



Quantifies – simultaneously in a single analysis – a broad spectrum of microorganisms and genes involved in biogeochemical processes

Diverse microbial communities comprise the biogeochemical (BGC) profile that carries out sulfate reduction, sulfur oxidation, iron reduction, metal oxidation, nitrification, denitrification, nitrogen fixation, fermentation, acetogenesis, methanogenesis, and various other processes. To evaluate these processes, *Microbial Insights Inc.* takes your samples collected from the field, extracts RNA or DNA, and performs **QuantArray®—BGC** analysis. **QuantArrays®** use nanoliter fluidics and solution-phase qPCR — to quantify, in parallel, numerous genes (see below) in individually monitored reactions, in this case to accurately and comprehensively assess biogeochemical processes.

- Sulfate Reduction**
Sulfate is the terminal electron acceptor for electrons from hydrogen produced by other organisms to produce H₂S.
- Iron Reducing Bacteria**
Reduce insoluble iron oxides to soluble ferrous iron byproducts. Some can also reduce insoluble manganese oxides to soluble manganese by-products. Many use hydrogen as an electron donor.
- Metal Oxidizing Bacteria**
Iron and manganese oxidizers oxidize soluble iron and manganese to form insoluble iron and manganese oxides.
- Sulfur Oxidation**
Oxidize sulfide and elemental sulfur producing sulfuric acid.
- Nitrogen Cycle**
Nitrogen fixers convert atmospheric N₂ to ammonia that nitrite oxidizers then convert to nitrate that the denitrifiers then convert back into N₂. Anammox bacteria can also anaerobically convert nitrite and ammonia into N₂.
- Methanogens**
Methanogens use fermentation products of other anaerobes as electron donors (H₂, formate, and alcohols) and acceptors (CO₂, methanol, methylamines, and methylsulfides) to produce methane.
- Fermenters**
Produce H₂ during fermentation that other organisms — acetogens, methanogens, sulfate reducers, iron and manganese reducers, and nitrate reducers — can use. Designed to quantify a broad spectrum of fermenting bacteria, most notably of the class Clostridia.

Sulfate Reduction <ul style="list-style-type: none"> •Sulfate Reducing Bacteria (APS) •Sulfate Reducing Archaea (SRA) 	Sulfur Oxidation <ul style="list-style-type: none"> •Sulfur Oxidizing Bacteria (SOB)
Iron Reducing Bacteria <ul style="list-style-type: none"> •Iron Reducing Archaea (IRA) •Iron Reducing bacteria (IRB) •Iron Reducing Geobacter (IRG) •Iron Reducing Shewanella (IRS) 	Nitrogen Cycle <ul style="list-style-type: none"> •Ammonia Oxidizing Bacteria (AMO) •Ammonia Oxidizing Archaea (AOA) •Nitrite Oxidizing Bacteria (NOR)
Metal Oxidizing Bacteria <ul style="list-style-type: none"> •Iron Oxidizing Bacteria (FEOB) •Manganese Oxidizing Bacteria (MnOB) 	Microorganisms Classes <ul style="list-style-type: none"> •Total Bacteria (EBAC) and (ARC) •Fermenters (FER) •Acetogens (AGN) •Acetylene Degraders (AHY)

- Microbial Population Summary**
Plots of concentrations of microbial populations (e.g., Sulfate reducing bacteria) and genes relative to typical values.
- Summary Tables**
Tables of concentrations of microbial populations grouped by metabolic activity or mechanism.
- Comparison Figures**
Changes in microbial populations over time or across the site (depending on the project).

