Application brief MICROBIAL GENOMICS WITHIN REACH AND 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 costs.



MICROBIAL WHOLE GENOME SEQUENCING

Obtain reference-grade high accuracy, closed chromosomes and plasmids with methylation signatures using the HiFi plex prep kit 96¹ 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.[†]



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 <\$5/sample* or *de novo* assemble large viral genomes.





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 kit² enables more samples per SMRT Cell (up to a 1,536plex) and/or more reads per sample for <\$5/sample* at >30k average reads per sample.⁺ PacBio GitHub analysis completes a seamless workflow.³



SHOTGUN METAGENOME SEQUENCING

Achieve richer functional information and profile species with high precision and recall with the HiFi plex prep kit 96¹ and PacBio GitHub workflows⁴ for analysis. Prep and sequence at <\$60/sample* or sequence deeper and recover many high-quality metagenome assembled genomes (HQ MAGs) and many circular, singlecontig MAGs, even at lower coverage.

* Prices, listed in USD, are approximate and may vary by region. Pricing includes library and sequencing reagents run on a Vega[™] 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



Microbial genomics within reach and at scale enabled by HiFi systems

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

Vega system

- \$1,100 USD per SMRT Cell for sequencing*
- One sequencing stage that generates 60 Gb per run
- Simultaneous epigenetic information from native DNA sequencing applications
- * US list price is \$1100 for sequencing reagents for one Vega SMRT Cell, which has an expected yield of 60 Gb.

Revio system with SPRQ[™] chemistry

- \$995 USD per SMRT Cell for sequencing*
- Four independent sequencing stages that generate 120 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 120 Gb with the SPRQ chemistry.

Recommended maximum samples per SMRT Cell, estimated yield per sample, and cost estimate per sample*





	Vega system 60 Gb × 1 SMRT Cell in 24 hr		Revio system with SPRQ chemistry 120 Gb × 4 SMRT Cells in 24 hr	
Microbial WGS (2 Gb total) [†]	384 isolates ~30× coverage ~\$42^a ~\$24^b ~\$15^c		384 isolates ~50× coverage ~\$42ª ~\$24^b ~\$15 ^c	
Metagenome profiling	64 communities ~0.75 Gb ~\$57 ° ~\$30 °		128 communities ∼0.75 Gb ~\$47ª ~\$20 °	
Metagenome assembly	8 communities ~7 Gb ~\$194^d ~\$159°		16 communities ~6 Gb ~\$119^d ~\$79 °	
Full-length 16S rRNA	Standard 16S 384 communities ~10k reads ~\$5	Kinnex 16S 1,152 communities ~30k reads ~\$4	Standard 16S 384 communities ~20k reads ~\$5	Kinnex 16S 1,536 communities ~45k reads ~\$4
Viral amplicon	>1000 amplicons <\$5		>1000 amplicons <\$5	

* Study design, sample type, and level of multiplexing may affect the number of SMRT Cells required. All prices are listed in USD and cost may vary by region. Pricing includes library and sequencing reagents run on your Vega or Revio systems and does not include instrument amortization, other reagents, or DNA extraction.

+ Currently available SMRTbell[®] barcoded adapter plates contains 384 SMRTbell barcoded adapters. Microbial *de novo* assembly assumes microbes with ~2 Gb of total genome size per SMRT Cell.

^a Using PacBio HiFi plex prep kit 96; ^b Using seqWell LongPlex Long Fragment Multiplexing Kit; ^c Using Ampli-Fi protocol (loss of methylation info); ^d Using PacBio HiFi prep kit 96

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

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