# Master the Microbiome

Obtain a complete picture of complex microbial communities

The ProxiMeta™ Metagenome Deconvolution Platform combines cost-effective proximity ligation data with short- or long-read shotgun sequencing data to assemble high-quality metagenomes, and accurately assign mobile genetic elements to their hosts. Venture beyond 16S-based techniques and conventional binning to discover more species, strains, genes, and gene functions.

Key features and benefits:

- Outperforms conventional binning methods to yield more complete and less contaminated metagenome-assembled fungal, bacterial, and viral genomes.

- Only technology that enables accurate host attribution accurate host attribution for phages, plasmids and anti-microbial resistance (AMR) genes.

- No microbial culturing or high molecular weight DNA extraction required.

- ProxiMeta bundles include user-friendly proximity ligation library prep and cloud-based analysis.

Metagenome assembled genomes (MAGs) generated by conventional binning approaches are often fragmented and contaminated. In contrast, proximity ligation provides direct, physical evidence of sequences co-located in the same cell. The ProxiMeta™ Platform uses this information to generate high-quality MAGs for eukaryotic, prokaryotic, and viral members of complex microbial populations, and to assign mobile genetic elements to their hosts with high sensitivity and specificity.
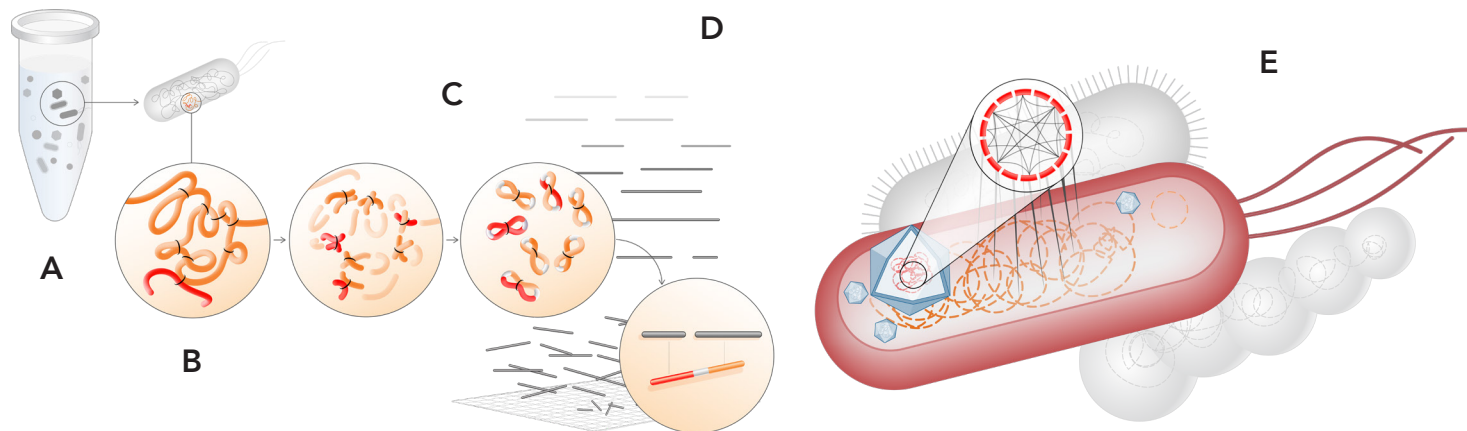
Overview of proximity-guided metagenome deconvolution and host attribution. Metagenomic samples are comprised of complex populations of archaea, bacteria and fungi (A). In addition to chromosomal DNA, cells contain genetic material such as plasmids, viruses or bacteriophages, transposons, integrons, and other mobile genetic elements. The first step in the generation of a proximity ligation library is crosslinking (B), which captures the physical interactions between DNA fragments in every individual cell. Digestion and ligation create chimeric junctions (C) that are sequenced and analyzed in combination with short- or long-read shotgun assemblies (D). The proximity ligation data provides an additional layer of information that is used to reconstruct more, high-quality bacterial and viral genomes than traditional binning approaches. In addition, the physical linkage information enables accurate viral-host attribution.

Applications

The long-range information obtained with proximity ligation technology takes the guesswork out of metagenomic deconvolution, and provides a more complete picture of complex microbial communities. Whether you are working with biological or environmental samples, the ProxiMeta Platform uniquely enables the discovery and characterization of more genomes, mobile genetic elements, and gene functions—as well as the relationships between them.

Employ this powerful platform to:

- discover new microbial species, strains, and genes
- study antibiotic resistance and improve surveillance
- reconstruct viral genomes, identify their hosts, and understand their biological roles
- analyze the human microbiome
- discover and annotate metabolic modules, and identify new metabolic and biosynthetic pathways

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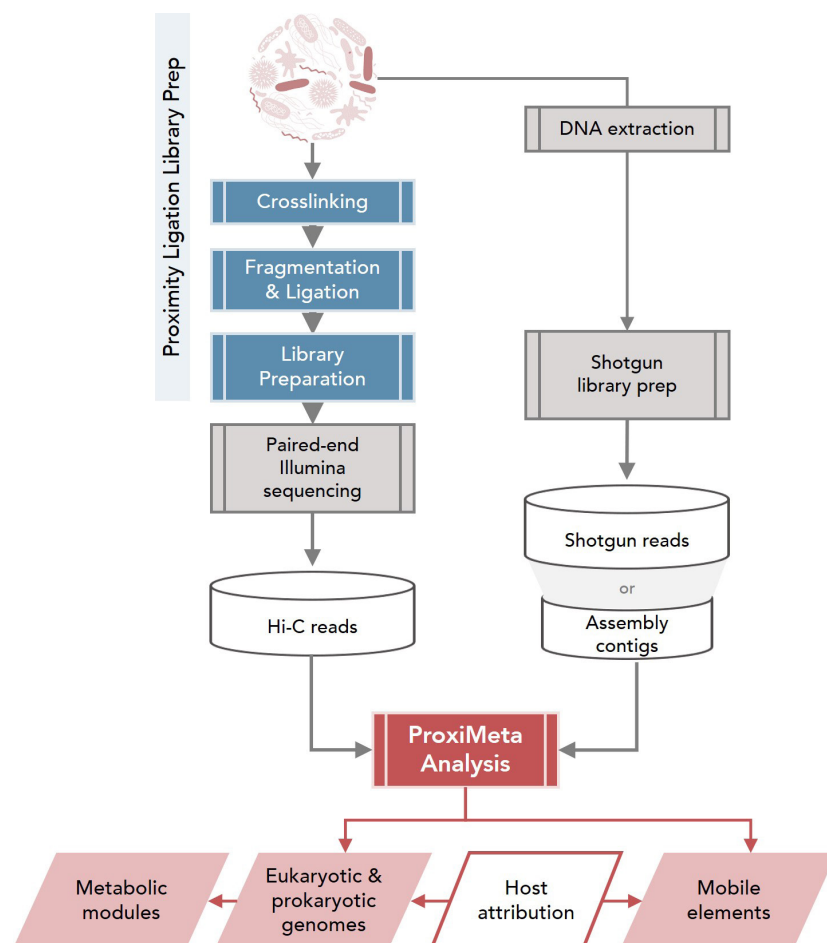
Download Application Notes

Complete Sample-to-Analysis Solution

The ProxiMeta™ Platform provides a complete sample-to-analysis solution that starts with a crude biological or environmental metagenomic sample, and ends with analyzed data.

The entire process (depicted on the right) is completed in a few weeks. ProxiMeta Kits provide all of the reagents and a streamlined protocol for the preparation of proximity ligation libraries.

- No culturing of microbes or extraction of high-molecular weight (HMW) DNA required.

- Processing guidelines for different types of metagenomic samples ensure robust results.

- Only three hours hands-on time required; convenient safe stopping points.

- Sequencing-ready libraries available within two working days.

- Reagents for shotgun library preparation are not included, and may be sourced from any suitable supplier.

All ProxiMeta Kits are now offered as bundles, including free online ProxiMeta Metagenome Deconvolution analysis. Visit proximeta.phasgenomics.com to register, upload your files, and download analyzed data and reports.

Proximity Ligation Library Prep

- Crosslinking
- Fragmentation & Ligation
- Library Preparation
- Paired-end Illumina sequencing
- Hi-C reads

- DNA extraction
- Shotgun library prep
- Shotgun reads
- or
- Assembly contigs

ProxiMeta Analysis

- Metabolic modules
- Eukaryotic & prokaryotic genomes
- Host attribution
- Mobile elements

Sample-to-analysis process. Proximity ligation (Hi-C) libraries are prepared with ProxiMeta Kits, directly from crude metagenomic samples. The proximity ligation library preparation workflow yields dual-indexed libraries for paired-end sequencing on the Illumina® platform. In a parallel workflow, DNA is extracted from the same sample, and used for shotgun library preparation, using any suitable library preparation method. Shotgun sequencing may be performed on a short- or long-read platform. The ProxiMeta analysis pipeline combines proximity ligation reads and shotgun reads/contigs to deconvolute samples, construct high-quality fungal, bacterial and viral genomes and mobile elements (phages, plasmids, AMR genes), and perform host attribution and metagenomic pathway analysis.

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ProxiMeta library prep and sequencing are also available as a service through our lab in Seattle, WA using the above workflow.

Contact us for more details about this option, and how you can ship samples directly to us.

Information-rich Analysis Reports

The ProxiMeta™ Platform is designed to yield more than just a taxonomic list of what is in your sample or a collection of genome FASTA files. Analysis reports provide more context, and allow for genome annotation, genome comparisons, and integration with several other industry-leading deconvolution tools. Visit proximeta.phasegenomics.com to view example reports.

Ordering Information

Description	Pack size
ProxiMeta Platform: ProxiMeta Kit + ProxiMeta Analysis	8 libraries
ProxiMeta Analysis: Metagenome Deconvolution Analysis (Computational Only)	≥1
ProxiMeta Service: Full Service Prep + ProxiMeta Analysis	≥1

Contact us to inquire about Plant & Animal Genomics or Human Genomics & Epigenomics applications and products, as well as other NGS services (incl. sequencing at competitive rates)

PHASE GENOMICS

info@phasegenomics.com
www.phasegenomics.com

Phone: 1-833-742-7436
Twitter: @PhaseGenomics