Phase Genomics Announces the Commercial Availability of ProxiMeta™ Hi-C

Revolutionary metagenomic discovery service assembles individual, reference-quality genomes from microbiome samples

Seattle, WA (PRWEB) May 16, 2017 -- Seattle-based Phase Genomics announced today the general availability of its newest ProxiMeta™ Hi-C metagenomic deconvolution service. ProxiMeta enables researchers to obtain complete, distinct genomes from microbiome samples easily and affordably—without culturing or high-molecular-weight DNA extraction—speeding research insights at lower cost.

“We’re very excited about the commercial launch of our newest service for metagenomic assembly,” said Dr. Ivan Liachko, CEO and Co-founder of Phase Genomics. “ProxiMeta will help researchers answer longstanding, fundamental questions about their microbial samples. We give customers a way to explore the dark matter of the microbiome by quickly assembling the many genomes contained in a sample, leading to answers they could not have found otherwise.”

Microbial communities are typically made up of many different species living together. Standard methods for sequencing these communities mix together information from all the microbes in the sample. The result is a hodgepodge of genes that is challenging to analyze, and unknown species in the sample are difficult to discover. The innovative ProxiMeta Hi-C method reveals which DNA sequences originated in the same cell, enabling the assembly of whole genomes from mixed microbial samples in their natural state.

"Phase Genomics' ProxiMeta Hi-C solution makes innovative use of Illumina reads to conduct metagenomic deconvolution and extract more complete sequence information from mixed microbiome samples,” said Gary Schroth, PhD, Vice President of Genomics Development and Distinguished Scientist for Illumina. “This technology promises to open many new metagenomic applications and we’re excited to see it come to market."

CLEAR RESEARCH BENEFITS

By combining Hi-C proximity data and metagenomic sequencing, ProxiMeta delivers benefits not available from other methods.

• Clarity. Gain a more detailed view of microbial communities using the only method that moves straight from a raw sample to scores, or hundreds, of individual, reference-quality genomes.
• Simplicity. Simply collect and send in a microbial sample. No culturing is required, saving time and cost.
• Velocity. With publication-ready data typically available in 30 days, researchers can find and publish new insights faster.

"ProxiMeta Hi-C facilitates the cultivation-independent assembly of bacterial genomes present in complex microbial communities. Of particular interest is its potential to associate plasmids with their host genomes. Without having to culture individual isolates, ProxiMeta offers a new approach to examine the reservoirs of mobile genetic elements that carry genes of interest, such as toxin or antimicrobial resistance genes,” said Professor Eva Top, Bioinformatics and Computational Biology Graduate Program Director at the University of Idaho.

A SIMPLE PROCESS

ProxiMeta Hi-C is based on capturing physical DNA proximity with in vivo Hi-C. This allows sequences from
the same species and/or strain to be grouped, yielding a large number of genomes for rare, unculturable, and novel microbes. The ProxiMeta Hi-C service is a straightforward process for researchers:

- Researchers contact Phase Genomics to obtain a quote
- Researchers collect a raw sample (for example, a fecal or soil sample) and send it to Phase Genomics
- Phase Genomics processes the sample, providing shotgun sequencing, assembly, and metagenomic deconvolution
- Phase Genomics delivers the resulting genomes, along with supplementary figures and reports, to a secure online location for customer access, typically within 30 days of receiving a sample

Interested parties can learn more about ProxiMeta and other Phase Genomics services by visiting the Phase Genomics table at the Sequencing, Finishing and Analysis in the Future (SFAF) conference May 16-18, or at www.phasegenomics.com.
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