PacBio

Application brief

WHAT CAN YOU DO WITH A REVIO™ SYSTEM?

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*
Whole genome sequencing		
***De novo* assembly**	1	4
Variant detection	Structural variants: 3 All variants: 1	Structural variants: 12 All variants: 4
Microbial *de novo* assembly	96	384
RNA sequencing		
Kinnex single-cell transcriptomics	1	4
Kinnex full-length RNA	4	16
Targeted sequencing		
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
Metagenomics		
Shotgun metagenomic profiling	96 communities	384 communities
Shotgun metagenomic assembly	12 communities	48 communities
Kinnex 16S rRNA	1,536 communities	6,144 communities

* 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. Full-length RNA assumes a total of 40M reads regardless of plexity. Amplicon sequencing assumes 12-hour movie time for 1–5 kb, 24-hour movie time for 5+ kb, and >50× per sample. Target enrichment assumes >50× per sample.

From sample prep to analysis, PacBio® has you covered




Sample prep	Library prep	Sequence	Analysis
Nanobind® DNA kits enable extraction of HMW gDNA from a variety of sample types	SMRTbell prep kit 3.0 supports manual and automated library prep for effortless SMRTbell library creation	The Revio system adds affordability, high throughput, and ease of use to a foundation of long reads, exceptional accuracy, and direct methylation	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 plates, and 6 Revio SMRT Cell trays	$23,880

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Learn about application-specific workflows
pacb.com/applications

Learn more about the Revio system
pacb.com/revio