MICROBIAL GENOMICS AT SCALE WITH PACBIO HIFI SEQUENCING

Microbial genomics with PacBio® long-read HiFi sequencing is accurate, scalable, and cost effective.

Automated end-to-end workflows from extraction to analysis and optimized kits drive greater throughput for HiFi microbial sequencing at lower cost.
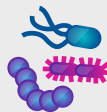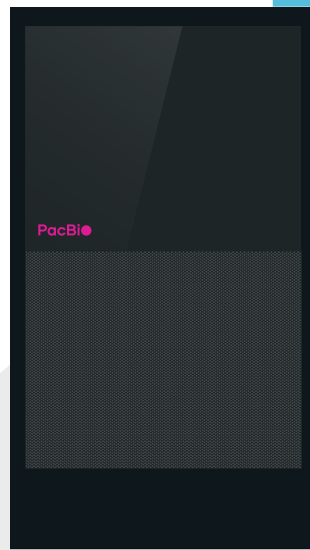
MICROBIAL WHOLE GENOME SEQUENCING

Obtain reference-grade high accuracy, closed chromosomes and plasmids with methylation signatures using the HiFi plex prep kit 96[1] and an end-to-end scalable workflow. Identify strain and functional characteristics, antimicrobial resistance (AMR) genes, and mobile vectors, all for <$50 USD/sample* with the ability to multiplex up to 384 libraries/SMRT® Cell.[†]

FULL-LENGTH 16S/ITS SEQUENCING

Sequence the entire gene to enable species- and strain-level taxonomy. Pairing full-length 16S sequencing with the Kinnex™ 16S rRNA kit[2] enables more samples per SMRT Cell (up to a 1,536-plex) and/or more reads per sample for <$5/amplicon* at >30k average reads per sample.[†] PacBio GitHub analysis completes a seamless workflow.[3]

VIRAL SEQUENCING

Sequence entire genes or genomes to deconvolute complex viral mixtures into quasispecies and unique haplotypes, identify and quantify minor variants linked to resistance or immunology, and track the evolution and phylogeny of viral populations. Use an amplicon or target enrichment approach for <$10/amplicon* or *de novo* assemble large viral genomes.

SHOTGUN METAGENOME SEQUENCING

Achieve richer functional information and profile species with high precision and recall with the HiFi plex prep kit 96[1] and PacBio GitHub workflows[4] for analysis. Prep and sequence at <$50/sample* or sequence deeper and recover many high-quality metagenome assembled genomes (HQ MAGs) and many circular, single-contig MAGs, even at lower coverage.

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* Prices, listed in USD, are approximate and may vary by region. Pricing includes library and sequencing reagents run on a Sequel® II/IIe or Revio™ system and does not include instrument amortization, other reagents, or DNA extraction.

† Reads per sample and number of samples per SMRT Cell and other sequencing performance results vary based on sample quality/type and insert size.

PacBio

Microbial genomics at scale enabled by the Revio™ system

HiFi sequencing on the Revio system with supporting products — Kinnex 16S rRNA and HiFi plex prep kits — brings higher throughput and lower costs for microbial genomics applications.

- $995 USD per SMRT Cell for sequencing*

- Four independent sequencing stages that generate 90 Gb per SMRT Cell for multi-application runs

- Simultaneous epigenetic information from native DNA sequencing applications

* US list price is $995 for sequencing reagents for one Revio SMRT Cell, which has an expected yield of 90 Gb, equivalent to a 30× human genome.

SMRT Cell 1	SMRT Cell 2	SMRT Cell 3	SMRT Cell 4
Microbial isolate whole genome sequencing	Viral targeted sequencing	Kinnex full-length 16S sequencing	Shotgun metagenome sequencing

Application	Samples per SMRT Cell	Samples per Revio run with 4 SMRT Cells	Estimated samples per year*
Microbial *de novo* assembly[†]	384	1,536	~499,200
Targeted amplicon sequencing[‡]	≥1,000	≥4,000	~2.6M for 1–5 kb ~1.3M for 5+ kb
Kinnex 16S rRNA	1,536	6,144	~2M
Shotgun metagenomic profiling	96	384	~124,800
Shotgun metagenomic assembly	12	48	~15,600

* Estimated samples per year calculated by assuming 1,300 SMRT Cells per year for each Revio system run using 4 SMRT Cells, 365 days in a year, and 90% utilization. Annual throughput is based on 1,300 Revio SMRT Cells. All sample throughputs are estimates per Revio run using 1 or 4 SMRT Cells. Coverage may vary based on sample quality, library quality, and fragment lengths.

† Currently available SMRTbell® barcoded adapter plates contains 384 SMRTbell barcoded adapters. Microbial *de novo* assembly assumes microbes with ~1.2 Gb of total genome size per SMRT Cell.

‡ Amplicon sequencing assumes 12-hour movie time for 1–5 kb, 24-hour movie time for 5+ kb, and >50× per sample.

Learn more about PacBio microbial genomics: pacb.com/microbial-genomics

KEY REFERENCES

1. Documentation — HiFi plex prep kit 96
2. Application note – Kinnex 16S rRNA kit for full-length 16S sequencing
3. https://github.com/PacificBiosciences/HiFi-16S-workflow
4. https://github.com/PacificBiosciences/pb-metagenomics-tools