



ProxiMeta™ Hi-C  
Metagenome Deconvolution



# DISCOVER

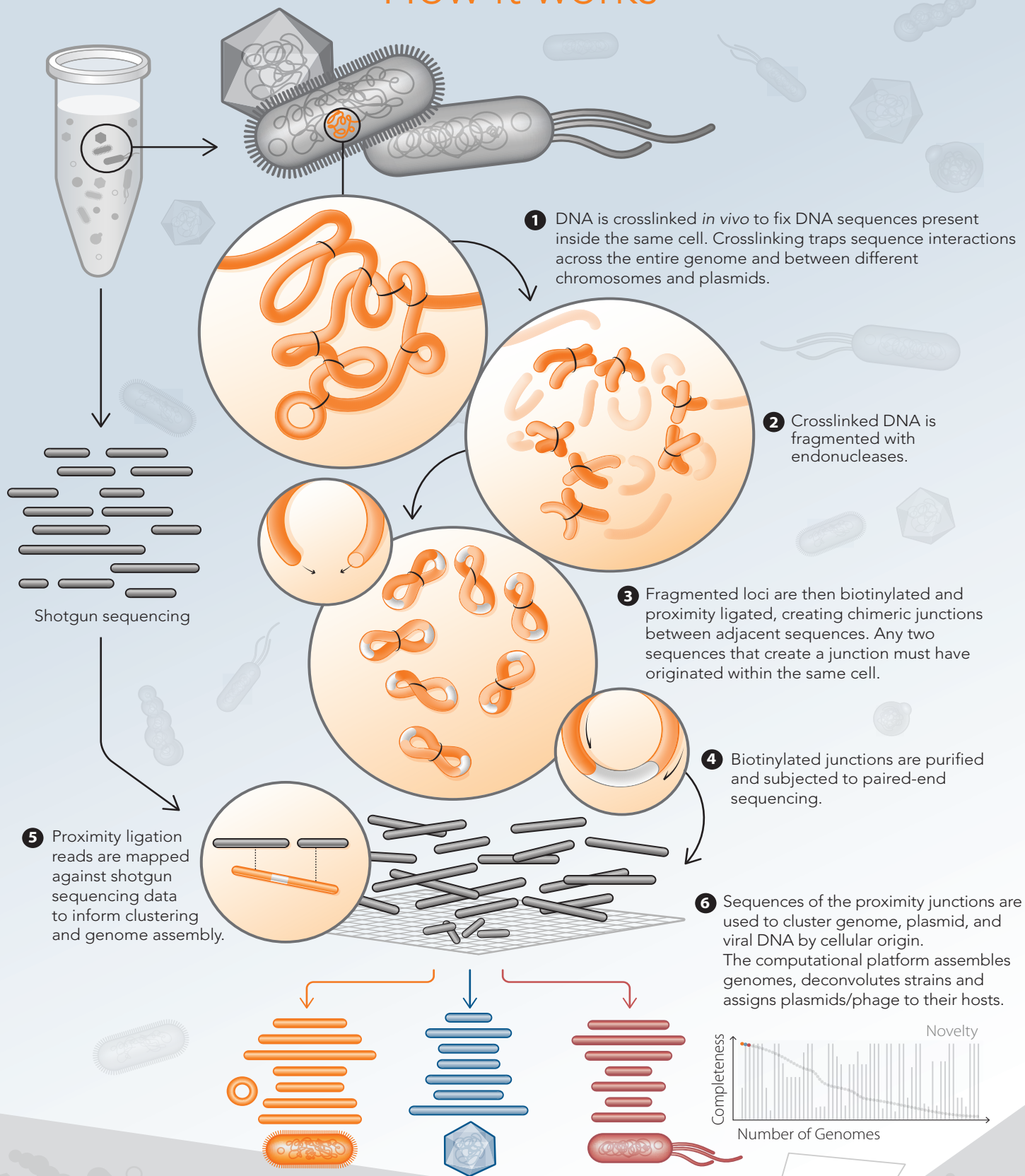
a shorter path to complete genomes.

The ProxiMeta Hi-C metagenomic deconvolution method employs proximity ligation data generated by *in vivo* Hi-C to enable true *de novo* assembly of microbial genomes directly from mixed samples

- Complete, novel genomes directly from complex microbiomes
- Associate plasmids and phage with their hosts
- No culturing, no HMW-DNA, no special equipment required
- User-friendly kit, computational analysis included

# ProxiMeta™ Hi-C

## How it works

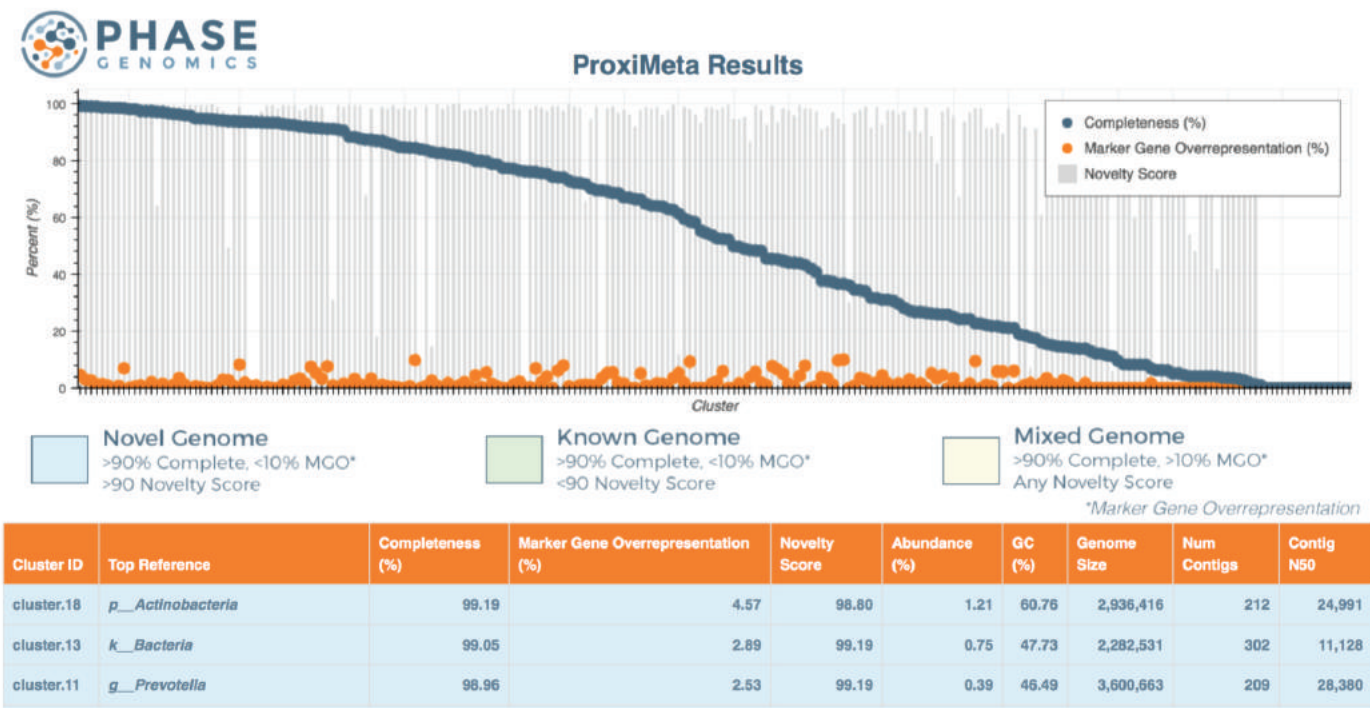
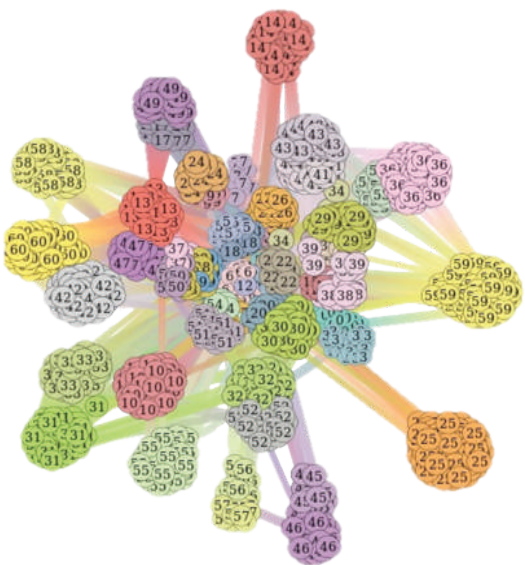


From communities to genomes.  
No culturing required.

Reference-quality genomes,  
directly from mixed populations

Unlike binning, *in vivo* proximity ligation provides direct physical evidence of sequences residing within the same cell. Data generated from a raw sample are used to deconvolve a mixed metagenomic dataset, creating genome clusters for eukaryotic and prokaryotic members of the population with no *a priori* species or strain information required.

Genome clusters include plasmids and phage, and can be used to search for query genes such as AMR and toxicity elements. This platform enables you to physically associate mobile DNA elements with host genomes directly from mixed communities.



Stewart et. al., Nature Commun., 2018 Feb28;9(1):870

Strains, species, genera

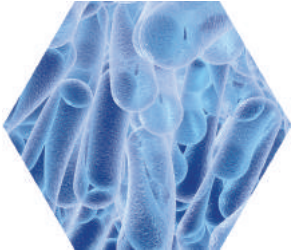
Genome data from ProxiMeta Hi-C is used to calculate completeness, novelty, abundance, and to assign taxonomic ID to resulting genome clusters. Novel genomes are identified and given the best matching phylogenetic assignment.

Our cloud-based computational platform makes analysis of the data fast and easy. Every project is handled by a team of dedicated computational biologists, helping you get the most from every dataset.



# Our Hi-C kits

Put the power of Hi-C in your hands.  
From sample to sequencer in one day with our kits.



## Microbiome Hi-C

- 250  $\mu$ L soil
- 100  $\mu$ L fecal
- 1-2 million cells



## Animal Hi-C

- 0.2 g tissue
- 1 mL blood
- 1-2 million cells



## Plant Hi-C

- 0.2 g leaf tissue
- 0.2 g seedling tissue
- 0.2 g flower tissue



## Human Hi-C

- 0.2 g human tissue
- 1 mL blood
- 1-2 million cells

# Our services

Take advantage of our genome assembly expertise.

### Hi-C Library Preparation

Let our experienced scientists handle your sample preparation and sequencing.

### Proximo™ Genome Scaffolding

Chromosome-scale genome scaffolds for virtually any organism, no HMW DNA required.

### ProxiMeta™ Metagenome Deconvolution

Go beyond 16S and binning techniques to obtain complete genomes from mixed communities.

### ProximoSV™

Identify large-scale structural variation and determine epigenetic changes using Hi-C data.



info@phasegenomics.com  
www.phasegenomics.com  
Twitter: @PhaseGenomics