

## Reveal more with accurate long-read sequencing

- Generate more complete genomes and detect more variant types, full-length transcripts, metagenomes, and direct methylation in native molecules.
- Achieve greater resolution in your projects with the exceptional HiFi accuracy of 90% of bases at Q30+.
- Enjoy on-instrument primary analysis with automatic conversion to the standard BAM format – so you can make meaningful insights faster.



**Vega™ system**  
HiFi within reach

1 SMRT® Cell



**Revio® system with SPRQ™ chemistry**  
HiFi at scale

1 SMRT Cell

4 SMRT Cells

**Application**

**Samples per run**

Application	1 SMRT® Cell	1 SMRT Cell	4 SMRT Cells
<b>Whole genome sequencing</b>			
Human genome (20x coverage)	1	2	8
Human methylation profiling (5x)	4	8	32
De novo assembly (1 Gb genome)	2	4	16
Microbial de novo assembly (2 Gb total)	384	384	1,536
<b>Targeted panels</b>			
Amplicon sequencing	>1,000	>1,000	>4,000
<b>Target enrichment</b>			
20 Mb panel	12	16	64
2 Mb panel	72	96	384
100 kb panel	288	384	1,536
PureTarget™ repeat expansion panel	48	48	192
<b>RNA sequencing</b>			
Kinnex™ single-cell RNA sequencing	1 (3,000–6,000 cells)	1 (6,000–10,000 cells)	4 (6,000–10,000 cells)
<b>Kinnex full-length RNA sequencing</b>			
5M reads	6	12	48
10M reads	3	6	24
<b>Microbial</b>			
Shotgun metagenomic profiling	64 communities	128 communities	512 communities
Shotgun metagenomic assembly	8 communities	16 communities	64 communities
Kinnex 16S rRNA	1,024 communities	1,536 communities	6,144 communities

All sample throughputs are estimates for either the Vega system with 1 SMRT Cell or the Revio system using SPRQ chemistry with both 1 or 4 SMRT Cells. Coverage may vary based on sample quality, library quality, and fragment lengths. Currently available SMRTbell® adapter index plates 96A-96D contain a total of 384 SMRTbell barcoded adapters. Microbial de novo assembly assumes microbes with 2 Gb of total genome size at 30x per sample. Single-cell transcriptomics assumes ≥80 million reads per library on the Revio system and ~50-60 million reads per library on the Vega system. Full-length RNA sequencing assumes a total of 60M reads for Revio SPRQ and 30M reads for Vega, regardless of plexity. Amplicon sequencing assumes a 12-hour movie time for 1–5 kb, 24-hour movie time for 5+ kb, and >50x per sample. Target enrichment assumes >50x per sample.

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



### Sample prep

The Nanobind® PanDNA kit provides all-in-one extraction of HMW gDNA from cultured cells, bacteria, whole blood, tissue, saliva, plant nuclei, and insect samples (~2 hrs)



### Library prep

SMRTbell® prep kit 3.0 and HiFi prep kits supports manual and automated library prep for effortless SMRTbell library creation (1 day)



### Sequence

The Vega and Revio systems add flexibility, high throughput, and ease of use to a foundation of long reads, exceptional accuracy, and simultaneous methylation (24 hrs)



### Analysis

On-instrument primary analysis and operate through SMRT® Link, a web-based workflow manager from sample setup to secondary analysis

## Ordering information

### Part number    Product

103-525-500    Vega system

103-517-600    Vega polymerase kit

103-274-300    Vega sequencing plate

103-406-700    Vega SMRT Cell tray

102-090-600    Revio system

103-520-100    Revio SPRQ polymerase kit

103-504-900    Revio SPRQ sequencing plate

102-202-200    Revio SMRT Cell tray

## Ready to start HiFi sequencing?

### Talk to a sales rep today.

North America: [nasales@pacb.com](mailto:nasales@pacb.com)

South America: [sasales@pacb.com](mailto:sasales@pacb.com)

EMEA: [emea@pacb.com](mailto:emea@pacb.com)

Asia Pacific: [apsales@pacb.com](mailto:apsales@pacb.com)



### Learn more about applications

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



### Learn more about the Vega system

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



### Learn more about the Revio system

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

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