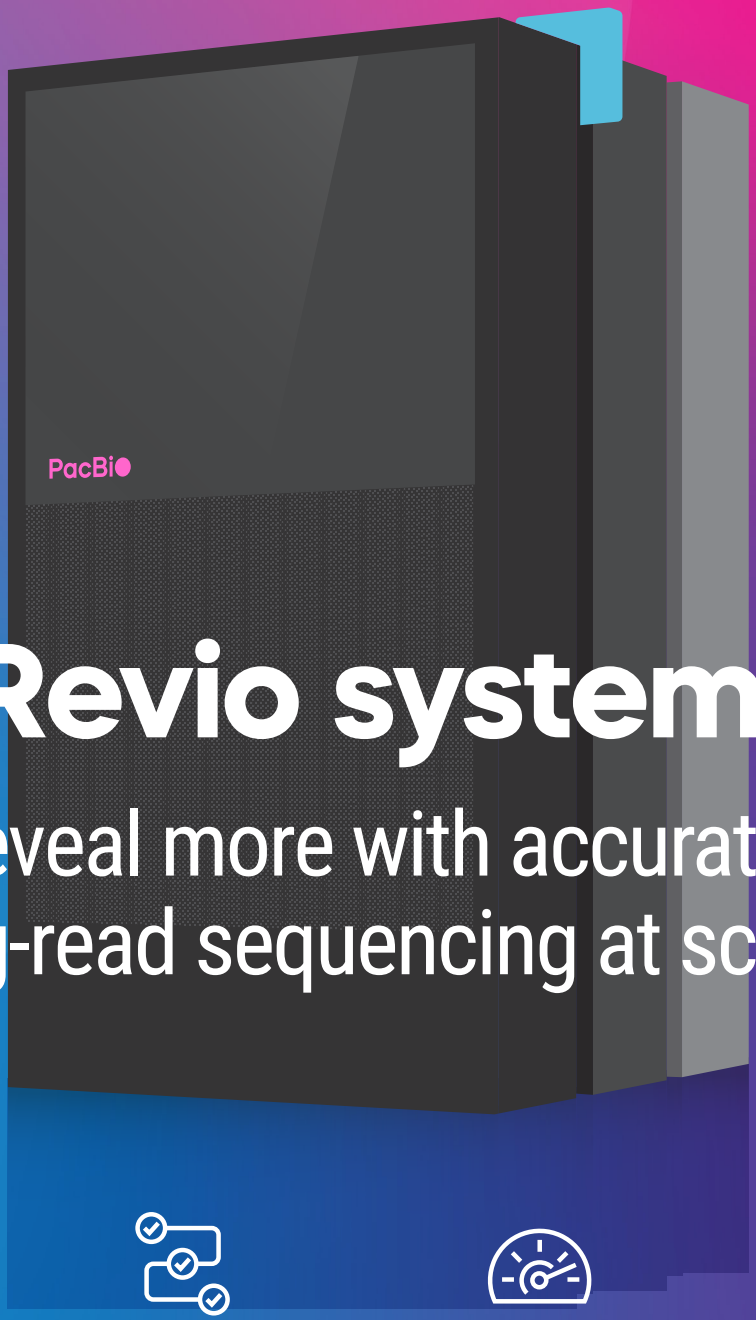
PacBio



Revio system

Reveal more with accurate long-read sequencing at scale

Scale
1,300 human HiFi genomes per year

Ease of use
Simplified consumables and flexible run setup

Compute power
Google DeepConsensus and more on board

Affordability
$1,000 per human HiFi genome

This is your moment for a more complete view of biology

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.[1]

Truly 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 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

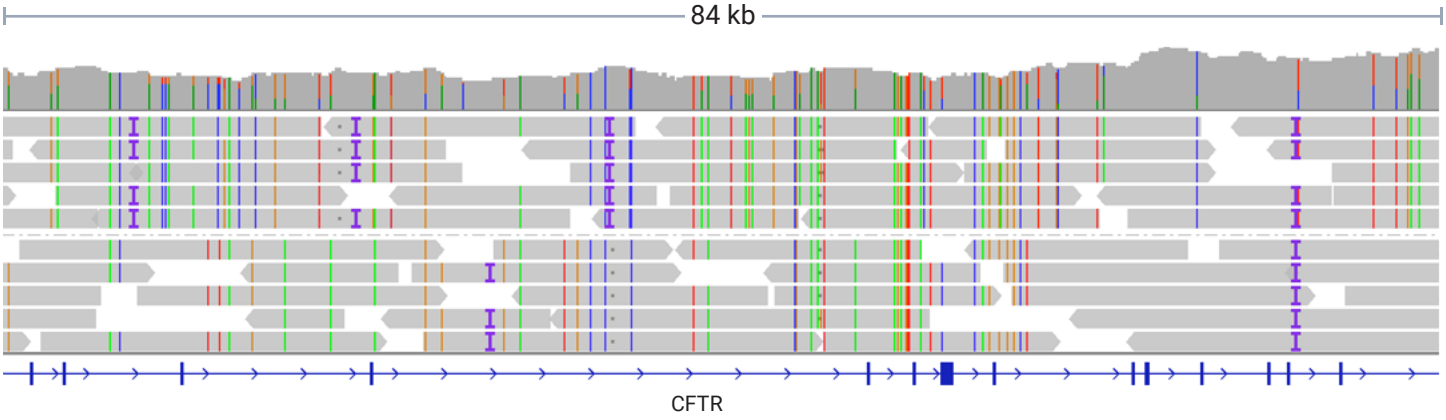
HiFi sequencing provides reliable answers through exceptional accuracy, with 90% of bases ≥Q30 and median read accuracy ≥Q30.

Direct methylation detection in native molecules

HiFi sequencing identifies base pair-level DNA methylation in all runs, without bisulfite treatment.

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.

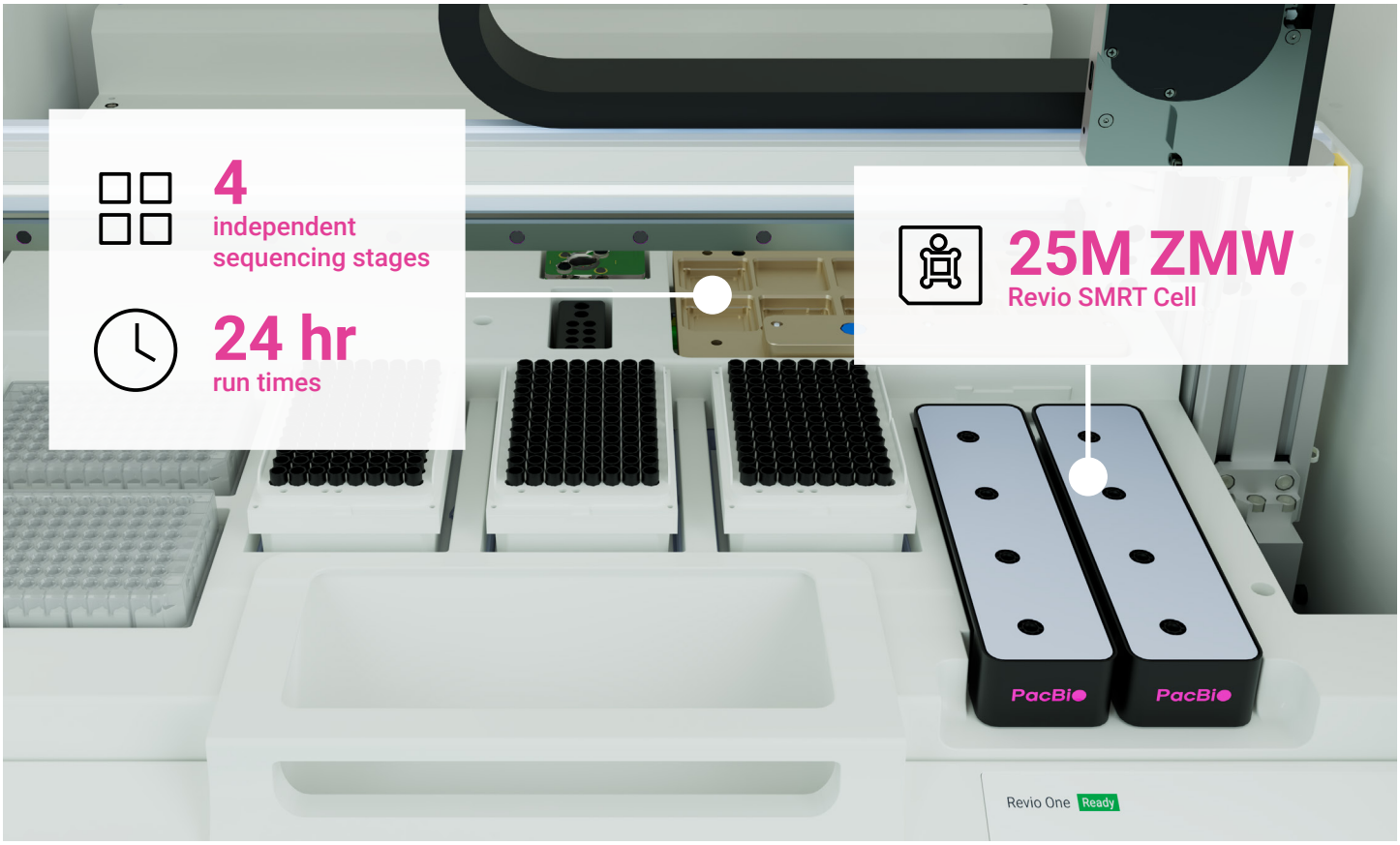


HiFi reads for the sample HG002 reveal accurate sequence of both maternal and paternal alleles, providing phasing that spans over 84 kb of the cystic fibrosis gene, *CFTR*.

Sequence with HiFi reads at high throughput

	Sequel® IIe system	Revio system	Increase
Higher density	8 million ZMWs	25 million ZMWs	3×
Independent stages	1	4	4×
Shorter run times	30 hours	24 hours	1.25×
30× HiFi human genomes/year	88	1,300	15× overall

Enjoy a fully automated sequencing workflow



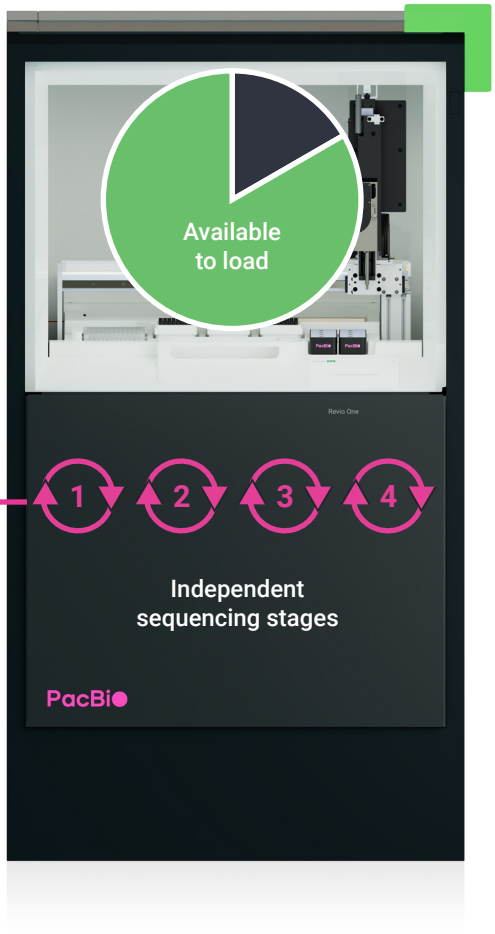
The easy-to-use Revio system fits your schedule

The Revio system offers 24 hour runs so that sequencing runs match the cadence of your lab's routine.

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.

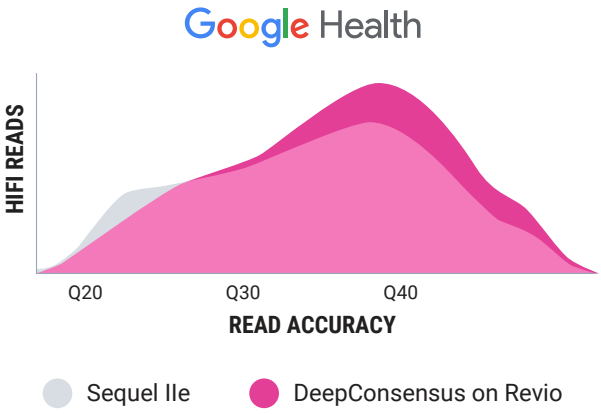


Set up runs instantly and use less plastic with smart consumables

- 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.
- The Revio sequencing plate combines what was previously four parts, eliminating extraneous plastics and making runs easier to manage. The single standard 96-well plate includes sample libraries, reagents, and space for mixing and waste.

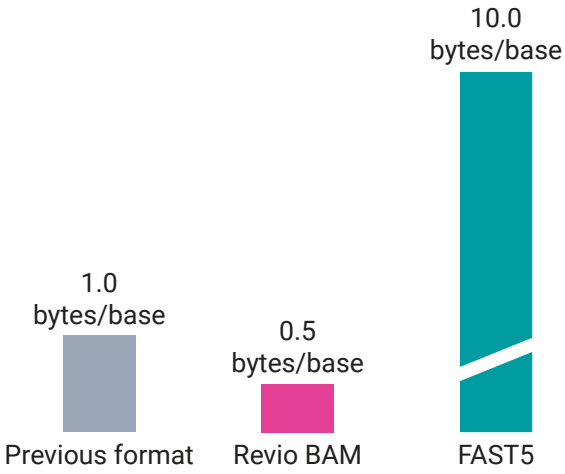
Get the most accurate reads — fast

- 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

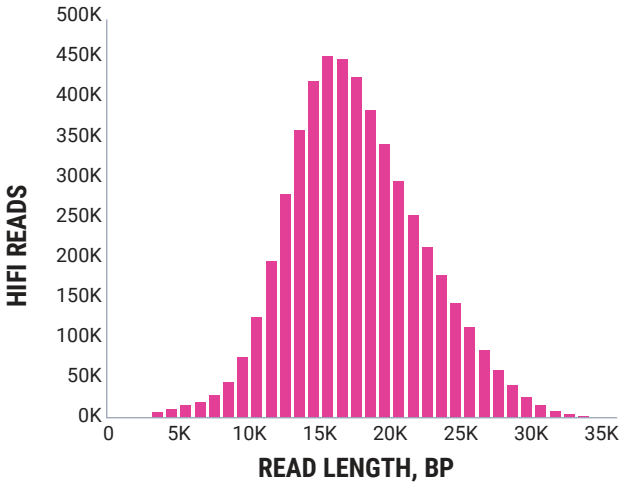
Add to what you love about HiFi sequencing with the Revio system

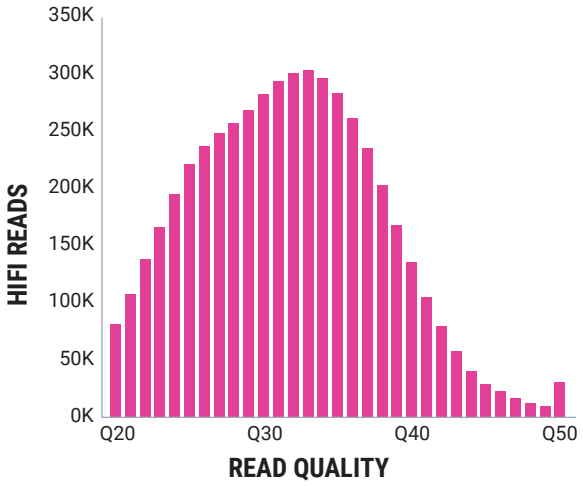
Keep what's great about HiFi sequencing

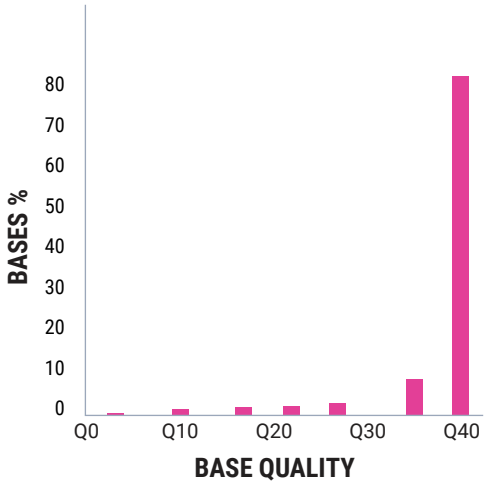
- Long, accurate reads of native DNA molecules
- Easy sample and library prep with the Nanobind® CBB kit and SMRTbell® prep kit 3.0
- On-instrument generation of HiFi reads + methylation calls, with demultiplexing
- Standard BAM file format compatible with downstream analysis tools

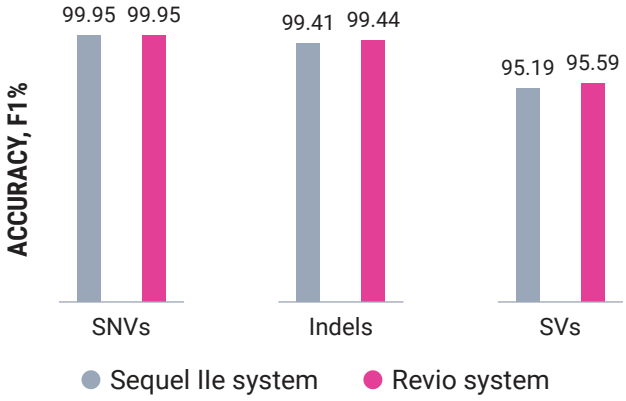
…and get even more on the Revio system

- High-throughput — up to 1,300 HiFi genomes per year
- Onboard Google DeepConsensus for the most accurate HiFi reads yet
- A simplified user experience including fewer consumables and rapid run setup
- 50% smaller output files to reduce storage costs









The Revio system produces the same — or better — read length, quality, and variant calling performance that have made HiFi sequencing so celebrated. Data shown is for a single Revio SMRT Cell for HG002/GM24385.[5]

Revio sequencing specifications

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

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

Revio application specifications

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×

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

Revio ordering information

Part number	Product	Description
102-090-600	Revio system	Sequencing instrument
102-301-900	Nanobind CBB kit	HMW DNA extraction for cells, bacteria, and blood (24 reactions)
102-182-700	SMRTbell prep kit 3.0	Library prep for 24 libraries
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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As a global company, we have offices in countries around the world. Visit **pacb.com/contact** for contact info.

What will you discover with Revio?

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

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EMEA: **emea@pacb.com**
Asia Pacific: **apsales@pacb.com**

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

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.

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