

Microbial Whole Genome Sequencing

Product Overview

Microbial whole genome sequencing (WGS) is a powerful technique enabling better understanding of the mechanisms underlying infectious diseases, antibiotic resistance, and the human microbiome — efforts that have resounding implications for personalized and global health. Broad Clinical Labs' Microbial WGS services leverage the power of multiplexing and the latest sequencing technologies to enable sequencing of hundreds of samples at once, powering large-scale comparative studies of microbial genomes and metagenomes, and identifying low frequency variants, genome rearrangements, and gene-level variation.

Due to the inherent variability in metagenomic samples, we process and sequence three different controls with each sample batch, including a negative control and two reference standards: an in-house developed standard consisting of a well-characterized microbial community, and a commercially available standard composed of a mixture of 10 microbial species.

We offer 2 sample preparation options: tagmentation-based and non-tagmentation-based. The tagmentation-based method enables efficient multiplexing with low input material. This library construction (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 the GC content of the sample which, in turn, can affect the resulting sequencing coverage. As such, the tagmentation-based LC method is generally most suitable for metagenomic community samples and most bacterial isolate samples, while the non-tagmentation-based LC method may be more suitable for whole genome assembly of low-GC isolate samples.

Summary of Product Offerings

Product	Utility	Expected Data Output (per sample)
Mid Output Non-tagmentation-based (Plasmodium and fungal)	Low GC content isolates	~1.5Gb
High Output Tagmentation-based -Available expedited	Large genome bacterial isolates, large/complex bacterial community metagenomics	~3Gb

What's Included

- Sample Receipt and incoming QC
- Library construction and QC
- 2x151bp paired-end Sequencing
- Data Delivery

Input Requirements

- 60 ng genomic DNA (minimum concentration: 2ng/μL)
- Stool: 75-150 mg (100mg preferred)
- Minimum sample data including collaborator participant ID and collaborator sample ID

Data Deliverable

- FASTQ files