

# HIFI SEQUENCING WITHOUT LIMITS ON THE REVIO SYSTEM



The [Revio™ system](#) empowers HiFi sequencing. It adds affordability, high throughput, and ease of use to a foundation of long reads, exceptional accuracy, and direct methylation detection. With the Revio system, you have access to long and accurate HiFi reads at the scale and price needed for large studies.



### 15× increase in HiFi read throughput<sup>1</sup>

With a high-density, 25 million ZMW SMRT® Cell, up to 4 SMRT Cells in parallel, and 24-hour run times, the Revio system delivers 360 Gb of HiFi reads per day, equivalent to 1,300 human whole genomes per year.



### A vastly simplified experience that eliminates extraneous consumables

Operating the Revio system is simple, thanks to a combined reagent and sample plate, rapid run setup, flexibility to queue runs while sequencing is in progress, and no external nitrogen supply.



### Google DeepConsensus and more on board

Advanced algorithms on the Revio system deliver the highest read accuracy plus methylation calling in every run. Its optimized file formats reduce data storage needs through quality value binning and smart read ordering.



### The \$1,000 complete, phased HiFi genome

HiFi sequencing provides small variants, structural variants, repeat expansions, methylation, and haplotype phasing from a single library and sequencing run.

## Sequencing specifications<sup>2</sup>

Library	Run time	HiFi yield		Base quality	Methylation
		1 Revio SMRT Cell	4 Revio SMRT Cells		
15–18 kb	24 hours	90 Gb	360 Gb	90% ≥Q30	5mC at CpG sites

## Application specifications<sup>3</sup>

Sample	Per Revio SMRT Cell	Per year	Expected coverage
Human genome	1	1,300	30×
Single-cell transcriptome	1	1,300	80 million reads
Large gene panel (20 Mb)	12	15,600	90% target positions ≥10×



# Reveal more with HiFi sequencing at scale

## Benefits of HiFi sequencing

[HiFi sequencing](#) gives you native long reads that are astonishingly accurate, free of systematic errors, unbiased by sequence context, and inclusive of epigenetic modifications like DNA methylation.



### Long reads

Reads tens of kilobases in length



### High accuracy

Sequencing free of systematic errors



### Uniform coverage

No bias based on GC content



### Native molecules

Direct sequencing of individual DNA molecules



### Epigenetics

DNA methylation without special library preparation

## Key applications of HiFi sequencing

HiFi sequencing enabled the first telomere-to-telomere genome assembly, the first directly phased methylomes, and the first catalogs of full-length isoforms at single-cell resolution. With the Revio system, you can unleash that power to move beyond fragmented views of biology to complete genomes + epigenomes and transcriptomes.



### HiFi genomes: sequence + methylation

Accurately profile all classes of variation — SNVs, indels, repeat expansions, structural variants — plus DNA methylation, all phased into chromosomal haplotypes.



### HiFi transcriptomes

Measure transcripts, not just isolated exons, with full-length isoform sequencing at the resolution of single cells.



Learn more about the Revio system:  
[pacb.com/revio](https://pacb.com/revio)



Connect with PacBio for more info:  
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### Ordering information

**102-090-600** Revio system  
**102-817-600** Revio polymerase kit  
**102-202-200** Revio SMRT Cell tray  
**102-587-400** Revio sequencing plate



### Instrument operating environment

**Temperature** 19–25°C (66–77°F)  
**Humidity** 20–80% relative humidity, non-condensing  
**Ventilation** 16,400 BTU/hr (4,800 W)  
**W × D × H** 36.5 × 35.5 × 68.7 in (92.7 × 90.2 × 174.5 cm)  
**Weight** 449 kg (989 lb)  
**Power** 200–240 VAC at 50–60 Hz, 30A  
**Network** 1 GbE or 10 GbE, copper

1. Compared to Sequel IIe system.

2. Run time specification is for the sequencing reaction. HiFi yield and base quality is based on HG002/GM24385 human DNA extracted with Nanobind CBB kit and prepared with SMRTbell prep kit 3.0.

3. Annual throughput is based on 1,300 Revio SMRT Cells. Expected coverages and throughputs are estimates. Coverage may vary based on library quality and fragment lengths.

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