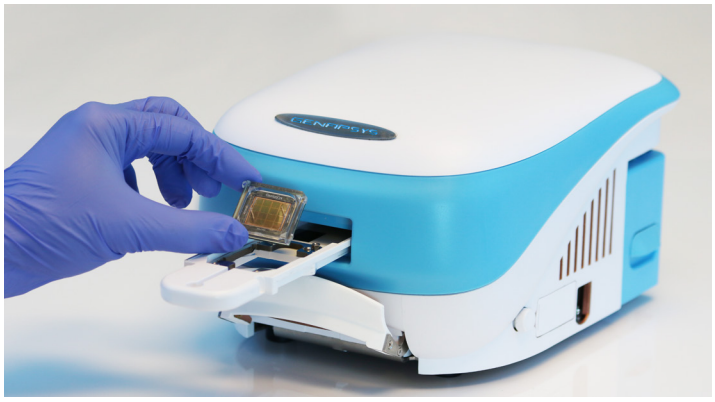
GenapSys™ Sequencing Platform: Small Genome Sequencing



- **Robust sequencing of whole genomes of bacteria, viruses, archaea, and other microorganisms**
- **Highly uniform genome coverage for viruses, bacteria, and other microbes**
- **Low price per run and low price per sample**
- **More than 1.2 Gb of highly accurate DNA sequence data per run**

Introduction

Advances in Next-Generation Sequencing have revolutionized the way biologists study organisms with small genomes (< 10 Mb), including viruses, bacteria, archaea, and other microorganisms. Applications of small genome sequencing include genome assembly, pathogen identification, comparative genomics, and analysis of biosynthetic pathways, just to name a few. The GenapSys Sequencing Platform that generates more than 1.2 Gb of highly accurate DNA sequence data per run is the ideal tool for addressing these applications.

Technology

The Genapsys™ Sequencer employs a novel electrical detection method that is capable of generating highly accurate DNA sequence information. With a CMOS-based detector, simple fluidics, and low computational requirements, the GenapSys instrument is small, affordable, and accessible even to novice genomic scientists. Inside the sequencing chip are millions of individual sensors, each loaded with a single bead coated in thousands of clonal copies of a particular DNA sequence. Individual nucleotides are flowed across the chip in succession and successful incorporation is detected by changes in impedance as the complementary DNA strand grows.

Experimental Methods

Genomic DNA from three different microbes was obtained from commercial sources. Sequencing libraries were generated by random shearing, end repair, A-tailing, and ligation of adapters. Libraries were size-selected for molecules with a median insert size of approximately 200 bp. Individual library molecules were clonally amplified onto beads, and beads were loaded onto the chip for sequencing on the GenapSys Sequencer.

Streamlined small genome sequencing workflow on the GenapSys Sequencing Platform

Library prep

Generate sequencing libraries. Size select. Enrich using capture panels.

Clonal Amplification

Clonally amplify libraries on the GenapSys Sequencing Prep System.

Sequencing

Load amplified beads into the chip and sequence using the GenapSys Sequencer.

Data Analysis

Basecall and generate FASTQ with GenapSys analysis software. Align to reference genomes using third-party tools.

Results

Sequencing data was processed using the GenapSys base-calling pipeline. The resulting FASTQ sequences were aligned to the reference genomes of the three sequenced microbes. Here, we show the coverage plots across each genome, highlighting deep and even coverage throughout. The three genomes sequenced have varying average GC contents. Distributions of reads segregated by GC content show even coverage across a wide range of sequence contexts.

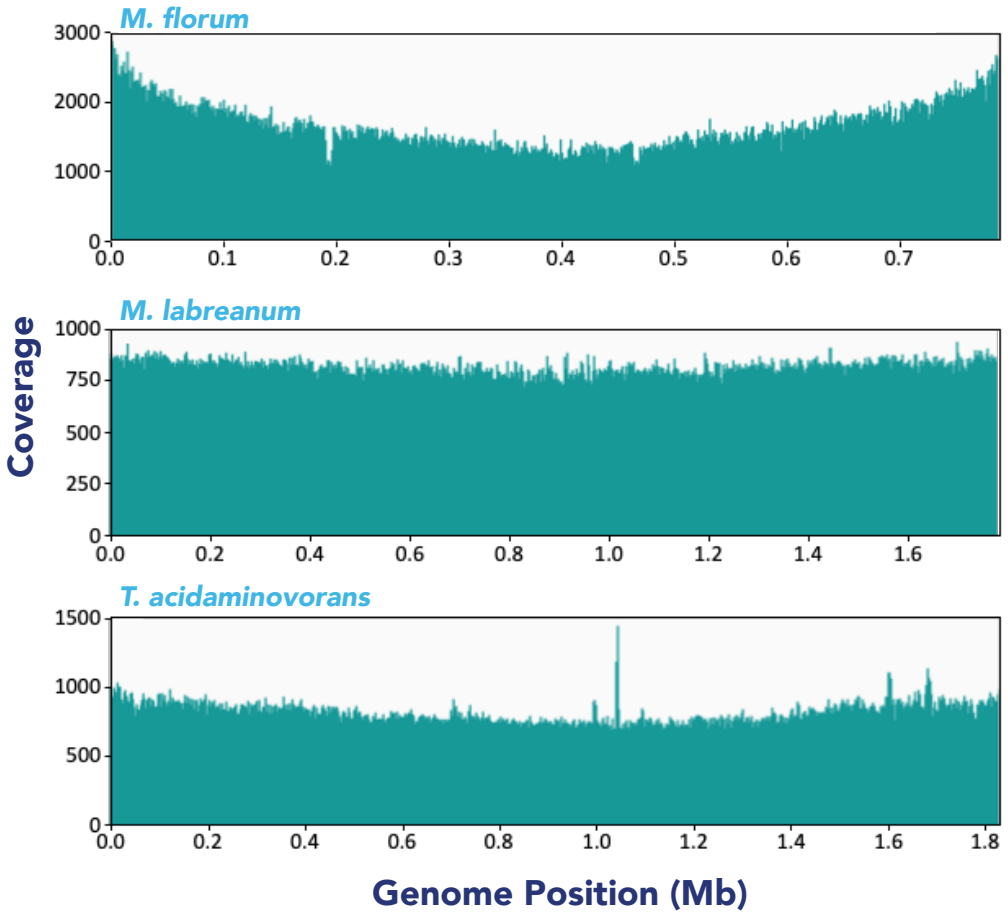
Conclusion

With highly accurate base calling and more than 1.2 Gb per run, the GenapSys Sequencing Platform allows microbiologists to address a wide range of biological questions for organisms with small genomes. Depending upon your coverage needs, multiple samples can be multiplexed into a single run. At a genome size of 5 Mb, up to 8 genomes can be sequenced to a depth of 30x in a single run.

Table 1: GC Content of Microbial Genomes Sequenced

	Mesoplasma florum	*Methanocorpusculum labreanum*	*Thermanaerovibrio acidaminovorans*
Genome Size	0.79 Mb	1.80 Mb	1.85 Mb
GC Content	~27%	~50%	~64%

Figure 1: Coverage Plots Across Three Reference Genomes



To learn more about the GenapSys Sequencing Platform, visit GenapSys.com

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Sequencing without compromise

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