

Metatranscriptomics Service

Capture the activity of the gut microbiome with gene expression profiling

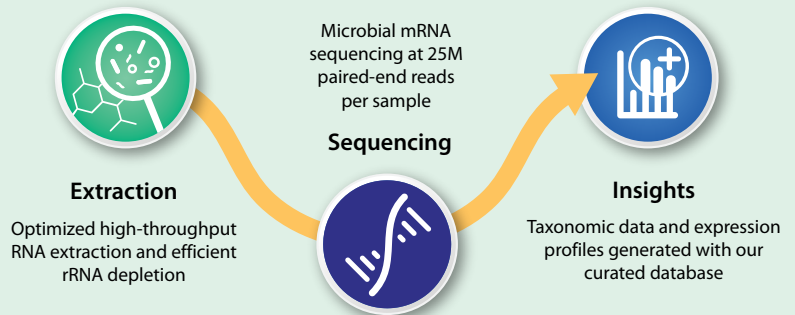
Features

- Comprehensive analysis, including gene expression profiles, taxonomic profiles and diversity metrics
- Curated database containing over 190,000 genomes and 100 million unique genes
- Optimized RNA extraction from stool with enhanced microbial mRNA recovery
- Sequencing at an average of 25M paired-end read depth per sample
- Project consultation
- Dedicated study coordinator
- Quality-controlled

The metatranscriptome represents an entire microbial community's gene expression profile, providing valuable information about the microbial activity, community dynamics and interaction between the microbes and the host.

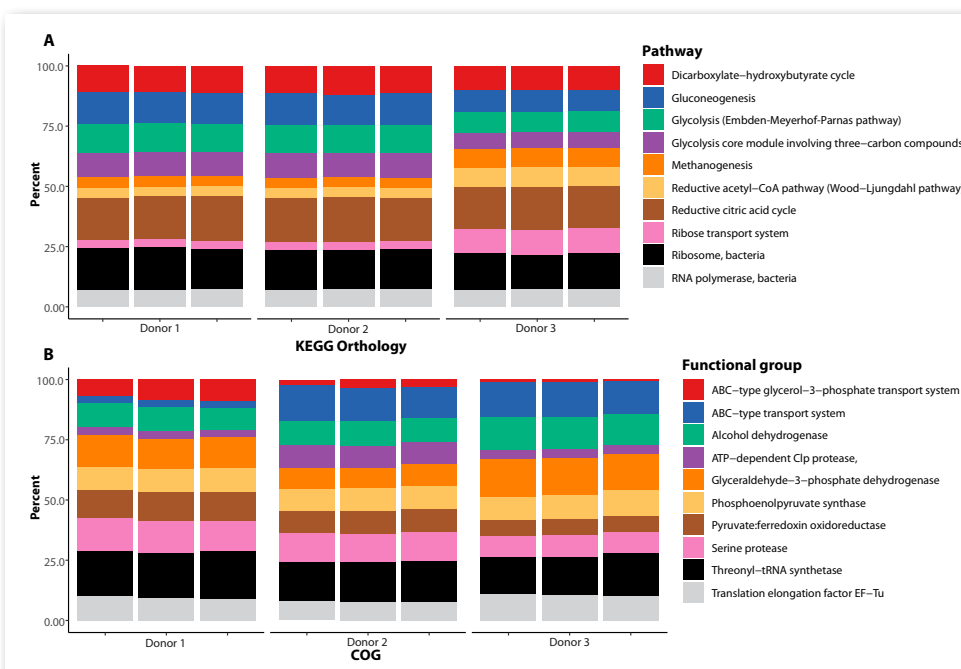
Diversigen's scientists developed the Metatranscriptomics Service to deliver valuable insights into microbial gene expression profiles, pathways, function and taxonomic information.

Your partner from sample to insight



Enhance the interpretation of the gut metatranscriptome:

- Optimized sample processing ensures microbial mRNA recovery
- Reproducible gene expression profiles at an average 25M paired-end read depth
- Accurate annotation based on a curated functional and taxonomic database
- Comprehensive analysis of gene expression, pathways and functions



Robust and reproducible gene expression profiles from stool at 25M paired-end reads

Figure 1. Metatranscriptomics Service enables robust and reproducible identification of KEGG Orthology pathways of the gut microbiome and COG functional groups in stool.
A) Top 10 KEGG Orthology pathways and B) Top 10 COG functional groups detected in 3 donors (N = 3 replicates per donor).

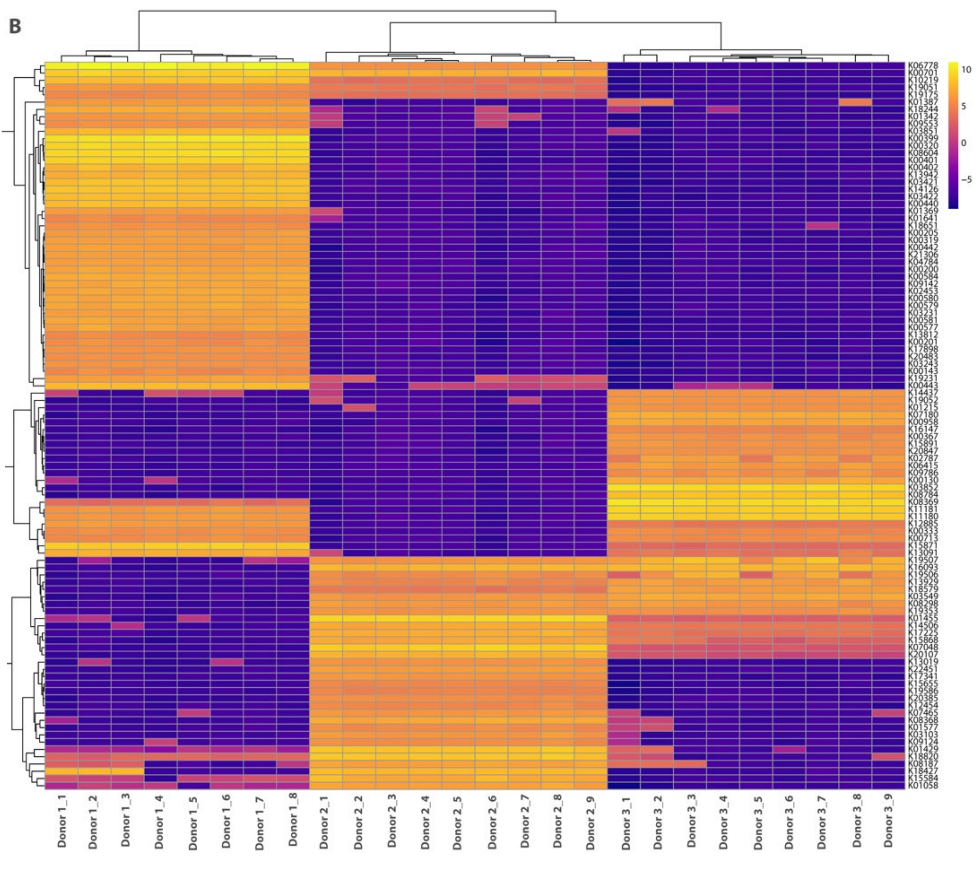
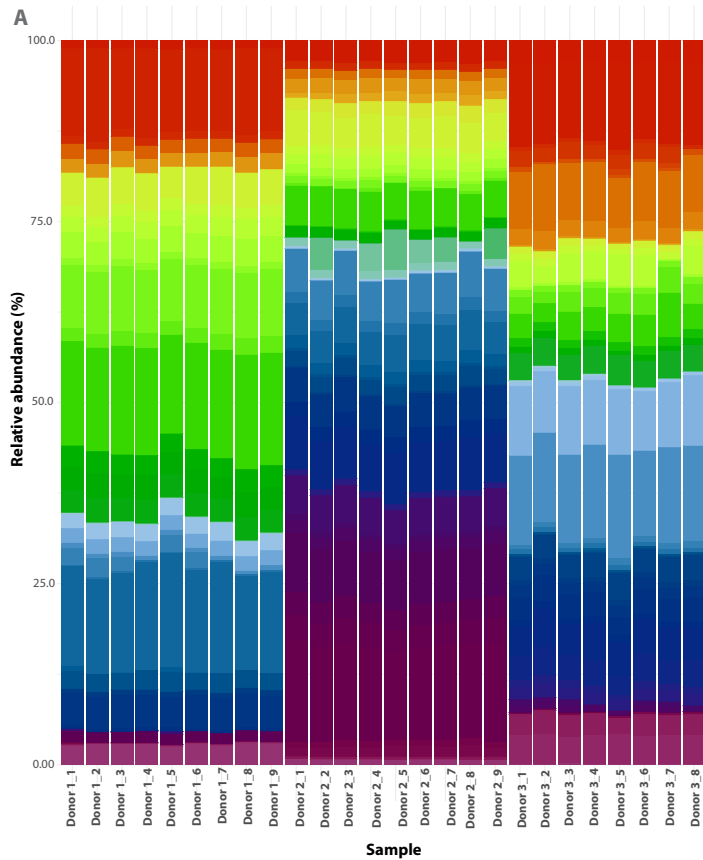
The Core Analysis Report includes taxonomic and gene expression profiles providing valuable insights into the gut microbial community

Figure 2. Taxonomic and gene expression data capture the activity of the gut microbiome.

A) Top 50 species identified and B) Relative abundance of ortholog groups (KO numbers) heat map from 3 donors at 9 time points.

Looking for more analytics?

Ask about CorePlus™ Analysis for custom bioinformatics and analytics to enable differential expression analysis, pathway enrichment, and correlation and association analyses.



Our team of scientists is ready to help at every step.

Interested in maximizing the value of your microbial metatranscriptomics project? Contact us at info@diversigen.com or www.diversigen.com