

Heat maps and other graphical outputs in Gene-Trac® NGS reports provide easy to interpret visualization of microbial community profiles

Gene-Trac® NGS uses leading edge next generation sequencing technology to achieve comprehensive microbial community characterization. Gene-Trac® NGS provides cost-effective insights into community function and dynamics which are simply not possible with qPCR methods that target specific microorganisms. Gene-Trac® NGS is ideal to gain insight into complex microbial systems including bioremediation sites, wastewater treatment systems and landfills to improve understanding and management of these systems.

Use Gene-Trac® NGS to:

- Understand dominant, and potential, microbial processes.
- Visualize microbial community spatial and temporal variability.
- Determine the impact of e⁻ donors, nutrients, pH buffers, bioaugmentation, etc.
- Identify inhibitory conditions and challenging site locations.
- Make informed decisions to manage bioremediation & other microbial systems.

Data Analysis to Leverage the Power of NGS

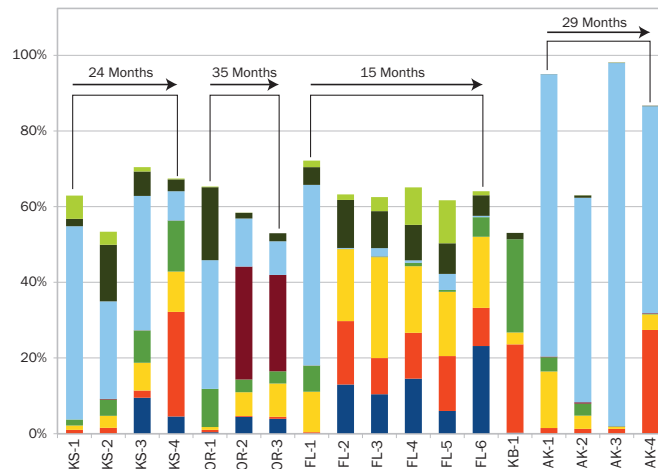
The complexity of NGS data means effective analysis, visualization and interpretation are essential to get the most out of this technology. SiREM, in collaboration with our research partners, has the in-depth knowledge and customized outputs required to effectively analyze and report NGS data sets using:

- Cluster analysis, interactive pie charts and heat maps to relate and characterize microbial communities.
- Functional analysis that provides easy to interpret plots of key microbial processes.
- Multivariate statistical methods to correlate metadata (e.g., remediation site parameters) to clarify factors driving microbial community composition.

Contact SiREM for a quotation or more information on Gene-Trac® tests for microbial community quantification and characterization.

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■ Sulfur Oxidizers ■ Aerobic / Facultatives ■ Metal Reducers ■ Dechlorinators
■ Sulfate Reducers ■ Methanotrophs ■ Fermenters ■ Methanogens



Functional analysis of NGS data for groundwater at chlorinated solvent remediation sites demonstrating a range of microbial processes between sites that vary over time and in response to bioremediation amendments