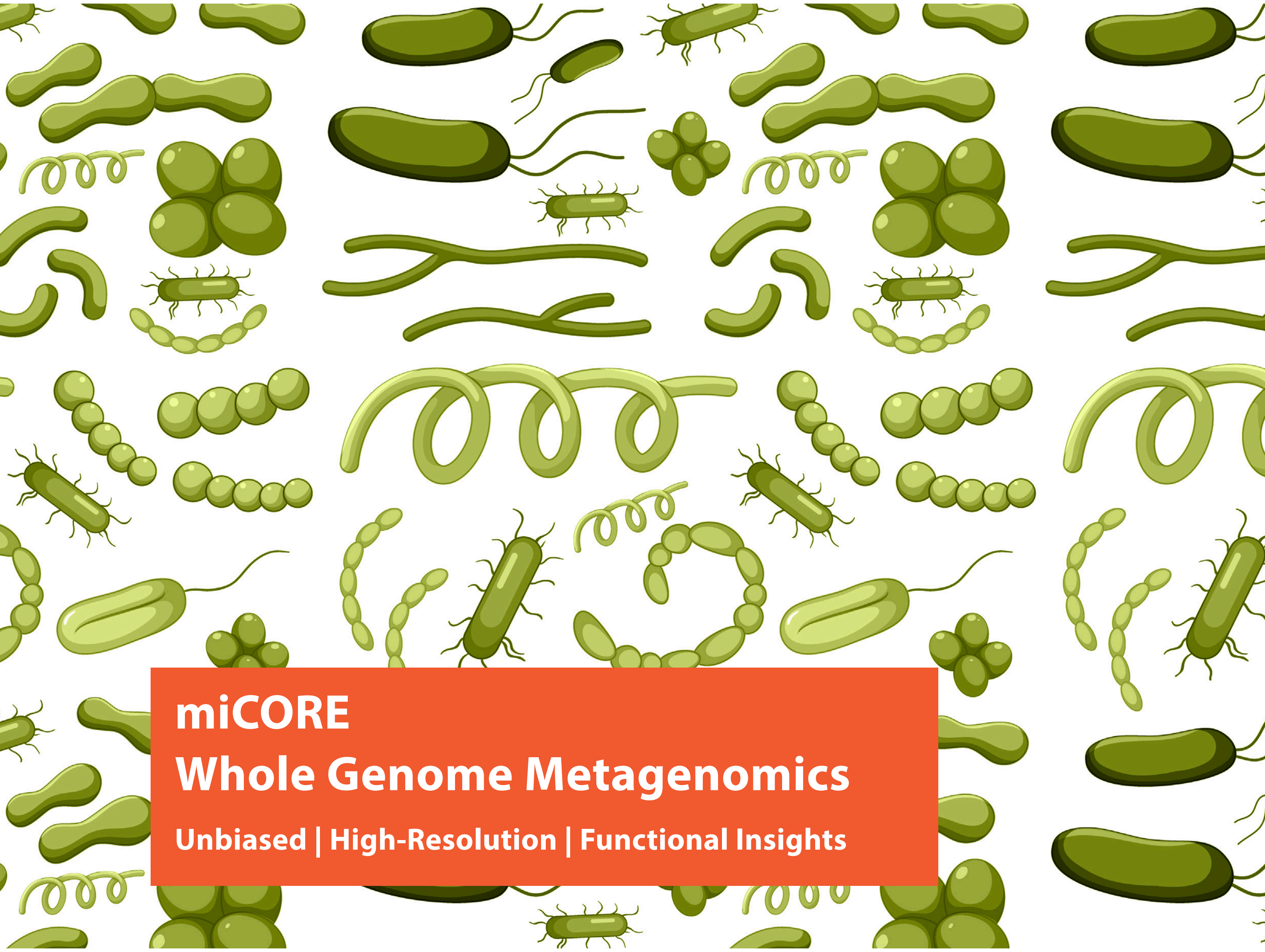


miCORE
Whole Genome Metagenomics

Unbiased | High-Resolution | Functional Insights

Unbiased Taxonomic Analysis
Comprehensively profile communities spanning all domains of life without marker gene biases.

High-Resolution Profiling
Identify organisms and estimate their relative abundances down to the species or even strain level.

Functional Insights
Uncover metabolic pathways, antibiotic resistance genes, virulence factors, and other functional genetic elements.

Overview of miCORE Whole Genome Metagenomics

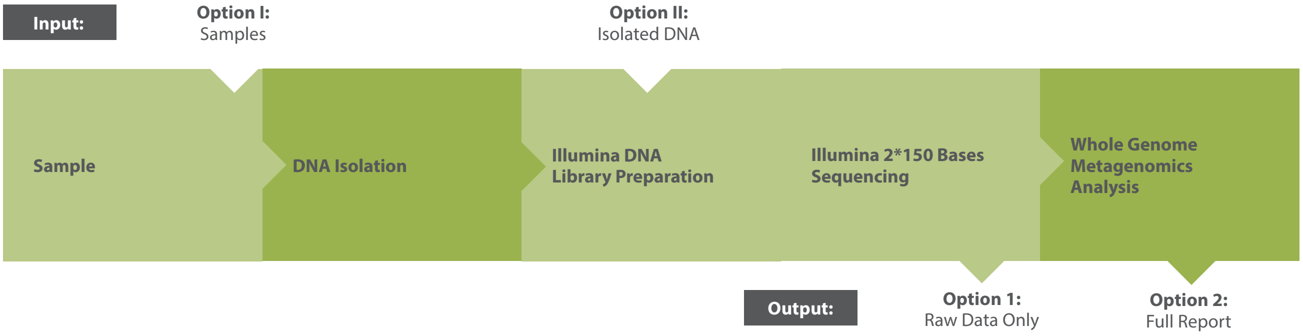
Microsynth's miCORE Whole Genome Metagenomics provides an unbiased comprehensive, high-resolution approach to studying biological communities. Unlike targeted methods, whole genome metagenomics sequencing — also known as shotgun metagenomics sequencing — captures the entire genetic content of a sample, facilitating unparalleled insights into microbial diversity, functional potential, and ecological interactions.

Unbiased Taxonomic Analysis – Explore the full spectrum of bacteria, archaea, viruses and eukaryotes beyond marker-gene limitations for a complete community profile across domain boundaries.

Functional Insights – Explore the functional potential, e.g. metabolic pathways, resistance genes and virulence factors, enabling deeper biological interpretation.

High-Resolution Profiling – Precisely determine relative abundances down to species or even strain level.

Workflow and Service Description



Input:

Option I: Samples

Option II: Isolated DNA

Sample → **DNA Isolation** → **Illumina DNA Library Preparation** → **Illumina 2*150 Bases Sequencing** → **Whole Genome Metagenomics Analysis**

Output:

Option 1: Raw Data Only

Option 2: Full Report

DNA Isolation (Optional): Outsource your DNA extraction to Microsynth with validated protocols for soil, water, feces, and clinical samples.

Library Preparation: Quality-controlled DNA samples are prepared using Illumina-stranded libraries for optimal sequencing performance.

Sequencing: High-throughput sequencing (2×150 bp Illumina reads) with flexible data output (1-5 Gb per sample), ensuring in-depth microbial analysis.

Bioinformatics: We offer two levels of analysis: Either only a taxonomic analysis or a full bioinformatics analysis. Full analysis includes: taxonomic and functional analysis, where reads are matched against nucleotide and protein databases, and analyzed for protein functions and relative abundance. For either service reads are quality filtered, raw data and interactive Krona charts are provided and selected NCBI taxonomic nodes (e.g., higher eukaryotes) can be included at an additional cost.

Turnaround Time

DNA Isolation (standard material)	**Library Preparation and Sequencing**	**Bioinformatics**
5 working days	**15 working days**	**15 working days (full analysis)** **5 working days (taxonomy only)**

We also offer an express service option for an additional fee to expedite the sequencing of your samples.

miCORE Whole Genome Metagenomics Products

Laboratory:

20008	Whole Genome Metagenomics - DNA Isolation
30003	Whole Genome Metagenomics - Library Preparation
30750	Illumina Sequencing (1 Gb Reads Package, 2×150)

Bioinformatics Analysis:

30128	Whole Genome Metagenomics - Bioinformatics (Full)
30129	Whole Genome Metagenomics - Bioinformatics (Taxonomy)
30228	Add-On Bioinformatics - Customized Database
30202	Add-On Bioinformatics - Comparative Analysis

Ready to Transform Your Microbiome Research?

Let's discuss your project! Contact us today to learn more.