

# 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 includes 384 unique dual molecular indices, enabling 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 (96 unique dual indices for this option).

## Summary of Product Offerings

Product	Utility	Expected Data Output (per sample)
<b>Low Output Tagmentation-based</b>	Bacterial isolates	~0.25Gb, ~1 million reads
<b>Mid Output Tagmentation-based</b> -Available expedited	Bacterial isolates and small/simple population metagenomics	~1.5Gb, ~6 million reads
<b>Mid Output Non-tagmentation-based</b> (Plasmodium and fungal)	Low GC content isolates	~1.5Gb, ~6 million reads
<b>High Output Tagmentation-based</b> -Available expedited	Large genome bacterial isolates, large/complex bacterial community metagenomics	~3Gb, ~12 million reads

## 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)
- Minimum sample data including collaborator participant ID and collaborator sample ID

## Data Deliverable

- De-multiplexed, aggregated, unaligned BAM file