SEQUENCE WITH CONFIDENCE

SMRT Sequencing — Delivering Highly Accurate Long Reads to Drive Discovery in Life Science
Our Core Technology

PacBio® Systems are powered by Single Molecule, Real-Time (SMRT®) Sequencing technology. This innovative approach enables simultaneous collection of data from millions of wells using the natural process of DNA replication to sequence long fragments of native DNA.

How SMRT Sequencing Works

- **Long Reads**: With reads tens of kilobases in length you can readily assemble complete genomes and sequence full-length transcripts
- **High Accuracy**: Sequencing free of systematic error achieves >99.999% consensus accuracy
- **Uniform Coverage**: No bias based on GC content means you can sequence through regions inaccessible to other technologies
- **Single-Molecule Resolution**: Capturing sequence data from native DNA or RNA molecules enables highly accurate long reads with >99.9% single-molecule accuracy
- **Epigenetics**: With no PCR amplification step, base modifications are directly detected during sequencing

Explore the SMRT Sequencing Advantages
Better Data for Better Biology with Highly Accurate Long Reads

As the foundation for advanced scientific discoveries, sequencing data must be accurate and complete. With highly accurate long reads - HiFi reads - you no longer need to compromise between long read lengths and high accuracy sequencing.

Use circular consensus sequencing (CCS) to generate HiFi reads and gain access to the most informative data available to answer your toughest biological questions.

The Benefits of HiFi Reads

- Long read lengths up to 25 kb
- High read accuracy >99.9%
- Easy library preparation
- Low coverage requirements
- Small file sizes to minimize compute time
- A single technology solution for a range of applications
- Unmatched data clarity for rapid interpretation
Our Solution

Based on our proven technology, PacBio Systems deliver exceptional results customers have come to expect.

Sequel® Ile System

Generates reliable high-throughput sequencing data

HiFi

Provides direct access to HiFi reads

Reduces project time for faster results

Makes sequencing more affordable

Supports the range of SMRT Sequencing applications

SMRT Consumables

Our complete set of consumables offers the ability to customize sequencing for your project

The SMRT® Cell 8M has 8 million ZMWs for unparalleled sequencing power

SMRT Software

Our analytical software tools support you at every step, from run design through analysis
Sequencing Data You Can Trust

Long Read Lengths
HiFi reads provide long read lengths up to 25 kb

Data from a 15 kb size-selected human library using the SMRTbell® Express Template Prep Kit 2.0 on a Sequel IIe System (2.0 Chemistry, Sequel IIe System Software v10, 30-hour movie.)

High Accuracy
HiFi reads are highly accurate with median accuracy of >99.9% (Q30)

Data from a 15 kb size-selected human library using the SMRTbell Express Template Prep Kit 2.0 on a Sequel IIe System (2.0 Chemistry, Sequel IIe System Software v10, 30-hour movie.)

Comprehensive Variant Detection
Only HiFi reads offer low error rates for detecting all variant types

Variant calling performance against Genome in a Bottle benchmarks for PacBio HiFi reads (35-fold, Sequel II System, 2.0 Chemistry); Illumina (35-fold, NovaSeq); Oxford Nanopore (60-fold, PromethION R9.4.1.)

Uniform Coverage
HiFi reads are generated without amplification and have no bias based on GC Content

Mean coverage per GC window across a human sample. Data generated with a 20 kb HiFi library (2.0 Chemistry, Sequel II System.)
SMRT Sequencing Applications

Gain comprehensive views of genomes, transcriptomes, and epigenomes.

**Whole Genome Sequencing**
Sequence and assemble complete, reference-quality genomes and phase haplotypes.

**VARIANT DETECTION**
Call all variants – single nucleotide, indel, and structural variants with high precision and recall.

**RNA Sequencing**
Characterize isoforms with direct sequencing of full-length transcripts, no assembly required.

**Targeted Sequencing**
Focus in on variation in even the most difficult regions of the genome.

**Complex Populations**
Resolve closely related sequences within a heterogeneous mixture.

**Epigenetics**
Directly detect DNA modifications during sequencing.

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Mega-base sized contigs assembled into a nearly complete human chromosome 1.

HiFi reads phased into haplotypes identified a homozygous insertion event and several single nucleotide variants.

Full-length transcripts generated with the Iso-Seq® method identified complex alternative splicing.
# Flexible Workflows

Use our end-to-end solutions to rapidly move from DNA to discovery.

## Generate a SMRTbell Library

<table>
<thead>
<tr>
<th>LIBRARY PREP</th>
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<tbody>
<tr>
<td>• Prepare templates in &lt;3 hours with easy-to-use kits</td>
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<tr>
<td>• Optional size selection for long inserts</td>
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<tr>
<td>• Multiplex and barcode samples to increase throughput</td>
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## Sequence on the Sequel Ile System

**With a single SMRT Cell 8M you can run experiments that:**

<table>
<thead>
<tr>
<th>SMRT SEQUENCING</th>
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<tbody>
<tr>
<td>• Produce reference-quality assemblies for genomes up to 2 Gb</td>
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<tr>
<td>• Detect structural variants for up to 2 samples with ~3 Gb genomes</td>
</tr>
<tr>
<td>• Characterize a whole transcriptome and identify alternative splicing</td>
</tr>
<tr>
<td>• Generate reference-quality assemblies for up to 48 microbial isolates</td>
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<tr>
<td>• Determine the composition of up to 96 microbiome samples</td>
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**With 2 SMRT Cells 8M you can run experiments that:**

<table>
<thead>
<tr>
<th>SMRT SEQUENCING</th>
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<tbody>
<tr>
<td>• Call single nucleotide, indel, and structural variants in a ~3 Gb genome</td>
</tr>
<tr>
<td>• Phase a diploid assembly of a ~3 Gb genome</td>
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## Enable Every User in the Lab with Our Analytical Portfolio

<table>
<thead>
<tr>
<th>DATA ANALYSIS</th>
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<tr>
<td>• <strong>SMRT Analysis:</strong> Explore intuitive GUI and command-line options</td>
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<tr>
<td>• <strong>PacBio DevNet:</strong> Discover community-developed tools</td>
</tr>
<tr>
<td>• <strong>SMRT Compatible Analysis Partners:</strong> Utilize solutions and services offered by trusted partners</td>
</tr>
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Learn More and Get Started with SMRT Sequencing

Products and Services
www.pacb.com/products

Documentation
www.pacb.com/documentation

Application-Specific Workflows
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