

Microbial Genome Sequencing

OVERVIEW

Microbial sequencing is a powerful technique enabling a better understanding of the mechanisms underlying infectious diseases, antibiotic resistance, and the workings of the human microbiome — efforts that have resounding implications for both personalized, and global health.

Our process leverages the power of multiplexing and the latest in sequencing technology to provide the ability to sequence hundreds of samples at once, enabling large-scale comparative studies of microbial species genomes and metagenomes, and to identify low frequency variants, genome rearrangements, and gene-level variation among isolates and metagenomes.

Due to the inherent variability found in many metagenomic samples, we process and sequence three different controls with every batch, including a negative control and two reference standards: an in-house developed standard consisting of a characterized microbial community, and a commercially available standard.

Sample preparation is achieved using a tagmentation method and includes 384 unique dual indexes, enabling us to multiplex efficiently with low input starting material. This LC method is not exclusive to microbial gDNA, and is suitable for other small genome projects with limited input material. Tagmentation can be affected by GC content, and though there is no significant effect on profiling metagenomic communities, additional coverage may be needed for genome assembly of isolates with less than ~25% GC content.

WHAT'S INCLUDED

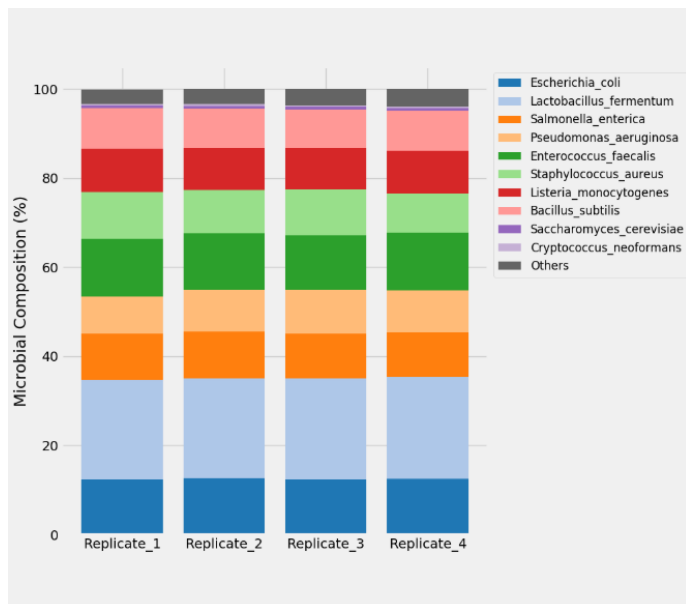
- Sample Receipt and Incoming QC
- Sample Preparation (LC) and QC
- 2x150bp Paired Sequencing
- ~0.25Gb, 1.5Gb, or 3Gb of Sequence Data per Sample*
- Data Delivery

*Samples submitted to this process are accepted at risk and billed accordingly. Gb estimates displayed here reflect ideal conditions.

	Utility	Sequence (per sample)
Microbial WGS - Low output	Bacterial isolates	~0.25 Gb, ~1m reads
Microbial WGS - Mid output -Available expedited	Bacterial isolates and small/simple population metagenomics	~1.5 Gb, ~6m reads
Microbial WGS - High output -Available expedited	Large genome bacterial isolates, large/complex bacterial community metagenomics	~3 Gb, ~12m reads
Microbial WGS - Very high output	Deep coverage of bacterial isolates, and very large/complex bacterial community metagenomics	>3 Gb, >12m reads

Designed for both bacterial isolates, and metagenomic analysis of complex bacterial communities

REPRODUCIBILITY OF STANDARDS



Species Abundance Across Control replicates.

Consistently reproducible taxonomic profiles from the commercially available Microbial Community DNA Standard are generated using bioBakery meta'omic profiling software.

INPUT REQUIREMENTS

- 60ng genomic DNA (@ 2ng/uL minimum concentration)
- Minimum sample data including Collaborator Participant ID and Collaborator Sample ID

DATA DELIVERABLE

- De-multiplexed, aggregated, unaligned BAM file

MORE INFORMATION

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