

REVIO SYSTEM SPECIFICATION SHEET

More HiFi reads, more samples, more discovery

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. Revio features advanced sequencing consumables, robotics, and massive compute power to deliver accurate long reads with methylation information directly from the sequencer in every run. Free yourself to discover more with a complete view of genomes, epigenomes, and transcriptomes on the Revio system.

System specifications

The Revio system utilizes nanofabricated Revio SMRT® Cells, each of which has 25 million zero-mode waveguide wells. Revio has four independent stages, allowing sequencing of multiple SMRT Cells in parallel. The onboard compute provides accurate basecalling with Google DeepConsensus, plus methylation calling in every run.

Library	Run time ¹	Q30+ bases	HiFi yield per SMRT Cell ²	Methylation
1–5 kb	12 hours	95%	6 million reads	5mC at CpG sites for native DNA
5–10 kb	24 hours	90%	30 Gb	
10–15 kb			60 Gb	
15–20 kb			90 Gb	
20–25 kb	30 hours	85%	90 Gb	

1. Run time refers to the data collection step, which determines the time between processing SMRT Cells.

2. HiFi yield is dependent on library quality and sequencing preparation procedures. Specified yield is based on high-quality samples prepared following best practices.

Key applications and sample throughput

The Revio system supports a variety of applications that benefit from accurate long HiFi reads. Its four independent stages allow different samples and applications to be sequenced in parallel. A subset of key applications is shown below:

Library	Sample	Per Revio SMRT Cell	Per year ³	Expected coverage ⁴
1–5 kb	Amplicon	>1,000	>2.6 million	50×
5–10 kb	Microbial genome	96	124,800	50×
15–20 kb	Human genome	1	1,300	30×
15–20 kb	Transcriptome with Kinnex™ full-length RNA kit	4	5,200	10 million reads

3. Annual throughput is based on 2,600 Revio SMRT Cells for 12 hour runs; 1,300 for 24 hour runs; and 1,050 for 30 hour runs. Adaptive loading – which increases the consistency of yield per SMRT Cell – adds about 4 hours to run time, affecting the maximum number of SMRT Cells per year.

4. Expected coverages are estimates.



Comprehensive variant calling with phasing + 5mC

Access high accuracy for all variant types – SNVs, indels, structural variants, tandem repeat expansions, and methylation – including in challenging regions.



Truly complete assembly of complex genomes

Accurately construct the full sequence of chromosomes, including telomeres and centromeres.



Targeted sequencing to study genes at scale

Focus the power of HiFi variant calling by enriching for regions of interest using hybrid capture or PCR amplification.



Single-cell transcriptome sequencing

Catalog RNA isoforms at single-cell resolution, moving beyond gene counting to catalog full-length transcripts.

Instrument specifications

Operating environment	
Temperature	19–25°C (66–77°F)
Humidity	20–80% relative humidity, non-condensing
Ventilation	13,000 BTU (3,800 W)
Altitude	Below 2,250 m (7,380 ft)
Air quality	Pollution degree 2, indoor use only
Dimensions	
W × D × H	92.7 cm (36.5 in) × 91.4 cm (36.0 in) × 174.5 cm (68.7 in)
Weight	465 kg (1,025 lb)
Floor space	243.8 cm (96.0 in) × 138.5 cm (54.5 in)
Crated W × D × H	125.7 cm (49.0 in) × 115.3 cm (45.4 in) × 220.4 cm (87.0 in)
Crated weight	635 kg (1,400 lb)
Electrical power	
Power requirements	200–240 VAC at 50-60 Hz, max 5 kVA / 4.8 kW / 24 A
Compute	
Network connection	1 GbE or 10 GbE, copper
ICC ⁵ operating system	Ubuntu 22
Output file format	hifi_reads.bam; ≈55 GB each, up to 72 TB per year

5. ICC = instrument control computer

Ordering information

Part number	Consumable	Description
102-090-600	Revio system	Sequencing instrument
102-817-600	Revio polymerase kit	Reagents for binding polymerase to 24 SMRTbell libraries
102-202-200	Revio SMRT Cell tray	Tray of 4 Revio SMRT Cells
102-587-400	Revio sequencing plate	Sequencing reagents supporting 4 Revio SMRT Cells



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