

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.

Sequencing 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	HiFi yield ²		Base quality ²	Methylation
		1 Revio SMRT Cell	4 Revio SMRT Cells		
15–18 kb	24 hours	90 Gb	360 Gb	90% ≥Q30	5mC at CpG sites

1. Run time specification is for the sequencing reaction.

2. 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.

Application specifications

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.

Sample	Per Revio SMRT Cell	Per year ³	Expected coverage ⁴
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×

3. Annual throughput is based on 1,300 Revio SMRT Cells.

4. Expected coverages and throughputs are estimates. Coverage may vary based on library quality and fragment lengths.



HiFi genomes

Achieve contiguous, complete, and correct genome assemblies

Profile variants comprehensively

- SNVs, indels, structural variants
- Complex tandem repeats
- Methylation
- Phased haplotypes



HiFi single-cell transcriptomes

See more complete transcriptomes, at single-cell resolution

- Beyond gene counting to full-length isoform information
- Characterize a 3,000–10,000 cell library with 80 million reads



HiFi gene panels

Target just the genes you need for comprehensive variant detection at scale

- SNVs and indels in hard-to-call regions
- Structural variants
- Direct phasing of haplotypes
- Ancestry-agnostic variant calling

Instrument specifications

Operating environment	
Temperature	19–25°C (66–77°F)
Humidity	20–80% relative humidity, non-condensing
Ventilation	16,400 BTU/hr (4,800 W)
Dimensions	
W × D × H	92.7 cm (36.5 in) × 90.2 cm (35.5 in) × 174.5 cm (68.7 in)
Weight	449 kg (989 lb)
Floor space	198.1 cm (78.0 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	612 kg (1,350 lb)
Electrical power	
Power requirements	200–240 VAC at 50-60 Hz, 30A
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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