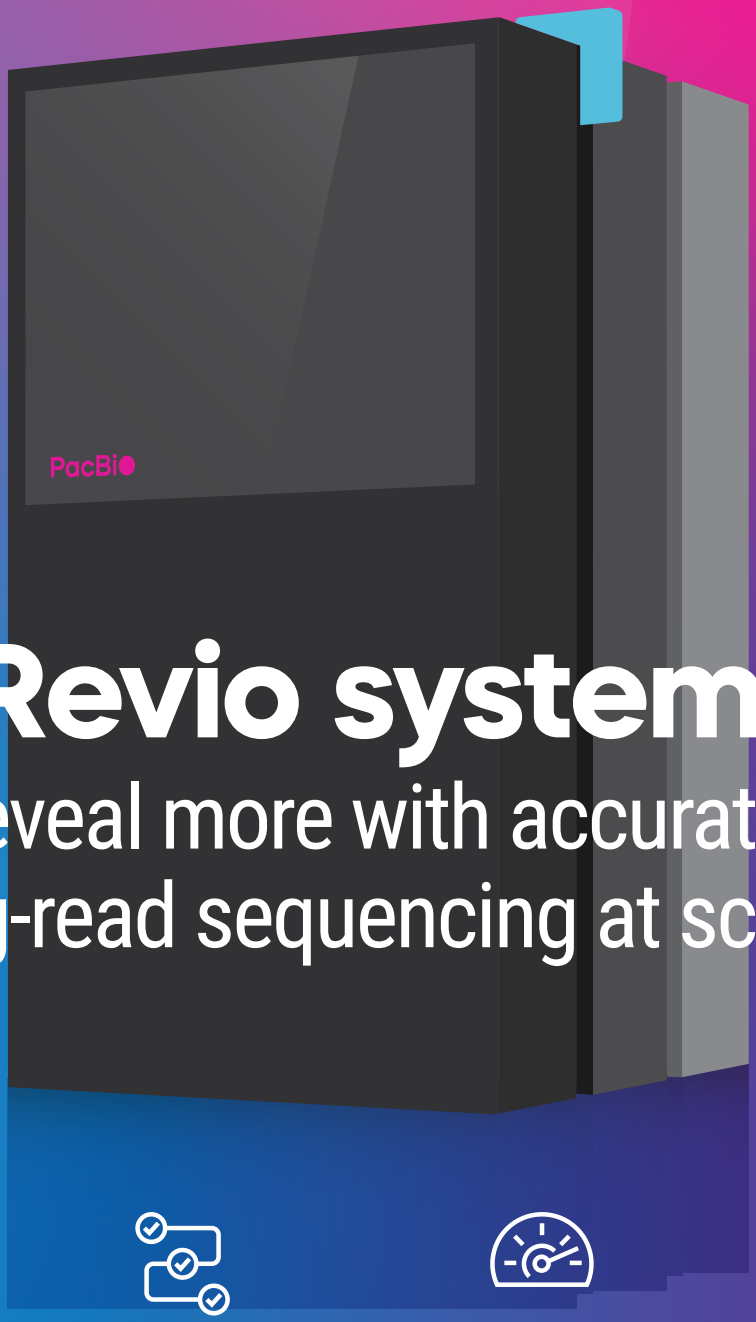
PacBio



Revio system

Reveal more with accurate long-read sequencing at scale

Scale

2,500 human HiFi genomes per year

Ease of use

Only 500 ng DNA input and flexible run setup

Compute power

Google DeepConsensus and more on board

Affordability

~$500 human HiFi genome

This is your moment for a more complete view of biology

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

Access high accuracy for all variant types — SNVs, indels, structural variants, tandem repeat expansions, and methylation — including in challenging regions.[1]

More complete assembly of complex genomes

Accurately construct the full sequence of chromosomes, including telomeres and centromeres.[2]

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 PCR amplification.

Single-cell transcriptome sequencing

Catalog RNA isoforms at single-cell resolution, moving beyond gene counting to catalog full-length transcripts.[3]

See it all with HiFi sequencing on the Revio system

Long reads

HiFi reads are tens of kilobases long, providing the ability to resolve large variants — like structural variants and tandem repeat expansions — and map to difficult, repetitive regions of the genome.

Exceptional accuracy

HiFi sequencing provides reliable answers through exceptional accuracy, with 90% of bases ≥Q30 and median read accuracy ≥Q30.

Direct methylation detection in native molecules

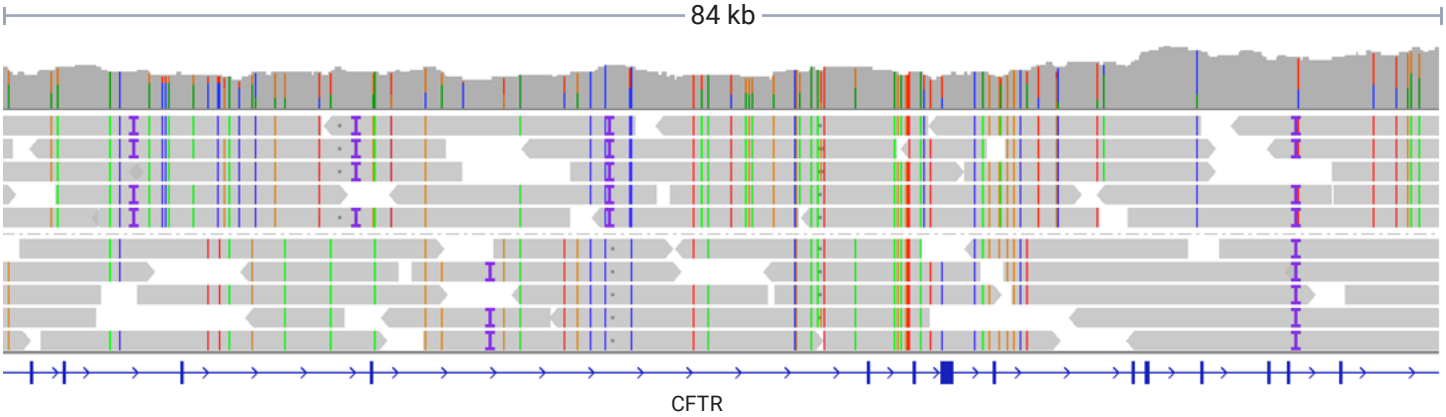
HiFi sequencing identifies base pair-level DNA methylation in all runs, without any additional library prep steps.

Low DNA input requirements

Each sample requires only 500 ng of DNA input, enabling HiFi sequencing for even the most precious samples on the Revio® system.

Uniform coverage across sequence contexts

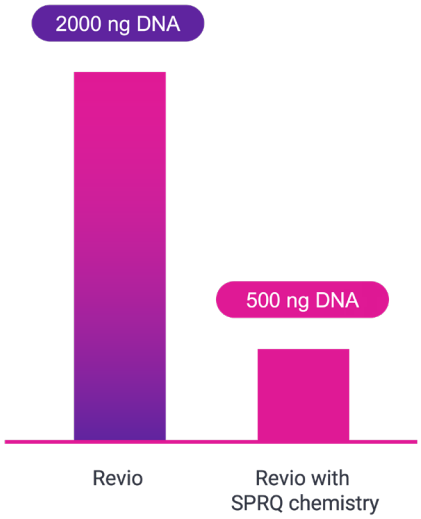
With an optimized polymerase and no amplification, HiFi sequencing provides uniform coverage even for high-GC regions and tandem repeats.



HiFi reads for the sample HG002 reveal accurate sequence of both maternal and paternal alleles, providing phasing that spans over 84 kb of the cystic fibrosis gene, *CFTR*.

Ignite your research with SPRQ chemistry

With SPRQ™ chemistry, the Revio system helps you achieve more with less DNA, increasing efficiency, maximizing output, and reducing costs—empowering you to make more discoveries faster and affordably.



Spark innovation:

- Resolve chromatin architecture with Fiber-seq, powered by on-instrument 5mC and 6mA calling, now with an increased 5mC CpG accuracy for even greater precision

Reduced input, expanded application possibilities:

- Only 500 ng DNA input
- 4× more efficient SMRT® Cell loading

Drive down genome costs:

- 33% increased HiFi yields
- 2 human genomes at 20× per SMRT Cell

Multiomics in every run

Independent stages enable simultaneous sequencing of 4 SMRT Cells, delivering high-quality, haplotype-resolved data for the genome, transcriptome, and epigenome – all from a single run.

SMRT Cell 1	SMRT Cell 2	SMRT Cell 3	SMRT Cell 4
2 whole human genome at 20×	384 microbial genomes	6 full-length transcriptomes at 10M reads	8 human methylation profiling at 5×

How Revio compares

	PacBio Revio with SPRQ	SBS short-read sequencing	Nanopore sequencing
Read length	15–20 kb	2×150 bp	10–100 kb
Read accuracy	99.95% (Q33)	99.92% (Q31)	99.26% (Q21)
Run time	24 hours	44 hours	72 hours
Yield	100–120 Gb	2,400–3,000 Gb	50–110 Gb
Variant calling—SNVs	✓	✓	✓
Variant calling—indels	✓	✓	×
Variant calling—SVs	✓	×	✓
Methylation	5mC, 6mA	×	5mC, 6mA
Phasing	✓	×	✓

The easy-to-use Revio system fits your schedule

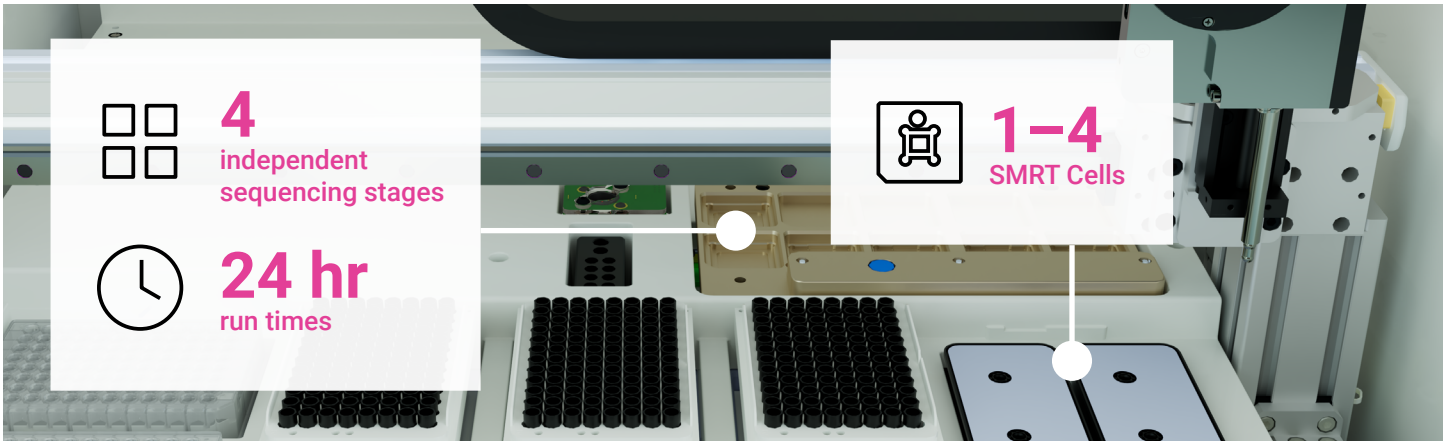
The Revio system offers configurable sequencing run times to tailor to your experiments.

The new flowcell design of the Revio SMRT Cell eliminates the need for a nitrogen supply, simplifying laboratory requirements.

The ability to load consumables while sequencing is in progress makes it easy to maximize instrument utilization without off-hours work.

The workdeck on the Revio system is isolated from the four sequencing stages. This leaves the system available for loading consumables up to 20 hours per day while keeping the stages fully utilized.

Enjoy a fully automated sequencing workflow



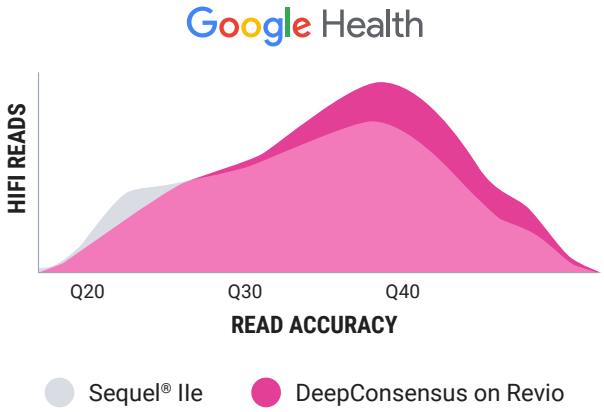
Simplified consumables

- The Revio system has only three workdeck consumables — a sequencing plate, a SMRT Cell tray, and pipette tips.
- Sequencing plates are linked automatically to run designs through an NFC tag, enabling rapid run setup on instrument.

- Now optimized with SPRQ chemistry, the Revio system adds a low DNA input requirement, enhanced affordability, and even higher throughput to a foundation of long reads, exceptional accuracy, direct methylation detection, and uniform coverage
- The Revio SPRQ sequencing plate combines what was previously four parts, eliminating extraneous plastic and making runs easier to manage. The single standard 96-well plate includes sample libraries, reagents, and space for mixing and waste.

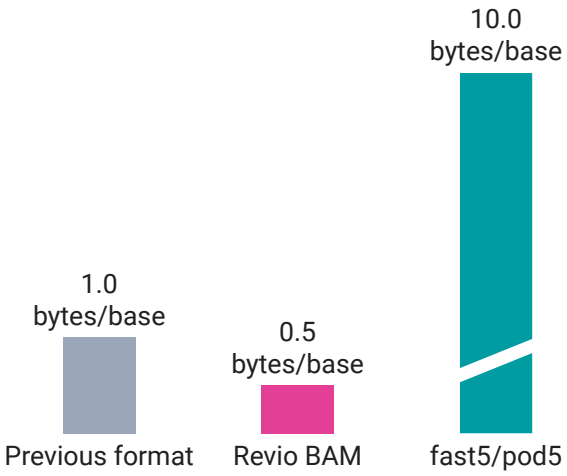
Get the most accurate reads — fast

- The Revio system features cutting-edge NVIDIA GPUs with >20× more compute power than the Sequel® IIe system.
- The GPUs provide rapid turnaround time for basecalling and HiFi read generation, keeping pace with the sequencing throughput of the Revio system.
- With Google DeepConsensus[4] on board, Revio is the most accurate PacBio long-read system to date. DeepConsensus uses advanced deep learning techniques to further extend the accuracy and yield of HiFi sequencing.



Reduce your compute and storage costs

- The Revio system is capable of much more than just basecalling. Every run also measures DNA methylation status, calculated with a deep learning algorithm that processes polymerase kinetics.
- All fundamental processing steps are performed on instrument, including barcode demultiplexing and conversion to the standard BAM format.
- A more efficient data representation reduces file size by 50% per base — 20× smaller than for other long-read technologies. Base quality scores are grouped into seven bins, and similar reads are sorted together for more effective compression.



	On instrument	Off instrument
Revio system	• Base calling • HiFi read generation with DeepConsensus • Methylation calling • Barcode demultiplexing • BAM file generation	• Variant calling • Genome assembly
Other long-read technology	• Signal collection • Initial base calling	• Additional base calling • Methylation calling • Barcode demultiplexing • BAM file generation • Variant calling • Genome assembly

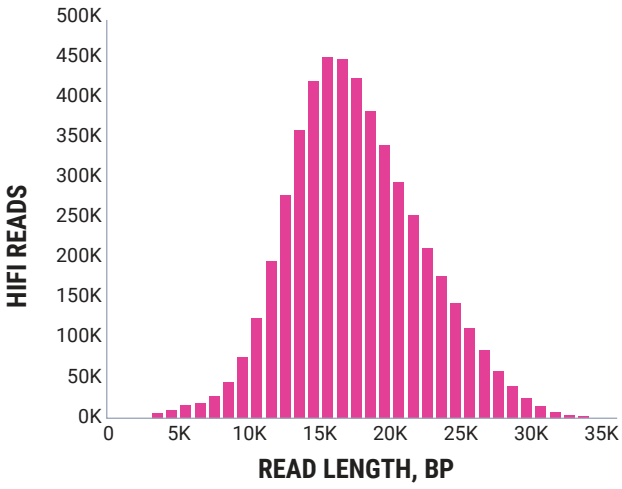
Add to what you love about HiFi sequencing with the Revio system

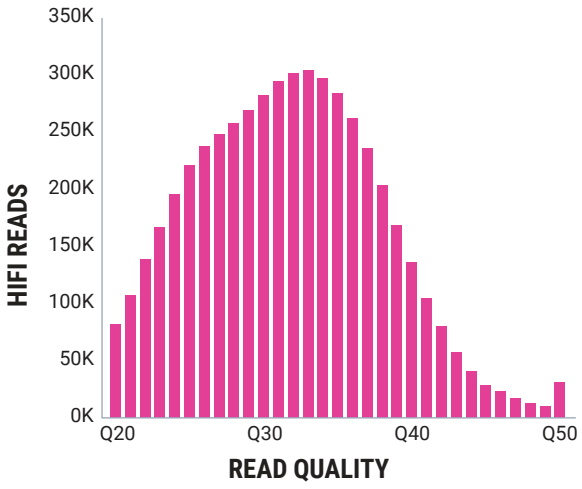
Keep what's great about HiFi sequencing

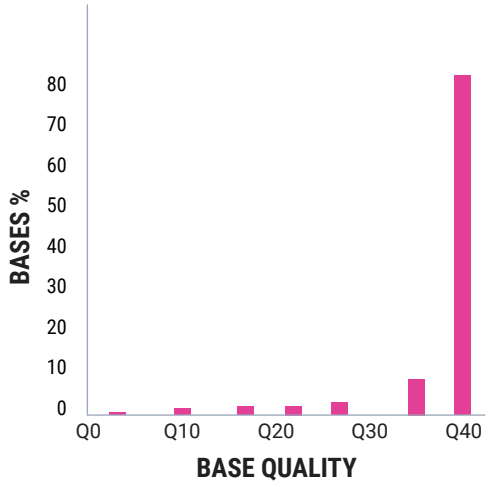
- Long, accurate reads of native DNA molecules
- Easy sample and library prep with options for manual and automated workflows
- On-instrument generation of HiFi reads + methylation calls (5mC and 6mA), with demultiplexing
- Standard BAM file format compatible with downstream analysis tools

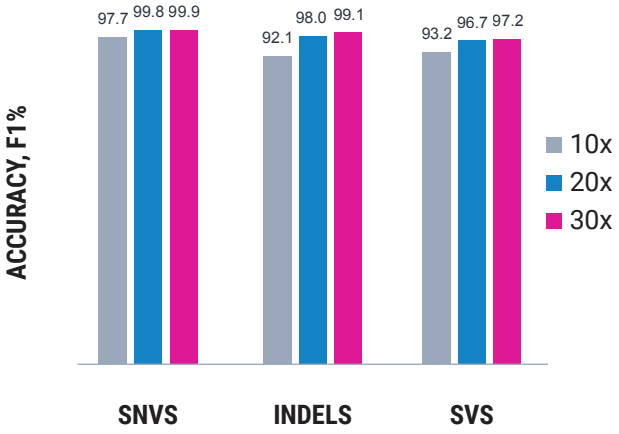
…and get even more on the Revio system

- High-throughput — up to 2,500 HiFi genomes per year
- 500 ng of DNA input per sample
- A simplified user experience, including adaptive loading, fewer consumables, rapid run setup, and real-time performance run previews
- Onboard Google DeepConsensus for the most accurate HiFi reads yet
- Reduce storage costs with smaller output files at only ~60 Gb each









Data shown is for a single Revio SMRT Cell for HG002/GM24385 sequenced with SPRQ chemistry.[5]

System specifications with SPRQ chemistry

The Revio system utilizes nanofabricated Revio SMRT Cells and has four independent stages, allowing sequencing of multiple SMRT Cells in parallel.

Library	Run time*	Q30+ bases	HiFi yield per SMRT Cell†	Methylation
0.5–5 kb	12 hours	95%	6–8 million reads	5mC at CpG sites and 6mA‡ for native DNA
5–10 kb	24 hours	90%	35–70 Gb	
10–15 kb			70–100 Gb	
15–20 kb			100–120 Gb	
20–25 kb	30 hours	85%	100–120 Gb	

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

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

‡ The Revio 6mA caller is designed to detect methylation in the context of the Fiber-seq chromatin assay.[6]

Key applications and sample throughput with SPRQ chemistry

The Revio system supports a variety of applications that benefit from accurate long HiFi reads and requires only 500 ng of input DNA per sample.

Library	Application	Per Revio SMRT Cell	Per year*	Expected coverage†
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 repeat expansion panel	48	60,000	200×
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

* 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.

†Expected coverages are estimates.

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What will you discover with Revio?

Learn more about the Revio system:
pacb.com/revio

Ordering information

Part number	Product
102-090-600	Revio system
103-260-000	Nanobind PanDNA kit
102-182-700	SMRTbell prep kit 3.0
103-520-100	Revio SPRQ polymerase kit
102-202-200	Revio SMRT Cell tray
103-504-900	Revio SPRQ sequencing plate

Instrument operating environment

Temperature	19–25°C (66–77°F)
Humidity	20–80% relative humidity, non-condensing
Ventilation	13,000 BTU (3,800 W)
W × D × H	92.7 × 91.4 × 174.5 cm (36.5 × 36.0 × 68.7 in)
Weight	465 kg (1,025 lb)
Power	200–240 VAC at 50–60 Hz, 30A
Network	1 GbE or 10 GbE, copper
Noise output	<75 dB at 3.3 m (10 ft 10 in) from instrument

KEY REFERENCES

1. Lincoln, S. E., et al. (2021). One in seven pathogenic variants can be challenging to detect by NGS: an analysis of 450,000 patients with implications for clinical sensitivity and genetic test implementation. *Genetics in Medicine*, 23(9), 1673–1680.
2. Nurk, S., et al. (2022). The complete sequence of a human genome. *Science*, 376(6588), 44–53.
3. Al'Khafaji, A. M., et al. (2021). High-throughput RNA isoform sequencing using programmable cDNA concatenation. bioRxiv, doi:10.1101/2021.10.01.462818.
4. Baid, G., et al. (2022). DeepConsensus improves the accuracy of sequences with a gap-aware sequence transformer. *Nature Biotechnology*, 1–7.
5. PacBio (2022). HG002 sequence data from Revio system.
6. Stergachis, A., et al. (2022). Single-molecule regulatory architectures captured by chromatin fiber sequencing. *Science* 368, 1449-1454.

$500 per human HiFi 20X genome assumes US list price of $995 for sequencing reagents for one Revio SMRT Cell, which has an expected yield of 120 Gb, equivalent to two 20x human genomes.

102-326-543 REV07 02APR2025