REVIO SYSTEM + SPRQ-NX CHEMISTRY SPECIFICATION SHEET

More HiFi reads, more samples, more discovery

The Revio® system powers HiFi sequencing on a foundation of long reads, exceptional accuracy, and direct methylation detection. Now optimized with SPRQ™-Nx chemistry, the Revio system offers enhanced affordability, throughput, and ease of use. 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 and has four independent stages, allowing sequencing of multiple SMRT Cells in parallel - while SPRQ-Nx chemistry enables multiple acquisitions per SMRT Cell. The onboard compute provides accurate basecalling with Google DeepConsensus, plus methylation calling in every run.

Library	Acquisition time[1]	Q30+ bases	HiFi yield[2]		Methylation detection
			Revio SMRT Cell (1 acquisition)	Revio SMRT Cell – Nx (3 acquisitions)	
0.5–5 kb	12 hours	95%	6–8 million reads	not supported[4]	5mC + 5hmC at CpG sites and 6mA[3] for native DNA
5–10 kb	24 hours	90%	35–70 Gb	105–210 Gb	
10–15 kb			70–100 Gb	210–300 Gb	
15–20 kb			100–120 Gb	300–360 Gb	
20–25 kb	30 hours	85%	100–120 Gb	300–360 Gb	

1. Acquisition 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.
3. The Revio 6mA caller is designed to detect methylation in the context of the Fiber-seq chromatin assay.
4. Libraries 0.5-5 kb are supported only with single acquisition Revio SMRT Cells with either SPRQ or SPRQ-Nx chemistry.

Key applications and sample throughput

The Revio system supports a variety of applications that benefit from accurate long HiFi reads and requires an input of 500 ng of DNA per sample. Its four independent stages allow different samples and applications to be sequenced in parallel. A subset of key applications is shown below:

Library	Application	Samples per Revio acquisition	Samples per year[5]	Expected coverage[6]
0.5–5 kb	Amplicon sequencing	>1,000	>2.5 million	50×
5–10 kb	Microbial genome	384	480,000	30×
5–10 kb	PureTarget panels	96	100,000	>100× mean per target
5–10 kb	Ampli-Fi human genome	1	1,250	20×
15–20 kb	Human genome	2	2,500	20×
15–20 kb	Human methylation profiling	8	10,000	5×
15–20 kb	Transcriptome with Kinnex™ full-length RNA kit	6	7,500	10 million reads

5. Annual throughput is based on 2,500 Revio SMRT Cells for 12 hour runs; 1,250 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.
6. Expected coverages are estimates.

More comprehensive variant calling with phasing and 5mC, 5hmC + 6mA methylation detection

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

More 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 PureTarget™, hybrid capture, or amplicon sequencing.

Single-cell transcriptome sequencing

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

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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
Noise output	<75 dB at 3.3 m (10 ft 10 in) from instrument
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 (49.5 in) × 115.3 cm (45.4 in) × 220.4 cm (86.8 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 / 30 A
Compute	
Network connection	1 GbE or 10 GbE, copper
Instrument operating system	Ubuntu 22
Output file format	hifi_reads.bam; ~60 GB each, up to 78 TB per year

Ordering information

Part number	Consumable	Description
102-090-600	Revio system	Sequencing instrument
103-520-100	Revio SPRQ polymerase kit	Reagents for binding polymerase supporting 24 Revio SMRT Cells
102-202-200	Revio SMRT Cell tray	Tray of 4 Revio SMRT Cells
103-483-800	Revio SMRT Cell tray – Nx	Tray of 4 Revio SMRT Cells – Nx
103-504-900	Revio SPRQ sequencing plate	Sequencing reagents supporting 4 Revio SMRT Cells
103-726-200	Revio SPRQ sequencing plate – Nx	Sequencing reagents supporting 4 Revio acquisitions

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