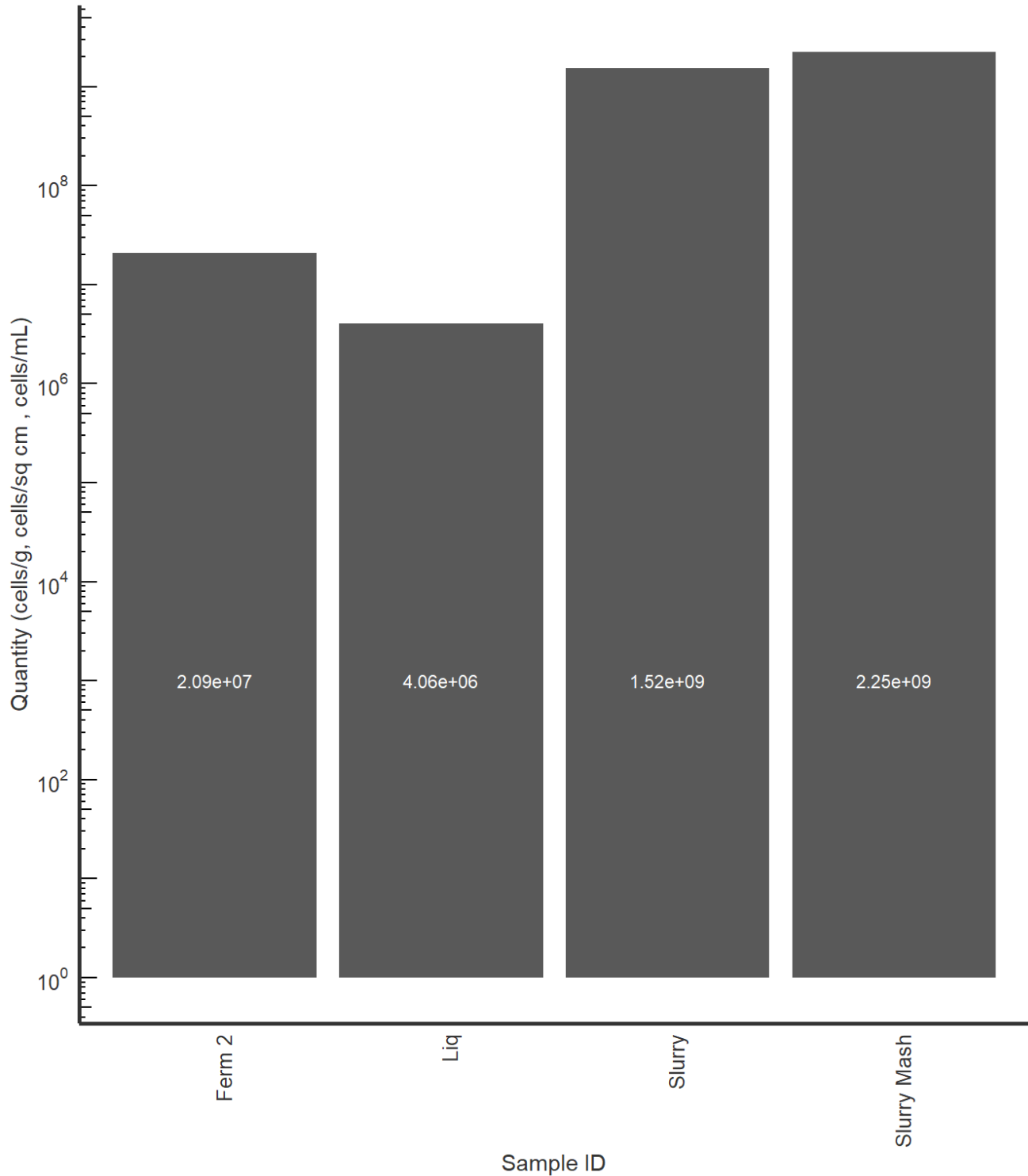


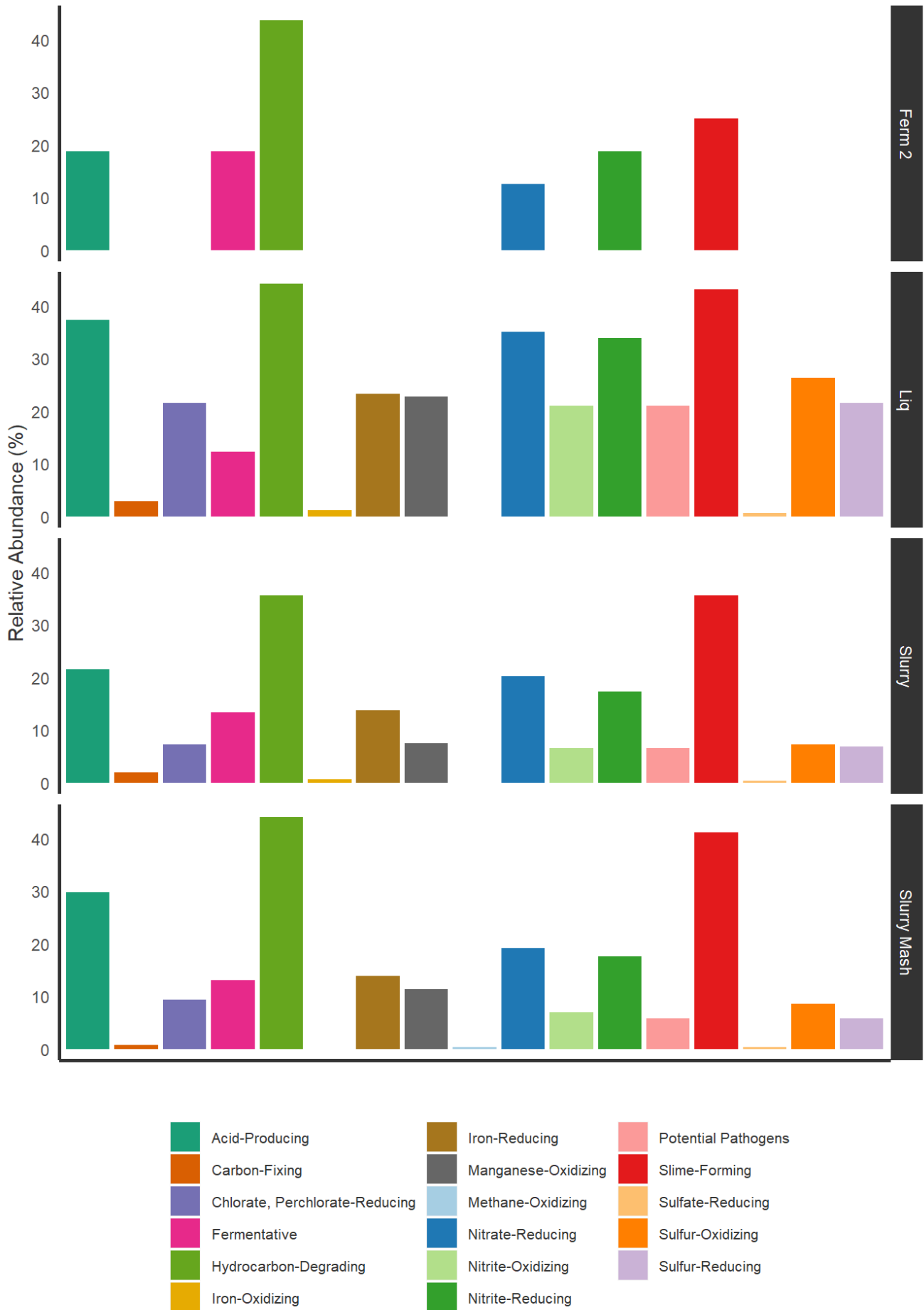
qPCR Data

This plot shows the total number of prokaryotes in the sample. Results of any additional qPCR assays will be provided in a separate report.



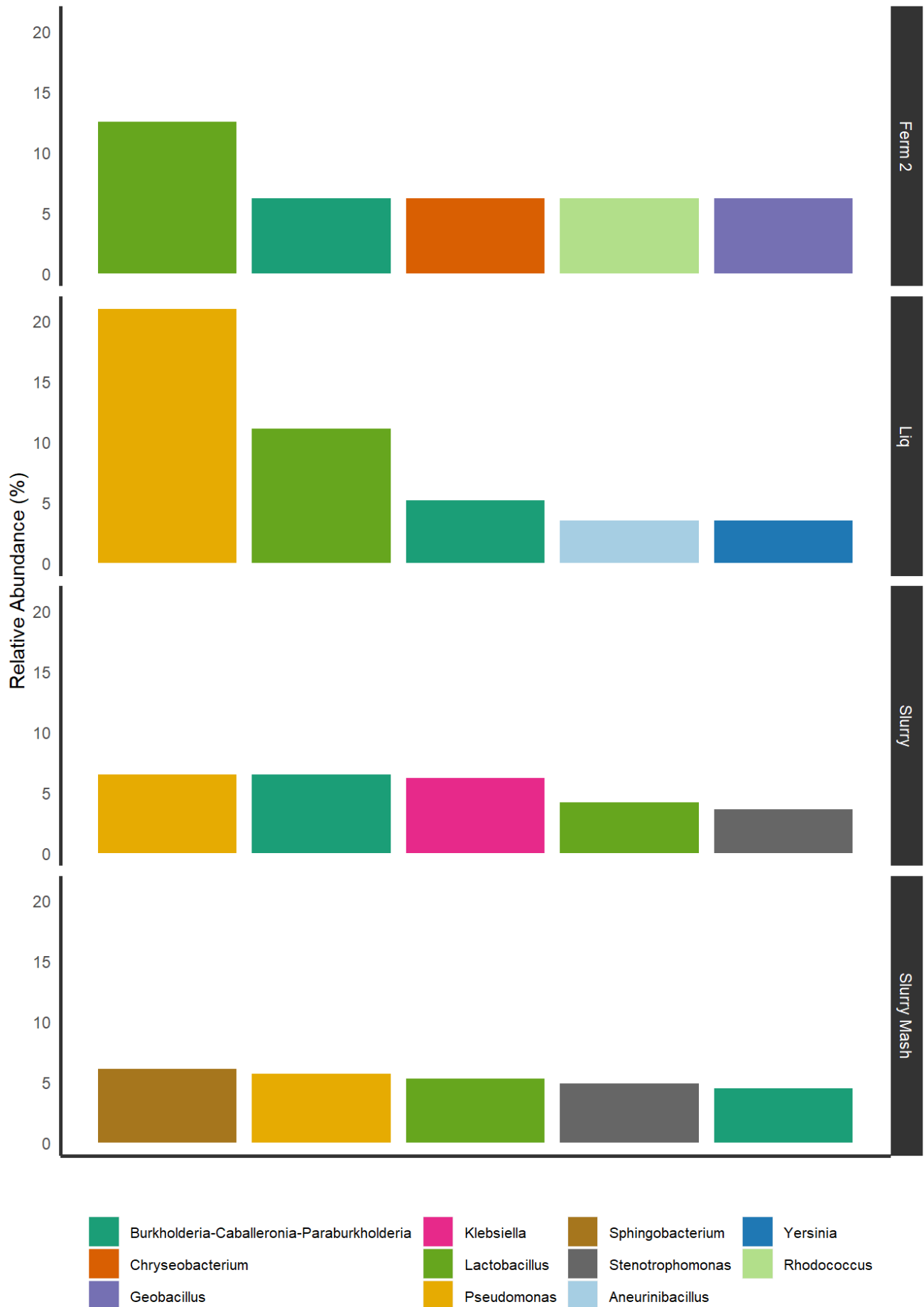
16S NGS Summary

This plot shows relative proportion of each metabolic group in the sample. Note: The cumulative abundance for each sample can exceed 100%, as organisms can have multiple metabolic associations



Top 5 Organisms

This plot shows the 5 most abundant organisms in the sample



- Burkholderia-Caballeronia-Paraburkholderia
- Klebsiella
- Spingobacterium
- Yersinia
- Chryseobacterium
- Lactobacillus
- Stenotrophomonas
- Rhodococcus
- Geobacillus
- Pseudomonas
- Aneurinibacillus

16S NGS Data by Metabolic Group

Results are given in cells/unit sampled (eg. g, sq cm, mL)

Group	Slurry	Liq	Ferm 2	Slurry Mash
Acid-Producing	328,884,520	1,519,967	3,921,474	670,049,999
Carbon-Fixing	29,884,732	118,264	0	18,225,000
Chlorate, Perchlorate-Reducing	109,628,173	879,062	0	211,275,000
Fermentative	204,313,982	498,662	3,921,474	293,624,999
Hydrocarbon-Degrading	542,804,308	1,802,821	9,150,106	990,449,997
Iron-Oxidizing	9,758,278	47,143	0	0
Iron-Reducing	209,345,595	949,776	0	312,524,999
Manganese-Oxidizing	114,812,261	926,205	0	256,724,998
Methane-Oxidizing	0	0	0	9e+06
Nitrate-Reducing	309,215,489	1,424,867	2,614,316	431,774,999
Nitrite-Oxidizing	99,869,895	855,491	0	156,375,000
Nitrite-Reducing	264,540,866	1,377,725	3,921,474	395,100,000
Potential Pathogens	99,869,895	855,491	0	128,925,000
Slime-Forming	543,109,255	1,756,086	5,228,632	9.27e+08
Sulfate-Reducing	4,879,139	23,571	0	9e+06
Sulfur-Oxidizing	109,628,173	1,068,448	0	192,600,000
Sulfur-Reducing	104,749,034	879,062	0	128,925,000

Description of Potential Metabolic Groups

Group	Description
Acid-Producing	Acid producing prokaryotes (APB) can produce organic and inorganic acids. APBs have been recognized as a major cause of corrosion because their activities can cause the pH, particularly in biofilms, to become acidic.
Ammonia-Oxidizing	Involved in the oxidizing of ammonia to nitrite. Commonly referred to as nitrifying prokaryotes.
Anammox	Anammox organisms are capable of converting ammonia and nitrite directly to nitrogen gas. They have very slow growth rates and prefer anoxic environments.
Carbon-Fixing	Various prokaryotes involved in the process of converting inorganic carbon (CO ₂) to organic compounds by living organisms.
Chlorate, Perchlorate-Reducing	Perchlorate-reducing bacteria (PRB) and chlorate-reducing bacteria (CRB) are microorganisms that can utilize perchlorate (ClO ₄ ⁻) or chlorate (ClO ₃ ⁻) as terminal electron acceptors.
Fermentative	Bacteria that use fermentation as a metabolic process to convert sugars into acids, gases, or alcohols.
Hydrocarbon-Degrading	Prokaryotes that are capable of degrading hydrocarbons to use as a food source.
Iron-Oxidizing	Prokaryotes that are capable of deriving energy by oxidizing dissolved ferrous iron (Fe ²⁺) into insoluble ferric iron (Fe ³⁺). Associated with MIC in the literature.
Iron-Reducing	Prokaryotes that are capable of reducing ferric iron (Fe ³⁺) by using this ion as a terminal electron acceptor in their metabolisms. Associated with MIC in the literature.
Manganese-Oxidizing	Characterized by the ability to catalyze the oxidation of divalent, soluble Mn(II) to insoluble manganese oxides of the general formula MnOx. Can result in the accumulation extracellular deposits of insoluble brown or black manganese oxides. Associated with MIC.
Methane-Oxidizing	Methane-oxidizing prokaryotes (methanotrophs) have the unique ability to grow using methane as their sole source of carbon and energy.
Methanogen	Archaea that produce methane as a metabolic byproduct in anoxic conditions.
Nitrate-Reducing	Prokaryotes that are capable of reducing nitrate. Generally multiple species are involved in the complete pathway for reducing nitrate to dinitrogen (N ₂).
Nitrite-Oxidizing	Involved in the oxidizing of nitrite to nitrate. Commonly referred to as nitrifying prokaryotes.
Nitrite-Reducing	Similar to Nitrate-Reducing but use nitrite as substrate.
Potential Pathogens	This group of microorganisms includes strains that are pathogenic, meaning they may cause disease. Routes of transmission may be through ingestion, aspiration or contact with open wounds or mucous membranes.
Slime-Forming	Prokaryotes that are capable of producing a variety of extracellular polysaccharide polymers. These long chain molecules act as the foundation and cement in the formation of biofilms.
Sulfate-Reducing	Bacteria and Archaea that can obtain energy by oxidizing organic compounds or molecular hydrogen (H ₂) while reducing sulfate (SO ₄ ²⁻), or other sulfur compounds such as thiosulfate, to hydrogen sulfide (H ₂ S). SRPs have been highly implicated in corrosion activities.
Sulfur-Oxidizing	Bacteria capable of oxidizing reduced sulfur compounds (such as sulfide H ₂ S), inorganic sulfur (S), and thiosulfate (S ₂ O ₃ ²⁻) to form sulfuric acid (H ₂ SO ₄).
Sulfur-Reducing	Bacteria that can derive energy by reducing elemental sulfur (S) to hydrogen sulfide (H ₂ S). Many SRPs also have this activity.

16S NGS Data by Genus

Note: Only organisms with a relative abundance greater than 1% are displayed. For all other organisms please refer to the accompanying datasheet. Results are given in cells/unit sampled (eg. g, sq cm, mL)

Genus	Slurry	Liq	Ferm 2	Slurry Mash
Acid-Producing				
Bacillus				27,450,000
Brevibacterium			1,307,158	
Corynebacterium				36,674,999
Flavobacterium				55,125,000
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Pseudomonas	99,869,895	855,491		128,925,000
Sphingobacterium	34,916,345			138,150,000
Yersinia		142,243		
Carbon-Fixing				
Anoxybacillus	29,884,732			
Cupriavidus		94,693		
Chlorate, Perchlorate-Reducing				
Acinetobacter				45,900,000
Bacillus				27,450,000
Pseudomonas	99,869,895	855,491		128,925,000
Fermentative				
Bacillus				27,450,000
Brevibacterium			1,307,158	
Corynebacterium				36,674,999
Gluconacetobacter	24,853,119			
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Hydrocarbon-Degrading				
Acinetobacter				45,900,000
Bacillus				27,450,000
Brevibacterium			1,307,158	
Chryseobacterium	44,979,571		1,307,158	64,350,000
Corynebacterium				36,674,999
Cupriavidus		94,693		
Dietzia			1,307,158	

Genus	Slurry	Liq	Ferm 2	Slurry Mash
Exiguobacterium		47,143		
Flavobacterium				55,125,000
Geobacillus			1,307,158	
Janthinobacterium	19,973,979			
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Paenibacillus	24,853,119	71,121		82,800,000
Pseudomonas	99,869,895	855,491		128,925,000
Rhodococcus			1,307,158	
Sphingomonas	34,916,345			36,674,999
Stenotrophomonas	54,890,324	47,143		110,475,000
Streptomyces				36,674,999
Iron-Oxidizing				
Paracoccus		47,143		
Iron-Reducing				
Bacillus				27,450,000
Pseudomonas	99,869,895	855,491		128,925,000
Sphingomonas	34,916,345			36,674,999
Stenotrophomonas	54,890,324	47,143		110,475,000
Manganese-Oxidizing				
Bacillus				27,450,000
Corynebacterium				36,674,999
Paracoccus		47,143		
Pseudomonas	99,869,895	855,491		128,925,000
Streptomyces				36,674,999
Nitrate-Reducing				
Bacillus				27,450,000
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Paracoccus		47,143		
Pseudomonas	99,869,895	855,491		128,925,000
Sphingomonas	34,916,345			36,674,999
Nitrite-Oxidizing				
Bacillus				27,450,000

Genus	Slurry	Liq	Ferm 2	Slurry Mash
Pseudomonas	99,869,895	855,491		128,925,000
Nitrite-Reducing				
Bacillus				27,450,000
Granulicatella			1,307,158	
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Paracoccus		47,143		
Pseudomonas	99,869,895	855,491		128,925,000
Potential Pathogens				
Pseudomonas	99,869,895	855,491		128,925,000
Slime-Forming				
Acinetobacter				45,900,000
Bacillus				27,450,000
Capnocytophaga			1,307,158	
Chryseobacterium	44,979,571		1,307,158	64,350,000
Corynebacterium				36,674,999
Enterococcus	29,884,732			
Flavobacterium				55,125,000
Janthinobacterium	19,973,979			
Klebsiella	94,838,282			82,800,000
Lactobacillus	64,953,550	451,520	2,614,316	119,700,000
Paenibacillus	24,853,119	71,121		82,800,000
Pseudomonas	99,869,895	855,491		128,925,000
Sphingomonas	34,916,345			36,674,999
Stenotrophomonas	54,890,324	47,143		110,475,000
Streptomyces				36,674,999
Yersinia		142,243		
Sulfur-Oxidizing				
Aneurinibacillus		142,243		
Bacillus				27,450,000
Paracoccus		47,143		
Pseudomonas	99,869,895	855,491		128,925,000
Sulfur-Reducing				
Pseudomonas	99,869,895	855,491		128,925,000

