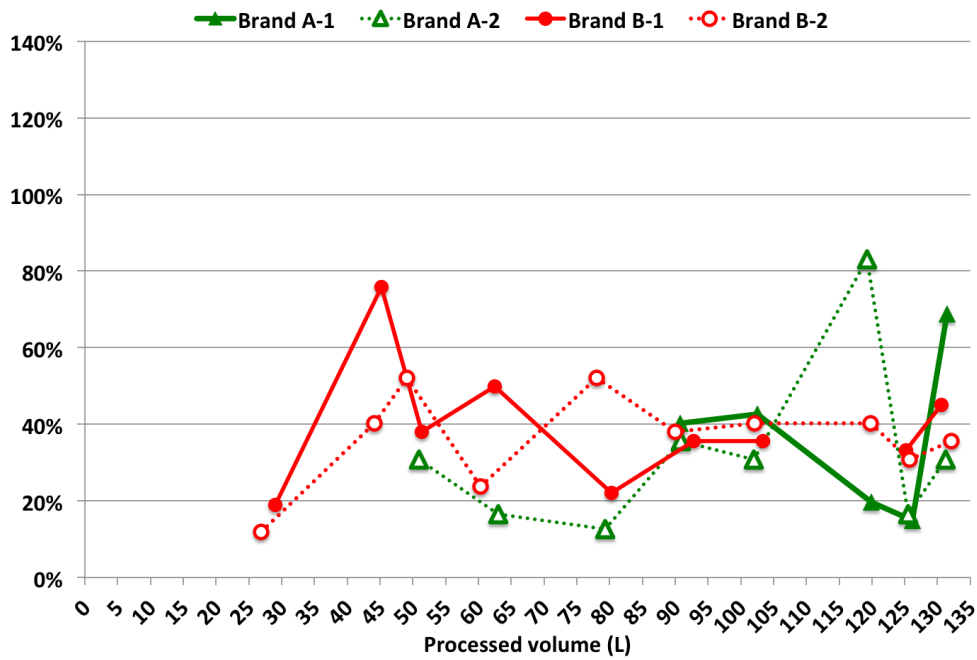


(B) Effluent

**Fig. S5-3 Flow cytometry dot plots of fluorescent microspheres.**

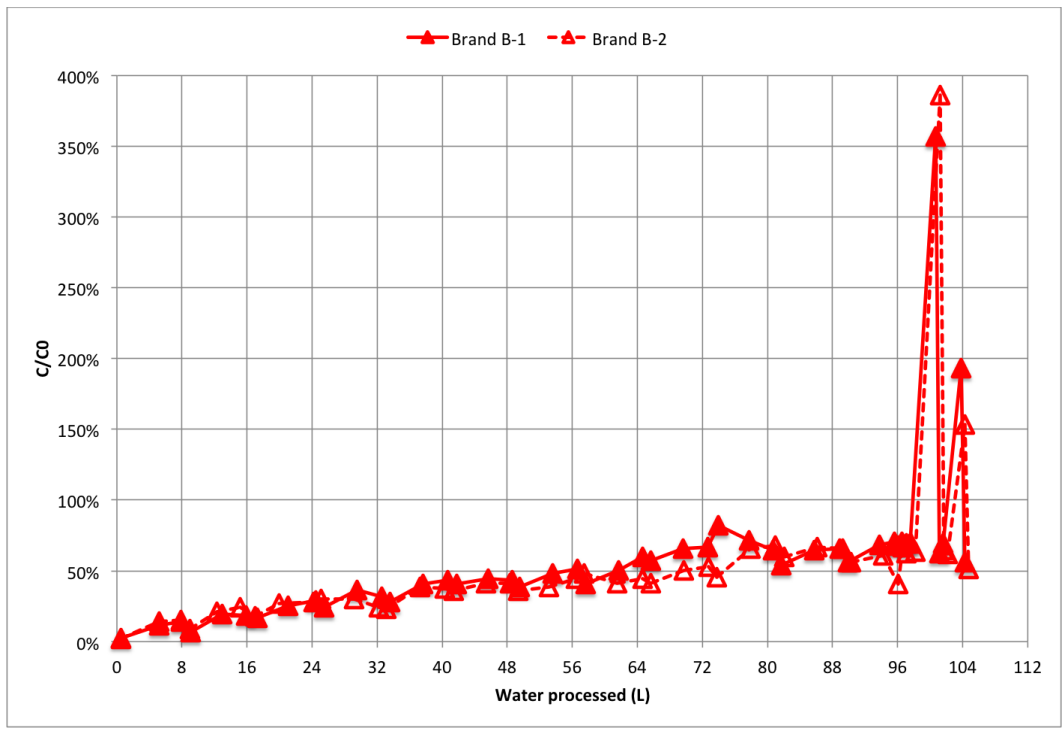
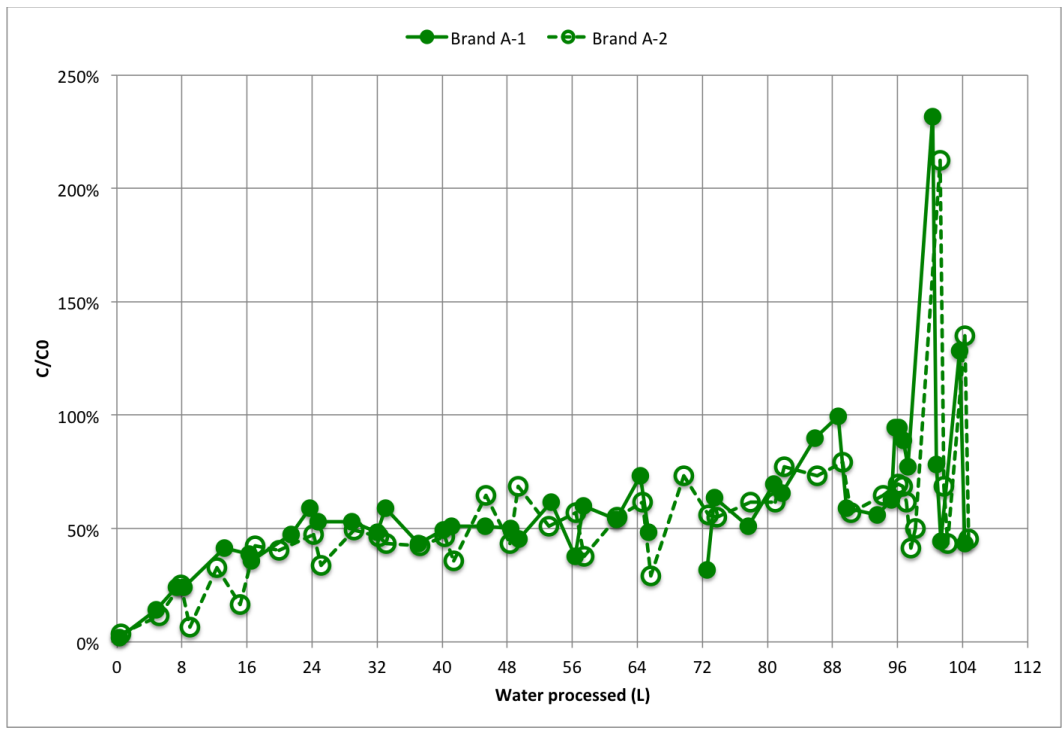


(A)



(B)

**Fig. S5-4 Ratio of effluent and influent concentration of (A) GFP-tagged *P. aeruginosa* and (B) mCherry-tagged *E. coli* through ACB PoU filters of Brand A (red) and Brand B (green).**



**Fig. S5-5 Microsphere breakthrough pattern in duplicates of Brand A (Top) and Brand B filters (Bottom). The curve included the hydraulic release events occurred at the end of operation.**

**Table S5-1 The rank of permeability of each ACB PoU filter tested.**

Filter label	Volume of water filtered at the initial 5 min (L)	Flow rate (L/min)	Rank of permeability*
Brand A-1	25	5.1	2
Brand A-2	25	5.1	2
Brand B-1	26	5.2	1
Brand B-2	24	4.9	3

\*Before first use, DI water was processed through each ACB PoU filter for 5 min. The rank of permeability was estimated by comparing the volume of water filtered at the first 5 min of each ACB PoU filter. The filter with more volume of water processed contained a more permeable ACB.



**Table S5-2 Mass balance of fluorescent bacteria across the filters.**

Parameters	GFP- <i>P. aeruginosa</i>				mCherry- <i>E. coli</i>			
	A-1	A-2	B-1	B-2	A-1	A-2	B-1	B-2
Influent loading <sup>a</sup> (No. of cell)	9.7×10 <sup>7</sup>				5.5×10 <sup>7</sup>			
Integrated cell counts in the effluent over the spiking phase (No. of cell)	1.1×10 <sup>8</sup>	1.3×10 <sup>8</sup>	1.7×10 <sup>8</sup>	2.3×10 <sup>8</sup>	6.8×10 <sup>6</sup>	1.2×10 <sup>7</sup>	1.8×10 <sup>7</sup>	1.7×10 <sup>7</sup>
Cell counts lost across the filters (No. of cell)	Not applicable				4.8×10 <sup>7</sup>	3.7×10 <sup>7</sup>	4.3×10 <sup>7</sup>	3.8×10 <sup>7</sup>
Estimated cell counts retained on fabric biofilm <sup>b</sup> (No. of cell each fabric)	5.0×10 <sup>3</sup>	2.1×10 <sup>4</sup>	2.5×10 <sup>3</sup>	6.6×10 <sup>4</sup>	5.3×10 <sup>4</sup>	7.3×10 <sup>4</sup>	3.1×10 <sup>4</sup>	1.8×10 <sup>5</sup>

<sup>a</sup> Determined from the average influent concentration multiplied with the volume of processed water (N = 9) .

<sup>b</sup> Estimated from the gene counts shown in Table 5-2. The estimated values pertain to the fabrics that were harvested after the washout period.

## **Appendix D.**

### **Relative abundance of OTUs in Ann Arbor PoU filter manifold system**

Table A. Relative abundance of OTUs in Anso Arbor P01 filter manifold system. All taxa observed were taken from influent (Infl), effluent (Eff), DNA samples collected from different operation days, and fabric (F) DNA replicates. Values represent abundance of each taxon as a percentage of all sequences obtained for each individual sample.

OTU number	Taxonomy	Sample code															
		11Infl	11Eff	12Infl	12Eff	12Infl	15Infl	15Eff	15Infl	15Eff	15Infl	15Eff	15Infl	15Eff	15Infl	15Eff	
Otu001	Sphingopyxis	0.33%	0.34%	0.19%	0.19%	0.34%	0.61%	0.57%	0.35%	0.77%							
Otu002	Acidovorax	2.19%	1.99%	1.57%	1.85%	2.02%	2.25%	1.89%	1.72%	2.51%							
Otu003	Mycobacterium	3.08%	19.07%	1.30%	17.82%	3.63%	0.60%	0.41%	0.79%	5.30%							
Otu004	Hydrogenophaga	17.99%	13.01%	18.79%	14.38%	17.47%	10.78%	8.96%	9.59%	17.07%							
Otu005	Aquabacterium	2.91%	3.13%	2.88%	2.68%	3.91%	2.97%	2.97%	2.74%	4.38%							
Otu006	Sphingomonas	0.50%	0.11%	0.18%	0.07%	0.21%	0.19%	0.37%	0.30%	0.13%							
Otu007	Unclassified Proteobacteria	0.00%	0.04%	0.06%	0.11%	0.84%	0.06%	0.22%	0.41%	1.35%							
Otu008	Unclassified Bradyrhizobiaceae	0.60%	0.27%	0.40%	0.26%	0.27%	0.57%	0.40%	0.30%	0.60%							
Otu009	Unclassified Bacteria	0.80%	0.22%	0.55%	0.26%	0.36%	0.82%	0.46%	0.49%	0.64%							
Otu010	Unclassified Betaproteobacteria	4.88%	4.95%	4.14%	4.12%	3.51%	5.06%	4.46%	4.07%	5.62%							
Otu011	Bosea	0.88%	1.27%	1.51%	1.27%	1.16%	1.21%	0.71%	0.99%	1.52%							
Otu012	Unclassified Bacteroidetes	1.85%	6.11%	3.19%	5.23%	1.79%	11.30%	9.76%	10.52%	3.08%							
Otu013	Unclassified Rhodobacteraceae	1.89%	2.24%	3.44%	1.96%	2.35%	2.10%	2.13%	2.28%	2.59%							
Otu014	Unclassified Sphingomonadaceae	0.00%	0.05%	0.02%	0.00%	0.06%	0.24%	0.00%	0.04%	0.08%							
Otu015	Unclassified Betaproteobacteria	0.14%	0.09%	0.19%	0.21%	0.31%	0.14%	0.23%	0.14%	0.37%							
Otu016	Unclassified Burkholderiales	2.27%	1.89%	1.53%	1.60%	1.70%	1.30%	1.42%	1.15%	1.96%							
Otu017	Unclassified Rhizobiales	0.15%	0.02%	0.07%	0.12%	0.43%	0.05%	0.09%	0.12%	0.24%							
Otu018	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%							
Otu019	Unclassified Bacteroidetes	4.29%	5.33%	5.85%	4.00%	3.72%	9.08%	9.10%	11.51%	4.13%							
Otu020	Nitrospira	0.36%	0.17%	0.65%	0.37%	0.30%	0.44%	0.44%	0.58%	0.31%							
Otu021	Unclassified Betaproteobacteria	0.43%	1.02%	0.94%	0.89%	0.54%	1.34%	1.72%	1.88%	0.63%							
Otu022	Unclassified Betaproteobacteria	0.74%	0.71%	0.77%	0.85%	0.51%	0.97%	0.68%	0.80%	0.81%							
Otu023	Unclassified Bacteria	7.18%	5.36%	1.15%	8.50%	8.97%	2.70%	3.88%	2.24%	1.90%							
Otu024	Pseudomonas	1.44%	1.77%	3.18%	1.59%	2.10%	1.09%	1.81%	1.35%	1.83%							
Otu025	Sediminibacterium	0.30%	0.50%	0.34%	0.68%	0.39%	0.43%	0.33%	0.49%	0.59%							
Otu026	Unclassified Betaproteobacteria	0.39%	1.00%	0.56%	1.00%	0.81%	0.60%	0.50%	0.38%	0.94%							
Otu027	Unclassified Rhodocyclaceae	0.03%	0.01%	0.04%	0.03%	0.00%	0.02%	0.10%	0.05%	0.06%							
Otu028	Chryseobacterium	0.14%	0.00%	0.02%	0.00%	0.00%	0.01%	0.07%	0.00%	0.00%							
Otu029	Unclassified Hyphomicrobiaceae	0.34%	0.09%	0.07%	0.13%	0.21%	0.13%	0.05%	0.12%	0.24%							
Otu030	Brevundimonas	3.66%	3.51%	4.41%	3.33%	2.35%	5.95%	4.27%	5.21%	3.57%							
Otu031	Methylobacterium	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.07%	0.01%	0.00%							
Otu032	Unclassified Proteobacteria	0.35%	0.16%	0.44%	0.48%	0.45%	0.61%	0.44%	0.55%	0.48%							
Otu033	Paraphysobacter	0.00%	0.00%	0.03%	0.03%	0.00%	0.03%	0.07%	0.10%	0.05%							
Otu034	Sphingopyxis	0.01%	0.24%	0.10%	0.12%	0.02%	0.23%	0.11%	0.15%	0.15%							
Otu035	Methylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%							
Otu036	Ralstonia	0.03%	0.05%	0.04%	0.15%	0.09%	0.04%	0.04%	0.01%	0.07%							
Otu037	Unclassified Rhizobiales	0.20%	0.16%	0.14%	0.14%	0.12%	0.06%	0.08%	0.07%	0.28%							
Otu038	Sediminibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%							
Otu039	Methylobacterium	0.16%	0.00%	0.04%	0.04%	0.13%	0.00%	0.01%	0.04%	0.11%							
Otu040	Unclassified Nitrosomonadaceae	0.00%	0.00%	0.01%	0.01%	0.01%	0.02%	0.00%	0.02%	0.00%							
Otu041	Bdellovibrio	0.06%	0.02%	0.03%	0.03%	0.07%	0.04%	0.02%	0.08%	0.00%							
Otu042	Unclassified Betaproteobacteria	0.44%	0.20%	0.21%	0.15%	0.24%	0.14%	0.08%	0.08%	0.58%							
Otu043	Herrnimonas	1.63%	1.91%	1.81%	1.25%	1.77%	1.48%	2.69%	2.30%	1.08%							
Otu044	Unclassified Proteobacteria	1.03%	0.73%	1.61%	0.93%	0.89%	1.27%	1.72%	1.65%	1.11%							
Otu045	Aminobacter	0.40%	0.28%	0.17%	0.11%	0.28%	0.24%	0.20%	0.11%	0.00%							
Otu046	Unclassified Bacteria	0.19%	0.69%	0.72%	0.52%	1.02%	1.31%	0.92%	0.66%	1.14%							
Otu047	Caulobacter	0.00%	0.00%	0.00%	0.00%	0.18%	0.00%	0.01%	0.00%	0.03%							
Otu048	Unclassified Bacteria	0.44%	0.12%	0.52%	0.26%	0.57%	0.09%	0.42%	0.17%	0.26%							
Otu049	Unclassified Bacteria	0.80%	0.64%	1.01%	0.43%	1.04%	0.56%	0.86%	0.82%	1.00%							
Otu050	Sphingomonas	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.04%	0.01%	0.00%							
Otu051	Unclassified Betaproteobacteria	0.48%	0.33%	0.47%	0.28%	0.26%	0.40%	0.28%	0.33%	0.42%							
Otu052	Unclassified Microbacteriaceae	0.29%	0.01%	0.09%	0.09%	0.16%	0.12%	0.04%	0.09%	0.17%							
Otu053	Pseudomonas	0.14%	0.05%	0.10%	0.38%	0.52%	0.04%	0.37%	0.02%	0.28%							
Otu054	Desulfobrio	0.27%	0.19%	0.08%	0.13%	0.00%	0.12%	0.09%	0.09%	0.12%							
Otu055	Unclassified Bacteria	0.25%	0.13%	0.34%	0.07%	0.19%	0.06%	0.13%	0.11%	0.27%							
Otu056	Unclassified Deltaproteobacteria	0.01%	0.00%	0.02%	0.03%	0.00%	0.04%	0.06%	0.04%	0.01%							
Otu057	Phenylobacterium	0.09%	0.01%	0.01%	0.01%	0.00%	0.01%	0.04%	0.20%	0.12%							
Otu058	Unclassified Comamonadaceae	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.02%	0.01%							
Otu059	Unclassified Chitinophagaceae	0.14%	0.18%	0.15%	0.09%	0.08%	0.15%	0.20%	0.15%	0.20%							
Otu060	Novosphingobium	0.08%	0.00%	0.02%	0.00%	0.02%	0.00%	0.07%	0.07%	0.00%							
Otu061	Unclassified Proteobacteria	0.05%	0.01%	0.14%	0.03%	0.06%	0.06%	0.04%	0.02%	0.11%							
Otu062	Bdellovibrio	1.63%	0.98%	2.18%	1.05%	2.16%	2.00%	2.68%	2.68%	1.55%							
Otu063	Bdellovibrio	0.79%	0.83%	1.08%	0.89%	0.86%	1.24%	1.01%	1.19%	0.81%							
Otu064	Hyphomicrobium	0.29%	0.22%	0.57%	0.36%	0.33%	0.30%	0.29%	0.33%	0.44%							
Otu065	Bdellovibrio	0.41%	0.08%	0.28%	0.12%	0.03%	0.17%	0.28%	0.24%	0.12%							
Otu066	Unclassified Rhizobiales	1.36%	0.42%	0.48%	0.84%	0.44%	0.35%	0.30%	0.92%								
Otu067	Unclassified Betaproteobacteria	0.00%	0.05%	0.13%	0.04%	0.02%	0.03%	0.09%	0.14%	0.16%							
Otu068	Acinetobacter	0.00%	0.00%	0.01%	0.02%	0.13%	0.02%	0.00%	0.00%	0.07%							
Otu069	Planctomyces	1.16%	0.96%	1.03%	0.83%	0.51%	0.71%	0.59%	0.68%	0.45%							
Otu070	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%							
Otu071	Unclassified Alphaproteobacteria	0.49%	0.33%	0.64%	0.30%	0.15%	0.47%	0.48%	0.27%	0.51%							
Otu072	Gemmatimonas	0.13%	0.01%	0.06%	0.05%	0.07%	0.03%	0.00%	0.04%	0.07%							
Otu073	Methylophilus	0.14%	0.16%	0.44%	0.20%	0.21%	0.84%	0.69%	0.61%	0.31%							
Otu074	Bacteriovorax	0.04%	0.18%	0.16%	0.12%	0.03%	2.62%	1.61%	1.30%	0.00%							
Otu075	Unclassified Proteobacteria	0.52%	0.23%	0.14%	0.31%	0.45%	0.32%	0.27%	0.21%	0.94%							
Otu076	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%							
Otu077	Limosbacter	1.97%	0.87%	0.72%	0.66%	0.98%	0.74%	0.86%	0.78%	2.03%							
Otu078	Unclassified Alphaproteobacteria	0.54%	0.11%	0.17%	0.11%	0.08%	0.13%	0.20%	0.13%	0.31%							
Otu079	Unclassified Bacteria	0.00%	0.03%	0.04%	0.02%	0.00%	0.03%	0.00%	0.01%	0.01%							
Otu080	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.17%	0.00%	0.00%	0.12%	0.00%	0.00%							
Otu081	Unclassified Bacteria	0.74%	0.48%	0.11%	0.67%	0.37%	0.47%	1.06%	0.76%	0.23%							
Otu082	Unclassified Bacteria	0.14%	0.05%	0.17%	0.16%	0.13%	0.02%	0.01%	0.04%	0.03%							



OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu0167	Unclassified Alphaproteobacteria	0.20%	0.11%	0.15%	0.21%	0.03%	0.14%	0.13%	0.09%	0.07%	
Otu0168	Unclassified Planctomycetaceae	0.07%	0.05%	0.14%	0.02%	0.26%	0.09%	0.04%	0.06%	0.09%	
Otu0169	Unclassified Sphingomonadaceae	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	0.01%	0.04%	
Otu0170	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0171	Unclassified Bacteria	0.22%	0.03%	0.08%	0.01%	0.01%	0.04%	0.04%	0.03%	0.04%	
Otu0172	Unclassified Bacteria	0.06%	0.05%	0.01%	0.07%	0.00%	0.09%	0.00%	0.05%	0.01%	
Otu0173	Methylomonas	0.13%	0.12%	0.22%	0.03%	0.01%	0.10%	0.12%	0.16%	0.07%	
Otu0174	Unclassified Rhodospirillales	0.05%	0.02%	0.02%	0.00%	0.06%	0.00%	0.07%	0.03%	0.03%	
Otu0175	Unclassified Bacteria	0.37%	0.11%	0.10%	0.14%	0.13%	0.12%	0.31%	0.24%	0.19%	
Otu0176	Microbacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0177	Unclassified Syntrophaceae	0.02%	0.05%	0.02%	0.04%	0.00%	0.03%	0.00%	0.01%	0.02%	
Otu0178	Unclassified Proteobacteria	0.01%	0.00%	0.06%	0.00%	0.00%	0.03%	0.01%	0.03%	0.03%	
Otu0179	Geothrix	0.00%	0.13%	0.02%	0.01%	0.00%	0.06%	0.01%	0.07%	0.13%	
Otu0180	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0181	Unclassified Bacteria	0.08%	0.27%	0.01%	0.34%	0.01%	0.01%	0.12%	0.03%	0.00%	
Otu0182	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	
Otu0183	Unclassified Gammaproteobacteria	0.16%	0.01%	0.02%	0.06%	0.15%	0.04%	0.17%	0.05%	0.07%	
Otu0184	Unclassified Caulobacteraceae	0.01%	0.11%	0.09%	0.03%	0.00%	0.09%	0.08%	0.07%	0.12%	
Otu0185	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0186	Unclassified Proteobacteria	0.13%	0.11%	0.02%	0.05%	0.12%	0.10%	0.19%	0.14%	0.00%	
Otu0187	Bdellovibrio	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0188	Unclassified Xanthomonadaceae	0.08%	0.09%	0.06%	0.08%	0.28%	0.08%	0.08%	0.04%	0.17%	
Otu0189	Unclassified Planctomycetaceae	0.10%	0.04%	0.07%	0.02%	0.04%	0.12%	0.04%	0.06%	0.03%	
Otu0190	Unclassified Sphingobacteriales	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.03%	0.02%	
Otu0191	Methylbacterium	0.18%	0.26%	0.19%	0.19%	0.21%	0.14%	0.16%	0.06%	0.29%	
Otu0192	Unclassified Comamonadaceae	0.09%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	
Otu0193	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0194	Gemmatimonas	0.05%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	
Otu0195	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.02%	0.00%	0.01%	0.03%	
Otu0196	Unclassified Proteobacteria	0.07%	0.00%	0.06%	0.00%	0.01%	0.00%	0.01%	0.02%	0.00%	
Otu0197	Gp6	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.05%	0.02%	0.00%	
Otu0198	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0199	Desulfosporosinus	0.00%	0.01%	0.06%	0.01%	0.00%	0.03%	0.02%	0.00%	0.00%	
Otu0200	Bdellovibrio	0.11%	0.00%	0.11%	0.03%	0.01%	0.00%	0.01%	0.05%	0.09%	
Otu0201	Gp4	0.00%	0.02%	0.16%	0.08%	0.00%	0.02%	0.08%	0.10%	0.04%	
Otu0202	Pseudomonas	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	
Otu0203	Stenotrophomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0204	Unclassified Alphaproteobacteria	0.03%	0.04%	0.00%	0.00%	0.00%	0.01%	0.04%	0.00%	0.00%	
Otu0205	Burkholderia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0206	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.01%	0.11%	0.02%	0.04%	0.00%	0.00%	
Otu0207	Unclassified Planctomycetaceae	0.14%	0.03%	0.01%	0.00%	0.00%	0.02%	0.02%	0.04%	0.02%	
Otu0208	Unclassified Betaproteobacteria	0.09%	0.24%	0.19%	0.11%	0.19%	0.18%	0.16%	0.11%	0.26%	
Otu0209	Gp3	0.36%	0.14%	0.27%	0.11%	0.12%	0.16%	0.14%	0.16%	0.19%	
Otu0210	Unclassified Rhodospirillales	0.01%	0.01%	0.03%	0.01%	0.02%	0.02%	0.00%	0.01%	0.00%	
Otu0211	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.01%	0.02%	0.01%	
Otu0212	Magnetospirillum	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	
Otu0213	Alkermansia	0.01%	0.00%	0.02%	0.01%	0.01%	0.00%	0.28%	0.00%	0.01%	
Otu0214	Prostheobacter	0.04%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.09%	
Otu0215	Roseburia	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.13%	0.00%	0.00%	
Otu0216	Unclassified Gammaproteobacteria	0.02%	0.08%	0.06%	0.01%	0.06%	0.05%	0.06%	0.09%	0.04%	
Otu0217	Unclassified Bacteria	0.13%	0.03%	0.01%	0.02%	0.11%	0.01%	0.07%	0.05%	0.00%	
Otu0218	Bacteroides	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.17%	0.00%	0.00%	
Otu0219	Bdellovibrio	0.19%	0.03%	0.13%	0.00%	0.09%	0.03%	0.00%	0.04%	0.07%	
Otu0220	Lewisella	0.05%	0.06%	0.31%	0.13%	0.30%	0.02%	0.15%	0.12%	0.07%	
Otu0221	Unclassified Bacteria	0.00%	0.01%	0.04%	0.00%	0.01%	0.03%	0.00%	0.03%	0.00%	
Otu0222	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0223	Unclassified Betaproteobacteria	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.04%	0.00%	0.00%	
Otu0224	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0225	Unclassified Gammaproteobacteria	0.00%	0.01%	0.04%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	
Otu0226	Unclassified Proteobacteria	0.18%	0.02%	0.08%	0.00%	0.00%	0.02%	0.03%	0.01%	0.00%	
Otu0227	Unclassified Gammaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.02%	
Otu0228	Unclassified Rhizobiales	0.06%	0.00%	0.04%	0.04%	0.07%	0.00%	0.02%	0.00%	0.06%	
Otu0229	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	
Otu0230	Unclassified Alphaproteobacteria	0.04%	0.03%	0.06%	0.01%	0.12%	0.05%	0.06%	0.04%	0.06%	
Otu0231	Unclassified Parachlamydiaceae	0.03%	0.01%	0.02%	0.01%	0.02%	0.02%	0.01%	0.00%	0.02%	
Otu0232	Shinella	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.01%	
Otu0233	Bdellovibrio	0.00%	0.02%	0.15%	0.05%	0.00%	0.00%	0.04%	0.00%	0.06%	
Otu0234	Bdellovibrio	0.23%	0.05%	0.15%	0.11%	0.10%	0.08%	0.07%	0.10%	0.38%	
Otu0235	Bdellovibrio	0.00%	0.02%	0.15%	0.00%	0.00%	0.01%	0.06%	0.01%	0.00%	
Otu0236	Unclassified Proteobacteria	0.05%	0.04%	0.08%	0.05%	0.07%	0.06%	0.04%	0.04%	0.05%	
Otu0237	Unclassified Planctomycetaceae	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0238	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0239	Unclassified Bacteroidetes	0.35%	0.13%	0.29%	0.08%	0.13%	0.04%	0.15%	0.10%	0.18%	
Otu0240	Planctomyces	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.08%	0.02%	
Otu0241	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0242	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0243	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.02%	0.10%	0.01%	
Otu0244	Gp4	0.08%	0.04%	0.17%	0.07%	0.00%	0.01%	0.08%	0.13%	0.02%	
Otu0245	Unclassified Deltaproteobacteria	0.00%	0.04%	0.04%	0.01%	0.00%	0.04%	0.02%	0.07%	0.00%	
Otu0246	Unclassified Bacteria	0.23%	0.11%	0.19%	0.00%	0.06%	0.03%	0.04%	0.04%	0.14%	
Otu0247	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0248	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0249	Unclassified Cryomorphaceae	0.00%	0.00%	0.04%	0.03%	0.00%	0.03%	0.04%	0.01%	0.00%	
Otu0250	Unclassified Bacteria	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.01%	0.04%	0.00%	





OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu0419	Unclassified Bacteria	0.02%	0.01%	0.00%	0.00%	0.04%	0.02%	0.04%	0.00%	0.00%	
Otu0420	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0421	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.01%	0.00%	
Otu0422	Hydrogenophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0423	Unclassified Rhizobiales	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0424	Thiomonas	0.03%	0.00%	0.04%	0.01%	0.00%	0.00%	0.02%	0.01%	0.00%	
Otu0425	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0426	Unclassified Gammaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0427	Unclassified Planctomycetaceae	0.04%	0.01%	0.02%	0.00%	0.00%	0.01%	0.01%	0.01%	0.01%	
Otu0428	Bdellovibrio	0.10%	0.00%	0.15%	0.05%	0.04%	0.03%	0.03%	0.05%	0.07%	
Otu0429	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0430	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0431	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0432	OD1_genus_incertae_sedis	0.01%	0.01%	0.04%	0.01%	0.01%	0.00%	0.00%	0.00%	0.02%	
Otu0433	Mycobacterium	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0434	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0435	Unclassified Gammaproteobacteria	0.14%	0.11%	0.03%	0.01%	0.22%	0.05%	0.03%	0.02%	0.13%	
Otu0436	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0437	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0438	Unclassified Gammaproteobacteria	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.06%	0.00%	0.01%	
Otu0439	Unclassified Myxococcales	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	
Otu0440	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	
Otu0441	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0442	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0443	Baukia	0.00%	0.00%	0.01%	0.00%	0.08%	0.01%	0.00%	0.01%	0.00%	
Otu0444	Unclassified Bacteria	0.00%	0.04%	0.04%	0.00%	0.00%	0.01%	0.01%	0.04%	0.02%	
Otu0445	Neisseria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0446	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0447	Pedomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0448	Unclassified Bacteroidetes	0.00%	0.00%	0.02%	0.04%	0.00%	0.01%	0.04%	0.00%	0.05%	
Otu0449	Unclassified Deltaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0450	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	
Otu0451	Acinetobacter	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0452	Unclassified Acetobacteraceae	0.02%	0.00%	0.05%	0.00%	0.07%	0.01%	0.01%	0.01%	0.02%	
Otu0453	Unclassified Bacteria	0.10%	0.03%	0.08%	0.07%	0.08%	0.04%	0.10%	0.10%	0.03%	
Otu0454	Flavicola	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.01%	0.02%	
Otu0455	Unclassified Gammaproteobacteria	0.00%	0.01%	0.00%	0.05%	0.07%	0.03%	0.02%	0.02%	0.01%	
Otu0456	Unclassified Phyllobacteriaceae	0.10%	0.00%	0.01%	0.03%	0.00%	0.00%	0.02%	0.00%	0.03%	
Otu0457	Vellbonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0458	Bdellovibrio	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0459	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0460	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0461	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0462	Unclassified Sphingobacteriales	0.06%	0.04%	0.07%	0.03%	0.00%	0.00%	0.13%	0.03%	0.02%	
Otu0463	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0464	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.03%	0.00%	
Otu0465	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0466	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0467	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0468	Unclassified Bacteria	0.02%	0.01%	0.03%	0.00%	0.00%	0.01%	0.00%	0.05%	0.00%	
Otu0469	OD1_genus_incertae_sedis	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0470	Unclassified Bacteria	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0471	Unclassified Gammaproteobacteria	0.00%	0.01%	0.01%	0.08%	0.00%	0.02%	0.07%	0.03%	0.01%	
Otu0472	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0473	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0474	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0475	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0476	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0477	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0478	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0479	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0480	Unclassified Betaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0481	Unclassified Bacteroidetes	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	
Otu0482	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0483	Peptostreptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0484	Gp3	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0485	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0486	Leptolinea	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0487	Unclassified Bacteria	0.22%	0.04%	0.08%	0.05%	0.00%	0.00%	0.08%	0.13%	0.11%	
Otu0488	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0489	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	
Otu0490	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0491	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0492	Unclassified Parachlamydiaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0493	Unclassified Bacteria	0.00%	0.01%	0.02%	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0494	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0495	Unclassified Bacteria	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0496	Unclassified Brucellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0497	Unclassified Proteobacteria	0.00%	0.01%	0.04%	0.00%	0.01%	0.00%	0.04%	0.01%	0.00%	
Otu0498	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0499	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0500	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0501	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0502	Gemmatimonas	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	



OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu0503	Unclassified Gammaproteobacteria	0.00%	0.05%	0.03%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0504	Unclassified Bacteria	0.00%	0.01%	0.00%	0.07%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0505	Bdellovibrio	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0506	Pasturia	0.00%	0.00%	0.00%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0507	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu0508	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0509	Unclassified Betaproteobacteria	0.00%	0.01%	0.09%	0.00%	0.07%	0.01%	0.00%	0.03%	0.01%	0.00%
Otu0510	Aureispira	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0511	Unclassified Rhizobiales	0.00%	0.01%	0.01%	0.00%	0.07%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0512	Unclassified Anaerolineaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0513	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0514	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0515	Spartobacteria_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0516	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0517	Gp16	0.03%	0.00%	0.04%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0518	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.10%	0.01%	0.01%	0.01%	0.06%	0.00%
Otu0519	Streptococcus	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Otu0520	Lactococcus	0.07%	0.00%	0.01%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%
Otu0521	Unclassified Myxococcales	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0522	Unclassified Planctomycetaceae	0.00%	0.01%	0.01%	0.00%	0.01%	0.02%	0.02%	0.01%	0.08%	0.00%
Otu0523	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0524	Unclassified Bacteria	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0525	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0526	Lactobacillus	0.02%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0527	Unclassified Bacteria	0.01%	0.00%	0.01%	0.03%	0.00%	0.03%	0.01%	0.01%	0.00%	0.00%
Otu0528	Unclassified Proteobacteria	0.08%	0.00%	0.00%	0.00%	0.00%	0.02%	0.04%	0.02%	0.00%	0.00%
Otu0529	Gp6	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0530	Unclassified Enterobacteriaceae	0.20%	0.00%	0.01%	0.13%	0.06%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0531	OD1_genus_incertae_sedis	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.01%	0.02%	0.00%
Otu0532	Chondromyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0533	Unclassified Bacteroidetes	0.07%	0.04%	0.01%	0.00%	0.00%	0.01%	0.03%	0.02%	0.00%	0.00%
Otu0534	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0535	Unclassified Nitrosomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0536	Ignavibacterium	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%
Otu0537	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0538	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0539	Unclassified Proteobacteria	0.00%	0.02%	0.07%	0.01%	0.08%	0.02%	0.00%	0.07%	0.00%	0.00%
Otu0540	Bryobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0541	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0542	OD1_genus_incertae_sedis	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0543	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0544	Unclassified Bacteria	0.04%	0.04%	0.02%	0.00%	0.00%	0.04%	0.04%	0.04%	0.01%	0.00%
Otu0545	Unclassified Rhizobiales	0.14%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.04%	0.00%
Otu0546	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%
Otu0547	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.02%	0.01%	0.01%	0.00%	0.03%	0.02%	0.00%
Otu0548	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0549	Unclassified Parachlamydiaceae	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0550	Ferruginibacter	0.08%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0551	Peredibacter	0.00%	0.02%	0.09%	0.05%	0.00%	0.01%	0.03%	0.05%	0.03%	0.00%
Otu0552	Unclassified Bacteria	0.00%	0.02%	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%
Otu0553	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0554	TM7_genus_incertae_sedis	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0555	Bacteriovorax	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0556	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0557	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0558	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0559	Unclassified Proteobacteria	0.00%	0.00%	0.05%	0.05%	0.00%	0.02%	0.04%	0.03%	0.00%	0.00%
Otu0560	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0561	Bdellovibrio	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0562	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.03%	0.00%	0.00%
Otu0563	Parachlamydia	0.06%	0.00%	0.02%	0.05%	0.07%	0.01%	0.02%	0.03%	0.03%	0.00%
Otu0564	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.07%	0.00%	0.00%
Otu0565	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0566	Unclassified Bacteroidetes	0.02%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.02%	0.03%	0.00%
Otu0567	Unclassified Rhodospirillaceae	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.03%	0.01%	0.02%	0.00%
Otu0568	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0569	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0570	Ophitulus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0571	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0572	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0573	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%
Otu0574	Unclassified Acidobacteria_Gp3	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0575	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
Otu0576	Unclassified Betaproteobacteria	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0577	Unclassified Bacteria	0.00%	0.01%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0578	Thiomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0579	Unclassified Bacteria	0.01%	0.00%	0.01%	0.05%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%
Otu0580	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0581	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Otu0582	Unclassified Betaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0583	Unclassified Gammaproteobacteria	0.00%	0.04%	0.01%	0.00%	0.00%	0.03%	0.08%	0.02%	0.02%	0.00%
Otu0584	Pedobacter	0.02%	0.00%	0.01%	0.00%	0.12%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0585	Ignavibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0586	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%

OTU number	Taxonomy	Sample code												
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3				
Otu0587	Unclassified Dehaloproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0588	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0589	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0590	Unclassified Bacteroidetes	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0591	Unclassified Rhodospirillales	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0592	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0593	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%
Otu0594	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0595	Neochlamydia	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0596	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0597	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0598	Aquaseta	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0599	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0600	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0601	Unclassified Proteobacteria	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0602	Ferribacterium	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0603	Unclassified Burkholderiales	0.00%	0.01%	0.02%	0.00%	0.07%	0.00%	0.04%	0.00%	0.04%	0.00%	0.03%	0.00%	0.00%
Otu0604	Unclassified Betaproteobacteria	0.00%	0.03%	0.02%	0.06%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.02%	0.00%
Otu0605	Unclassified Rhodospirillales	0.03%	0.02%	0.02%	0.05%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%
Otu0606	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0607	Unclassified Alphaproteobacteria	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0608	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0609	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0610	Conexibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0611	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0612	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0613	Unclassified Bacillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0614	Clostridium_III	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0615	Hydrogenisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0616	Hermisimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0617	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0618	Unclassified Gammaproteobacteria	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu0619	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0620	Bifidobacterium	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0621	Bdellovibrio	0.09%	0.04%	0.15%	0.00%	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.04%	0.00%
Otu0622	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0623	Unclassified Intrasporangiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0624	Aurantimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0625	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0626	Unclassified Bacteria	0.00%	0.00%	0.01%	0.01%	0.02%	0.01%	0.00%	0.02%	0.01%	0.00%	0.02%	0.01%	0.00%
Otu0627	Unclassified Clostridia	0.00%	0.00%	0.01%	0.06%	0.00%	0.01%	0.01%	0.01%	0.01%	0.02%	0.00%	0.00%	0.00%
Otu0628	OD1_genus_incertae_sedis	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.03%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0629	Unclassified Rhodocyclaceae	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0630	Unclassified Alphaproteobacteria	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0631	Unclassified Bacteria	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0632	Unclassified Bacteria	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0633	Bdellovibrio	0.00%	0.07%	0.08%	0.00%	0.15%	0.00%	0.00%	0.00%	0.01%	0.07%	0.00%	0.00%	0.00%
Otu0634	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0635	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0636	Unclassified Bacteria	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0637	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0638	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0639	Geobacillus	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0640	Unclassified Bacteria	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0641	Unclassified Bacteria	0.00%	0.01%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0642	Rheinheimera	0.00%	0.00%	0.06%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0643	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0644	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0645	Unclassified Bacteria	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0646	Ilumatobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu0647	Enterococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0648	Bdellovibrio	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0649	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0650	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0651	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0652	Pedobacter	0.00%	0.00%	0.00%	0.04%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0653	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0654	Unclassified Hyphomicrobiaceae	0.01%	0.00%	0.00%	0.00%	0.06%	0.00%	0.04%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0655	Unclassified Bacteria	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0656	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0657	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0658	Rhizobium	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0659	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.02%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0660	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0661	Unclassified Bacterioviraceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0662	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0663	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0664	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0665	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.03%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0666	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0667	Unclassified Proteobacteria	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0668	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0669	Ochrobactrum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0670	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code											
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3			
Otu0671	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0672	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0673	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0674	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0675	Moraxella	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0676	Unclassified Proteobacteria	0.02%	0.00%	0.04%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0677	Ilumatobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0678	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0679	Gp3	0.00%	0.00%	0.04%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0680	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0681	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0682	Unclassified Sphingobacteriales	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0683	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0684	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.01%	0.00%
Otu0685	Bdellovibrio	0.14%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0686	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0687	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.04%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0688	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0689	Dietzia	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.05%	0.00%	0.00%
Otu0690	Unclassified Bacteria	0.00%	0.03%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0691	Unclassified Sphingomonadales	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0692	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0693	Desulfobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0694	Unclassified Bacteria	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0695	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0696	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0697	Unclassified Gammaproteobacteria	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.07%	0.13%	0.01%	0.00%	0.00%	0.00%
Otu0698	OD1_genus_incertae_sedis	0.06%	0.01%	0.01%	0.00%	0.03%	0.02%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
Otu0699	Bdellovibrio	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0700	Unclassified Alphaproteobacteria	0.00%	0.01%	0.00%	0.01%	0.03%	0.01%	0.00%	0.00%	0.00%	0.01%	0.03%	0.00%
Otu0701	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0702	Unclassified Rhodocyclaceae	0.05%	0.01%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%	0.02%	0.00%
Otu0703	Pseudoxanthomonas	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%
Otu0704	Ilumatobacter	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0705	Gp3	0.00%	0.00%	0.06%	0.03%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0706	l_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0707	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0708	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0709	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0710	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0711	Unclassified Bacteria	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0712	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0713	Bdellovibrio	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0714	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0715	Unclassified Bacteria	0.00%	0.03%	0.08%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0716	Novosphingobium	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0717	Rothia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0718	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0719	OD1_genus_incertae_sedis	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0720	Unclassified Cryomorphaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0721	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0722	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0723	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0724	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0725	Unclassified Bacteroidetes	0.02%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%
Otu0726	Porphyromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0727	Unclassified Alphaproteobacteria	0.00%	0.02%	0.00%	0.00%	0.09%	0.02%	0.01%	0.01%	0.04%	0.00%	0.00%	0.00%
Otu0728	Gemmatimonas	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0729	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0730	Peredibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.04%	0.02%	0.00%	0.00%	0.00%
Otu0731	Bdellovibrio	0.00%	0.00%	0.05%	0.01%	0.00%	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%
Otu0732	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0733	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0734	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0735	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0736	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0737	Unclassified Sphingomonadaceae	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0738	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0739	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0740	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0741	Besza	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0742	Unclassified Parachlamydiaceae	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0743	Fusobacterium	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0744	Unclassified Bacteria	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Otu0745	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0746	Unclassified Bradyrhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0747	Unclassified Bacteroidetes	0.00%	0.01%	0.02%	0.05%	0.00%	0.03%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%
Otu0748	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0749	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0750	Unclassified Planococcaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0751	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0752	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0753	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0754	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code										
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3		
Otu0755	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0756	Unclassified Firmicutes	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0757	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0758	Unclassified Proteobacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0759	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0760	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0761	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0762	Desulfovibrio	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0763	Butyrivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0764	Trichococcus	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0765	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0766	Unclassified Bacteria	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0767	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0768	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0769	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0770	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0771	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0772	Unclassified Proteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0773	Bdellovibrio	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0774	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0775	Unclassified Burkholderiales	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.05%	0.00%
Otu0776	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0777	Polynucleobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0778	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu0779	Unclassified Bacteria	0.05%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0780	Barnesiella	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0781	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0782	Celhdrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0783	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0784	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0785	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0786	Phenylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0787	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0788	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0789	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0790	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0791	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0792	Actinomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0793	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0794	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%
Otu0795	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0796	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0797	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0798	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0799	Geebacter	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0800	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0801	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0802	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0803	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0804	Aerococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0805	Unclassified Alphaproteobacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0806	OD1_genus_incertae_sedis	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0807	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0808	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0809	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0810	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0811	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0812	Neochlamydia	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0813	Williamsia	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0814	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0815	Unclassified Opitutae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0816	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0817	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0818	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0819	Legionella	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Otu0820	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0821	Unclassified Bacteria	0.05%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%
Otu0822	Unclassified Deltaproteobacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0823	Unclassified Alphaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0824	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0825	Gp13	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0826	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0827	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0828	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.04%	0.00%	0.00%	0.00%
Otu0829	Unclassified Rhodospirillales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0830	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0831	Sneathia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0832	Unclassified Bacteroidetes	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0833	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0834	Unclassified Betaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0835	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%
Otu0836	Unclassified Ktedonobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0837	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0838	Unclassified Prevotellaceae	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code											
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3			
Otu0839	Unclassified Rhodocyclaceae	0.07%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0840	OD1_genus_incertae_sedis	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0841	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0842	Aquabacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0843	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0844	Methylobacter	0.11%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0845	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0846	Unclassified Veillonellaceae	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0847	Conexibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0848	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0849	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0850	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0851	Unclassified Bacteria	0.03%	0.11%	0.01%	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0852	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu0853	Unclassified Chloroflexi	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0854	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0855	Unclassified Pseudomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0856	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0857	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0858	Unclassified Porphyromonadaceae	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0859	Fusobacterium	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0860	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0861	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0862	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0863	Bosea	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0864	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0865	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0866	Singuliphæra	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0867	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0868	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0869	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0870	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0871	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0872	Arcobacter	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0873	Unclassified Gammaproteobacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0874	Unclassified Rhizobiales	0.00%	0.00%	0.02%	0.00%	0.04%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0875	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0876	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0877	Unclassified Bacteria	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0878	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu0879	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0880	Unclassified Cytophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0881	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0882	Unclassified Bacteria	0.05%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0883	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0884	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0885	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0886	Halomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0887	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0888	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0889	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0890	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0891	Unclassified Alcaligenaceae	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0892	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0893	Unclassified Spartobacteria_family_incerta	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0894	Unclassified Bacteria	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0895	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0896	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0897	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0898	Unclassified Bacteria	0.00%	0.02%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0899	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0900	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0901	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0902	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0903	Chryseobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0904	Unclassified Rhodospirillales	0.00%	0.01%	0.01%	0.03%	0.00%	0.03%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%
Otu0905	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0906	Anaerorhabdus	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0907	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0908	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0909	Arenimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0910	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0911	Unclassified Bradyrhizobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0912	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0913	Citricoccus	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0914	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0915	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0916	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0917	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0918	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0919	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0920	Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0921	Bacteriovorax	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0922	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu923	Unclassified Myxococcales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu924	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu925	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu926	Unclassified Micromonosporaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu927	Unclassified Fusobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu928	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu929	Gardnerella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu930	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu931	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu932	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu933	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu934	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu935	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu936	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu937	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu938	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu939	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu940	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu941	Unclassified Pasteurellales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu942	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.02%	0.01%	0.01%	0.03%	0.01%	0.02%	0.00%
Otu943	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu944	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu945	Unclassified Spartobacteria_family_incerta	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu946	OD1_genus_incertae_sedis	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu947	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu948	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu949	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu950	Unclassified Bacteria	0.00%	0.00%	0.01%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu951	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu952	Devesia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu953	Bejerinckia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu954	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu955	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu956	Desulfuromonas	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu957	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu958	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu959	Armatimonadetes_gp5	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu960	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu961	Methylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu962	Holophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu963	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu964	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu965	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu966	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu967	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu968	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.07%	0.00%	0.00%
Otu969	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu970	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu971	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu972	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu973	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu974	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu975	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu976	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu977	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu978	Unclassified Acetobacteraceae	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu979	Tolumonas	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu980	Unclassified Bacteroidetes	0.00%	0.04%	0.03%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu981	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu982	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu983	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu984	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu985	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu986	Curvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu987	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu988	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu989	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu990	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu991	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu992	Unclassified Bacteria	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu993	Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu994	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu995	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu996	Unclassified Rhizobiales	0.07%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu997	Exiguobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu998	Unclassified Rhizobiales_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu999	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1000	Peptoniphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1001	Nesterenkonia	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1002	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1003	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1004	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1005	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1006	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%

OTU number	Taxonomy	Sample code										
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3		
Otu1007	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1008	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1009	Sphingomonas	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1010	Mansuriyantis	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu1011	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1012	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%
Otu1013	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1014	Clostridium_XI	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.22%	0.00%	0.00%	0.00%
Otu1015	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1016	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu1017	_3_genus_incertae_sedis	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1018	Unclassified Bacteria	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1019	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1020	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1021	Unclassified Bacteria	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1022	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1023	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1024	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1025	Unclassified Gammaproteobacteria	0.00%	0.02%	0.04%	0.00%	0.00%	0.01%	0.04%	0.04%	0.00%	0.00%	0.00%
Otu1026	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.07%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1027	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1028	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1029	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1030	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1031	Planctomyces	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1032	Algoriphagus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1033	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1034	Unclassified Desulfobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1035	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1036	Turibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1037	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1038	Pseudonocardia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1039	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1040	Mycobacterium	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu1041	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1042	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1043	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1044	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1045	Labrys	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1046	Geothrix	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1047	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1048	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1049	Perucidibaca	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1050	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1051	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1052	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1053	Unclassified Bacteria	0.02%	0.01%	0.01%	0.04%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1054	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1055	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%
Otu1056	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1057	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1058	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1059	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1060	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1061	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1062	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1063	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1064	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu1065	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%
Otu1066	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1067	Unclassified Nitrospirobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1068	Unclassified Bacteria	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1069	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1070	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1071	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1072	Gp7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1073	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1074	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1075	Unclassified Bacteria	0.00%	0.00%	0.00%	0.04%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1076	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1077	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1078	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1079	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1080	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1081	Unclassified Verrucomicrobiaeae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1082	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1083	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%
Otu1084	Agamomas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1085	Cupriavidus	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%
Otu1086	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1087	Dyadobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1088	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1089	Cloacibacterium	0.00%	0.00%	0.00%	0.00%	1.86%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1090	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%











OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu1429	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1430	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1431	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1432	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1433	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1434	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1435	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1436	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1437	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1438	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1439	Acholeplasma	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1440	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1441	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1442	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1443	Parachlamydia	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1444	Elizabethkingia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1445	Unclassified Deltaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu1446	Fangia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1447	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1448	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1449	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1450	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1451	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1452	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1453	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1454	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1455	Unclassified Alteromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1456	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.11%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1457	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1458	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1459	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1460	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1461	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1462	Enhydrobacter	0.00%	0.00%	0.00%	0.00%	0.46%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1463	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1464	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1465	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1466	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1467	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1468	Ornithinimicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1469	Unclassified Bacteroidales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1470	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1471	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.12%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1472	Blastococcus	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1473	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1474	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1475	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1476	Barnesiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1477	Arcobacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1478	Dyadobacter	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1479	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1480	Bdelovirio	0.00%	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1481	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1482	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1483	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1484	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1485	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1486	Unclassified Flavobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1487	Unclassified unclassified	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1488	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1489	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1490	SR1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1491	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1492	Aeromonas	0.00%	0.05%	0.00%	0.05%	0.11%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1493	Bilophila	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1494	Opitulus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1495	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1496	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1497	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1498	Gjk	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1499	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%
Otu1500	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1501	Blastopirellula	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1502	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1503	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1504	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1505	Fusobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%
Otu1506	Singuliphæra	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1507	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1508	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1509	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1510	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1511	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu1512	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

















OTU number	Taxonomy	Sample code											
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3			
Otu2101	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2102	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2103	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2104	Unclassified Planctomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2105	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2106	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2107	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu2108	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2109	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu2110	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2111	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2112	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2113	Corneliobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2114	Armatimonas_Armatimonadetes_gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2115	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2116	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2117	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2118	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2119	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2120	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2121	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2122	Niastella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2123	Pedobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2124	Nitriiruptor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu2125	Gp18	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2126	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2127	Angustibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2128	Dphtus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2129	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2130	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu2131	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2132	Asticcacaulis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2133	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2134	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2135	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2136	Rhodomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2137	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2138	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2139	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2140	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2141	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2142	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2143	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2144	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2145	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2146	Solirubrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2147	Gp17	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2148	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2149	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2150	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2151	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2152	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2153	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2154	Byssovora	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2155	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2156	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu2157	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2158	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2159	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2160	Vampirovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2161	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2162	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2163	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2164	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2165	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2166	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2167	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2168	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2169	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2170	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2171	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2172	Bdelovibrio	0.00%	0.00%	0.09%	0.01%	0.10%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%	0.00%
Otu2173	OD1_genus_incertae_sedis	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu2174	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu2175	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2176	Chthonomonas_Armatimonadetes_gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2177	Pseudoflavonifractor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2178	Rhazomonrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2179	Legionella	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2180	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2181	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2182	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2183	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.07%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2184	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%





OTU number	Taxonomy	Sample code											
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3			
Otu2353	Unclassified Bacteria	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2354	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2355	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2356	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2357	Proteus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2358	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2359	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2360	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2361	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2362	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2363	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2364	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2365	Unclassified Planctomycetaceae	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2366	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2367	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2368	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2369	Unclassified Bacteroidetes	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2370	Flavobacterium	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2371	Aquabacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2372	Unclassified Bacteroidetes	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2373	Unclassified Hyphomicrobiae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2374	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2375	Cellulomonas	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2376	Caedibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2377	Unclassified Hyphomicrobiae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2378	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2379	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2380	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2381	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2382	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2383	Desulfomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2384	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2385	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2386	Novosphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2387	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2388	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2389	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2390	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2391	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2392	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2393	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2394	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2395	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2396	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2397	Caldilinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2398	Unclassified Alcaligenaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2399	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2400	Unclassified Acetobacteraceae	0.00%	0.02%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2401	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2402	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu2403	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2404	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2405	Unclassified Gracilbacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2406	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2407	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2408	Unclassified Proteobacteria	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2409	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2410	Caldilinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2411	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2412	Unclassified Bacteria	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2413	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2414	Opitutus	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2415	Unclassified Gammaproteobacteria	0.09%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2416	Nitrospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2417	Unclassified unclassified	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2418	Flavosolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2419	Unclassified unclassified	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2420	Unclassified Bacteria	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2421	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2422	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2423	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2424	Unclassified Veillonellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2425	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2426	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2427	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2428	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2429	Legionella	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2430	Unclassified Firmicutes	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2431	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2432	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2433	Unclassified Bacteroidetes	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2434	Veillonella	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2435	Unclassified Bacteria	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2436	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code									
		11inf2	11inf3	12inf1	12inf2	12inf3	15inf1	15inf2	15inf3	30inf3	
Otu2437	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu2438	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu2439	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Otu2440	Pasteuria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu2441	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2442	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2443	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2444	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2445	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2446	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2447	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2448	Unclassified Alphaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2449	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2450	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2451	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2452	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2453	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2454	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2455	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2456	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2457	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2458	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2459	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2460	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2461	Unclassified Thermomicrobia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2462	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2463	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2464	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2465	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2466	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2467	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2468	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2469	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2470	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2471	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2472	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2473	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2474	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2475	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2476	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2477	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2478	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2479	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2480	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2481	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2482	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2483	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2484	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2485	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2486	Unclassified Alphaproteobacteria	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2487	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2488	Methylocella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2489	Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2490	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2491	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2492	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2493	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2494	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2495	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2496	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2497	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2498	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2499	Catenulispora	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2500	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2501	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2502	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2503	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2504	Unclassified Bacteriivora	0.00%	0.00%	0.01%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2505	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2506	Rhizomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2507	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2508	Singuliphaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2509	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2510	Terrimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2511	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2512	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2513	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2514	Actinoallomurus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2515	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2516	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2517	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2518	Vogesella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu2519	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%
Otu2520	Unclassified Methylocystaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%





OTU number	Taxonomy	Sample code															
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3	
Otu0001	Sphingopyxis	21.44%	21.51%	21.45%	22.08%	20.59%	23.87%	21.71%	22.55%	22.53%	22.08%	25.68%	26.15%	22.48%	21.53%	20.84%	
Otu0002	Acidovorax	6.29%	6.55%	6.49%	6.00%	6.39%	6.50%	6.77%	6.64%	7.54%	7.36%	8.02%	8.53%	7.42%	7.31%	7.22%	
Otu0003	Mycobacterium	17.80%	17.54%	16.39%	15.43%	20.35%	17.69%	19.08%	19.93%	21.17%	21.17%	18.04%	18.67%	24.89%	24.07%	26.57%	
Otu0004	Hydrogenophaga	1.60%	1.29%	1.30%	1.37%	1.25%	1.22%	1.42%	1.38%	1.24%	0.63%	1.24%	1.32%	1.42%	1.21%	1.30%	
Otu0005	Aquabacterium	8.11%	8.61%	9.22%	9.44%	5.49%	5.59%	5.86%	5.53%	3.00%	3.29%	3.52%	3.77%	3.01%	2.88%	2.71%	
Otu0006	Sphingomonas	4.97%	4.32%	4.24%	3.77%	3.76%	4.21%	4.69%	3.81%	8.91%	10.70%	8.33%	8.25%	8.72%	9.31%	8.30%	
Otu0007	Unclassified Proteobacteria	0.01%	0.07%	0.08%	0.01%	0.04%	0.07%	0.04%	0.04%	0.11%	0.05%	0.14%	0.19%	0.10%	0.09%	0.15%	
Otu0008	Unclassified Bradyrhizobiales	0.81%	1.08%	1.17%	1.19%	1.62%	1.97%	1.68%	1.63%	2.28%	1.89%	1.92%	2.00%	1.41%	1.63%	1.37%	
Otu0009	Unclassified Bacteria	4.54%	4.24%	3.86%	3.88%	3.26%	3.72%	3.46%	3.55%	4.28%	4.17%	4.03%	3.88%	3.62%	3.40%	3.71%	
Otu0010	Unclassified Betaproteobacteria	0.48%	0.54%	0.63%	0.50%	0.43%	0.54%	0.61%	0.69%	0.45%	0.43%	0.69%	0.60%	0.51%	0.66%	0.53%	
Otu0011	Bosea	1.20%	1.34%	0.99%	1.10%	1.84%	1.92%	1.77%	1.40%	1.04%	0.77%	1.11%	1.29%	1.08%	1.15%	0.92%	
Otu0012	Unclassified Bacteroidetes	1.99%	1.51%	1.33%	1.81%	2.06%	1.62%	1.85%	1.80%	3.08%	1.89%	2.99%	2.65%	2.36%	3.08%	2.90%	
Otu0013	Unclassified Rhodobacteraceae	0.41%	0.21%	0.30%	0.11%	0.20%	0.22%	0.29%	0.25%	0.51%	0.43%	0.48%	0.48%	0.36%	0.39%	0.49%	
Otu0014	Unclassified Sphingomonadaceae	5.64%	6.09%	6.54%	6.59%	5.65%	5.59%	5.73%	5.27%	1.15%	1.45%	1.37%	1.10%	1.24%	1.23%	0.97%	
Otu0015	Unclassified Betaproteobacteria	0.03%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.00%	0.03%	0.01%	0.02%	0.01%	0.01%	
Otu0016	Unclassified Burkholderiales	0.34%	0.28%	0.25%	0.40%	0.20%	0.38%	0.31%	0.22%	0.12%	0.16%	0.18%	0.18%	0.19%	0.17%	0.21%	
Otu0017	Unclassified Rhizobiales	0.66%	0.62%	0.60%	0.73%	1.34%	1.11%	1.13%	1.10%	1.73%	1.72%	1.26%	1.25%	0.82%	0.64%	0.65%	
Otu0018	Unclassified Comamonadaceae	0.08%	0.09%	0.04%	0.06%	0.13%	0.09%	0.15%	0.01%	0.12%	0.05%	0.01%	0.11%	0.20%	0.10%	0.10%	
Otu0019	Unclassified Bacteroidetes	2.65%	2.16%	2.61%	1.96%	2.78%	2.08%	2.36%	2.32%	2.98%	2.31%	2.49%	2.38%	2.96%	3.13%	2.48%	
Otu0020	Nitrospira	0.15%	0.36%	0.38%	0.56%	0.37%	0.33%	0.29%	0.29%	0.24%	0.18%	0.28%	0.20%	0.19%	0.21%	0.12%	
Otu0021	Unclassified Betaproteobacteria	0.37%	0.70%	0.88%	0.77%	0.52%	0.73%	0.69%	0.62%	0.55%	0.78%	0.51%	0.84%	0.46%	0.57%	0.43%	
Otu0022	Unclassified Betaproteobacteria	0.10%	0.11%	0.11%	0.08%	0.11%	0.10%	0.10%	0.08%	0.10%	0.08%	0.14%	0.08%	0.14%	0.09%	0.11%	
Otu0023	Unclassified Bacteria	0.00%	0.03%	0.10%	0.07%	0.06%	0.09%	0.08%	0.07%	0.12%	0.00%	0.00%	0.05%	0.08%	0.04%	0.09%	
Otu0024	Pseudomonas	1.57%	1.46%	1.80%	1.43%	1.55%	1.27%	1.48%	1.22%	0.12%	0.79%	0.30%	0.34%	0.55%	0.40%	0.31%	
Otu0025	Sediminibacterium	0.09%	0.16%	0.16%	0.23%	0.11%	0.05%	0.17%	0.18%	0.33%	0.50%	0.39%	0.28%	0.26%	0.20%	0.19%	
Otu0026	Unclassified Betaproteobacteria	0.03%	0.12%	0.11%	0.12%	0.15%	0.08%	0.17%	0.15%	0.08%	0.08%	0.16%	0.14%	0.10%	0.13%	0.14%	
Otu0027	Unclassified Rhodocyclaceae	0.16%	0.26%	0.28%	0.14%	0.30%	0.31%	0.27%	0.30%	0.14%	0.29%	0.22%	0.16%	0.17%	0.23%	0.19%	
Otu0028	Chryseobacterium	4.88%	4.26%	4.38%	4.86%	3.71%	4.07%	4.53%	4.51%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0029	Unclassified Hyphomicrobiales	0.34%	0.08%	0.18%	0.11%	0.13%	0.13%	0.10%	0.13%	0.16%	0.27%	0.11%	0.11%	0.19%	0.15%	0.12%	
Otu0030	Brevundimonas	0.66%	0.80%	0.80%	0.85%	0.81%	0.57%	0.56%	0.55%	0.53%	0.37%	0.48%	0.65%	0.56%	0.49%	0.63%	
Otu0031	Methylbacterium	0.03%	0.07%	0.12%	0.07%	0.02%	0.07%	0.04%	0.03%	0.66%	0.97%	0.54%	0.64%	0.87%	1.19%	1.37%	
Otu0032	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.04%	0.05%	0.04%	0.00%	0.02%	0.00%	0.04%	0.01%	0.03%	0.02%	0.01%	
Otu0033	Porphyrobacter	0.17%	0.08%	0.11%	0.08%	0.07%	0.07%	0.08%	0.08%	0.12%	0.48%	0.27%	0.31%	0.24%	0.29%	0.36%	
Otu0034	Sphingopyxis	0.04%	0.11%	0.09%	0.08%	0.05%	0.07%	0.00%	0.01%	1.10%	1.44%	1.54%	1.39%	0.35%	0.24%	0.20%	
Otu0035	Methylbacterium	0.38%	0.45%	0.40%	0.33%	0.68%	0.61%	0.62%	0.71%	0.66%	0.58%	0.43%	0.58%	0.90%	0.86%	0.97%	
Otu0036	Rabstonia	0.11%	0.06%	0.10%	0.02%	0.09%	0.04%	0.05%	0.06%	0.10%	0.02%	0.11%	0.10%	0.06%	0.04%	0.08%	
Otu0037	Unclassified Rhizobiales	0.01%	0.03%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.01%	
Otu0038	Sediminibacterium	0.07%	0.02%	0.05%	0.00%	0.10%	0.04%	0.03%	0.03%	0.36%	0.13%	0.30%	0.31%	0.09%	0.04%	0.10%	
Otu0039	Methylbacterium	0.01%	0.05%	0.04%	0.00%	0.05%	0.02%	0.05%	0.03%	0.55%	0.48%	0.48%	0.48%	0.91%	1.25%	1.52%	
Otu0040	Unclassified Nitrospomonadaceae	0.08%	0.04%	0.07%	0.12%	0.09%	0.03%	0.09%	0.07%	0.03%	0.01%	0.01%	0.06%	0.07%	0.03%	0.08%	
Otu0041	Bdellovibrio	0.00%	0.02%	0.03%	0.07%	0.03%	0.03%	0.02%	0.01%	0.03%	0.01%	0.01%	0.01%	0.01%	0.02%	0.02%	
Otu0042	Unclassified Betaproteobacteria	0.17%	0.16%	0.27%	0.22%	0.24%	0.14%	0.19%	0.17%	0.32%	0.49%	0.41%	0.33%	0.45%	0.54%	0.34%	
Otu0043	Hermimonas	0.02%	0.14%	0.14%	0.15%	0.01%	0.10%	0.17%	0.17%	0.13%	0.06%	0.13%	0.15%	0.11%	0.26%	0.23%	
Otu0044	Unclassified Proteobacteria	0.55%	0.38%	0.25%	0.27%	0.62%	0.36%	0.26%	0.34%	0.40%	0.22%	0.27%	0.30%	0.30%	0.32%	0.27%	
Otu0045	Aminobacter	0.59%	0.63%	0.31%	0.48%	0.56%	0.32%	0.46%	0.43%	0.20%	0.60%	0.36%	0.21%	0.21%	0.28%	0.22%	
Otu0046	Unclassified Bacteria	0.00%	0.03%	0.04%	0.00%	0.05%	0.03%	0.03%	0.05%	0.03%	0.29%	0.05%	0.03%	0.04%	0.03%	0.04%	
Otu0047	Caulobacter	0.30%	0.33%	0.32%	0.35%	0.27%	0.22%	0.24%	0.23%	0.85%	0.64%	0.68%	0.77%	0.55%	0.54%	0.60%	
Otu0048	Unclassified Bacteria	0.12%	0.14%	0.10%	0.12%	0.04%	0.12%	0.10%	0.09%	0.04%	0.15%	0.02%	0.04%	0.03%	0.06%	0.04%	
Otu0049	Unclassified Bacteria	0.21%	0.35%	0.33%	0.50%	0.38%	0.42%	0.39%	0.33%	0.29%	0.14%	0.15%	0.14%	0.17%	0.26%	0.19%	
Otu0050	Sphingomonas	0.27%	0.46%	0.44%	0.59%	0.52%	0.49%	0.37%	0.41%	0.65%	0.76%	0.71%	0.64%	0.44%	0.35%	0.43%	
Otu0051	Unclassified Betaproteobacteria	0.10%	0.04%	0.05%	0.11%	0.10%	0.11%	0.05%	0.07%	0.07%	0.05%	0.10%	0.06%	0.06%	0.07%	0.04%	
Otu0052	Unclassified Microbacteriaceae	0.03%	0.03%	0.04%	0.04%	0.04%	0.03%	0.04%	0.03%	0.02%	0.04%	0.10%	0.03%	0.07%	0.09%	0.04%	
Otu0053	Pseudomonas	0.04%	0.03%	0.01%	0.03%	0.01%	0.02%	0.01%	0.03%	0.03%	0.08%	0.05%	0.01%	0.03%	0.03%	0.05%	
Otu0054	Desulfobrio	0.09%	0.04%	0.04%	0.02%	0.03%	0.04%	0.02%	0.02%	0.02%	0.00%	0.02%	0.01%	0.00%	0.05%	0.01%	
Otu0055	Unclassified Bacteria	0.03%	0.03%	0.13%	0.18%	0.06%	0.14%	0.06%	0.09%	0.03%	0.00%	0.00%	0.07%	0.03%	0.04%	0.04%	
Otu0056	Unclassified Deltaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.02%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.00%	
Otu0057	Phenylobacterium	0.03%	0.07%	0.04%	0.01%	0.03%	0.05%	0.03%	0.02%	0.45%	0.62%	0.55%	0.42%	0.32%	0.28%	0.18%	
Otu0058	Unclassified Comamonadaceae	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	
Otu0059	Unclassified Chthonophagaceae	0.02%	0.23%	0.15%	0.12%	0.10%	0.19%	0.20%	0.13%	0.12%	0.05%	0.15%	0.08%	0.09%	0.12%	0.11%	
Otu0060	Novosphingobium	0.59%	0.75%	0.79%	0.82%	0.64%	0.65%	0.57%	0.62%	0.57%	0.49%	0.80%	0.60%	0.67%	0.73%	0.85%	
Otu0061	Unclassified Proteobacteria	0.21%	0.15%	0.11%	0.15%	0.29%	0.15%	0.20%	0.17%	0.25%	0.08%	0.24%	0.20%	0.37%	0.25%	0.30%	
Otu0062	Bdellovibrio	0.48%	0.49%	0.48%	0.58%	0.52%	0.79%	0.46%	0.57%	0.33%	0.29%	0.57%	0.45%	0.47%	0.41%	0.46%	
Otu0063	Bdellovibrio	0.45%	0.27%	0.32%	0.35%	0.74%	0.37%	0.33%	0.31%	0.27%	0.06%	0.18%	0.18%	0.20%	0.20%	0.33%	
Otu0064	Hyphomicrobium	0.20%	0.08%	0.05%	0.08%	0.02%	0.04%	0.04%	0.04%	0.06%	0.03%	0.09%	0.05%	0.06%	0.04%	0.07%	
Otu0065	Bdellovibrio	0.02%	0.04%	0.04%	0.05%	0.02%	0.03%	0.03%	0.02%	0.04%	0.19%	0.06%	0.07%	0.02%	0.05%	0.03%	
Otu0066	Unclassified Rhizobiales	0.04%	0.02%	0.07%	0.05%	0.05%	0.02%	0.03%	0.11%	0.03%	0.03%	0.01%	0.02%	0.05%	0.03%	0.08%	
Otu0067	Unclassified Betaproteobacteria	0.07%	0.01%	0.01%	0.01%	0.02%	0.00%	0.01%	0.04%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0068	Acetobacter	0.00%	0.00%	0.04%	0.00%	0.05%	0.00%	0.01%	0.01%	0.02%	0.11%	0.01%	0.02%	0.02%	0.04%	0.04%	
Otu0069	Planctomyces	0.61%	0.53%	0.57%	0.51%	0.43%	0.63%	0.38%	0.60%	0.43%	0.01%	0.24%	0.46%	0.37%	0.34%	0.42%	
Otu0070	Unclassified Comamonadaceae	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0071	Unclassified Alphaproteobacteria	0.08%	0.19%	0.14%	0.04%	0.09%	0.13%	0.07%	0.07%	0.08%	0.02%	0.05%	0.03%	0.05%	0.04%	0.04%	
Otu0072	Gemmatimonas	0.02%	0.00%	0.01%	0.03%	0.00%	0.02%	0.03%	0.01%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0073	Methylphilus	0.00%	0.04%	0.01%	0.02%	0.00%	0.06%	0.03%	0.03%	0.10%	0.11%	0.03%	0.03%	0.07%	0.09%	0.09%	
Otu0074	Bacteriovora	0.06%	0.07%	0.07%	0.05%	0.02%	0.09%	0.06%	0.10%	0.55%	0.32%	0.18%	0.14%	0.11%	0.20%	0.17%	
Otu0075	Unclassified Proteobacteria	0.03%	0.03%	0.07%	0.05%	0.02%	0.03%	0.01%	0.04%	0.00%	0.00%	0.04%	0.04%	0.04%	0.03%	0.04%	
Otu0076	Unclassified Alphaproteobacteria	0.02%	0.01%	0.04%	0.00%	0.01%											

OTU number	Taxonomy	Sample code															
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3	
Otu0083	Peredibacter	0.01%	0.01%	0.05%	0.11%	0.08%	0.07%	0.10%	0.03%	0.05%	0.01%	0.12%	0.04%	0.05%	0.09%	0.02%	
Otu0084	Bdellovibrio	0.13%	0.02%	0.01%	0.01%	0.02%	0.02%	0.03%	0.00%	0.04%	0.00%	0.00%	0.03%	0.05%	0.03%	0.06%	
Otu0085	Unclassified Rhizobiales	0.00%	0.04%	0.01%	0.00%	0.01%	0.01%	0.02%	0.02%	0.02%	0.00%	0.03%	0.00%	0.01%	0.03%	0.02%	
Otu0086	Unclassified Actinomycetales	0.01%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.04%	0.01%	0.01%	0.04%	0.03%	
Otu0087	Phenylbacterium	0.03%	0.01%	0.04%	0.02%	0.02%	0.02%	0.01%	0.01%	0.01%	0.00%	0.02%	0.01%	0.00%	0.01%	0.02%	
Otu0088	Hypomicrobium	0.13%	0.07%	0.05%	0.05%	0.09%	0.10%	0.06%	0.06%	0.03%	0.06%	0.10%	0.06%	0.08%	0.07%	0.04%	
Otu0089	Roseomonas	0.04%	0.08%	0.08%	0.06%	0.07%	0.10%	0.03%	0.05%	0.05%	0.16%	0.01%	0.04%	0.09%	0.08%	0.13%	
Otu0090	Unclassified Proteobacteria	0.05%	0.06%	0.10%	0.05%	0.02%	0.06%	0.08%	0.10%	0.06%	0.02%	0.06%	0.04%	0.02%	0.05%	0.10%	
Otu0091	Bacteroides	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0092	Unclassified Gammaproteobacteria	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.01%	
Otu0093	Pasteuria	0.14%	0.20%	0.25%	0.21%	0.25%	0.30%	0.23%	0.28%	0.24%	0.11%	0.43%	0.19%	0.26%	0.40%	0.27%	
Otu0094	Unclassified Sphingomonadales	0.05%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.00%	0.02%	
Otu0095	Unclassified Xanthomonadales	0.07%	0.00%	0.01%	0.02%	0.00%	0.01%	0.02%	0.01%	0.01%	0.03%	0.00%	0.01%	0.01%	0.01%	0.03%	
Otu0096	Unclassified Rhizobiales	0.00%	0.00%	0.01%	0.05%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%	
Otu0097	Unclassified Bacteroidetes	0.08%	0.05%	0.04%	0.01%	0.07%	0.07%	0.04%	0.05%	0.03%	0.09%	0.02%	0.03%	0.08%	0.01%	0.05%	
Otu0098	Flavobacterium	0.01%	0.01%	0.03%	0.06%	0.02%	0.03%	0.04%	0.03%	0.01%	0.22%	0.01%	0.04%	0.03%	0.02%	0.05%	
Otu0099	Sphingomonas	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.02%	0.02%	0.02%	0.00%	0.03%	
Otu0100	Unclassified Bacteria	0.01%	0.01%	0.03%	0.01%	0.01%	0.01%	0.01%	0.02%	0.01%	0.00%	0.04%	0.02%	0.03%	0.02%	0.01%	
Otu0101	Unclassified Rhizobiales	0.01%	0.09%	0.06%	0.05%	0.02%	0.07%	0.03%	0.08%	0.03%	0.02%	0.04%	0.05%	0.05%	0.09%	0.03%	
Otu0102	Unclassified Bacteria	0.00%	0.02%	0.02%	0.01%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	
Otu0103	Unclassified Acidimicrobiales	0.00%	0.04%	0.03%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.02%	0.02%	
Otu0104	Dewesia	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.01%	0.00%	0.02%	
Otu0105	Cupriavidus	0.08%	0.22%	0.19%	0.12%	0.21%	0.19%	0.17%	0.26%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0106	Unclassified Planctomycetales	0.00%	0.10%	0.15%	0.16%	0.00%	0.19%	0.18%	0.12%	0.03%	0.00%	0.09%	0.03%	0.00%	0.02%	0.07%	
Otu0107	Sphingomonas	0.05%	0.04%	0.04%	0.02%	0.07%	0.04%	0.08%	0.02%	0.05%	0.02%	0.04%	0.08%	0.16%	0.07%	0.07%	
Otu0108	Unclassified Planctomycetales	0.16%	0.11%	0.15%	0.11%	0.17%	0.27%	0.16%	0.29%	0.26%	0.08%	0.14%	0.15%	0.33%	0.51%	0.25%	
Otu0109	Unclassified Bacteria	0.02%	0.03%	0.05%	0.04%	0.10%	0.05%	0.06%	0.03%	0.04%	0.00%	0.01%	0.02%	0.03%	0.02%	0.04%	
Otu0110	Unclassified Rhizobiales	0.01%	0.01%	0.01%	0.00%	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.03%	0.01%	0.00%	0.01%	0.02%	
Otu0111	Unclassified Proteobacteria	0.01%	0.01%	0.02%	0.02%	0.00%	0.03%	0.02%	0.03%	0.01%	0.17%	0.00%	0.01%	0.01%	0.02%	0.03%	
Otu0112	Unclassified Enterobacteriaceae	0.01%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0113	Splanomias	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	
Otu0114	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.01%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.02%	0.02%	
Otu0115	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0116	Unclassified Proteobacteria	0.00%	0.06%	0.05%	0.10%	0.12%	0.06%	0.03%	0.11%	0.05%	0.02%	0.05%	0.03%	0.04%	0.02%	0.07%	
Otu0117	Unclassified Alphaproteobacteria	0.00%	0.01%	0.02%	0.00%	0.00%	0.01%	0.04%	0.02%	0.02%	0.04%	0.02%	0.02%	0.02%	0.04%	0.01%	
Otu0118	Unclassified Hypomicrobiales	0.00%	0.00%	0.01%	0.02%	0.00%	0.01%	0.01%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0119	Unclassified Acetivibrioaceae	0.00%	0.00%	0.01%	0.00%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.01%	0.02%	0.00%	0.02%	
Otu0120	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.03%	0.02%	
Otu0121	OD1_genus_incertae_sedis	0.05%	0.01%	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	0.03%	0.00%	0.00%	0.01%	0.01%	0.02%	0.03%	
Otu0122	Brevundimonas	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.04%	0.01%	0.04%	0.00%	0.03%	0.00%	0.00%	0.01%	
Otu0123	Roseomonas	0.00%	0.01%	0.00%	0.01%	0.00%	0.02%	0.05%	0.00%	0.00%	0.00%	0.02%	0.01%	0.01%	0.01%	0.00%	
Otu0124	Unclassified Acetivibrioaceae	0.00%	0.02%	0.01%	0.00%	0.02%	0.01%	0.00%	0.00%	0.02%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	
Otu0125	Unclassified Betaproteobacteria	0.08%	0.06%	0.09%	0.02%	0.13%	0.06%	0.08%	0.04%	0.06%	0.04%	0.05%	0.05%	0.07%	0.04%	0.01%	
Otu0126	Unclassified Bacteria	0.01%	0.08%	0.07%	0.20%	0.08%	0.06%	0.09%	0.09%	0.06%	0.08%	0.07%	0.04%	0.05%	0.00%	0.06%	
Otu0127	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.02%	0.02%	0.04%	0.02%	0.01%	0.00%	0.00%	0.01%	0.03%	0.03%	0.04%	
Otu0128	Unclassified Bradyrhizobiales	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0129	Methylphilus	0.04%	0.05%	0.03%	0.04%	0.08%	0.06%	0.11%	0.06%	0.06%	0.02%	0.10%	0.08%	0.11%	0.10%	0.19%	
Otu0130	Dongia	0.00%	0.00%	0.00%	0.04%	0.00%	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	
Otu0131	Unclassified Alphaproteobacteria	0.07%	0.01%	0.01%	0.01%	0.00%	0.03%	0.02%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.03%	
Otu0132	Unclassified Proteobacteria	0.01%	0.01%	0.00%	0.10%	0.03%	0.05%	0.02%	0.01%	0.00%	0.00%	0.02%	0.01%	0.03%	0.01%	0.02%	
Otu0133	Unclassified Proteobacteria	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	
Otu0134	Unclassified Bacteria	0.00%	0.03%	0.01%	0.08%	0.04%	0.01%	0.00%	0.00%	0.02%	0.00%	0.08%	0.01%	0.00%	0.00%	0.00%	
Otu0135	Unclassified Alphaproteobacteria	0.05%	0.02%	0.02%	0.05%	0.00%	0.02%	0.02%	0.03%	0.01%	0.00%	0.03%	0.03%	0.01%	0.01%	0.03%	
Otu0136	Unclassified Betaproteobacteria	0.01%	0.01%	0.00%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0137	Mesorhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0138	Unclassified Bacteria	0.00%	0.01%	0.03%	0.02%	0.02%	0.03%	0.00%	0.09%	0.02%	0.00%	0.00%	0.03%	0.02%	0.06%	0.04%	
Otu0139	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.02%	0.02%	0.01%	0.01%	
Otu0140	Unclassified Bacteria	0.00%	0.02%	0.04%	0.07%	0.01%	0.02%	0.04%	0.00%	0.04%	0.00%	0.00%	0.01%	0.03%	0.04%	0.01%	
Otu0141	Spartobacteria_genera_incertae_sedis	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.12%	0.01%	0.04%	0.05%	0.03%	
Otu0142	Unclassified Rhodospirillales	0.05%	0.00%	0.04%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0143	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0144	Unclassified Proteobacteria	0.00%	0.01%	0.00%	0.07%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.01%	0.01%	0.01%	
Otu0145	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.01%	
Otu0146	Unclassified Proteobacteria	0.00%	0.01%	0.01%	0.00%	0.09%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	
Otu0147	Unclassified Bacterivora	0.02%	0.06%	0.09%	0.05%	0.09%	0.06%	0.09%	0.07%	0.07%	0.00%	0.08%	0.04%	0.08%	0.06%	0.06%	
Otu0148	Sulfuricella	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0149	Bdellovibrio	0.07%	0.08%	0.08%	0.03%	0.00%	0.06%	0.01%	0.15%	0.07%	0.00%	0.02%	0.04%	0.05%	0.03%	0.08%	
Otu0150	Unclassified Bacteria	0.00%	0.01%	0.00%	0.01%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0151	Unclassified Acetivibrioaceae	0.00%	0.01%	0.02%	0.02%	0.02%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	
Otu0152	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	
Otu0153	Unclassified Deltaproteobacteria	0.05%	0.10%	0.04%	0.21%	0.13%	0.10%	0.06%	0.07%	0.00%	0.00%	0.04%	0.07%	0.05%	0.02%	0.07%	
Otu0154	Unclassified Sphingobacteriales	0.01%	0.00%	0.00%	0.02%	0.04%	0.02%	0.22%	0.25%	0.17%	0.13%	0.14%	0.15%	0.09%	0.13%	0.14%	
Otu0155	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.01%	0.00%	
Otu0156	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0157	Unclassified Rhodocyclales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0158	Unclassified Alphaproteobacteria	0.00%	0.01%	0.01%	0.01%												



OTU number	Taxonomy	Sample code															
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3	
Otu0251	Unclassified Desulfobacterales	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.01%	
Otu0252	Bdellovibrio	0.15%	0.08%	0.07%	0.08%	0.16%	0.17%	0.07%	0.19%	0.01%	0.00%	0.10%	0.03%	0.05%	0.04%	0.04%	
Otu0253	Unclassified Proteobacteria	0.02%	0.08%	0.00%	0.03%	0.01%	0.03%	0.03%	0.07%	0.00%	0.00%	0.01%	0.01%	0.01%	0.02%	0.01%	
Otu0254	Unclassified Eriobacteriaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0255	Azospira	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0256	Terrimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0257	Unclassified Bacteria	0.00%	0.03%	0.00%	0.02%	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0258	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0259	Unclassified Proteobacteria	0.00%	0.02%	0.01%	0.06%	0.02%	0.02%	0.01%	0.02%	0.05%	0.00%	0.00%	0.03%	0.02%	0.03%	0.04%	
Otu0260	Rhodobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0261	Unclassified Bacteria	0.01%	0.00%	0.02%	0.01%	0.00%	0.02%	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0262	Unclassified Phyllobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0263	Hydrotaea	0.12%	0.02%	0.05%	0.01%	0.02%	0.08%	0.01%	0.02%	0.02%	0.07%	0.09%	0.05%	0.00%	0.01%	0.04%	
Otu0264	Unclassified Bacteroidetes	0.00%	0.02%	0.02%	0.05%	0.00%	0.02%	0.02%	0.09%	0.00%	0.00%	0.00%	0.02%	0.05%	0.02%	0.04%	
Otu0265	Unclassified Bacteroidetes	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0266	Unclassified Bacteria	0.01%	0.00%	0.01%	0.02%	0.03%	0.00%	0.01%	0.03%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0267	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	
Otu0268	Unclassified Bacteroidetes	0.00%	0.09%	0.07%	0.14%	0.02%	0.06%	0.05%	0.16%	0.00%	0.00%	0.01%	0.03%	0.03%	0.01%	0.02%	
Otu0269	Unclassified Bacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	
Otu0270	TM7 genus incertae sedis	0.00%	0.01%	0.01%	0.00%	0.02%	0.01%	0.00%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	
Otu0271	O01 genus incertae sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0272	Gp4	0.00%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0273	Unclassified Bacteria	0.00%	0.02%	0.03%	0.03%	0.18%	0.00%	0.02%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.02%	0.02%	
Otu0274	Unclassified Gammaproteobacteria	0.06%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0275	Rheinheimera	0.00%	0.01%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0276	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0277	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0278	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0279	Opiatus	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0280	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0281	Lactobacillus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0282	Unclassified Proteobacteria	0.00%	0.03%	0.00%	0.00%	0.01%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0283	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0284	Unclassified Burkholderiales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0285	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	
Otu0286	Unclassified Bacteria	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.02%	0.01%	0.04%	
Otu0287	Gp1	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0288	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0289	Hyphomonas	0.04%	0.00%	0.00%	0.06%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	
Otu0290	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0291	Unclassified Proteobacteria	0.08%	0.09%	0.11%	0.05%	0.06%	0.08%	0.06%	0.06%	0.06%	0.07%	0.01%	0.03%	0.02%	0.04%	0.05%	
Otu0292	Unclassified Rhizobiales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0293	Unclassified Bacteria	0.06%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.04%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0294	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0295	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0296	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	
Otu0297	Singuliphora	0.01%	0.04%	0.01%	0.00%	0.04%	0.02%	0.01%	0.03%	0.11%	0.44%	0.12%	0.05%	0.08%	0.04%	0.05%	
Otu0298	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0299	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0300	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0301	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	
Otu0302	Acinetobacter	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0303	Magnetospirillum	0.00%	0.02%	0.01%	0.00%	0.04%	0.00%	0.00%	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.01%	
Otu0304	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0305	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.02%	0.02%	0.02%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0306	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%	0.00%	0.02%	0.01%	
Otu0307	Unclassified Bacteria	0.00%	0.01%	0.02%	0.01%	0.01%	0.01%	0.01%	0.01%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0308	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0309	Unclassified Bacteria	0.24%	0.00%	0.01%	0.02%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	
Otu0310	Thiobacillus	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0311	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0312	Planimicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0313	Unclassified Betaproteobacteria	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.02%	0.02%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	
Otu0314	Unclassified Mycococcales	0.00%	0.01%	0.00%	0.01%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0315	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	
Otu0316	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0317	Unclassified Bacteroidetes	0.01%	0.03%	0.01%	0.02%	0.00%	0.06%	0.05%	0.02%	0.00%	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0318	Unclassified Flavobacteriaceae	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0319	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.07%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	
Otu0320	Unclassified Sphingobacteriales	0.00%	0.00%	0.01%	0.01%	0.02%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	
Otu0321	Unclassified Bacteria	0.12%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0322	Unclassified Alphaproteobacteria	0.00%	0.01%	0.05%	0.01%	0.02%	0.03%	0.03%	0.01%	0.01%	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%	
Otu0323	Unclassified Parachlamydiaceae	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0324	Unclassified Bacteria	0.01%	0.01%	0.05%	0.01%	0.03%	0.01%	0.04%	0.02%	0.02%	0.00%	0.02%	0.03%	0.03%	0.02%	0.02%	
Otu0325	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0326	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%										



OTU number	Taxonomy	Sample code														
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3
Otu0419	Unclassified Bacteria	0.11%	0.00%	0.01%	0.00%	0.09%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0420	Sphingopyria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0421	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0422	Hydrogenisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0423	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0424	Thiomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0425	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0426	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0427	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
Otu0428	Bdellovibrio	0.00%	0.04%	0.00%	0.09%	0.00%	0.02%	0.02%	0.02%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.02%
Otu0429	Bdellovibrio	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0430	Unclassified Deltaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0431	Unclassified Planctomycetaceae	0.00%	0.01%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0432	OD1_genus_incertae_sedis	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.01%	0.22%	0.02%	0.00%	0.02%	0.00%	0.00%
Otu0433	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0434	Gemmatimonas	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0435	Unclassified Gammaproteobacteria	0.08%	0.04%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.03%	0.01%	0.03%	0.00%	0.03%
Otu0436	Gemmatimonas	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0437	Sphingopyria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0438	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0439	Unclassified Myxoscoales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0440	Unclassified Bacteroidetes	0.22%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0441	Unclassified Bacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0442	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0443	Bauldia	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0444	Unclassified Bacteria	0.01%	0.01%	0.01%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%
Otu0445	Neisseria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0446	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0447	Pedimicrobium	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.10%	0.00%	0.01%	0.01%	0.00%	0.03%
Otu0448	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0449	Unclassified Deltaproteobacteria	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0450	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0451	Acinetobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0452	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0453	Unclassified Bacteria	0.00%	0.00%	0.03%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%
Otu0454	Flavicola	0.01%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0455	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0456	Unclassified Phyllobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0457	Veillonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0458	Bdellovibrio	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0459	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0460	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0461	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu0462	Unclassified Sphingobacteriales	0.00%	0.00%	0.04%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu0463	Spartobacteria genera incertae sec	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0464	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0465	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu0466	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0467	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0468	Unclassified Bacteria	0.00%	0.03%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0469	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0470	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%
Otu0471	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0472	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0473	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0474	Spartobacteria genera incertae sec	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0475	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0476	3 genus incertae sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0477	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0478	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0479	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.37%	0.17%	0.14%	0.19%	0.14%	0.25%	0.15%	0.14%	0.11%	0.16%	0.04%
Otu0480	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0481	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0482	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0483	Peptostreptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0484	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0485	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0486	Leptolinea	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0487	Unclassified Bacteria	0.02%	0.05%	0.03%	0.04%	0.02%	0.05%	0.03%	0.02%	0.00%	0.00%	0.00%	0.02%	0.02%	0.01%	0.02%
Otu0488	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0489	Unclassified Bacteroidetes	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0490	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0491	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0492	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0493	Unclassified Bacteria	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0494	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%											

OTU number	Taxonomy	Sample code															
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3	
Otu0503	Unclassified Gammaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.02%	0.01%	0.00%	
Otu0504	Unclassified Bacteria	0.00%	0.01%	0.03%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	
Otu0505	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	
Otu0506	Pasteuria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0507	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0508	Unclassified Chitinophagaceae	0.00%	0.01%	0.00%	0.04%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	
Otu0509	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0510	Aureispira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	
Otu0511	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0512	Unclassified Anaerolineaceae	0.00%	0.02%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.01%	
Otu0513	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0514	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0515	Spartobacteria_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0516	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0517	Gp16	0.01%	0.02%	0.02%	0.03%	0.01%	0.02%	0.00%	0.02%	0.02%	0.10%	0.02%	0.03%	0.03%	0.00%	0.02%	
Otu0518	Unclassified Bacteria	0.00%	0.03%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0519	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0520	Lactococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0521	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0522	Unclassified Planctomycetaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	
Otu0523	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0524	Unclassified Bacteria	0.00%	0.01%	0.00%	0.02%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0525	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0526	Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0527	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0528	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	
Otu0529	Gp6	0.00%	0.00%	0.02%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	
Otu0530	Unclassified Enterobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0531	OD1_genus_incertae_sedis	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0532	Chondromyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0533	Unclassified Bacteroidetes	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.04%	0.01%	0.01%	0.00%	0.03%	0.01%	
Otu0534	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0535	Unclassified Nitrospomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0536	Ignavibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Otu0537	Unclassified Burkholderiales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0538	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0539	Unclassified Proteobacteria	0.00%	0.01%	0.03%	0.05%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	
Otu0540	Braybacter	0.00%	0.00%	0.03%	0.05%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0541	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0542	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0543	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0544	Unclassified Bacteria	0.01%	0.01%	0.01%	0.02%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0545	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0546	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0547	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0548	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0549	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0550	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0551	Pereidibacter	0.00%	0.01%	0.01%	0.03%	0.00%	0.02%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	
Otu0552	Unclassified Bacteria	0.00%	0.01%	0.01%	0.02%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0553	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0554	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0555	Bacteriovora	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0556	Unclassified Bacteroidetes	0.00%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	
Otu0557	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0558	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0559	Unclassified Proteobacteria	0.00%	0.01%	0.00%	0.00%	0.03%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0560	Unclassified Bacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0561	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0562	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	
Otu0563	Parachlamydia	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.02%	0.00%	0.07%	0.00%	0.00%	0.03%	0.00%	
Otu0564	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0565	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0566	Unclassified Bacteroidetes	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0567	Unclassified Rhodospirillaceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0568	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0569	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0570	Opitutus	0.00%	0.01%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0571	Gemmata	0.00%	0.01%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0572	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0573	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0574	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0575	Unclassified Alphaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0576	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0577	Unclassified Bacteria	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0578	Thiomonas	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%										



OTU number	Taxonomy	Sample code															
		F1A1	F1A2	F1A3	F1A4	F1B1	F1B2	F1B3	F1B4	F2A1	F2A2	F2A3	F2A4	F2B1	F2B2	F2B3	
Otu0587	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0588	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0589	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0590	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0591	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0592	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0593	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0594	Sphingomonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0595	Nesochlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0596	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0597	Unclassified Betaproteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0598	Aquificia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0599	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0600	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0601	Unclassified Proteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0602	Ferribacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0603	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	
Otu0604	Unclassified Betaproteobacteria	0.00%	0.02%	0.00%	0.00%	0.01%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0605	Unclassified Rhodospirillales	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	
Otu0606	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0607	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0608	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0609	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0610	Coneixibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0611	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0612	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0613	Unclassified Bacillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0614	Clostridium III	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0615	Hydrogenisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0616	Herminimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0617	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0618	Unclassified Gammaproteobacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	
Otu0619	Spartobacteria_genera_incertae_sed	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0620	Bifidobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0621	Bdellovibrio	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%	0.03%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Otu0622	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0623	Unclassified Intraparvngicaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0624	Aurantimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0625	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0626	Unclassified Bacteria	0.00%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0627	Unclassified Clostridia	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	
Otu0628	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0629	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0630	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0631	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0632	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0633	Bdellovibrio	0.00%	0.02%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0634	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0635	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0636	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0637	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0638	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0639	Geobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0640	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0641	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0642	Rheinheimera	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0643	Unclassified Planctomycetaceae	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.03%	0.00%	0.00%	
Otu0644	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0645	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0646	Ilumatobacter	0.03%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0647	Enterococcus	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	
Otu0648	Bdellovibrio	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0649	Unclassified Bacteria	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0650	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0651	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0652	Pedobacter	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0653	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0654	Unclassified Hyphomicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0655	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0656	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0657	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0658	Rhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0659	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0660	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Otu0661	Unclassified Bacterioviracaceae	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Otu0662	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.0										





















































OTU number	Taxonomy	Sample code																			
		F3B4	F3A1	F3A2	F3A3	F3A4	F3B1	F3B2	F3B3	F3B4	F1E10B8	F1E10D2	F1E10D8	F2E10A1	F2E10B1	F2E10D2	F2E10D8	F2E10D4	F2E10F1		
Otu0001	Sphingopyxis	21.49%	24.21%	22.53%	24.13%	23.62%	23.40%	25.06%	24.25%	23.07%	1.74%	4.25%	3.55%	4.71%	1.45%	2.33%	4.33%	3.51%	3.27%	4.97%	2.20%
Otu0002	Acidovorax	8.00%	10.23%	11.05%	12.18%	11.85%	10.19%	8.98%	8.81%	9.41%	5.47%	5.70%	6.19%	6.51%	3.16%	5.86%	7.24%	6.84%	6.79%	7.55%	1.69%
Otu0003	Mycobacterium	24.82%	28.62%	24.11%	24.81%	22.73%	21.84%	24.00%	25.70%	29.14%	1.00%	0.93%	1.16%	2.38%	0.09%	0.30%	1.61%	1.65%	1.36%	3.03%	0.07%
Otu0004	Hydrogenophaga	1.25%	1.51%	1.45%	1.08%	1.37%	1.34%	1.05%	1.75%	1.33%	29.14%	23.31%	22.81%	21.77%	20.16%	20.56%	16.92%	15.78%	19.41%	16.10%	14.31%
Otu0005	Aquabacterium	2.52%	2.22%	2.13%	2.00%	2.47%	2.43%	2.04%	2.09%	2.21%	2.24%	3.69%	3.59%	2.99%	5.19%	2.72%	3.87%	3.34%	1.44%	3.60%	5.24%
Otu0006	Sphingomonas	8.80%	7.69%	8.34%	8.02%	8.38%	8.02%	8.00%	8.53%	7.72%	0.38%	0.17%	0.11%	0.15%	0.01%	0.08%	0.14%	0.16%	0.11%	0.15%	0.00%
Otu0007	Unclassified Proteobacteria	0.12%	0.06%	0.17%	0.14%	0.14%	0.32%	0.09%	0.06%	0.15%	29.98%	27.40%	29.30%	27.69%	30.15%	27.52%	27.34%	34.28%	31.99%	22.04%	32.07%
Otu0008	Unclassified Bradyrhizobaceae	1.53%	0.23%	0.41%	0.37%	0.46%	0.73%	0.51%	0.33%	0.33%	0.85%	2.51%	2.65%	0.82%	0.81%	1.60%	3.33%	2.13%	1.33%	0.51%	0.93%
Otu0009	Unclassified Bacteria	3.83%	2.49%	2.95%	2.35%	2.93%	2.46%	2.02%	1.92%	2.53%	6.83%	9.34%	6.89%	7.93%	7.35%	8.57%	2.89%	7.53%	11.74%	8.24%	5.54%
Otu0010	Unclassified Betaproteobacteria	0.40%	0.56%	0.56%	0.40%	0.66%	0.57%	0.71%	0.11%	0.66%	0.45%	0.34%	0.44%	2.12%	1.28%	0.61%	0.26%	0.19%	0.18%	2.55%	0.77%
Otu0011	Rosea	0.88%	1.12%	1.09%	1.05%	0.95%	1.50%	1.62%	1.92%	0.99%	3.26%	7.67%	9.46%	5.22%	2.51%	2.50%	4.78%	4.10%	2.90%	4.74%	4.59%
Otu0012	Unclassified Bacteroidetes	2.96%	2.09%	2.79%	2.71%	3.53%	2.63%	2.71%	3.46%	2.71%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Otu0013	Unclassified Rhodobacteraceae	0.31%	0.54%	0.27%	0.63%	0.52%	0.52%	0.59%	0.74%	0.38%	1.89%	1.80%	1.73%	2.64%	1.80%	2.30%	2.26%	1.93%	2.99%	2.71%	1.19%
Otu0014	Unclassified Sphingomonadaceae	1.30%	0.14%	0.09%	0.11%	0.12%	0.09%	0.19%	0.21%	0.20%	1.21%	0.24%	0.16%	0.05%	0.79%	1.89%	0.74%	0.70%	0.03%	0.07%	0.48%
Otu0015	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.01%	0.03%	0.03%	0.04%	0.00%	0.01%	6.11%	0.51%	2.18%	2.68%	9.94%	6.68%	1.87%	4.00%	2.32%	5.96%	10.15%
Otu0016	Unclassified Burkholderiales	0.27%	0.24%	0.18%	0.20%	0.20%	0.21%	0.23%	0.19%	0.07%	0.05%	0.06%	0.07%	0.05%	0.02%	0.02%	0.06%	0.04%	0.02%	0.10%	0.03%
Otu0017	Unclassified Rhizobiales	0.69%	0.49%	0.33%	0.35%	0.33%	0.43%	0.54%	0.50%	0.44%	0.98%	0.98%	0.30%	0.38%	0.84%	1.28%	1.91%	0.72%	0.52%	0.82%	2.30%
Otu0018	Unclassified Comamonadaceae	0.11%	0.06%	0.21%	0.27%	0.01%	0.01%	0.04%	0.00%	0.00%	0.01%	0.02%	0.02%	0.02%	0.00%	0.06%	0.02%	0.02%	0.00%	0.00%	0.00%
Otu0019	Unclassified Bacteroidetes	3.19%	2.17%	3.99%	2.62%	2.97%	3.10%	3.04%	1.40%	2.93%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0020	Nitrosira	0.22%	0.00%	0.12%	0.24%	0.35%	0.20%	0.22%	0.14%	0.05%	0.92%	0.77%	0.73%	1.21%	1.81%	7.21%	6.79%	4.68%	4.54%	4.74%	7.57%
Otu0021	Unclassified Betaproteobacteria	0.44%	1.45%	0.91%	0.37%	0.59%	0.52%	0.56%	0.93%	0.54%	0.37%	0.87%	0.32%	0.41%	0.17%	0.34%	0.65%	0.37%	0.31%	0.58%	0.32%
Otu0022	Unclassified Betaproteobacteria	0.02%	0.03%	0.06%	0.12%	0.10%	0.09%	0.10%	0.01%	0.03%	0.01%	0.04%	0.06%	0.09%	0.02%	0.00%	0.06%	0.03%	0.02%	0.08%	0.00%
Otu0023	Unclassified Bacteria	0.10%	0.29%	0.07%	0.10%	0.24%	0.21%	0.06%	0.16%	0.07%	0.01%	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.04%	0.00%
Otu0024	Pseudomonas	0.31%	0.57%	0.79%	0.60%	0.90%	0.41%	0.41%	0.40%	0.33%	0.72%	0.04%	0.09%	0.53%	0.32%	0.82%	0.05%	0.04%	1.05%	0.83%	0.10%
Otu0025	Sedimentibacterium	0.159%	0.03%	0.17%	0.36%	0.10%	0.23%	0.18%	0.07%	0.02%	0.16%	0.44%	0.65%	0.43%	0.14%	0.20%	0.68%	0.62%	0.29%	0.43%	0.39%
Otu0026	Unclassified Betaproteobacteria	0.05%	0.12%	0.16%	0.09%	0.12%	0.11%	0.14%	0.04%	0.45%	0.04%	0.02%	0.05%	0.06%	0.02%	0.02%	0.06%	0.04%	0.03%	0.08%	0.02%
Otu0027	Unclassified Rhodocyclaceae	0.11%	0.05%	0.06%	0.15%	0.10%	0.11%	0.20%	0.09%	0.15%	0.32%	0.12%	0.40%	0.22%	0.31%	0.31%	0.22%	0.45%	0.27%	0.39%	0.12%
Otu0028	Chryseobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.13%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0029	Unclassified Hyphomicrobiaceae	0.20%	0.06%	0.08%	0.14%	0.18%	0.09%	0.15%	0.06%	0.27%	0.15%	0.08%	0.11%	0.15%	0.16%	0.06%	0.07%	0.05%	0.07%	0.40%	0.00%
Otu0030	Brevundimonas	0.43%	0.91%	0.56%	0.86%	0.70%	0.64%	0.58%	0.79%	0.77%	0.28%	0.29%	0.31%	0.39%	0.32%	0.37%	0.42%	0.36%	0.33%	0.57%	0.29%
Otu0031	Methylbacterium	0.65%	0.00%	0.05%	0.02%	0.07%	0.02%	0.05%	0.00%	0.17%	0.00%	0.01%	0.04%	0.01%	0.00%	0.02%	0.06%	0.07%	0.01%	0.02%	0.00%
Otu0032	Unclassified Proteobacteria	0.00%	0.00%	0.02%	0.01%	0.00%	0.03%	0.02%	0.00%	0.01%	0.03%	0.03%	0.04%	0.03%	0.01%	0.02%	0.00%	0.03%	0.05%	0.06%	0.13%
Otu0033	Paraphrobacter	0.31%	0.87%	0.65%	0.77%	0.75%	1.05%	1.18%	1.71%	0.94%	0.01%	0.04%	0.07%	0.89%	0.03%	0.02%	0.18%	0.18%	0.13%	0.68%	0.00%
Otu0034	Sphingopyxis	0.06%	0.21%	0.14%	0.05%	0.04%	0.14%	0.23%	0.17%	0.14%	0.00%	0.34%	0.07%	0.00%	0.01%	0.00%	0.24%	0.09%	0.01%	0.03%	0.00%
Otu0035	Methylbacterium	1.02%	1.13%	0.60%	0.76%	0.50%	0.58%	0.94%	0.89%	0.83%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.03%	0.03%	0.05%	0.04%	0.00%
Otu0036	Ralstonia	0.02%	0.12%	0.10%	0.11%	0.13%	0.28%	0.13%	0.05%	0.40%	0.14%	0.44%	0.17%	0.31%	0.29%	0.19%	0.24%	0.18%	0.22%	0.28%	0.42%
Otu0037	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.02%	0.01%	0.02%	0.01%	0.00%	0.00%	0.08%	0.90%	0.16%	0.09%	0.17%	0.05%	0.32%	0.11%	0.02%	0.43%	0.14%
Otu0038	Sedimentibacterium	0.08%	0.00%	0.08%	0.13%	0.11%	0.12%	0.20%	0.03%	0.30%	0.02%	0.90%	0.65%	0.44%	0.22%	0.35%	1.75%	1.00%	0.98%	1.25%	0.05%
Otu0039	Methylbacterium	0.95%	0.36%	0.82%	0.60%	0.55%	0.61%	0.83%	1.01%	1.42%	0.01%	0.26%	0.09%	0.23%	0.05%	0.03%	0.13%	0.10%	0.25%	0.27%	0.00%
Otu0040	Unclassified Nitrosomonadaceae	0.08%	0.11%	0.14%	0.04%	0.12%	0.09%	0.07%	0.09%	0.02%	0.14%	0.10%	0.07%	0.96%	0.19%	0.15%	0.14%	0.22%	1.12%	0.24%	0.68%
Otu0041	Belleflovirio	0.01%	0.00%	0.01%	0.02%	0.00%	0.01%	0.02%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0042	Unclassified Betaproteobacteria	0.64%	0.03%	0.28%	0.07%	0.18%	0.21%	0.23%	0.10%	0.48%	0.89%	1.48%	1.18%	0.67%	1.07%	0.75%	0.83%	0.80%	0.34%	0.53%	1.25%
Otu0043	Hermismonas	0.07%	0.18%	0.10%	0.09%	0.12%	0.00%	0.17%	0.29%	0.00%	0.01%	0.13%	0.07%	0.00%	0.01%	0.07%	0.16%	0.11%	0.01%	0.22%	0.00%
Otu0044	Unclassified Proteobacteria	0.30%	0.13%	0.41%	0.21%	0.29%	0.58%	0.36%	0.18%	0.44%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0045	Aminobacter	0.33%	0.39%	0.35%	0.45%	0.39%	0.14%	0.19%	0.24%	0.06%	0.33%	0.30%	0.32%	0.40%	0.62%	0.61%	0.57%	0.35%	0.65%	0.33%	0.17%
Otu0046	Unclassified Bacteria	0.00%	0.01%	0.05%	0.03%	0.12%	0.05%	0.04%	0.00%	0.09%	0.22%	0.20%	0.13%	0.24%	0.06%	0.11%	0.20%	0.29%	0.18%	0.29%	0.05%
Otu0047	Caulobacter	0.74%	0.13%	0.53%	0.62%	0.63%	0.53%	0.50%	0.43%	0.98%	0.03%	0.09%	0.11%	0.21%	0.08%	0.10%	0.13%	0.14%	0.13%	0.32%	0.00%
Otu0048	Unclassified Bacteria	0.02%	0.18%	0.10%	0.05%	0.03%	0.11%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0049	Unclassified Bacteria	0.21%	0.20%	0.18%	0.16%	0.15%	0.24%	0.26%	0.10%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0050	Sphingomonas	0.49%	0.35%	0.34%	0.49%	0.41%	0.50%	0.46%	0.36%	0.37%	0.07%	0.23%	0.26%	0.20%	0.04%	0.12%	0.08%	0.09%	0.05%	0.13%	0.00%
Otu0051	Unclassified Betaproteobacteria	0.05%	0.00%	0.13%	0.04%	0.02%	0.06%	0.05%	0.00%	0.02%	0.01%	0.00%	0.01%	0.01%	0.00%	0.01%	0.01%	0.01%	0.01%	0.02%	0.00%
Otu0052	Unclassified Microbacteriaceae	0.02%	0.10%	0.05%	0.10%	0.07%	0.08%	0.01%	0.08%	0.03%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%
Otu0053	Pseudomonas	0.07%	0.16%	0.04%	0.05%	0.06%	0.01%	0.03%	0.00%	0.03%	0.00%	0.01%	0.03%	0.01%	0.01%	0.01%	0.01%	0.03%	0.00%	0.02%	0.01%
Otu0054	Desulfobrio	0.01%	0.00%	0.00%	0.00%	0.01%	0.04%	0.02%	0.01%	0.00%	0.01%	0.01%	0.03%	0.02%	0.01%	0.02%	0.02%	0.02%	0.02%	0.02%	0.00%
Otu0055	Unclassified Bacteria	0.01%	0.02%	0.22%	0.03%	0.10%	0.06%	0.05%	0.03%	0.02%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0056	Unclassified Deltaproteobacteria	0.01%	0.05%	0.00%	0.01%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0057	Phenylobacterium	0.37%	0.04%	0.08%	0.01%	0.07%	0.00%	0.03%	0.01%	0.00%	0.23%	0.10%	0.05%	0.00%	0.04%	0.03%	0.12%	0.08%	0.01%	0.01%	0.05%
Otu0058	Unclassified Comamonadaceae	0.01%	0.01%	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.03%	0.03%	0.13%	0.02%	0.33%	0.03%	0.02%	0.66%	0.00%	0.02%	0.57%
Otu0059	Unclassified Chitinophagaceae	0.04%	0.11%	0.14%	0.09%	0.18%	0.13%	0.03%	0.11%	0.27%	0.01%	0.00%	0.								



































































OTU number	Taxonomy	Sample code								
		15EFM1A	15EFM2A	15EFM3A	15EFM4A	15EFM5A	15EFM6A	15EFM7A	15EFM8A	
Otu001	Sphingopyxis	2.15%	3.99%	3.77%	3.81%	3.26%	4.95%	4.18%		
Otu002	Acidovorax	2.69%	4.98%	4.02%	4.69%	5.09%	7.37%	5.81%		
Otu003	Mycobacterium	0.39%	1.67%	1.64%	0.79%	0.92%	2.12%	1.99%		
Otu004	Hydrogenophaga	16.28%	12.43%	12.41%	16.51%	12.90%	18.16%	21.01%		
Otu005	Aquabacterium	2.65%	2.08%	3.20%	0.59%	1.98%	3.80%	2.01%		
Otu006	Sphingomonas	0.16%	0.07%	0.16%	0.14%	0.79%	0.16%	0.09%		
Otu007	Unclassified Proteobacteria	32.22%	30.67%	35.97%	37.21%	24.30%	23.11%	31.52%		
Otu008	Unclassified Bradyrhizobiales	1.06%	2.12%	2.33%	1.15%	0.34%	0.48%	1.09%		
Otu009	Unclassified Bacteria	9.57%	10.54%	9.36%	11.27%	11.66%	6.52%	8.28%		
Otu010	Unclassified Betaproteobacteria	0.66%	0.36%	0.32%	0.19%	1.99%	3.04%	1.02%		
Otu011	Bosea	4.28%	3.42%	3.26%	2.53%	4.49%	6.13%	5.06%		
Otu012	Unclassified Bacteroidetes	0.00%	0.00%	0.06%	0.07%	0.00%	0.00%	0.00%		
Otu013	Unclassified Rhodobacteraceae	2.30%	2.23%	2.10%	3.39%	3.92%	3.90%	3.37%		
Otu014	Unclassified Sphingomonadaceae	1.93%	2.02%	0.75%	0.09%	0.01%	0.04%	0.04%		
Otu015	Unclassified Betaproteobacteria	8.10%	1.67%	4.31%	4.15%	7.78%	4.89%	2.15%		
Otu016	Unclassified Burkholderiales	0.01%	0.00%	0.11%	0.07%	0.06%	0.04%	0.03%		
Otu017	Unclassified Rhizobiales	2.03%	3.98%	1.01%	0.67%	1.19%	0.72%	0.74%		
Otu018	Unclassified Comamonadaceae	0.00%	0.01%	0.02%	0.02%	0.02%	0.02%	0.01%		
Otu019	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu020	Nitrospira	9.01%	7.06%	6.72%	3.60%	8.06%	3.53%	1.91%		
Otu021	Unclassified Betaproteobacteria	0.11%	1.47%	0.66%	0.28%	1.01%	0.74%	0.61%		
Otu022	Unclassified Betaproteobacteria	0.02%	0.03%	0.03%	0.03%	0.07%	0.06%	0.04%		
Otu023	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%		
Otu024	Pseudomonas	0.08%	0.00%	0.01%	0.63%	0.70%	0.81%	0.60%		
Otu025	Sediminibacterium	0.16%	0.60%	1.08%	0.69%	0.13%	0.36%	0.35%		
Otu026	Unclassified Betaproteobacteria	0.00%	0.00%	0.03%	0.01%	0.07%	0.05%	0.06%		
Otu027	Unclassified Rhodocyclaceae	0.12%	0.02%	0.18%	0.04%	0.17%	0.26%	0.19%		
Otu028	Chryseobacterium	0.41%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%		
Otu029	Unclassified Hyphomicrobiaceae	0.15%	0.01%	0.18%	0.09%	0.08%	0.43%	0.36%		
Otu030	Brevundimonas	0.30%	0.36%	0.34%	0.17%	0.22%	0.33%	0.26%		
Otu031	Methylobacterium	0.00%	0.00%	0.05%	0.01%	0.03%	0.01%	0.02%		
Otu032	Unclassified Proteobacteria	0.02%	0.00%	0.00%	0.01%	0.01%	0.03%	0.06%		
Otu033	Porphyrobacter	0.02%	0.14%	0.14%	0.75%	0.74%	1.09%	0.61%		
Otu034	Sphingopyxis	0.02%	0.71%	0.25%	0.00%	0.01%	0.02%	0.00%		
Otu035	Methylobacterium	0.01%	0.02%	0.03%	0.00%	0.02%	0.02%	0.01%		
Otu036	Ralstonia	0.20%	0.34%	0.34%	0.02%	0.14%	0.25%	0.25%		
Otu037	Unclassified Rhizobiales	0.13%	0.60%	0.27%	0.00%	0.75%	0.41%	0.06%		
Otu038	Sediminibacterium	0.19%	0.97%	0.37%	1.55%	0.66%	0.76%	0.53%		
Otu039	Methylobacterium	0.01%	0.22%	0.15%	0.13%	0.14%	0.18%	0.30%		
Otu040	Unclassified Nitrospiradaceae	0.31%	0.14%	0.31%	2.34%	0.64%	0.33%	1.41%		
Otu041	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu042	Unclassified Betaproteobacteria	0.43%	1.32%	0.79%	0.06%	1.11%	1.10%	0.58%		
Otu043	Hermismonas	0.00%	0.00%	0.00%	0.09%	0.14%	0.00%	0.00%		
Otu044	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.01%	0.00%	0.02%	0.00%		
Otu045	Aminobacter	0.32%	0.37%	0.35%	0.05%	0.18%	0.22%	0.44%		
Otu046	Unclassified Bacteria	0.01%	0.30%	0.12%	0.00%	0.21%	0.27%	0.22%		
Otu047	Caulobacter	0.01%	0.05%	0.18%	0.10%	0.31%	0.20%	0.09%		
Otu048	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu049	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu050	Sphingomonas	0.07%	0.04%	0.15%	0.00%	0.04%	0.22%	0.15%		
Otu051	Unclassified Betaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%	0.01%		
Otu052	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%		
Otu053	Pseudomonas	0.00%	0.04%	0.01%	0.19%	0.00%	0.01%	0.02%		
Otu054	Desulfovibrio	0.01%	0.02%	0.00%	0.01%	0.01%	0.01%	0.01%		
Otu055	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%		
Otu056	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu057	Phenylobacterium	0.07%	0.02%	0.08%	0.00%	0.01%	0.01%	0.02%		
Otu058	Unclassified Comamonadaceae	0.05%	0.00%	0.08%	0.01%	0.00%	0.01%	0.00%		
Otu059	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%		
Otu060	Novosphingobium	0.02%	0.46%	0.03%	0.00%	0.00%	0.00%	0.00%		
Otu061	Unclassified Proteobacteria	0.08%	0.00%	0.09%	0.03%	0.03%	0.02%	0.04%		
Otu062	Bdellovibrio	0.00%	0.00%	0.00%	0.01%	0.11%	0.00%	0.00%		
Otu063	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu064	Hyphomicrobium	0.01%	0.00%	0.12%	0.05%	0.04%	0.07%	0.06%		
Otu065	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu066	Unclassified Rhizobiales	0.09%	0.08%	0.04%	0.01%	0.10%	0.12%	0.12%		
Otu067	Unclassified Betaproteobacteria	0.14%	0.39%	0.14%	0.22%	0.03%	0.08%	0.13%		
Otu068	Acinetobacter	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%		
Otu069	Planctomyces	0.01%	0.00%	0.00%	0.00%	0.07%	0.02%	0.01%		
Otu070	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%		
Otu071	Unclassified Alphaproteobacteria	0.00%	0.00%	0.02%	0.01%	0.00%	0.04%	0.00%		
Otu072	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu073	Methylophilus	0.02%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%		
Otu074	Bacteriovorax	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%		
Otu075	Unclassified Proteobacteria	0.00%	0.05%	0.01%	0.00%	0.02%	0.00%	0.06%		
Otu076	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%		
Otu077	Limnobacter	0.00%	0.00%	0.00%	0.02%	0.04%	0.02%	0.03%		
Otu078	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%		
Otu079	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu080	Unclassified Sphingomonadaceae	0.00%	0.26%	0.19%	0.01%	0.00%	0.12%	0.05%		
Otu081	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		
Otu082	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%		



OTU number	Taxonomy	Sample code						
		15EFH18	15EFH2A	15EFH2B	15EFH3A	15EFH3B	15EFH3B	
Otu0083	Peridibacter	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0084	Bdellovibrio	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%
Otu0085	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0086	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%
Otu0087	Phenylobacterium	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0088	Hyphomicrobium	0.01%	0.00%	0.01%	0.00%	0.06%	0.04%	0.02%
Otu0089	Roseomonas	0.07%	0.01%	0.01%	0.19%	0.01%	0.06%	0.09%
Otu0090	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0091	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%
Otu0092	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.04%
Otu0093	Pasteuria	0.02%	0.00%	0.08%	0.00%	0.00%	0.09%	0.13%
Otu0094	Unclassified Sphingomonadales	0.00%	0.16%	0.06%	0.03%	0.13%	0.01%	0.00%
Otu0095	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0096	Unclassified Rhizobiales	0.02%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Otu0097	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0098	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0099	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.16%	0.00%	0.00%
Otu0100	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0101	Unclassified Rhizobiales	0.02%	0.00%	0.00%	0.00%	0.01%	0.01%	0.02%
Otu0102	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0103	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0104	Devosia	0.03%	0.00%	0.01%	0.00%	0.00%	0.01%	0.02%
Otu0105	Cupriavidus	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0106	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0107	Sphingomonas	0.02%	0.01%	0.00%	0.01%	0.01%	0.05%	0.06%
Otu0108	Unclassified Planctomycetaceae	0.04%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%
Otu0109	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0110	Unclassified Rhizobiales	0.00%	0.00%	0.06%	0.00%	0.00%	0.01%	0.00%
Otu0111	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0112	Unclassified Enterobacteriaceae	0.00%	0.08%	0.00%	0.03%	0.01%	0.00%	0.00%
Otu0113	Silanimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0114	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0115	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0116	Unclassified Proteobacteria	0.05%	0.05%	0.02%	0.04%	0.07%	0.12%	0.09%
Otu0117	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0118	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0119	Unclassified Acetobacteraceae	0.01%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%
Otu0120	Unclassified Rhizobiales	0.01%	0.00%	0.01%	0.01%	0.08%	0.04%	0.03%
Otu0121	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0122	Brevandimonas	0.02%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%
Otu0123	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0124	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0125	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0126	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0127	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%
Otu0128	Unclassified Bradyrhizobiaceae	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%
Otu0129	Methylophilus	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.02%
Otu0130	Dongia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0131	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu0132	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0133	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0134	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0135	Unclassified Alphaproteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0136	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0137	Mesorhizobium	0.01%	0.02%	0.40%	0.00%	0.56%	0.24%	0.03%
Otu0138	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Otu0139	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0140	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.05%	0.01%	0.01%
Otu0141	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Otu0142	Unclassified Rhodospirillales	0.01%	0.00%	0.00%	0.00%	0.01%	0.03%	0.01%
Otu0143	Unclassified Betaproteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0144	Unclassified Proteobacteria	0.01%	0.00%	0.00%	0.20%	0.09%	0.01%	0.00%
Otu0145	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0146	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0147	Unclassified Bacterioviraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0148	Sulfuricella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0149	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0150	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0151	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0152	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%
Otu0153	Unclassified Delphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.04%	0.01%	0.00%
Otu0154	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0155	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0156	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0157	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%
Otu0158	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0159	Hyphomicrobium	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0160	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0161	Legionella	0.00%	0.00%	0.00%	0.21%	0.00%	0.05%	0.05%
Otu0162	Unclassified Planctomycetaceae	0.00%	0.00%	0.04%	0.00%	0.00%	0.02%	0.01%
Otu0163	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%
Otu0164	Bacteriovirax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0165	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0166	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code						
		15EFH18	15EFH24	15EFH28	15EFH34	15EFH38	15EFH39	
Otu0167	Unclassified Alphaproteobacteria	0.00%	0.03%	0.00%	0.10%	0.02%	0.07%	0.03%
Otu0168	Unclassified Planctomycetaceae	0.00%	0.50%	0.00%	0.00%	0.05%	0.02%	0.00%
Otu0169	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0170	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0171	Unclassified Bacteria	0.02%	0.00%	0.00%	0.01%	0.00%	0.01%	0.01%
Otu0172	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0173	Methylomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0174	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0175	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0176	Microbacterium	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0177	Unclassified Syntrophaceae	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%
Otu0178	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0179	Geothrix	0.00%	0.00%	0.00%	0.08%	0.02%	0.00%	0.00%
Otu0180	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0181	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0182	Unclassified Caulobacteraceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.04%	0.01%
Otu0183	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.14%	0.00%	0.01%
Otu0184	Unclassified Caulobacteraceae	0.01%	0.00%	0.04%	0.01%	0.03%	0.02%	0.01%
Otu0185	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0186	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0187	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0188	Unclassified Xanthomonadaceae	0.02%	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%
Otu0189	Unclassified Planctomycetaceae	0.01%	0.00%	0.00%	0.00%	0.01%	0.02%	0.01%
Otu0190	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0191	Methylbacterium	0.00%	0.01%	0.00%	0.00%	0.09%	0.04%	0.01%
Otu0192	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0193	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0194	Gemmalimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0195	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.03%	0.02%	0.00%
Otu0196	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0197	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0198	Bosea	0.00%	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Otu0199	Desulfosporosinus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0200	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0201	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0202	Pseudomonas	0.00%	0.23%	0.02%	0.11%	0.26%	0.00%	0.00%
Otu0203	Sinetriphomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0204	Unclassified Alphaproteobacteria	0.00%	0.00%	0.04%	0.00%	0.00%	0.01%	0.01%
Otu0205	Burkholderia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0206	Unclassified Proteobacteria	0.00%	0.11%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0207	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.01%
Otu0208	Unclassified Betaproteobacteria	0.00%	0.00%	0.04%	0.00%	0.00%	0.01%	0.00%
Otu0209	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0210	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0211	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0212	Magnetspirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0213	Alkermansia	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.01%
Otu0214	Prostheobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0215	Roseburia	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0216	Unclassified Gammaproteobacteria	0.03%	0.00%	0.07%	0.00%	0.00%	0.06%	0.04%
Otu0217	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0218	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0219	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0220	Lewinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0221	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0222	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0223	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0224	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0225	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0226	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0227	Unclassified Gammaproteobacteria	0.00%	0.14%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0228	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0229	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0230	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.01%
Otu0231	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0232	Shinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0233	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0234	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0235	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0236	Unclassified Proteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Otu0237	Unclassified Planctomycetaceae	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0238	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0239	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0240	Planctomyces	0.00%	0.00%	0.12%	0.00%	0.08%	0.02%	0.01%
Otu0241	Bosea	0.00%	0.00%	0.01%	0.00%	0.03%	0.00%	0.00%
Otu0242	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0243	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.21%	0.00%	0.00%
Otu0244	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0245	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0246	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0247	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0248	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0249	Unclassified Cryomorphaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0250	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFH18	15EFH24	15EFH28	15EFH34	15EFH38	15EFH39
Otu0251	Unclassified Desulfobacteriales	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0252	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0253	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0254	Unclassified Enterobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0255	Azospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0256	Terribomas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0257	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0258	Unclassified Oxalobacteraceae	0.00%	0.01%	0.00%	0.03%	0.00%	0.00%
Otu0259	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0260	Rhodobacter	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0261	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0262	Unclassified Phyllobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0263	Hydrotales	0.00%	0.01%	0.00%	0.01%	0.00%	0.02%
Otu0264	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0265	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0266	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0267	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0268	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0269	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0270	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0271	OT1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0272	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0273	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0274	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0275	Rheinheimera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0276	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0277	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0278	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0279	Opilinus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0280	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0281	Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0282	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Otu0283	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0284	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0285	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0286	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0287	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0288	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0289	Hyphomonas	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0290	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0291	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0292	Unclassified Rhizobiales	0.00%	0.01%	0.00%	0.00%	0.00%	0.02%
Otu0293	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0294	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0295	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0296	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0297	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0298	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0299	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0300	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0301	Unclassified Caulobacteraceae	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0302	Acinetobacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0303	Magnetospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0304	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0305	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Otu0306	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0307	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0308	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0309	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0310	Thiobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0311	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0312	Planomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0313	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0314	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0315	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
Otu0316	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0317	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0318	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0319	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0320	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0321	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0322	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0323	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%
Otu0324	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0325	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0326	Unclassified Bacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0327	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0328	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0329	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0330	Inhella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0331	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0332	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%
Otu0333	Rhizobium	0.00%	0.00%	0.00%	0.15%	0.00%	0.22%
Otu0334	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code						
		15EFH18	15EFH24	15EFH28	15EFH34	15EFH38	15EFH39	
Otu0335	Legionella	0.01%	0.00%	0.01%	0.01%	0.00%	0.00%	0.03%
Otu0336	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0337	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0338	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0339	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0340	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0341	Sulfuricurvum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0342	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0343	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0344	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0345	Unclassified Bacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Otu0346	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0347	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0348	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0349	Unclassified Chitinophagaceae	0.00%	0.00%	0.11%	0.00%	0.00%	0.00%	0.00%
Otu0350	Syntrophomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0351	Unclassified Bradyrhizobiaceae	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0352	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0353	Legionella	0.00%	0.00%	0.01%	0.00%	0.01%	0.02%	0.00%
Otu0354	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0355	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0356	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0357	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0358	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0359	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0360	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0361	Algoriphagus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0362	Rhodanobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0363	Unclassified Syntrophaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0364	Sphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0365	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0366	Planctomyces	0.04%	0.00%	0.00%	0.00%	0.04%	0.04%	0.03%
Otu0367	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0368	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0369	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0370	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0371	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0372	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0373	Psychrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0374	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0375	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0376	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0377	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0378	Turneriella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0379	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0380	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0381	Blastopirellula	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0382	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0383	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0384	Meliothermus	0.00%	0.00%	0.00%	0.01%	0.00%	0.01%	0.02%
Otu0385	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0386	Parachlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0387	Alkalibacter	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0388	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0389	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0390	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0391	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0392	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0393	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0394	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0395	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0396	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0397	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0398	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0399	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0400	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0401	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0402	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0403	Unclassified Actinomycetales	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0404	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0405	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0406	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0407	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0408	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0409	Lacbacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0410	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0411	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0412	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0413	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0414	Neosphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0415	Roseococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0416	Unclassified Leptotrichiaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0417	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0418	Staphylococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFH18	15EFH24	15EFH28	15EFH34	15EFH38	15EFH39
Otu0419	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0420	Sphingopyxis	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0421	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0422	Hydrogenispha	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0423	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0424	Thiomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0425	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0426	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0427	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0428	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0429	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0431	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0432	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0433	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0434	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0435	Unclassified Gammaproteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%
Otu0436	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0437	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0438	Unclassified Gammaproteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0439	Unclassified Myxococcia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0440	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0441	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0442	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0443	Bauldia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0444	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0445	Neisseria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0446	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0447	Pedomicrobium	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%
Otu0448	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0449	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0450	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0451	Acinetobacter	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%
Otu0452	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0453	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0454	Fluvivivola	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0455	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0456	Unclassified Phyllobacteriaceae	0.00%	0.02%	0.00%	0.00%	0.00%	0.01%
Otu0457	Veillonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0458	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0459	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0460	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0461	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0462	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0463	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0464	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0465	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0466	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu0467	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0468	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0469	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0470	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0471	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0472	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0473	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0474	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0475	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0476	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0477	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0478	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0479	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0480	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0481	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0482	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0483	Peptostreptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0484	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0485	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0486	Leptolinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0487	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0488	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0489	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0490	Unclassified Comamonadaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0491	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0492	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0493	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0494	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0495	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0496	Unclassified Brucellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0497	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0498	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0499	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0500	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0501	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0502	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFH18	15EFH24	15EFH28	15EFH34	15EFH38	15EFH39
Otu0503	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0504	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0505	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0506	Plancteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0507	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0508	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0509	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0510	Aureispira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0511	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0512	Unclassified Anaerolineaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0513	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0514	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0515	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0516	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0517	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0518	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0519	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0520	Lactococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0521	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0522	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0523	Ga3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0524	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0525	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0526	Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0527	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0528	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0529	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0530	Unclassified Enterobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0531	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0532	Chondromyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0533	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0534	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0535	Unclassified Nitrosomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0536	Ignavibacterium	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%
Otu0537	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0538	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0539	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0540	Bryobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0541	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0542	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0543	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0544	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Otu0545	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0546	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0547	Unclassified Caulobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0548	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0549	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0550	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0551	Peredibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0552	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0553	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0554	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0555	Bacteriovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0556	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0557	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0558	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0559	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0560	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0561	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0562	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0563	Parachlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0564	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0565	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0566	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0567	Unclassified Rhodospirillaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0568	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0569	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0570	Opitutus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0571	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0572	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0573	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.15%	0.00%
Otu0574	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0575	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0576	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0577	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0578	Thiomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0579	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0580	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0581	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0582	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0583	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0584	Pedobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0585	Ignavibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0586	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu0587	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0588	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0589	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0590	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0591	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0592	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0593	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0594	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0595	Neochlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0596	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0597	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0598	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0599	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0600	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0601	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0602	Ferribacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0603	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0604	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0605	Unclassified Rhodospirillales	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0606	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0607	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0608	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0609	Unclassified Acidobacteria_Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0610	Coneixibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0611	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0612	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0613	Unclassified Bacillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0614	Clostridium_III	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0615	Hydrogenophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0616	Hermimionas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0617	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0618	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0619	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0620	Bifidobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0621	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0622	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0623	Unclassified Intrasporangiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0624	Aurantimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0625	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0626	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0627	Unclassified Clostridia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0628	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0629	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0630	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0631	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0632	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0633	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0634	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0635	Unclassified Actinobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0636	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0637	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0638	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0639	Geobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0640	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0641	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0642	Rheinheimeria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0643	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0644	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0645	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0646	Ilumotobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0647	Enterococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0648	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0649	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0650	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0651	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0652	Pedobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0653	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0654	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0655	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0656	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0657	Legionella	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%
Otu0658	Rhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0659	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0660	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0661	Unclassified Bacteriovoracaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0662	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0663	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0664	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0665	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0666	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0667	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0668	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0669	Ochrobactrum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0670	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu0671	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0672	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0673	Unclassified Cytiobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0674	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0675	Moraxella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0676	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0677	Ilumatobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0678	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0679	Gp3	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%
Otu0680	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0681	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0682	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0683	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0684	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0685	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0686	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0687	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0688	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0689	Dietzia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0690	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0691	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0692	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0693	Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0694	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0695	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0696	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0697	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0698	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0699	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0700	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0701	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0702	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0703	Pseudoxanthomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0704	Ilumatobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0705	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0706	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0707	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0708	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0709	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0710	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0711	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0712	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0713	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0714	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0715	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0716	Nevoosphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0717	Rothia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0718	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0719	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0720	Unclassified Cryomorphaceae	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0721	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0722	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0723	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0724	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0725	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0726	Porphyromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0727	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0728	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0729	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0730	Peredibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0731	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0732	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0733	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0734	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0735	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0736	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0737	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0738	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0739	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0740	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0741	Bosea	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0742	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0743	Fusobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0744	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0745	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0746	Unclassified Bradyrhizobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0747	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0748	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0749	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0750	Unclassified Planococcaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0751	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0752	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0753	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0754	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%



OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu0755	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0756	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0757	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0758	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0759	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0760	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0761	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0762	Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0763	Butyrivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0764	Trichococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0765	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0766	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0767	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0768	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0769	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0770	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0771	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0772	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0773	Bifidobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0774	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0775	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0776	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0777	Polynucleobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0778	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0779	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0780	Barnesiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0781	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0782	Cellvibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0783	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0784	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0785	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0786	Phenylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0787	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0788	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0789	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0790	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0791	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0792	Actinomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0793	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0794	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0795	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0796	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0797	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0798	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0799	Beobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0800	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0801	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0802	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0803	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0804	Aerococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0805	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0806	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0807	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0808	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0809	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0810	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0811	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0812	Neochlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0813	Williamsia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0814	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0815	Unclassified Opilutae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0816	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0817	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0818	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0819	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0820	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0821	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0822	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0823	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0824	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0825	Gp13	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0826	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0827	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0828	Unclassified Bacteria	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0829	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0830	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0831	Sneathia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0832	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0833	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0834	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0835	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0836	Unclassified Ktedonobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0837	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0838	Unclassified Prevotellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu0839	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0840	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0841	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0842	Aquabacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0843	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0844	Methylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0845	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0846	Unclassified Veillonellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0847	Coneixibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0848	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0849	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0850	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0851	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0852	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0853	Unclassified Chloroflexi	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0854	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0855	Unclassified Pseudomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0856	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0857	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0858	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0859	Fusobacterium	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0860	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0861	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0862	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0863	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0864	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0865	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0866	Singuliphera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0867	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0868	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0869	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0870	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0871	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0872	Arcobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0873	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0874	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0875	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0876	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0877	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0878	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0879	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0880	Unclassified Cytophagaceae	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0881	Unclassified Bacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu0882	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.12%	0.00%
Otu0883	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0884	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0885	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0886	Halomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0887	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0888	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0889	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0890	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0891	Unclassified Alkaligenaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0892	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0893	Unclassified Spartobacteria_family_incerta	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0894	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0895	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0896	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0897	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0898	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0899	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0900	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0901	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0902	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0903	Chryseobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0904	Unclassified Rhodospirillales	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0905	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0906	Anaerorhabdus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0907	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0908	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0909	Arenimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu0910	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0911	Unclassified Bradyrhizobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0912	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0913	Citricoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0914	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0915	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0916	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0917	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0918	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu0919	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0920	Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0921	Bacteriovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0922	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM18	15EM2A	15EM2B	15EM3A	15EM3B	15EM3B
Otu0923	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0924	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0925	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0926	Unclassified Micromonosporaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0927	Unclassified Fusobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0928	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0929	Gardnerella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0930	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0931	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0932	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0933	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0934	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0935	Unclassified Alphaproteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu0936	Unclassified Bradyrhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0937	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0938	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0939	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0940	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0941	Unclassified Pasteurellales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0942	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu0943	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0944	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0945	Unclassified Spartobacteria_family_incerta	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0946	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0947	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0948	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0949	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0950	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0951	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0952	Devosia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0953	Beijerinckia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0954	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0955	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0956	Desulfuromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0957	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0958	Unclassified Cytophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0959	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0960	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0961	Methylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0962	Holophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0963	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0964	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0965	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0966	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0967	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0968	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0969	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0970	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0971	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0972	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0973	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0974	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0975	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0976	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0977	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0978	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0979	Tolomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0980	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0981	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0982	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0983	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0984	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0985	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0986	Curvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0987	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0988	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0989	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0990	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0991	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0992	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0993	Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0994	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0995	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0996	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0997	Exiguobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0998	Unclassified Rhizobiales_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu0999	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1000	Peptoniphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1001	Nesterenkonia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1002	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1003	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1004	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1005	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1006	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code						
		15EM18	15EM24	15EM28	15EM34	15EM38	15EM39	15EM38
Otu1007	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1008	Unclassified Planctomycetacia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1009	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1010	Nitrospirilla	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1011	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1012	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1013	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1014	Clostridium_XI	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1015	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1016	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1017	_3_genus_inferae_sed5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1018	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1019	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1020	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1021	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1022	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1023	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1024	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1025	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1026	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1027	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1028	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1029	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1030	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1031	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1032	Algoriphagus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1033	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1034	Unclassified Desulfobacteraceae	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
Otu1035	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1036	Turicibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1037	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1038	Pseudonocardia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1039	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1040	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1041	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1042	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1043	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1044	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1045	Labrys	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1046	Geothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1047	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1048	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1049	Perluvidbaca	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1050	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1051	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1052	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1053	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1054	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1055	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1056	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1057	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1058	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1059	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1060	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1061	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1062	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1063	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1064	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1065	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1066	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1067	Unclassified Ktedonobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1068	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1069	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1070	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1071	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1072	Gp7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1073	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1074	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1075	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1076	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1077	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1078	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1079	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1080	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1081	Unclassified Verrucomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1082	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1083	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1084	Aquomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1085	Cuipavidus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1086	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1087	Dyadobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1088	Unclassified Proteobacteria	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.01%
Otu1089	Cloacibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1090	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM18	15EM24	15EM28	15EM34	15EM38	15EM38
Otu1091	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1092	Sanguibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1093	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1094	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1095	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1096	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1097	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1098	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1099	Anaeroplasm	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1100	Faecalibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1101	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1102	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1103	Simkania	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1104	Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1105	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1106	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1107	Pedomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1108	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1109	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1110	Diplulus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1111	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1112	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1113	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1114	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1115	Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1116	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1117	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1118	Parabacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1119	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1120	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1121	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1122	Neochlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1123	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1124	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1125	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1126	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1127	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1128	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1129	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1130	Unclassified Clostridiales Incertae Sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1131	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1132	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1133	Singuliphæra	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1134	Sulfurospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1135	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1136	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1137	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1138	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1139	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1140	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1141	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1142	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1143	Prevotella	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Otu1144	Unclassified Bacteroidales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1145	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1146	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1147	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1148	Wingradskyella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1149	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1150	Unclassified Clostridiales_1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1151	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1152	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1153	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1154	Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1155	Unclassified Bacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1156	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1157	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1158	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1159	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1160	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1161	Skermanella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1162	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1163	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1164	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1165	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1166	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1167	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1168	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1169	Sphingosinella	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1170	Subdoligranulum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1171	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1172	Unclassified Betaproteobacteria	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1173	Methylobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1174	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM18	15EM24	15EM28	15EM34	15EM38	15EM38
Otu175	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu176	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu177	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu178	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu179	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu180	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu181	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu182	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu183	Unclassified Desulfobubaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu184	Labrys	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu185	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu186	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu187	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu188	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu189	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu190	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu191	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu192	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu193	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu194	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu195	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu196	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu197	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu198	Hyphomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu199	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu200	Unclassified Polyangiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu201	Ktedonobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu202	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu203	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu204	Clostridium_XIVa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu205	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu206	Unclassified Verrucomicrobia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu207	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu208	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu209	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu210	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu211	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu212	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu213	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu214	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu215	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu216	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu217	Geothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu218	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu219	Rhizosium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu220	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu221	Unclassified Clostridiaceae_1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu222	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu223	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu224	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu225	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu226	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu227	Unclassified Rhodocyclaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu228	Unclassified Thermomonosporaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu229	Unclassified Chloroflexi	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu230	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu231	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu232	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu233	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu234	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu235	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu236	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu237	Planococcaceae_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu238	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu239	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu240	Unclassified Sphingobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu241	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu242	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu243	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu244	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu245	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu246	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu247	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu248	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu249	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu250	Campylobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu251	Zwarrzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu252	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu253	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu254	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu255	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu256	Phenylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu257	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu258	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1259	Anaerorhabdus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1260	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1261	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1262	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1263	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1264	Haloferula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1265	Gp7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1266	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1267	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1268	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1269	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1270	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1271	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1272	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1273	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1274	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1275	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1276	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1277	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1278	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1279	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1280	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1281	Gp7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1282	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1283	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1284	Clostridium_sensu_stricto	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1285	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1286	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1287	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1288	Rhizomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1289	Corynebacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1290	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1291	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1292	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1293	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1294	Unclassified Rhodospirillaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1295	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1296	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1297	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1298	Arenicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1299	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1300	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1301	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1302	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1303	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1304	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1305	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1306	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1307	Simkania	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1308	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1309	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1310	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1311	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1312	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1313	Unclassified Algalginaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%
Otu1314	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1315	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1316	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1317	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1318	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1319	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1320	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1321	Unclassified Algalginaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1322	Nitrospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1323	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1324	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1325	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1326	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1327	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1328	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1329	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1330	Unclassified Phyllobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1331	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1332	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1333	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1334	Sutterella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1335	Truepera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1336	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1337	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1338	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1339	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1340	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1341	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1342	Bdelovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1343	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1344	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1345	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1346	Arcobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1347	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1348	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1349	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1350	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1351	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1352	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1353	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1354	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1355	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1356	Unclassified Spingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1357	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1358	Phascocartobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1359	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1360	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1361	Prosthecoacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1362	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1363	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1364	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1365	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1366	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1367	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1368	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1369	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1370	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1371	Novosphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1372	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1373	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1374	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1375	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1376	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1377	Unclassified Verrucomicrobia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1378	Pasteuria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1379	Unclassified Spingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1380	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1381	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1382	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1383	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1384	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1385	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1386	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1387	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1388	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1389	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1390	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1391	Oplutus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1392	Fluviolca	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1393	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1394	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1395	Unclassified Desulfuovibrionales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1396	Unclassified Beijerinckiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1397	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1398	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1399	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1400	Blastomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1401	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1402	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1403	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1404	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1405	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1406	Unclassified Spingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1407	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1408	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1409	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1410	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1411	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1412	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1413	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1414	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1415	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1416	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1417	Pseudomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1418	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1419	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1420	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1421	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1422	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1423	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1424	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1425	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1426	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1427	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1428	Unclassified Spingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%



OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1429	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1430	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1431	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1432	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1433	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1434	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1435	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1436	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1437	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1438	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1439	Acholeplasma	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1440	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1441	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1442	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1443	Parachlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1444	Elizabethkingia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1445	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1446	Fangia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1447	Unclassified Bacteroidetes	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu1448	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1449	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1450	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1451	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1452	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1453	Unclassified Microbacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1454	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1455	Unclassified Alteromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1456	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1457	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1458	Streptococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1459	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1460	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1461	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1462	Enhydrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1463	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1464	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1465	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1466	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1467	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1468	Ornithinimicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1469	Unclassified Bacteroidales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1470	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1471	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1472	Blastococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1473	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1474	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1475	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1476	Barnesiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1477	Arcobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1478	Dyadobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1479	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1480	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1481	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1482	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1483	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1484	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1485	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1486	Unclassified Flavobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1487	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1488	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1489	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1490	SR1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1491	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1492	Aeromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1493	Bilophila	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1494	Opitutus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1495	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1496	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1497	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1498	Gs4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1499	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1500	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1501	Blastopirellula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1502	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1503	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1504	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1505	Fusobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1506	Singuliphera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1507	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1508	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1509	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1510	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1511	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1512	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM118	15EM124	15EM128	15EM134	15EM138	15EM138
Otu1513	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1514	Unclassified Bacteroidales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1515	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1516	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1517	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1518	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1519	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1520	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1521	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1522	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1523	Moryella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1524	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1525	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1526	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1527	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1528	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1529	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1530	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1531	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1532	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1533	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1534	Unclassified Opitutae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1535	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1536	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1537	Actinobaculum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1538	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1539	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1540	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1541	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1542	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1543	Paludibacter	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu1544	Unclassified Anaerolineaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1545	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1546	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1547	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1548	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1549	Oxidibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1550	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1551	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1552	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1553	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1554	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1555	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1556	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1557	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1558	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1559	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1560	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1561	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1562	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1563	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1564	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1565	Desulfobacula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1566	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1567	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1568	Unclassified Lactobacillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1569	Limnobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1570	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1571	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1572	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1573	Unclassified Neisseriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1574	Caldivrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1575	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1576	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1577	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1578	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1579	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1580	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1581	Hydrotales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1582	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1583	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1584	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1585	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1586	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1587	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1588	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1589	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1590	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1591	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1592	Unclassified Enterobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1593	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1594	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1595	Acinetobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1596	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM13B	15EM12A	15EM12B	15EM13A	15EM13B	15EM13B
Otu1597	Maikla	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1598	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1599	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1600	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1601	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1602	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1603	Herminimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1604	Unclassified Veillonellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1605	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1606	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1607	Unclassified Ruminococcaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1608	Unclassified Aerococcaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1609	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1610	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1611	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1612	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1613	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1614	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1615	Muricauda	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1616	Unclassified Erythrorhizaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1617	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1618	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1619	Phenylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Otu1620	Unclassified Erythrobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1621	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1622	Unclassified Mycococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1623	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1624	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1625	Porphyromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1626	Alistipes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1627	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1628	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1629	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1630	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1631	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1632	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1633	OTU1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1634	Unclassified Desulfobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1635	Phenylobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1636	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1637	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1638	Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1639	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1640	Thiocystis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1641	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1642	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1643	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1644	Unclassified Fusobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1645	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1646	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1647	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1648	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1649	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1650	Simkania	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1651	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1652	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1653	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1654	Blastomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1655	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1656	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1657	Unclassified Ruminococcaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1658	Anaerostipes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1659	Helcococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1660	Pasteuria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1661	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1662	Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1663	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1664	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1665	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1666	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1667	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1668	Parvimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1669	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1670	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1671	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1672	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1673	Unclassified Sphingomonadales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1674	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1675	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1676	Delta	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1677	Nitrospira	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1678	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1679	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1680	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1681	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1682	Peptoniphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1683	Armatimonadetes_ga2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1684	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1685	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1686	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1687	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1688	Caulobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1689	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1690	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1691	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1692	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1693	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1694	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1695	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1696	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1697	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1698	Psychrobacter	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1699	Unclassified Aerococaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1700	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1701	TN7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1702	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1703	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1704	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1705	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1706	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1707	Unclassified Flavobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1708	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1709	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1710	Hydrogenophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1711	Unclassified Camamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1712	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1713	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1714	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1715	Oleispira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1716	Rosebacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1717	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1718	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1719	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1720	Rhodopirellula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1721	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1722	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1723	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1724	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1725	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1726	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1727	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1728	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1729	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1730	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1731	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1732	Rothia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1733	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1734	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1735	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Otu1736	Sphingomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1737	Dialister	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1738	Unclassified Verrucomicrobia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1739	Lutibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1740	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1741	Saccharofermentans	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1742	Gemella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1743	Desulfomonile	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1744	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1745	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1746	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1747	Unclassified Bradyrhizobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1748	Desulfocapsa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1749	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1750	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1751	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1752	Unclassified Camamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1753	Prevotella	0.00%	0.00%	0.12%	0.00%	0.00%	0.00%
Otu1754	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1755	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1756	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1757	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1758	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1759	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1760	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1761	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1762	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1763	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1764	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu1765	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1766	Armatimonas_Armatimonadetes_gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1767	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1768	Saccharofermentans	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1769	Hydrogenophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1770	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1771	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1772	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1773	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1774	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1775	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1776	Unclassified Proteobacteria	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1777	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1778	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1779	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1780	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1781	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1782	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1783	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1784	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1785	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1786	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1787	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu1788	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1789	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1790	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1791	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1792	Catellibacterium	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Otu1793	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1794	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1795	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1796	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1797	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1798	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1799	Aminobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1800	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1801	Lactobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1802	Unclassified Bacteria	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
Otu1803	Fluvicola	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1804	Hyphomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1805	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1806	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1807	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1808	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1809	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1810	Unclassified Beijerinckiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1811	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1812	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1813	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1814	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1815	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1816	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1817	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1818	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1819	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1820	Unclassified Clostridiales_Incertae_Sedis_)	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1821	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1822	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1823	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1824	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1825	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1826	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1827	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1828	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1829	Curvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1830	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1831	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1832	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1833	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1834	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1835	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1836	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1837	Corynebacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1838	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1839	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1840	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1841	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1842	Murdobdella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1843	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1844	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1845	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1846	Unclassified Proteobacteria	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Otu1847	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1848	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1849	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1850	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1851	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1852	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1853	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1854	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1855	Unclassified Pseudomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1856	Unclassified Bradyrhizobaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1857	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1858	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1859	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1860	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1861	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1862	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1863	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1864	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1865	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1866	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1867	Corynebacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1868	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1869	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1870	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1871	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1872	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1873	Simkania	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1874	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1875	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1876	Capnocytophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1877	Blastomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1878	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1879	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1880	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1881	Exiguobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1882	Unclassified Pseudomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1883	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
Otu1884	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1885	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1886	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1887	Unclassified Pseudomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1888	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1889	Clostridium_XIVa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1890	Brevundimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1891	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1892	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1893	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1894	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1895	Unclassified Comamonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1896	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1897	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1898	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1899	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1900	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1901	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1902	Hydrogenophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1903	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1904	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1905	Cloacibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1906	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1907	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1908	Arthrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1909	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1910	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1911	Catonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1912	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1913	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1914	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1915	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1916	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1917	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1918	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1919	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1920	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1921	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1922	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1923	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1924	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1925	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1926	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1927	Unclassified Chloroflexi	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1928	Unclassified Ruminococcaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1929	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1930	Ktedonobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1931	Cytophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1932	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu1933	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1934	Atopobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1935	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1936	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1937	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1938	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1939	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1940	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1941	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1942	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1943	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1944	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1945	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1946	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1947	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1948	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1949	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1950	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1951	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1952	Parhyphomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1953	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1954	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1955	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1956	Unclassified Sphingobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1957	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1958	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1959	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1960	Mucilagibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1961	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1962	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1963	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1964	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1965	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1966	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1967	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1968	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1969	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1970	Arenimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1971	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1972	Geminicoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1973	Unclassified Flavobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1974	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1975	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1976	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1977	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1978	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1979	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1980	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1981	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1982	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1983	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1984	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1985	Unclassified Bradyrhizobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1986	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1987	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1988	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1989	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1990	Collinsella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1991	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1992	Opitulus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1993	Treponema	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1994	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1995	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1996	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1997	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1998	Dongia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu1999	Duganella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2000	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2001	Clostridium_xi	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2002	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2003	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2004	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2005	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2006	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2007	Selenomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2008	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2009	Barnesiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2010	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2011	Pirevella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2012	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2013	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2014	Anaerococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2015	Enterorhabdus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2016	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu2017	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2018	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2019	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2020	Unclassified Polyangiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2021	Gemmata	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2022	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2023	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2024	Alkanindiges	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2025	Azoarcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2026	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2027	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2028	Unclassified Methylcoccaeae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2029	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2030	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2031	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2032	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2033	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2034	Gp17	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2035	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2036	Simkania	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2037	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2038	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2039	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2040	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2041	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2042	Singulisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2043	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2044	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2045	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2046	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2047	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2048	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2049	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2050	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2051	Unclassified Solirubrobacterales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2052	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2053	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2054	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2055	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2056	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2057	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2058	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2059	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2060	Alitipes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2061	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2062	Clostridium_sensu_stricto	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2063	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2064	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2065	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2066	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2067	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2068	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2069	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2070	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2071	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2072	Varivoxax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2073	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2074	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2075	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2076	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2077	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2078	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2079	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2080	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2081	Rhizomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2082	Gp13	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2083	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2084	Unclassified Kineosporiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2085	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2086	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2087	Actinallomurus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2088	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2089	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2090	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2091	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2092	Unclassified Xanthomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2093	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2094	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2095	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2096	Chitinophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2097	Devosia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2098	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2099	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2100	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%



OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu2101	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2102	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2103	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2104	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2105	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2106	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2107	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2108	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2109	Unclassified Spingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2110	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2111	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2112	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2113	Coneisbacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2114	Armatimonas_Armatimonadetes_gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2115	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2116	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2117	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2118	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2119	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2120	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2121	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2122	Niastella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2123	Pedobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2124	Nitriiruptor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2125	Gp18	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2126	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2127	Angustibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2128	Opitubus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2129	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2130	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2131	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2132	Asticcacaulis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2133	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2134	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2135	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2136	Rhodomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2137	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2138	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2139	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2140	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2141	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2142	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2143	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2144	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2145	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2146	Solirubrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2147	Gp17	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2148	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2149	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2150	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2151	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2152	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2153	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2154	Byssovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2155	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2156	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2157	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2158	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2159	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2160	Vampirovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2161	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2162	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2163	Zwarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2164	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2165	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2166	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2167	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2168	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2169	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2170	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2171	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2172	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2173	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2174	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2175	Gp6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2176	Chthonomonas_Armatimonadetes_gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2177	Pseudoflavonifactor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2178	Rhodomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2179	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2180	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2181	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2182	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2183	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2184	Unclassified Spingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu2185	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2186	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2187	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2188	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2189	Gemmatimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2190	Sulfurospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2191	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2192	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2193	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2194	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2195	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2196	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2197	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2198	Capnocytophaga	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2199	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2200	Blastopirellula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2201	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2202	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2203	Neochlamydia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2204	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2205	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2206	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2207	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2208	Bacteriovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2209	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2210	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2211	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2212	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2213	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2214	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2215	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2216	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2217	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2218	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2219	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2220	Mycobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2221	Unclassified Saprospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2222	Longilinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2223	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2224	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2225	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2226	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2227	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2228	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2229	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2230	Vibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2231	Leptotrichia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2232	Unclassified Ophitae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2233	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2234	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2235	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2236	Unclassified Lactobacillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2237	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2238	Unclassified Burkholderiales_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2239	Unclassified Clostridia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2240	Parvibaculum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2241	Bosea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2242	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2243	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2244	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2245	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2246	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2247	Actinomycetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2248	Flavobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2249	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2250	Clostridium_sensu_stricto	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2251	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2252	Magnetospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2253	Unclassified Saprospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2254	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2255	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2256	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2257	Unclassified Oxalobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2258	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2259	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2260	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2261	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2262	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2263	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2264	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2265	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2266	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2267	Unclassified Prevotellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2268	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu2269	Blastomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2270	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2271	Nocardia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2272	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2273	Beijerinckia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2274	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2275	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2276	Unclassified Peptococaceae_1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2277	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2278	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2279	Cateflibacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2280	Singulivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2281	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2282	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2283	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2284	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2285	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2286	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2287	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2288	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2289	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2290	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2291	Unclassified Rhodobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2292	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2293	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2294	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2295	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2296	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2297	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2298	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2299	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2300	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2301	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2302	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2303	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2304	Sphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2305	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2306	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2307	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2308	Armatimonadetes_gp5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2309	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2310	Caloramator	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2311	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2312	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2313	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2314	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2315	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2316	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2317	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2318	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2319	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2320	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2321	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2322	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2323	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2324	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2325	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2326	Sphingisnicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2327	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2328	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2329	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2330	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2331	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2332	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2333	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2334	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2335	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2336	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2337	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2338	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2339	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2340	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2341	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2342	Deinococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2343	Gp16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2344	Unclassified Clostridia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2345	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2346	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2347	Leucostomic	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2348	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2349	Clostridium_XIVa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2350	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2351	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2352	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM24	15EFM28	15EFM34	15EFM38	15EFM38
Otu2353	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2354	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2355	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2356	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2357	Proteus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2358	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2359	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2360	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2361	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2362	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2363	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2364	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2365	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2366	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2367	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2368	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2369	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2370	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2371	Aquabacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2372	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2373	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2374	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2375	Cellulomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2376	Caedibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2377	Unclassified Hyphomicrobiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2378	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2379	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2380	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2381	Unclassified Springbacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2382	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2383	Desulfomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2384	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2385	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2386	Novosphingobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2387	Bacteroides	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2388	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2389	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2390	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2391	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2392	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2393	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2394	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2395	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2396	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2397	Caldilinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2398	Unclassified Alcaligenaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2399	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2400	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2401	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2402	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2403	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2404	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2405	Unclassified Gracilbacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2406	Bifida	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2407	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2408	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2409	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2410	Caldilinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2411	Bdellovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2412	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2413	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2414	Opilutius	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2415	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2416	Nitrospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2417	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2418	Flavisolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2419	Unclassified unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2420	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2421	Roseomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2422	Unclassified Actinomycetales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2423	Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2424	Unclassified Veillonellaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2425	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2426	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2427	Unclassified Parachlamydiaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2428	Unclassified Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2429	Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2430	Unclassified Firmicutes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2431	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2432	Flavobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2433	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2434	Veillonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2435	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2436	Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EM118	15EM124	15EM128	15EM134	15EM138	15EM138
Otu2437	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2438	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2439	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2440	Pasteuria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2441	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2442	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2443	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2444	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2445	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2446	Unclassified Cystobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2447	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2448	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2449	Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2450	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2451	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2452	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2453	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2454	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2455	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2456	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2457	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2458	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2459	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2460	TM7_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2461	Unclassified Thermomicrobia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2462	Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2463	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2464	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2465	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2466	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2467	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2468	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2469	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2470	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2471	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2472	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2473	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2474	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2475	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2476	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2477	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2478	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2479	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2480	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2481	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2482	OD1_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2483	Unclassified Lachnospiraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2484	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2485	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2486	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2487	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2488	Methylocella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2489	Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2490	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2491	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2492	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2493	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2494	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2495	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2496	Unclassified Deltaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2497	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2498	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2499	Catenulispora	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2500	Unclassified Acetobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2501	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2502	Spartobacteria_genera_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2503	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2504	Unclassified Bacteriovoraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2505	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2506	Rhizomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2507	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2508	Singuliphpera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2509	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2510	Terimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2511	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2512	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2513	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2514	Actinobolomurus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2515	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2516	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2517	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2518	Vogesella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2519	Unclassified Chlamydiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2520	Unclassified Methylocystaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

OTU number	Taxonomy	Sample code					
		15EFM18	15EFM2A	15EFM2B	15EFM3A	15EFM3B	15EFM3B
Otu2521	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2522	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2523	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2524	Armatimonadetes_gg5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2525	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2526	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2527	Phenylbacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2528	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2529	Gp3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2530	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2531	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2532	Ferruginibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2533	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2534	Unclassified Rhodocytales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2535	Pseudomonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2536	Unclassified Rhodospirillales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2537	Unclassified Rhodospirillaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2538	Unclassified Chitinophagaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2539	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2540	Alphabacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2541	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2542	Oscillibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2543	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2544	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2545	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2546	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2547	Zavarzinella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2548	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2549	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2550	Byssovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2551	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2552	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2553	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2554	Unclassified Acidimicrobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2555	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2556	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2557	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2558	Hallcomenobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2559	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2560	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2561	Unclassified Sphingobacteriales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2562	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2563	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2564	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2565	Byssovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2566	Unclassified Bacteroidetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2567	Unclassified Proteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2568	Unclassified Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2569	Unclassified Caulobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2570	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2571	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2572	Unclassified Myxococcales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2573	Facklamia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2574	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2575	Planctomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2576	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2577	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2578	Gp2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2579	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2580	Unclassified Rhizobiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2581	3_genus_incertae_sedis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2582	Unclassified Actinobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2583	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2584	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2585	Gp4	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2586	Streptomyces	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2587	Unclassified Clostridiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2588	Unclassified Sphingomonadaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2589	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2590	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2591	Unclassified Betaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2592	Unclassified Planctomycetaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2593	Unclassified Gammaproteobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2594	Prevotella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2595	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2596	Anaeromyobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2597	Gp1	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2598	Unclassified Burkholderiales	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Otu2599	Unclassified Bacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%