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

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

Enjoy a fully automated sequencing workflow

- 4 independent sequencing stages
- 24 hr run times

25M ZMW
Revio SMRT Cell
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 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.

<table>
<thead>
<tr>
<th>On instrument</th>
<th>Off instrument</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Revio system</strong></td>
<td><strong>Variant calling</strong></td>
</tr>
<tr>
<td>• Base calling</td>
<td>• Genome assembly</td>
</tr>
<tr>
<td>• HiFi read generation with DeepConsensus</td>
<td></td>
</tr>
<tr>
<td>• Methylation calling</td>
<td></td>
</tr>
<tr>
<td>• Barcode demultiplexing</td>
<td></td>
</tr>
<tr>
<td>• BAM file generation</td>
<td></td>
</tr>
<tr>
<td><strong>Other long-read technology</strong></td>
<td><strong>Additional base calling</strong></td>
</tr>
<tr>
<td>• Signal collection</td>
<td>• Methylation calling</td>
</tr>
<tr>
<td>• Initial base calling</td>
<td>• Barcode demultiplexing</td>
</tr>
<tr>
<td></td>
<td>• BAM file generation</td>
</tr>
<tr>
<td></td>
<td>• Variant calling</td>
</tr>
<tr>
<td></td>
<td>• Genome assembly</td>
</tr>
</tbody>
</table>
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. ²
**Revio sequencing specifications**

<table>
<thead>
<tr>
<th>Library</th>
<th>Run time †</th>
<th>1 Revio SMRT Cell</th>
<th>4 Revio SMRT Cells</th>
<th>Base quality ‡</th>
<th>Methylation</th>
</tr>
</thead>
<tbody>
<tr>
<td>15–18 kb</td>
<td>24 hours</td>
<td>90 Gb</td>
<td>360 Gb</td>
<td>90% ≥Q30</td>
<td>5mC at CpG sites</td>
</tr>
</tbody>
</table>

*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.
†Run time specification is for the sequencing reaction.

**Revio application specifications**

<table>
<thead>
<tr>
<th>Sample</th>
<th>Per Revio SMRT Cell</th>
<th>Per year ‡</th>
<th>Expected coverage ‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human genome</td>
<td>1</td>
<td>1,300</td>
<td>30×</td>
</tr>
<tr>
<td>Single-cell transcriptome</td>
<td>1</td>
<td>1,300</td>
<td>80 million reads</td>
</tr>
<tr>
<td>Large gene panel (20 Mb)</td>
<td>12</td>
<td>15,600</td>
<td>90% target positions ≥10×</td>
</tr>
</tbody>
</table>

‡ 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**

<table>
<thead>
<tr>
<th>Part number</th>
<th>Product</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>102-090-600</td>
<td>Revio system</td>
<td>Sequencing instrument</td>
</tr>
<tr>
<td>102-301-900</td>
<td>Nanobind CBB kit</td>
<td>HMW DNA extraction for cells, bacteria, and blood (24 reactions)</td>
</tr>
<tr>
<td>102-182-700</td>
<td>SMRTbell prep kit 3.0</td>
<td>Library prep for 24 libraries</td>
</tr>
<tr>
<td>102-817-600</td>
<td>Revio polymerase kit</td>
<td>Reagents for binding polymerase to 24 SMRTbell libraries</td>
</tr>
<tr>
<td>102-202-200</td>
<td>Revio SMRT Cell tray</td>
<td>Tray of 4 Revio SMRT Cells</td>
</tr>
<tr>
<td>102-587-400</td>
<td>Revio sequencing plate</td>
<td>Sequencing reagents supporting 4 Revio SMRT Cells</td>
</tr>
</tbody>
</table>
What will you discover with Revio?

Learn more about the Revio system:
[pacb.com/revio](http://pacb.com/revio)

Connect with PacBio for more info:
North America: nasales@pacb.com
South America: sasales@pacb.com
EMEA: emea@pacb.com
Asia Pacific: apsales@pacb.com

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**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.

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$1,000 per human HiFi genome assumes US list price of $995 for sequencing reagents for one Revio SMRT Cell, which has an expected yield of 90 Gb, equivalent to a 30× human genome.

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