

The outstanding accuracy of HiFi long-read sequencing allows you to get the most out of each Revio run. Discover how you can access more information at reduced cost and higher throughput for each of your sequencing projects.

- HiFi sequencing provides reliable answers through exceptional accuracy, with 90% of bases Q30+. Maximize genetic information and detect more variant types including direct methylation in native molecules.
- Perform on-board primary analysis including barcode demultiplexing, methylation calling, and Google DeepConsensus.
- Optimize your workflow with simplified consumables and rapid run setup. Take advantage of four independent sequencing stages to perform multiomic experiments in one sequencing run.
- **Generate a \$1,000 complete, phased human genome.\***

## More samples, more discovery

Application	Samples per SMRT® Cell†	Samples per Revio run using 4 SMRT Cells†
<b>Whole genome sequencing</b>		
<i>De novo</i> assembly	1	4
Variant detection	Structural variants: 3 All variants: 1	Structural variants: 12 All variants: 4
Microbial <i>de novo</i> assembly	96	384
<b>RNA sequencing</b>		
Single-cell transcriptomics	1	4
<b>Targeted sequencing</b>		
Amplicon sequencing	≥1,000	≥4,000
Target enrichment	20 Mb panel: 12 2 Mb panel: 72 100 kb panel: 288	20 Mb panel: 48 2 Mb panel: 288 100 kb panel: 1,152
<b>Metagenomics</b>		
Shotgun metagenomic profiling	96 communities	384 communities
Shotgun metagenomic assembly	12 communities	48 communities

\* 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. Your local sales representative can provide detailed pricing in your currency.

† 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 plate 3.0 contains 96 SMRTbell barcoded adapters. Whole genome sequencing for a 3 Gb human-like genome at >15× per haplotype for *de novo* assembly, >10× coverage for structural variants, and >30× coverage to detect more variants. Microbial *de novo* assembly assumes microbes with ~1.2 Gb of total genome size per SMRT Cell at >50× per sample. Single cell transcriptomics assumes ≥80 million reads per library. Amplicon sequencing assumes amplicon fragments (>3 kb) and >50× per sample. Target enrichment assumes >50× per sample.

## From sample prep to analysis, PacBio® has you covered



### Sample prep

Nanobind® DNA kits enable extraction of HMW gDNA from a variety of sample types



### Library prep

SMRTbell prep kit 3.0 supports manual and automated library prep for effortless SMRTbell library creation



### Sequence

The Revio system adds affordability, high throughput, and ease of use to a foundation of long reads, exceptional accuracy, and direct methylation



### Analysis

On-board SMRT® Link primary analysis, methylation calling, and Google DeepConsensus

## Ordering information

Part number	Product	Description	List price (USD)
102-090-600	Revio system	Sequencing instrument	\$779,000
102-817-600	Revio polymerase kit	Reagents for binding polymerase to 24 SMRTbell libraries	\$1,800
102-587-400	Revio sequencing plate	Sequencing reagents supporting 4 SMRT Cells	\$720
102-202-200	Revio SMRT Cell tray	Tray of 4 Revio SMRT Cells	\$2,960
102-817-900	Revio reagent kit, 24-pack	(1) Revio polymerase kit, (6) Revio sequencing plate, and (6) Revio SMRT Cell tray	\$23,880



### Connect with PacBio

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### Learn about application-specific workflows

[pacb.com/applications](https://pacb.com/applications)



### Learn more about the Revio system

[pacb.com/revio](https://pacb.com/revio)

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