



Microbial Analysis Report

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Submitted to
Sample Wastewater Client

METAGENOMICS • DATA SCIENCE • BIOBANKING

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Disclaimer

The information provided in this report is based on the latest DNA sequencing methodologies and is for research purposes only. Microbe Detectives takes no responsibility for decisions made based upon this information.

Executive Summary

Tetrasphaera was found, indicating biological phosphorus removal activity. The abundance of this bacteria increased through fall 2015 and spring 2016, peaking in March 2106 but remaining relatively high through May 2016.

Nitrosomonas was found to be the primary ammonia oxidizing bacteria while *Nitrospira* and a new bacteria, *Nitrotoga*, both contributed to nitrite oxidation. The October and November 2015 samples, however had very low levels of any AOB or NOB bacteria, indicating ammonia removal by other bacteria, possibly *Paraococcus*, which is known to perform simultaneous nitrification denitrification and increased in abundance in these samples.

The centrifuge feed samples indicate a high thermophilic digester environment dominated by the methanogens, *Methanosarcina* (methane production from acetate) and *Methanothermus* (methane production from hydrogen). A small amount of sulfate reducing bacteria were found in these samples as well indicating the presence of sulfate which can interfere with methane production and can result in the formation of hydrogen sulfide gas.

The digester sample was much different than the centrifuge feed samples and did not contain methanogens.

Microthrix was found in all MLSS samples, reaching peak abundance in the October and November 2015 samples, potentially causing issues with foaming and settling. Other filaments such as *Haliscomenobacter*, *Flexibacter*, and *Trichococcus* were also found in the MLSS samples.

Background

The following samples were received:

Client: Date Received: 08/06/15, Sample Group: MLSS, Sample ID: MLSS/080615

Client: Date Received: 10/19/15, Sample Group: MLSS, Sample ID: MLSS/101915

Client: Date Received: 11/30/15, Sample Group: MLSS, Sample ID: MLSS/113015

Client: Date Received: 03/28/16, Sample Group: MLSS, Sample ID: MLSS/032816

Client: Date Received: 05/04/16, Sample Group: MLSS, Sample ID: MLSS/050416

Client: Date Received: 10/18/15, Sample Group: FinalEffluent, Sample ID: FinalEffluent/101815

Client: Date Received: 05/04/16, Sample Group: Dig4, Sample ID: Dig4/050416

Client: Date Received: 05/04/16, Sample Group: CentFeed, Sample ID: CentFeed/050416

Client: Date Received: 11/30/15, Sample Group: CentFeed, Sample ID: CentFeed/113015

DNA results and analysis are presented below.

Results

DNA data are displayed in Figure 5 and the Microbe Detectives tables. The data in these tables is a subset of the total data, focusing on bacteria that are typically important in wastewater systems. The full data is also provided in a spreadsheet. Data presented are bacterial relative abundance (% of total bacteria in the sample). For example 0.12% Actinobacteria means that 0.12% of bacteria in the sample are Actinobacteria.

Please note, the raw data spreadsheet identifies each bacteria with a taxonomic string comprised of Domain>Kingdom>Phylum>Class>Order>Family>Genus>Species. Typically, most bacteria are identified to the genus level. If there is a strong match with our database they may be identified to the species level. On the other hand, if there are weaker matches to our database, they may be identified only to the family, order or class level. Many bacteria remain unstudied and unknown to science, but our database continues to grow and improve with the rapid advancement of DNA-based microbiology.

Phylum

Figure 5 shows the phylum distribution for the sample. The predominant phyla were Proteobacteria, Bacteroidetes which contain many common environmental bacteria.

Gram-Negative

Sample ID: MLSS/080615 - Proteobacteria 30.93%, Actinobacteria 23.25%, Bacteroidetes 18.87%, Firmicutes 6.92%, Chloroflexi 0.8%, Verrucomicrobia 0.1% and Cyanobacteria 0% were detected in this sample.

Sample ID: MLSS/101915 - Proteobacteria 29.76%, Actinobacteria 20.15%, Bacteroidetes 10.1%, Firmicutes 3.36%, Chloroflexi 0.82%, Verrucomicrobia 0.82% and Cyanobacteria 0% were detected in this sample.

Sample ID: MLSS/113015 - Proteobacteria 24.7%, Bacteroidetes 17.2%, Actinobacteria 13%, Firmicutes 3.23%, Chloroflexi 2.37%, Verrucomicrobia 1.04% and Cyanobacteria 0% were detected in this sample.

Sample ID: MLSS/032816 - Proteobacteria 36.51%, Actinobacteria 17.86%, Bacteroidetes 16.07%, Firmicutes 4.38%, Chloroflexi 2.59%, Verrucomicrobia 1.04% and Cyanobacteria 0% were detected in this sample.

Sample ID: MLSS/050416 - Proteobacteria 29.24%, Actinobacteria 24.37%, Bacteroidetes 20.23%, Firmicutes 6.85%, Chloroflexi 0.93%, Verrucomicrobia 0.9% and Cyanobacteria 0% were detected in this sample.

Sample ID: FinalEffluent/101815 - Proteobacteria 26.12%, Bacteroidetes 6.61%, Actinobacteria 4.15%, Verrucomicrobia 2.17%, Firmicutes 1.34%, Chloroflexi 0.18% and Cyanobacteria 0% were detected in this sample.

Sample ID: Dig4/050416 - Firmicutes 49.16%, Proteobacteria 30.82%, Bacteroidetes 4.93%, Actinobacteria 2.88%, Verrucomicrobia 0.37% and Chloroflexi 0% were detected in this sample.

Sample ID: CentFeed/050416 - Firmicutes 11.55%, Actinobacteria 3.67%, Proteobacteria 2.24%, Bacteroidetes 0.98% and Verrucomicrobia 0% were detected in this sample.

Sample ID: CentFeed/113015 - Firmicutes 12.71%, Bacteroidetes 4.04%, Proteobacteria 2.11%, Actinobacteria 1.27%, Chloroflexi 0.16% and Verrucomicrobia 0% were detected in this sample.

These are gram negative bacteria that include many environmental bacteria, especially freshwater and marine bacteria. This phyla includes anaerobic, aerobic and facultative bacteria (facultative means they can survive in aerobic or anaerobic environments). Many bacteria important in wastewater treatment fall into the Proteobacteria phyla including ammonia oxidizing bacteria, sulfate-reducing bacteria, and phosphorus accumulating bacteria.

Bacteroidetes is a very common phyla of gram negative environmental bacteria that includes both aerobic and anaerobic bacteria. One of the most well-studied genera in this phyla is *Bacteroides* a very common inhabitant of the human large intestine. The presence of *Bacteroides* in particular likely indicates the presence of fecal matter from warm-blooded animals and possibly humans.

Cyanobacteria are gram-negative bacteria that obtain most or all of their energy from sunlight and typically utilize inorganic carbon to build cell materials. These bacteria are commonly called blue-green algae, though they are actually bacteria, not eukaryotic algae. Most “algal blooms” are caused by Cyanobacteria. Some of these bacteria such as *Microcystis* contain neurotoxins. As a result, algal blooms can be dangerous to mammals. Algal blooms are typically triggered by warm, stagnant water and high nutrients (nitrogen and phosphorus). These blooms produce oxygen during daylight but consume oxygen during night-time and as cells die and decay. This decay can lead to oxygen-starved waters like those found in the Gulf of Mexico dead zone which is inhospitable to fish and most life forms.

Nitrospirae are a phyla of gram-negative bacteria that are important in the nitrogen cycle. These bacteria are very important in wastewater treatment and other freshwater and marine environments where they oxidize nitrite to nitrate and play a crucial role in removing ammonia from wastewater. These bacteria are able to compete well at low concentrations of nitrite and oxygen. In the past, it was thought that *Nitrobacter* was the primary nitrite-oxidizing bacteria found in wastewater treatment plants. This mistake was based upon culture studies that were able to grow *Nitrobacter* from wastewater samples. However, scientists have more recently learned (based on DNA methods) that *Nitrobacter* is not typically common in wastewater treatment plants and doesn't compete well at low concentrations of nitrite even though it grows well in culture (which usually contains high concentrations of nitrite).

Synergistetes are a phyla of bacteria involved in methane production. These bacteria are frequently symbionts with methanogenic archaea.

Chloroflexi are a somewhat new and unstudied phyla. Some of these bacteria may be important filaments in wastewater treatment.

Verrucomicrobia are a somewhat new and unstudied phyla. These bacteria are frequently correlated with cyanobacterial blooms in freshwaters and likely consume simple carbohydrates released from cyanobacteria or other sources. They tend to be fast growing bacteria.

Planctomycetes are a unique phyla of bacteria that are ovoid and reproduce by budding. This phyla includes most or all of the bacteria capable of performing anammox (anaerobic ammonia oxidation) in wastewater treatment which is a novel method to remove ammonia with substantially lower energy consumption than conventional processes that rely on nitrifiers and denitrifiers.

Gram-Positive

Firmicutes are gram-positive and are generally rod-like (bacilli) or round (cocci) cells. Many Firmicutes produce endospores that are resistant to drying and can survive extreme conditions. One example is *Clostridia tetani*, the bacteria that survives in soil and can cause tetanus. Firmicutes are important in beer, wine and cider spoilage. The primary subgroups of Firmicutes include the *Clostridia* class which are strictly anaerobic and the *Bacilli* which are obligate or facultative aerobes. In wastewater treatment, the presence of Firmicutes may indicate anaerobic conditions and could also indicate the presence of fermenting bacteria which are important for the production of volatile fatty acids necessary for biological phosphorus removal.

Actinobacteria are gram-positive and are frequently soil-dwelling bacteria, though a major portion of freshwater bacteria also fall into this phyla. Actinobacteria are known for producing secondary metabolites (compounds not directly necessary for the cell's survival) such as antibiotics and they are also known for degrading complex organics as part of the natural decay process. *Streptomyces* is one example which is famous for producing the majority of antibiotics used in medicine. In wastewater treatment, these bacteria are mostly known for causing problems such as filamentous bulking and foaming. *Microthrix* and *Gordonia* (aka *Nocardia*) are the two most-well known problematic Actinobacteria. The Actinobacteria are known for creating filamentous forms that can cause settling issues in wastewater treatment plants.

Fermenting Bacteria

Sample ID: MLSS/080615 - *Tetrasphaera* 1.18% was detected in the sample.

Sample ID: MLSS/101915 - *Tetrasphaera* 2.02%, *Streptococcus* 0.14%, *Lactococcus* 0.13% and *Lactobacillus* 0.06% were detected in this sample.

Sample ID: MLSS/113015 - *Tetrasphaera* 3.37%, *Streptococcus* 0.26%, *Lactococcus* 0.12% and *Lactobacillus* 0.1% were detected in this sample.

Sample ID: MLSS/032816 - *Tetrasphaera* 5.77% was detected in the sample.

Sample ID: MLSS/050416 - *Tetrasphaera* 3.17% and *Streptococcus* 0.08% were detected in this sample.

Sample ID: FinalEffluent/101815 - *Tetrasphaera* 0.15% and *Propionivibrio* 0.06% were detected in this sample.

Sample ID: Dig4/050416 - *Lactococcus* 2.66%, *Streptococcus* 1.68% and *Propionivibrio* 0.29% were detected in this sample.

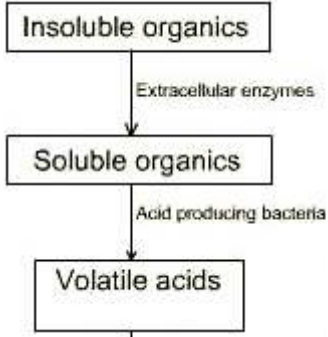
Sample ID: CentFeed/050416 - *Tetrasphaera* 0.26% was detected in the sample.

Sample ID: CentFeed/113015 - None were detected in this sample.

Fermenting bacteria produce volatile fatty acids (such as acetic acid) necessary for biological phosphorus removal. Fermentation can also occur upstream in sewer systems that have extended residence times.

Fermenting bacteria are generally anaerobic bacteria. Figure 1 demonstrates the steps involved in fermentation in wastewater. The first step may be hydrolysis of large insoluble organics with extracellular microbial enzyme to break down the organics and produce soluble compounds that can be taken into a cell. The next step is production of volatile fatty acids in anaerobic conditions.

FIGURE 1. DIAGRAM DEMONSTRATING HYDROLYSIS THROUGH FERMENTATION IN WASTEWATER TREATMENT



Phosphorus Bacteria

Sample ID: MLSS/080615 - Tetrasphaera 1.18% and Dechloromonas 0.21% were detected in this sample.

Sample ID: MLSS/101915 - Tetrasphaera 2.02% was detected in the sample.

Sample ID: MLSS/113015 - Tetrasphaera 3.37% was detected in the sample.

Sample ID: MLSS/032816 - Tetrasphaera 5.77% was detected in the sample.

Sample ID: MLSS/050416 - Tetrasphaera 3.17% was detected in the sample.

Sample ID: FinalEffluent/101815 - Tetrasphaera 0.15% and Dechloromonas 0.1% were detected in this sample.

Sample ID: Dig4/050416 - None were detected in this sample.

Sample ID: CentFeed/050416 - Tetrasphaera 0.26% was detected in the sample.

Sample ID: CentFeed/113015 - None were detected in this sample.

Phosphorus accumulating organisms (PAOs) are Proteobacteria with a unique metabolic ability to take up and store volatile fatty acids (VFAs) such as acetic acid during anaerobic conditions. The PAOs consume polyphosphate for energy during anaerobic conditions and take up organics and store them as PHA (polyhydroxyacetate). They then consume PHA for energy during aerobic conditions and take up phosphate to store energy as a polyphosphate granule (Figure 2). Figure 3 shows how this metabolism can be harnessed in wastewater treatment to remove phosphorus biologically rather than using chemicals.

FIGURE 2. BIOLOGICAL PHOSPHORUS REMOVAL MECHANISM

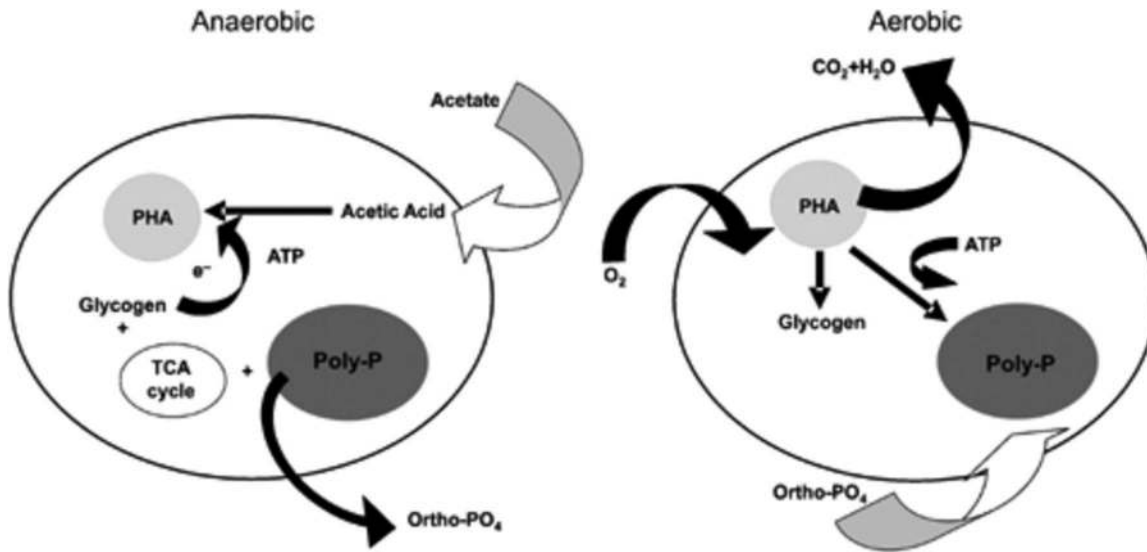
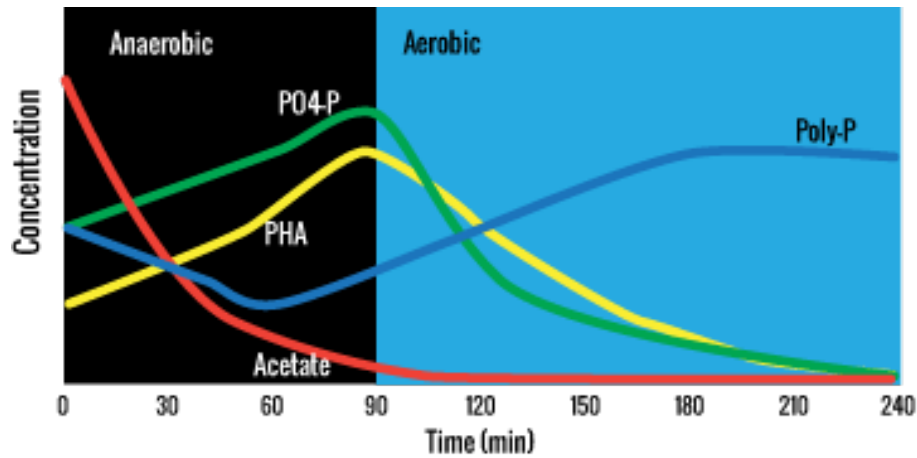


FIGURE 3. BIOLOGICAL PHOSPHORUS REMOVAL IN WASTEWATER TREATMENT



Nitrogen Bacteria

Sample ID: MLSS/080615 - Thauera 0.73%, Thauera 0.73%, Nitrotoga 0.73%, Nitrosomonas 0.31%, Dechloromonas 0.21% and Nitrospira 0.21% were detected in this sample.

Sample ID: MLSS/101915 - Nitrosomonas 0.1% and Paracoccus 0.09% were detected in this sample.

Sample ID: MLSS/113015 - Paracoccus 0.1%, Nitrosomonas 0.06%, Thauera 0.06% and Thauera 0.06% were detected in this sample.

Sample ID: MLSS/032816 - Nitrosomonas 0.22%, Paracoccus 0.14% and Pseudomonas 0.13% were detected in this sample.

Sample ID: MLSS/050416 - Nitrosomonas 0.58%, Nitrotoga 0.45%, Thauera 0.24%, Thauera 0.24%, Nitrospira 0.21% and Paracoccus 0.09% were detected in this sample.

Sample ID: FinalEffluent/101815 - Pseudomonas 0.14%, Dechloromonas 0.1%, Thauera 0.08% and Thauera 0.08% were detected in this sample.

Sample ID: Dig4/050416 - Pseudomonas 1.11%, Thauera 0.59%, Thauera 0.59% and Paracoccus 0.11% were detected in this sample.

Sample ID: CentFeed/050416 - None were detected in this sample.

Sample ID: CentFeed/113015 - None were detected in this sample.

The Microbe Detectives table includes several groups of bacteria important in nitrogen processes. The first group labelled SND includes bacteria important in simultaneous nitrification and denitrification. This is a unique process which is usually operated at low dissolved oxygen concentrations (<0.5 mg/L) which results in aerobic conditions in the outside of the floc but anoxic conditions inside, allowing these bacteria to both oxidize ammonia aerobically and perform nitrate reduction in anoxic conditions. This process can save energy over conventional nitrification-denitrification if the bacteria utilize the nitrite shunt, in which they oxidize ammonia to nitrite then reduce nitrite to nitrogen gas without ever producing nitrate. It's essentially a shortcut.

The second group in the table are the AOBs (ammonia oxidizing bacteria). These bacteria are autotrophs (i.e. fix inorganic carbon into organic carbon) that obtain energy by oxidizing ammonia to nitrite (Figure 4). Nitrosomonas is the most common of these bacteria.

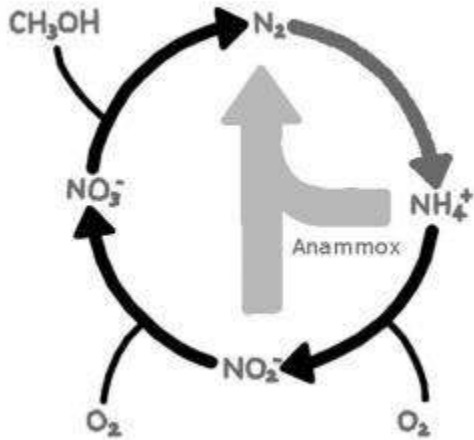
The third group are the NOBs (nitrite oxidizing bacteria). These bacteria are autotrophs (i.e. fix inorganic carbon into organic carbon) that obtain energy by oxidizing nitrite to nitrate (Figure 4). Nitrospira is the most common of these bacteria in wastewater treatment plants.

The next group includes nitrogen fixing bacteria such as Bradyrhizobium. The presence of these bacteria may indicate nitrogen-limiting conditions (i.e. plenty COD and P but not enough N to produce proteins for growth).

Next in the table are the denitrifiers. Thauera is the most well-known denitrifier in wastewater treatment systems. However, denitrification is not a truly unique function. Many aerobic bacteria are capable of this metabolic function.

The final group in the table are the anammox bacteria. These are very unique bacteria capable of oxidizing ammonia and reducing nitrite in anaerobic conditions (Figure 4). This is the most energy efficient method of removing ammonia in wastewater treatment. These bacteria are very slow growing and are typically present only if retention times are in excess of 50 days. As a result, biofilm retention is one method of keeping these bacteria in a system.

FIGURE 4. NITROGEN REMOVAL PROCESSES



Foaming Bacteria

Sample ID: MLSS/080615 - Mycobacterium 0.63% and Microthrix 0.45% were detected in this sample.

Sample ID: MLSS/101915 - Microthrix 1.34% and Mycobacterium 0.7% were detected in this sample.

Sample ID: MLSS/113015 - Microthrix 2.58% and Mycobacterium 1% were detected in this sample.

Sample ID: MLSS/032816 - Microthrix 0.61% and Mycobacterium 0.47% were detected in this sample.

Sample ID: MLSS/050416 - Microthrix 0.39% and Mycobacterium 0.2% were detected in this sample.

Sample ID: FinalEffluent/101815 - Mycobacterium 2.48% and Microthrix 0.23% were detected in this sample.

Sample ID: Dig4/050416 - None were detected in this sample.

Sample ID: CentFeed/050416 - Mycobacterium 0.27% was detected in the sample.

Sample ID: CentFeed/113015 - Mycobacterium 0.61% was detected in the sample.

Foaming bacteria are typically caused by the presence of FOG (fats, oils and grease). Most of these bacteria are mycolic-acid producing bacteria in the Acidomicrobiales or Actinomycetales orders of Actinobacteria. They are hydrophobic bacteria (water repellent) and thus naturally cling to air bubbles present in wastewater. As a result they float to the surface where they entrap air into bubbles and create a foamy broth that can become several feet thick. This foam layer can overflow basins, creating high effluent TSS, permit violation and a difficult mess to clean up.

Filamentous Bacteria

Sample ID: MLSS/080615 - Flexibacter 4.17%, Haliscomenobacter 2.47%, Tetrasphaera 1.18%, Trichococcus 1.18%, Caldilinea 0.8% and Zoogloea 0.63% were detected in this sample.

Sample ID: MLSS/101915 - Flexibacter 2.37%, Tetrasphaera 2.02%, Haliscomenobacter 1.6%, Microthrix 1.34%, Trichococcus 1.3% and Caldilinea 0.6% were detected in this sample.

Sample ID: MLSS/113015 - Haliscomenobacter 11.56%, Tetrasphaera 3.37%, Microthrix 2.58%, Caldilinea 1.93%, Flexibacter 1.85% and Trichococcus 1.2% were detected in this sample.

Sample ID: MLSS/032816 - Tetrasphaera 5.77%, Flexibacter 2.67%, Caldilinea 2.38%, Trichococcus 1.85%, Haliscomenobacter 1.77% and Microthrix 0.61% were detected in this sample.

Sample ID: MLSS/050416 - Haliscomenobacter 6.82%, Tetrasphaera 3.17%, Flexibacter 2.34%, Caldilinea 0.79%, Microthrix 0.39% and Trichococcus 0.28% were detected in this sample.

Sample ID: FinalEffluent/101815 - Haliscomenobacter 0.68%, Zoogloea 0.55%, Microthrix 0.23%, Sphaerotilus 0.18%, Acinetobacter 0.17% and Tetrasphaera 0.15% were detected in this sample.

Sample ID: Dig4/050416 - Trichococcus 29.98%, Acinetobacter 3.52%, Sphaerotilus 2.77% and Thiothrix 0.16% were detected in this sample.

Sample ID: CentFeed/050416 - Tetrasphaera 0.26% was detected in the sample.

Sample ID: CentFeed/113015 - None were detected in this sample.

Table 1 indicates the potential cause of each possible filament.

Filamentous bacteria are necessary for bridging between flocs to create a strong floc and blanket necessary for clear effluent. However, an abundance of filaments can prevent flocs from coalescing, resulting in a condition called bulking in which the sludge blanket does not thicken well. This condition can limit plant hydraulic capacity and cause high effluent TSS if the blanket goes over the clarifier weir.

TABLE 1. CAUSES OF FILAMENTS

Bacterial Genus	Description/Potential Cause
<i>Zoogloea</i>	Slime, typically caused by low nutrients
<i>Thiothrix</i>	Type 021N, Sulfur
<i>Meganema</i>	Unknown
<i>Acinetobacter</i>	Type 1863, FOG (fats, oils, grease)
<i>Flexibacter</i>	Unknown
<i>Microthrix</i>	FOG (fats, oils, grease); can also produce foam
<i>Ranella</i>	Type 0411; septicity/organic acids
<i>Gordonia</i>	Nocardia; FOG (fats, oils, grease)
<i>Sphaerotilus</i>	Low DO
<i>Haliscomenobacter</i>	Low DO, Low P
<i>Trichococcus</i>	Nostocoida Limnicola II, septicity/organic acids
<i>Leptolinea</i>	Unknown
<i>Tetrasphaera</i>	Nostocoida Limnicola I; Septicity/organic acids
<i>Isosphaera</i>	Nostocoida Limnicola III; Septicity/organic acids
<i>Caldilinea</i>	Eikelboom Type 803; Low F:M
<i>Skermania piniformis</i>	PTLO - Pine tree like organisms, can cause foam; possibly FOG (fats, oils, grease)
<i>Beggiatoa</i>	Unknown
<i>Brachythrix</i>	Unknown
<i>Kouleothrix</i>	Unknown
<i>Unnamed SJA-15</i>	Unknown

Iron Bacteria

Sample ID: MLSS/080615 - None were detected in this sample.

Sample ID: MLSS/101915 - None were detected in this sample.

Sample ID: MLSS/113015 - None were detected in this sample.

Sample ID: MLSS/032816 - None were detected in this sample.

Sample ID: MLSS/050416 - None were detected in this sample.

Sample ID: FinalEffluent/101815 - None were detected in this sample.

Sample ID: Dig4/050416 - None were detected in this sample.

Sample ID: CentFeed/050416 - None were detected in this sample.

Sample ID: CentFeed/113015 - None were detected in this sample.

Iron oxidizing bacteria consume reduced iron for energy in aerobic conditions, typically producing a rust color in the water. These bacteria can also play a role in corrosion. Gallionella is one of the most well-known iron oxidizing which is frequently found in drinking water wells. The presence of iron oxidizing bacteria indicates the presence of dissolved iron.

Sulfur Bacteria

Sample ID: MLSS/080615 - None were detected in this sample.

Sample ID: MLSS/101915 - None were detected in this sample.

Sample ID: MLSS/113015 - None were detected in this sample.

Sample ID: MLSS/032816 - None were detected in this sample.

Sample ID: MLSS/050416 - None were detected in this sample.

Sample ID: FinalEffluent/101815 - None were detected in this sample.

Sample ID: Dig4/050416 - Desulfovibrio 0.18% was detected in the sample.

Sample ID: CentFeed/050416 - None were detected in this sample.

Sample ID: CentFeed/113015 - Desulfomicrobium 0.24% was detected in the sample.

The presence of sulfate reducing or sulfur oxidizing bacteria indicates the presence of sulfur. Sulfur can hinder ammonia removal and can also cause filamentous issues such as Thiothrix (aka 021N). Sulfate reduction can also produce hydrogen sulfide gas which may cause aesthetic issues due to the rotten egg odor. The presence of sulfur-associated bacteria could increase corrosion in certain environments such as sewers as these bacteria oxidizing hydrogen sulfide in the head space and produce corrosive sulfuric acid.

Figure 5-1 MLSS/08-06-15

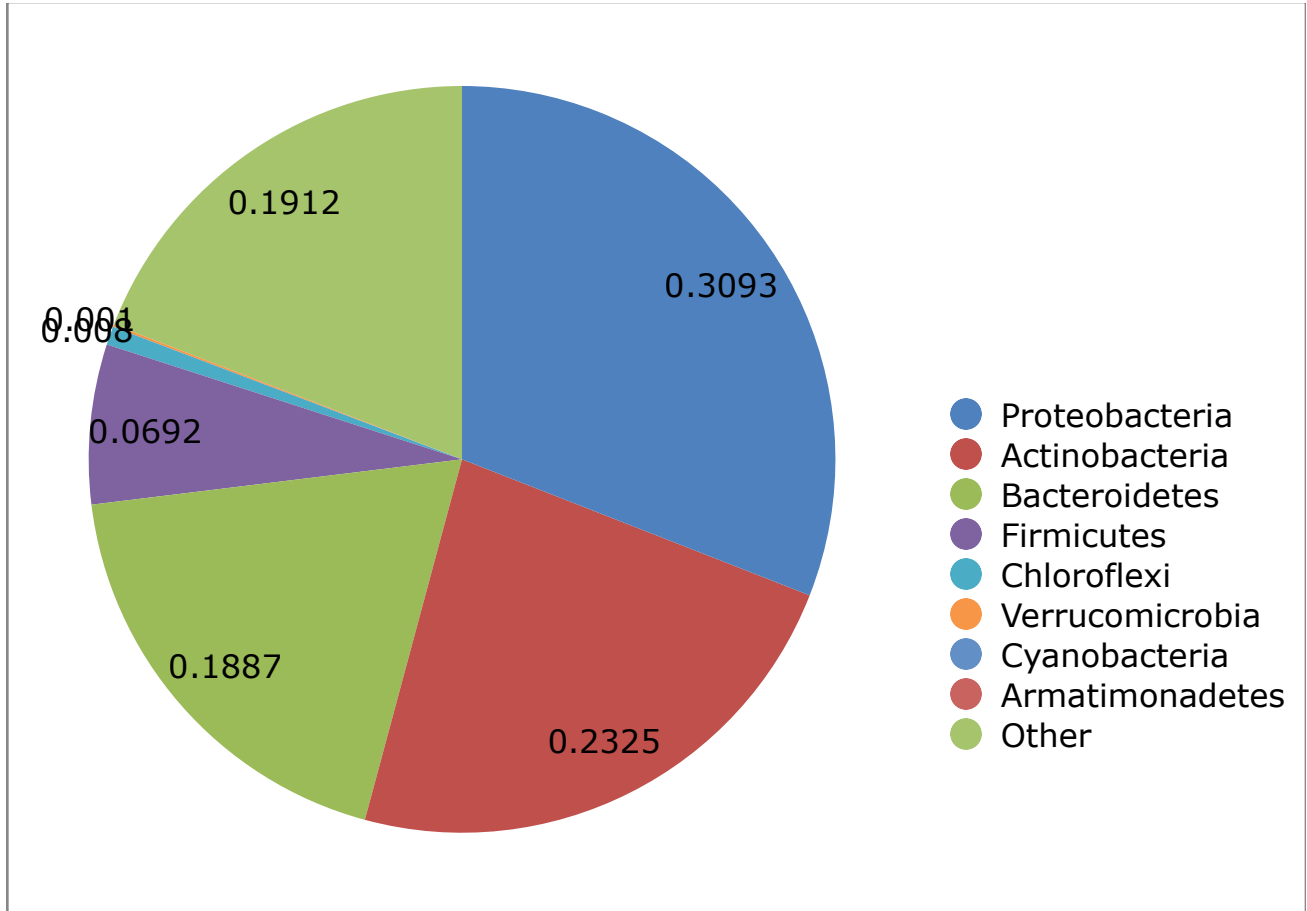


Figure 5-2 MLSS/10-19-15

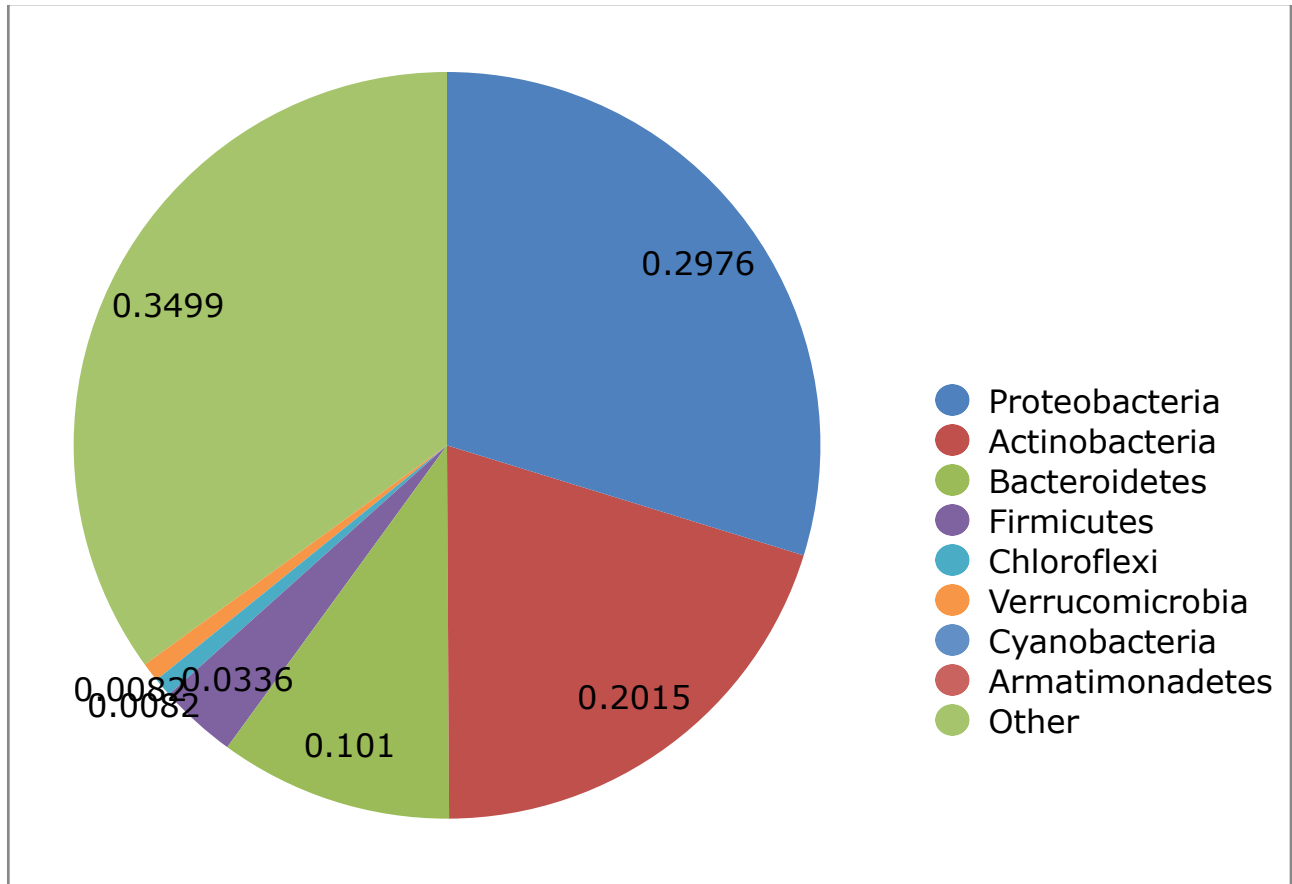


Figure 5-3 MLSS/11-30-15

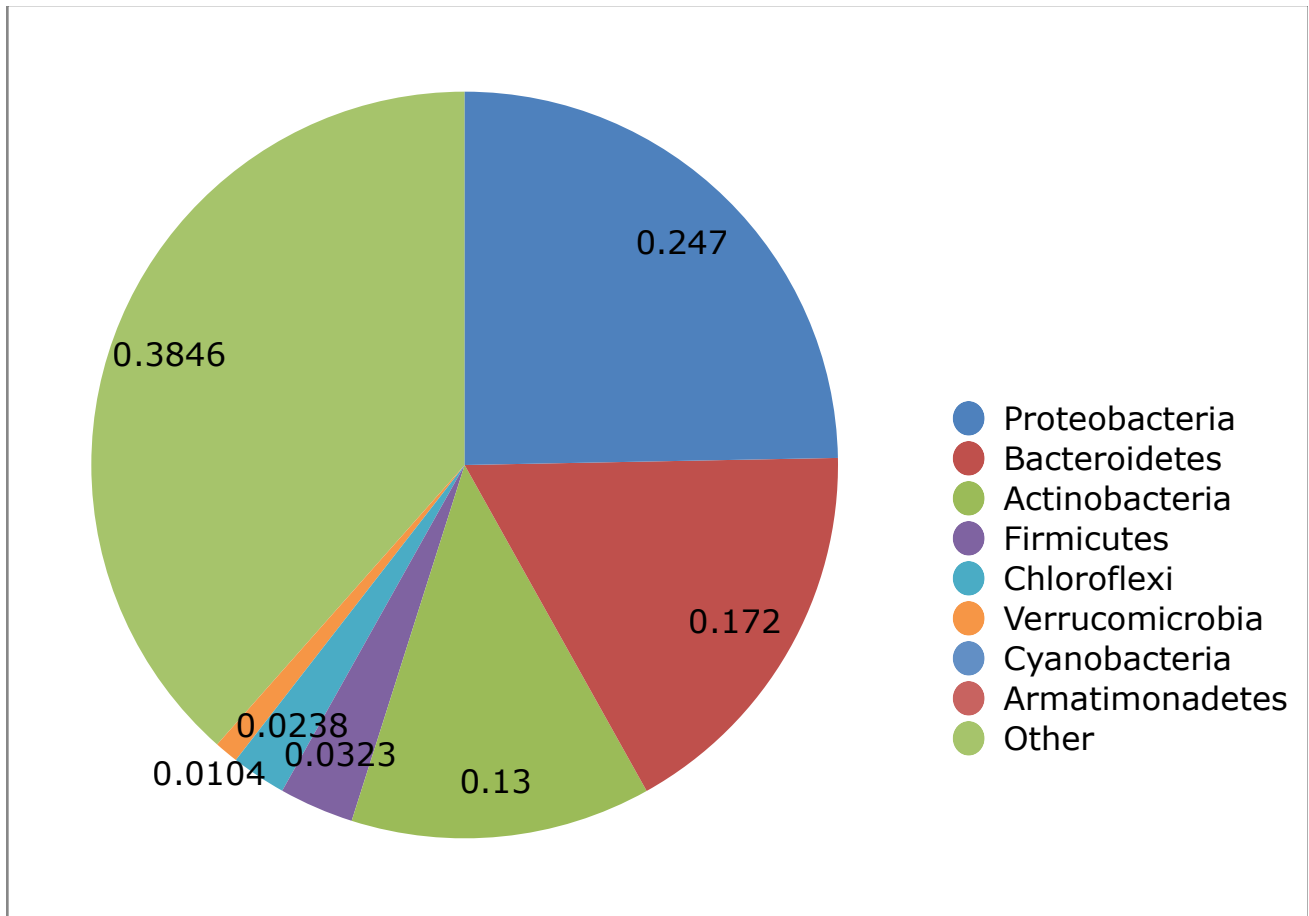


Figure 5-4 MLSS/03-28-16

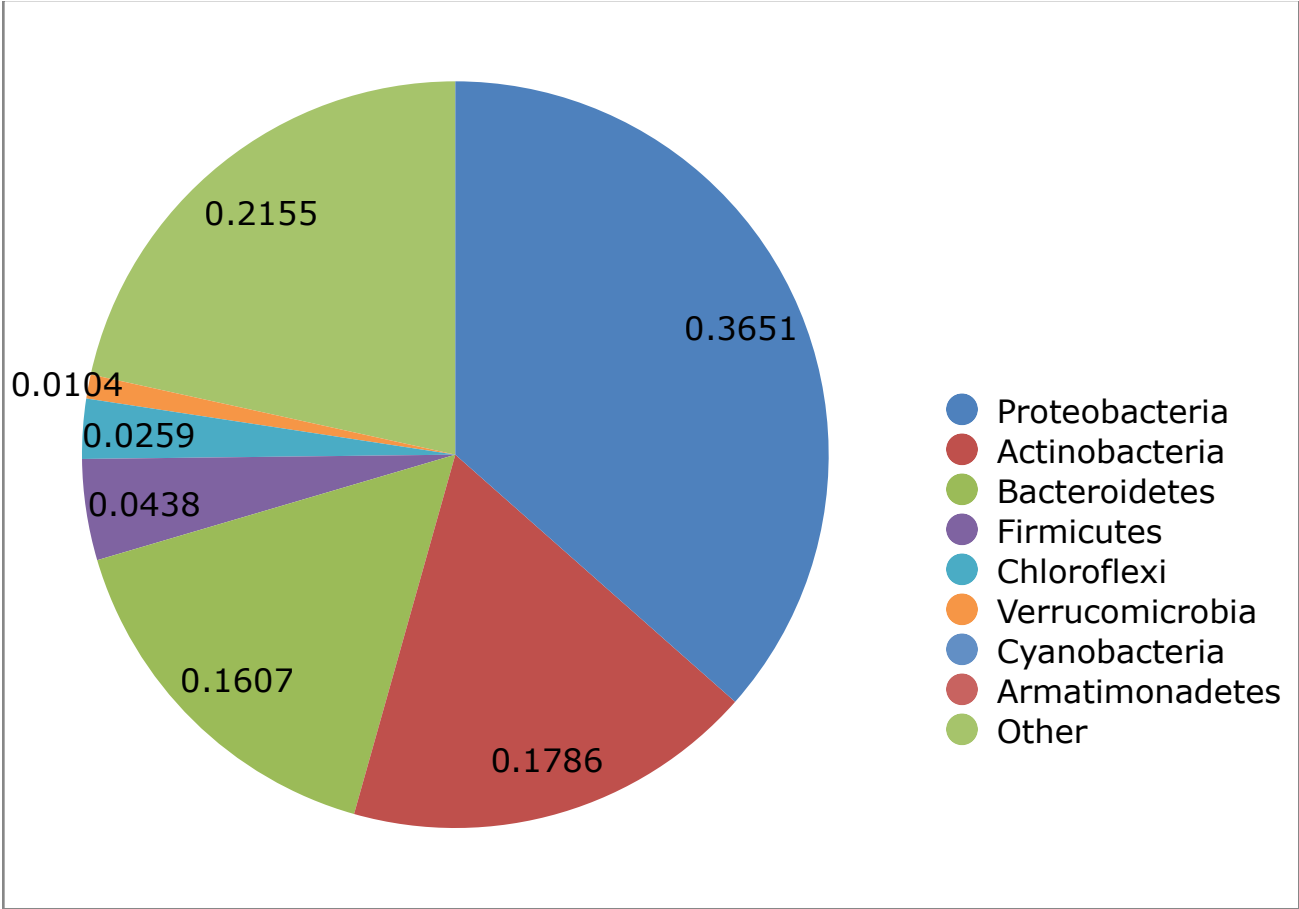


Figure 5-5 MLSS/05-04-16

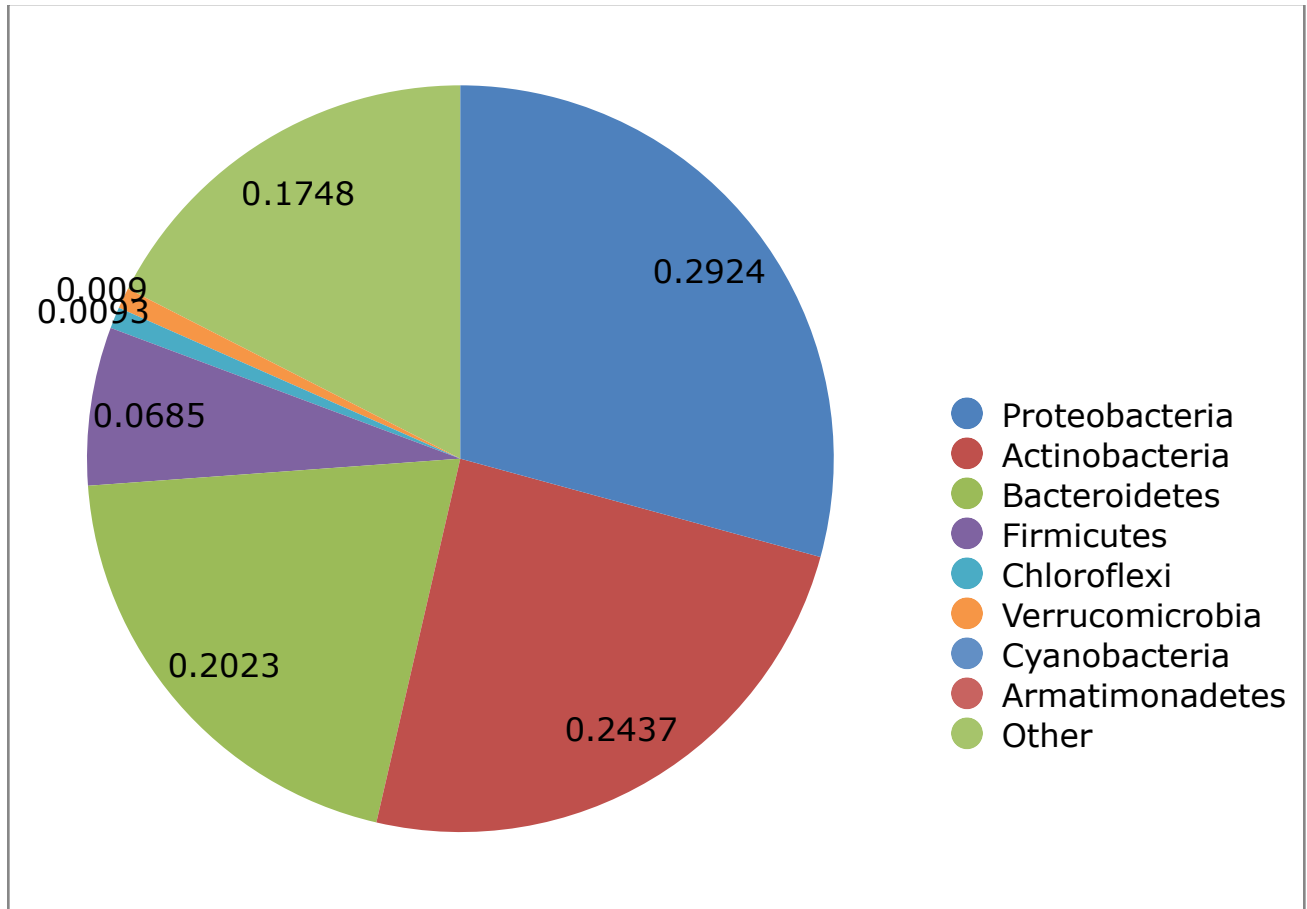


Figure 5-6 Final Effluent/10-18-15

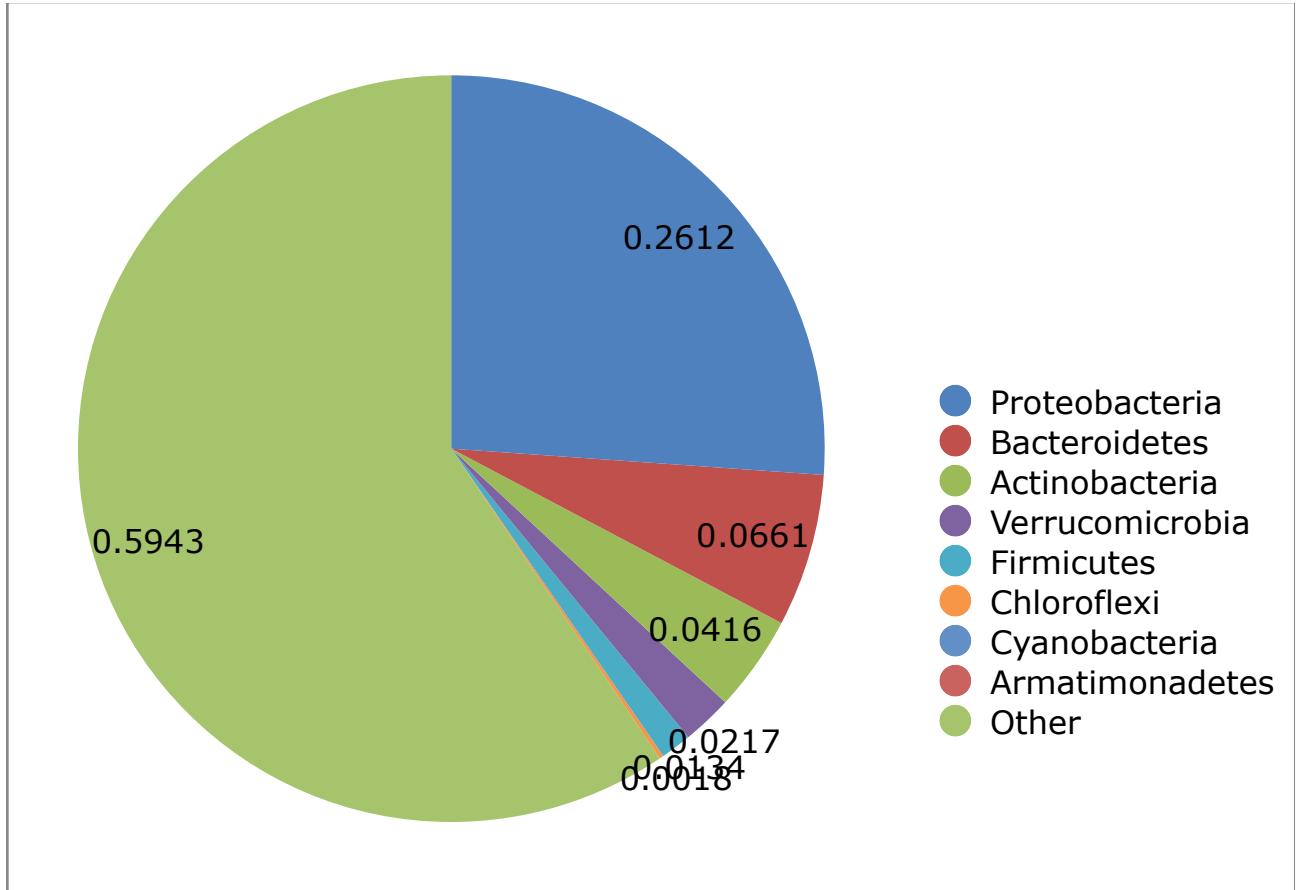


Figure 5-7 Dig4/05-04-16

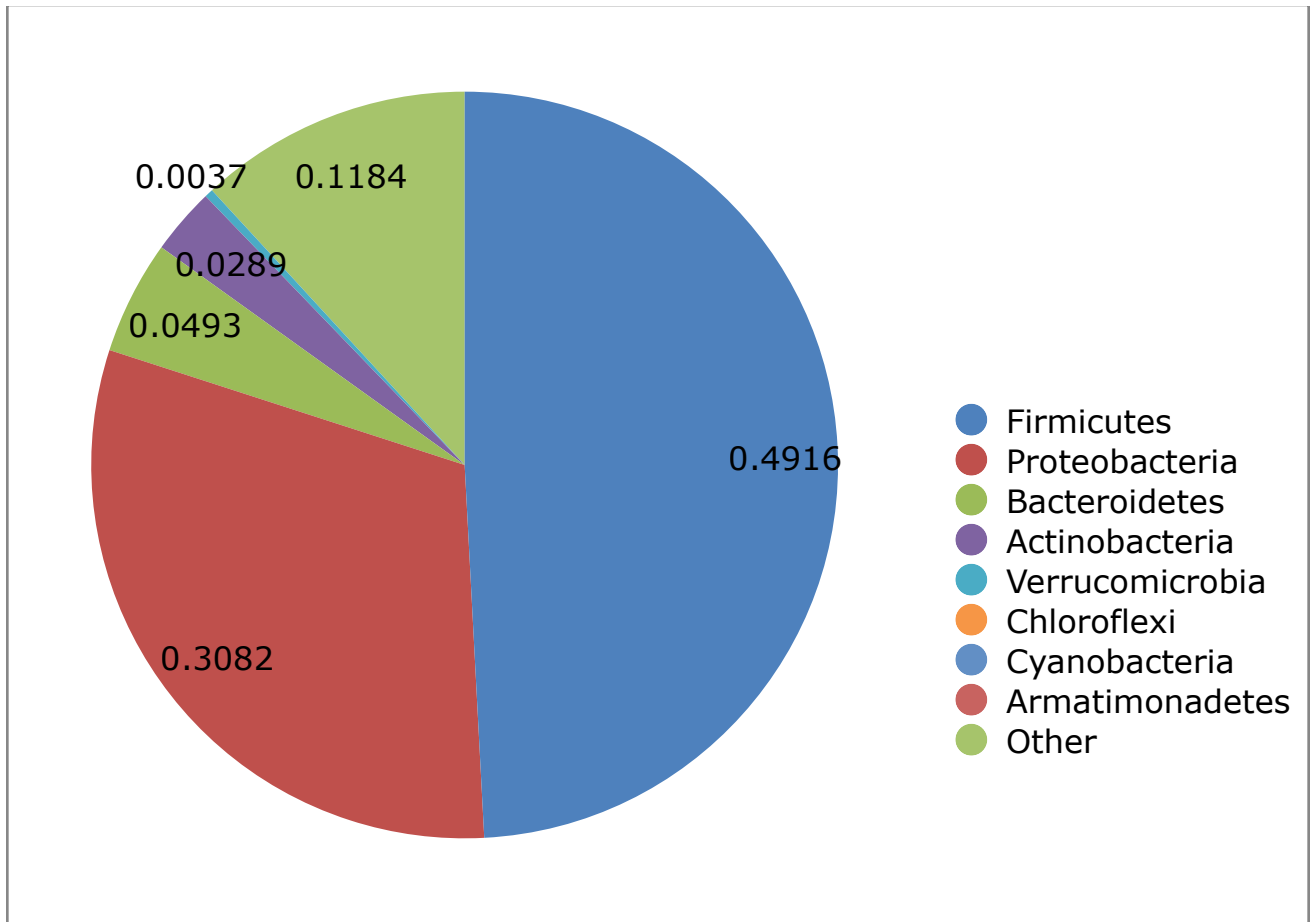


Figure 5-8 CentFeed/05-04-16

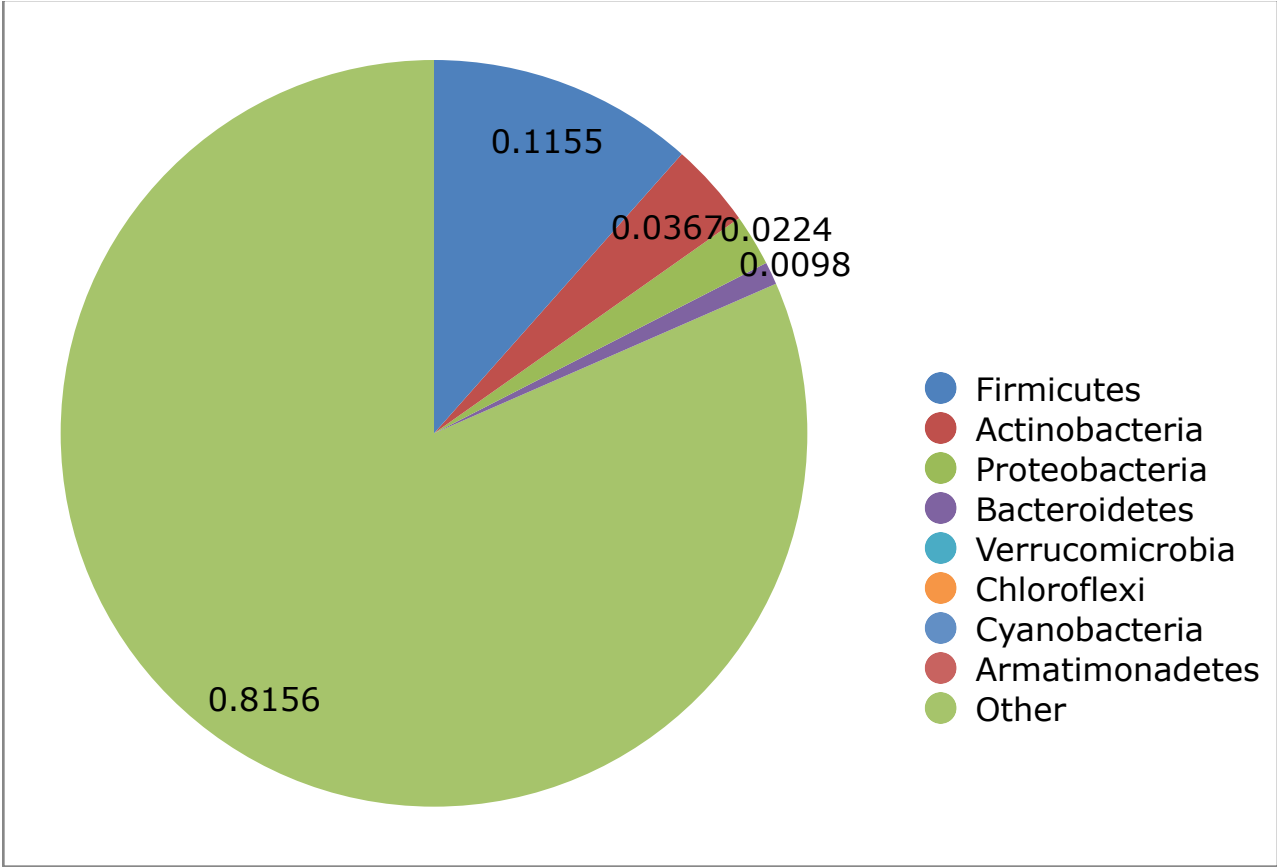
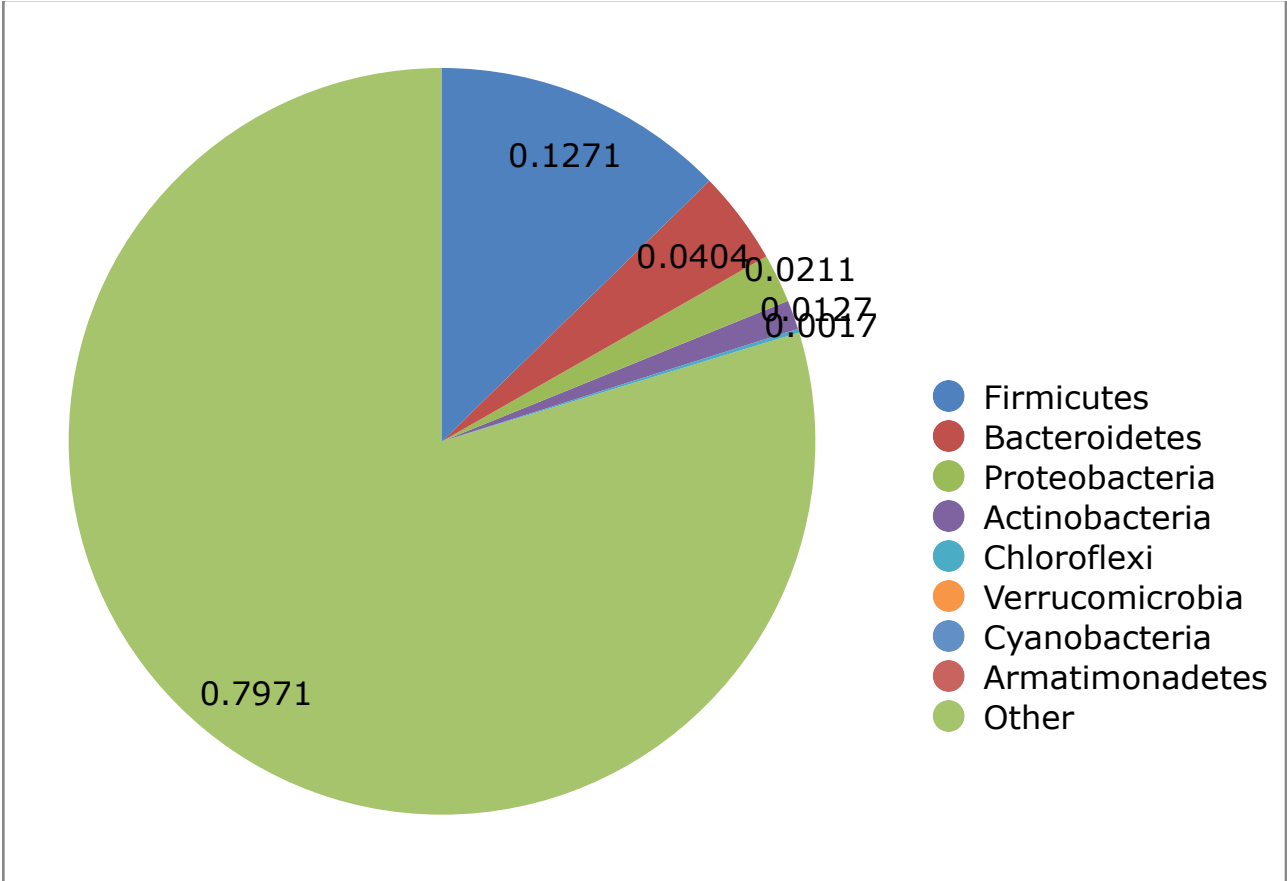
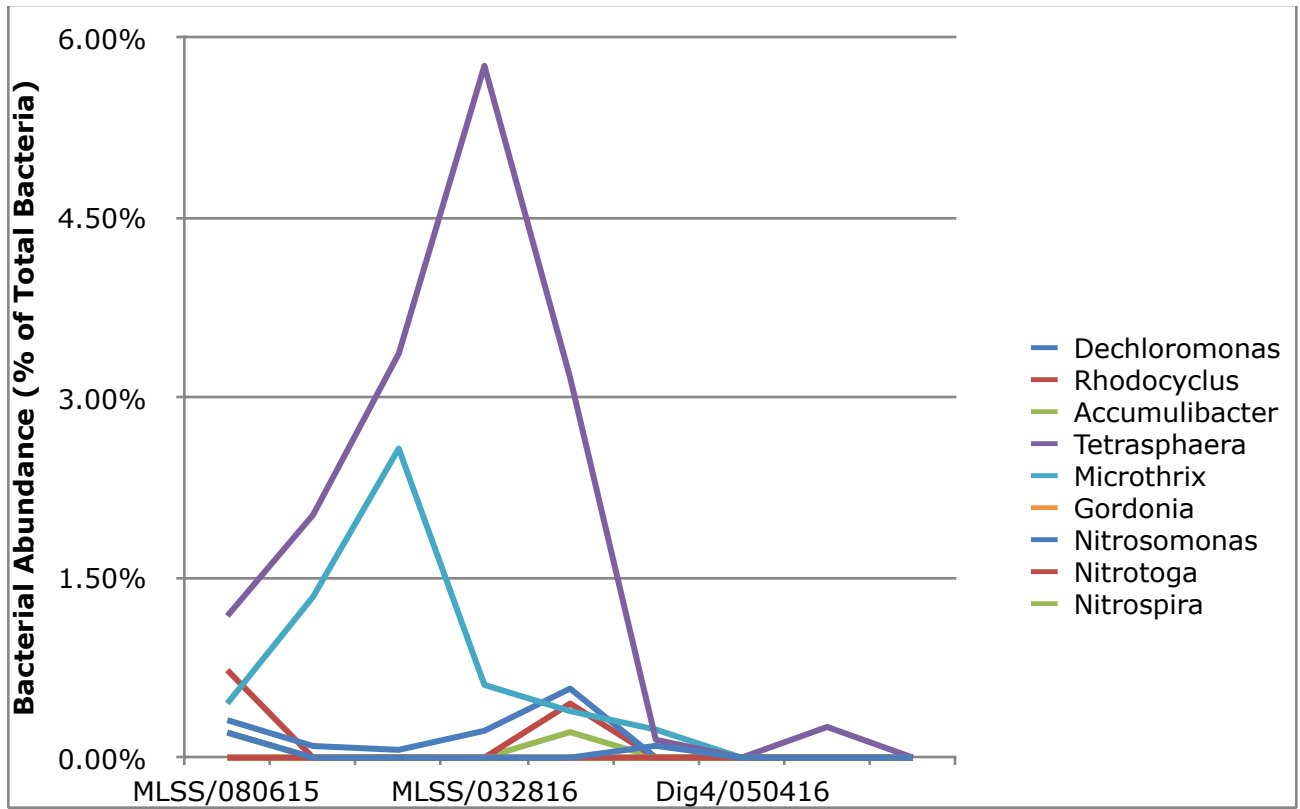


Figure 5-9 CentFeed/11-30-15



Bacterial Abundance Chart



Bacterial Relative Abundance Tables

Bolded or highlighted text indicates bacteria that were found greater than 0.2% of total bacteria.

Bacteria Name									
Phylum	MLSS/ 080615	MLSS/ 101915	MLSS/ 113015	MLSS/ 032816	MLSS/ 050416	FinalEffluent/ 101815	Dig4/05 0416	CentFeed/ 050416	CentFeed/ 113015
Actinobacteria	23.25%	20.15%	13.00%	17.86%	24.37%	4.16%	2.89%	3.67%	1.27%
Armatimonadetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bacteroidetes	18.87%	10.10%	17.20%	16.07%	20.23%	6.61%	4.93%	0.98%	4.04%
Chloroflexi	0.80%	0.82%	2.38%	2.59%	0.93%	0.18%	0.00%	0.00%	0.17%
Cyanobacteria	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes	6.92%	3.36%	3.23%	4.38%	6.85%	1.34%	49.16%	11.55%	12.71%
Proteobacteria	30.93%	29.76%	24.70%	36.51%	29.24%	26.12%	30.82%	2.24%	2.11%
Verrucomicrobia	0.10%	0.82%	1.04%	1.04%	0.90%	2.17%	0.37%	0.00%	0.00%
Other	19.12%	34.99%	38.46%	21.55%	17.48%	59.43%	11.84%	81.56%	79.71%
Fermenters									
Lactobacillus	0.00%	0.06%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Lactococcus	0.00%	0.13%	0.13%	0.00%	0.00%	0.00%	2.67%	0.00%	0.00%
Propionimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Propionivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.06%	0.29%	0.00%	0.00%
Streptococcus	0.00%	0.14%	0.26%	0.00%	0.08%	0.00%	1.68%	0.00%	0.00%
Tetrasphaera	1.18%	2.02%	3.37%	5.77%	3.17%	0.15%	0.00%	0.26%	0.00%
Phosphorus									
Accumulibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
CandidatusCompetibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Dechloromonas	0.21%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
Defluviicoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Rhodocyclus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Tetrasphaera	1.18%	2.02%	3.37%	5.77%	3.17%	0.15%	0.00%	0.26%	0.00%
Nitrogen									
Anammoxoglobus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Aromatoleum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Brocadia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Candidatus_Nitrosoarchaeum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Dechloromonas	0.21%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
Jettenia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Kueninia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitratireductor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitratiruptor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrotoga	0.73%	0.00%	0.00%	0.00%	0.45%	0.00%	0.00%	0.00%	0.00%
Nitrosocaldus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrosococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrosomonas	0.31%	0.10%	0.07%	0.22%	0.58%	0.00%	0.00%	0.00%	0.00%
Nitrosopumilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrososphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrosovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrospira	0.21%	0.00%	0.00%	0.00%	0.21%	0.00%	0.00%	0.00%	0.00%
Paracoccus	0.00%	0.09%	0.10%	0.14%	0.09%	0.00%	0.11%	0.00%	0.00%
Pseudomonas	0.00%	0.00%	0.00%	0.13%	0.00%	0.14%	1.11%	0.00%	0.00%
Rhodococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Scalindua	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Thauera	0.73%	0.00%	0.07%	0.00%	0.24%	0.09%	0.59%	0.00%	0.00%
Foaming									
Microthrix	0.45%	1.34%	2.58%	0.61%	0.39%	0.23%	0.00%	0.00%	0.00%
Dietzia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Gordonia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Mycobacterium	0.63%	0.70%	1.00%	0.47%	0.20%	2.48%	0.00%	0.27%	0.61%
Rhodococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Skermania piniformis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Tsukamurella pseudospumae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Filaments									
Acinetobacter	0.00%	0.00%	0.00%	0.31%	0.00%	0.17%	3.52%	0.00%	0.00%
Beggiatoa	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Brachytrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Caldilinea	0.80%	0.60%	1.93%	2.38%	0.79%	0.11%	0.00%	0.00%	0.00%
Microthrix	0.45%	1.34%	2.58%	0.61%	0.39%	0.23%	0.00%	0.00%	0.00%
Flexibacter	4.17%	2.37%	1.85%	2.67%	2.34%	0.07%	0.00%	0.00%	0.00%
Gordonia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Haliscomenobacter	2.47%	1.61%	11.56%	1.77%	6.82%	0.68%	0.00%	0.00%	0.00%
Isosphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Kouleoethrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Leptolinea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Leucothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Meganema	0.00%	0.45%	0.18%	0.18%	0.21%	0.09%	0.00%	0.00%	0.00%
Runella	0.00%	0.06%	0.00%	0.12%	0.18%	0.00%	0.00%	0.00%	0.00%
Skermania piniformis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sphaerotilus	0.00%	0.00%	0.87%	0.23%	0.00%	0.18%	2.77%	0.00%	0.00%
Tetrasphaera	1.18%	2.02%	3.37%	5.77%	3.17%	0.15%	0.00%	0.26%	0.00%
Thiothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.11%	0.16%	0.00%	0.00%
Trichococcus	1.18%	1.30%	1.20%	1.85%	0.28%	0.09%	29.98%	0.00%	0.00%
Unnamed SJA-15	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Zoogloea	0.63%	0.00%	0.00%	0.00%	0.00%	0.55%	0.00%	0.00%	0.00%
Iron									
Crenothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Gallionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Geobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Leptothrix	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sideroxydans	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sulfur									
Desulfarculaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfatibacillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfobacteraceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.24%
Desulfonatronospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfonatronum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulforegula	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulforudis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfosalsimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Desulfovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.18%	0.00%	0.00%
Sulfuricella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sulfuricurvum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sulfurimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sulfuritalea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sulfurospirillum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Syntrophobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Thermodesulforhabdus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Thiobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Thiorhodospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

	Dig4/050416	CentFeed/050416	CentFeed/113015
Hydrogenesis			
Clostridium	0.0%	0.0%	0.0%
Variovorax	0.1%	0.0%	0.0%
Methanoculleus	0.0%	0.0%	0.0%
Janthinobacterium	0.0%	0.0%	0.0%
Fermentation/Acetogenesis			
Paludibacter	0.0%	0.0%	0.5%
Propioniceella	0.1%	0.0%	0.0%
Anaerovirgula	0.1%	0.2%	0.2%
Acetivibrio	0.1%	0.4%	0.9%
Acetivibrio	0.1%	0.4%	0.9%
Streptococcus	1.7%	0.0%	0.0%
Gelria	0.0%	0.9%	0.3%
Syntrophomonas	0.0%	0.0%	0.0%
Anaerobaculum	0.0%	2.2%	4.2%
Coprothermobacter	0.0%	4.8%	5.6%
Clostridium	0.0%	0.0%	0.0%
Garciella	0.0%	0.0%	0.0%
Butyrivibrio	0.0%	0.0%	0.0%
Tissierella	0.0%	0.0%	0.0%
Methane Production - Aceticlastic			
Methanosaeta	0.0%	0.0%	0.0%
Methanosarcina	0.1%	16.3%	16.5%
Methanobrevibacter	0.0%	0.0%	0.0%
Methanomicrobium	0.0%	0.0%	0.0%
Methane Production - Hydrogenoclastic			
Methanothermus	0.0%	4.8%	9.4%
Methanobacterium	0.0%	0.0%	0.0%
Methanothermobacter	0.0%	0.3%	0.8%
Methanomicrobiales	0.0%	0.0%	0.0%
Methanoculleus	0.0%	0.0%	0.0%
Methane Consumption (typically aerobic)			
Methylothera	0.0%	0.0%	0.0%
Methylacidiphilum	0.0%	0.0%	0.0%
Methylosinus	0.0%	0.0%	0.0%
Methylobacterium	0.0%	0.0%	0.0%
Methylibium	0.0%	0.0%	0.0%
Methylophilaceae	0.0%	0.0%	0.0%

Syntrophs			
Aminobacterium	0.0%	0.0%	0.0%
Smithella	0.0%	0.0%	0.0%
Geobacter	0.0%	0.0%	0.0%
Syntrophobacter	0.0%	0.0%	0.0%
Syntrophus	0.0%	0.0%	0.0%
Sulfate Reducing Bacteria (SRB)			
Desulfomicrobium	0.0%	0.0%	0.2%
Desulfovibrio	0.2%	0.0%	0.0%
Thermodesulfobium	0.0%	1.3%	1.7%
Foaming			
Microthrix	0.0%	0.0%	0.0%
Mycobacterium fortuitum	0.0%	0.0%	0.0%
Gordonia	0.0%	0.0%	0.0%
Rhodococcus globerulus	0.0%	0.0%	0.0%
Rhodococcus ruber	0.0%	0.0%	0.0%
Dietzia	0.0%	0.0%	0.0%
Skermania piniformis	0.0%	0.0%	0.0%
Tsukamurella pseudospumae	0.0%	0.0%	0.0%