PACBIO®

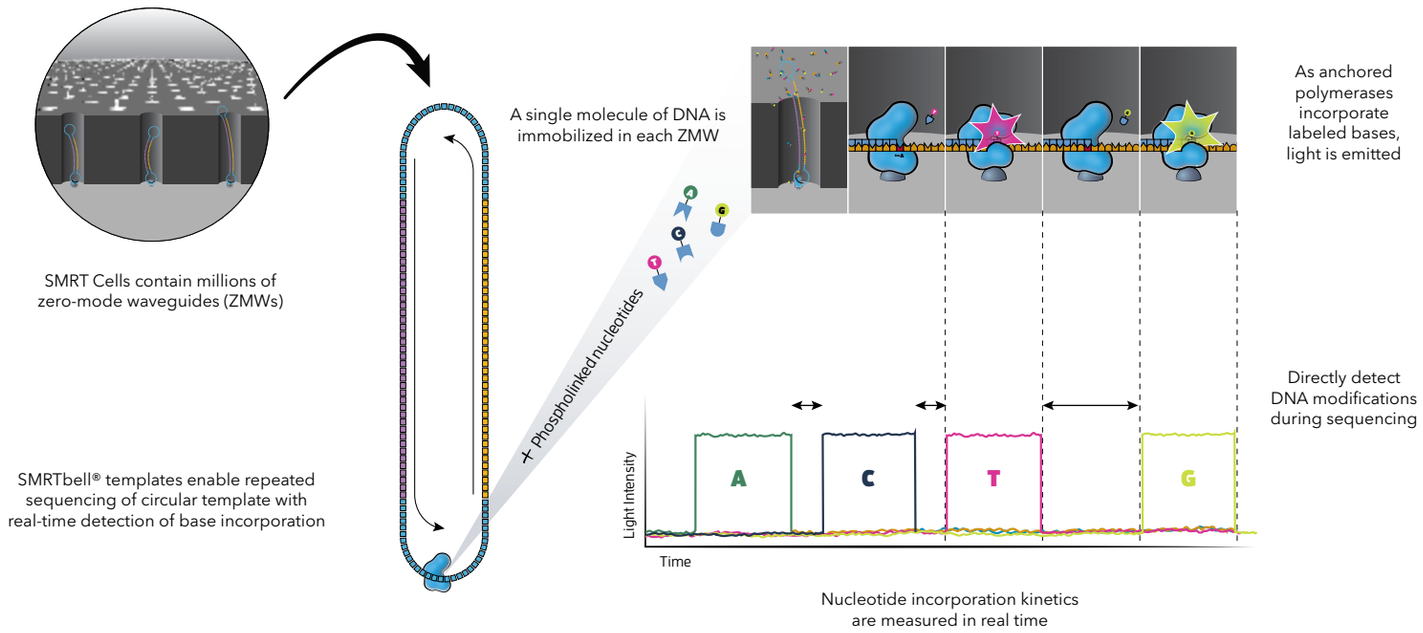
SEQUENCE WITH CONFIDENCE

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

Our Core Technology

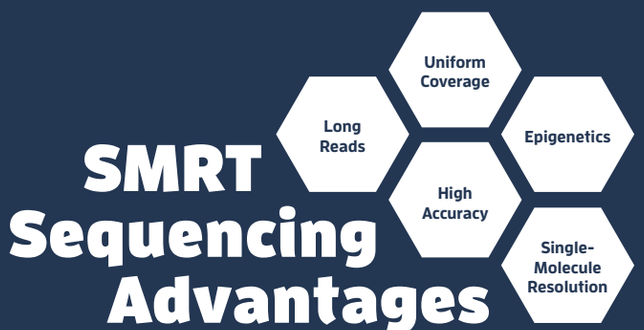
PacBio® Systems are powered by Single Molecule, Real-Time (SMRT®) Sequencing technology. This innovative approach enables simultaneous collection of data from millions of wells using the natural process of DNA replication to sequence long fragments of native DNA.

How SMRT Sequencing Works



Explore the SMRT Sequencing Advantages

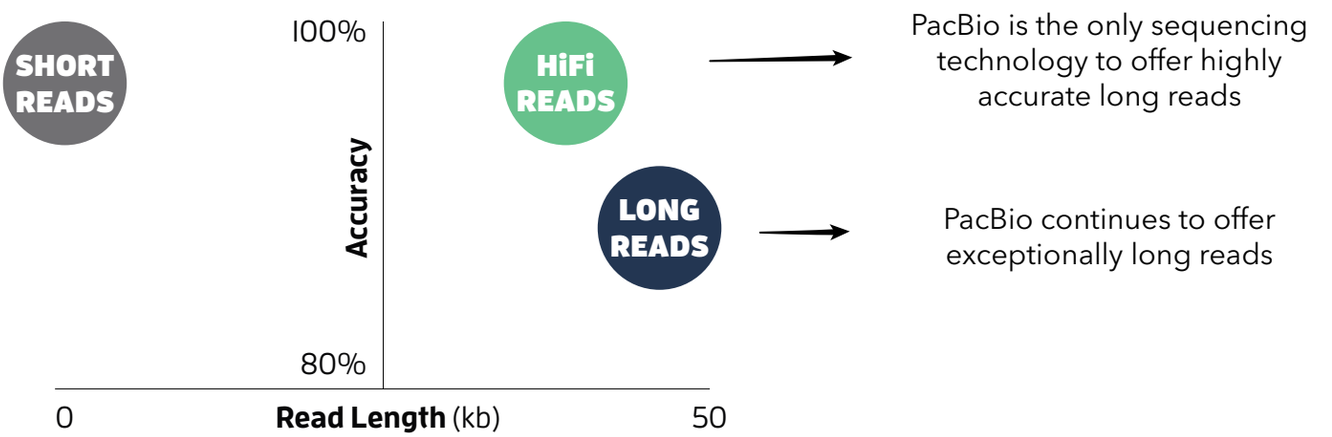
- **Long Reads:** With reads tens of kilobases in length you can readily assemble complete genomes and sequence full-length transcripts
- **High Accuracy:** Sequencing free of systematic error achieves >99.999% accuracy for Sanger-quality reads
- **Uniform Coverage:** No bias based on GC content means you can sequence through regions inaccessible to other technologies



- **Single-Molecule Resolution:** Capturing sequence data from native DNA or RNA molecules enables unparalleled read lengths with 99% single-molecule accuracy
- **Epigenetics:** With no PCR amplification step, base modifications are directly detected during sequencing

Better Data for Better Biology

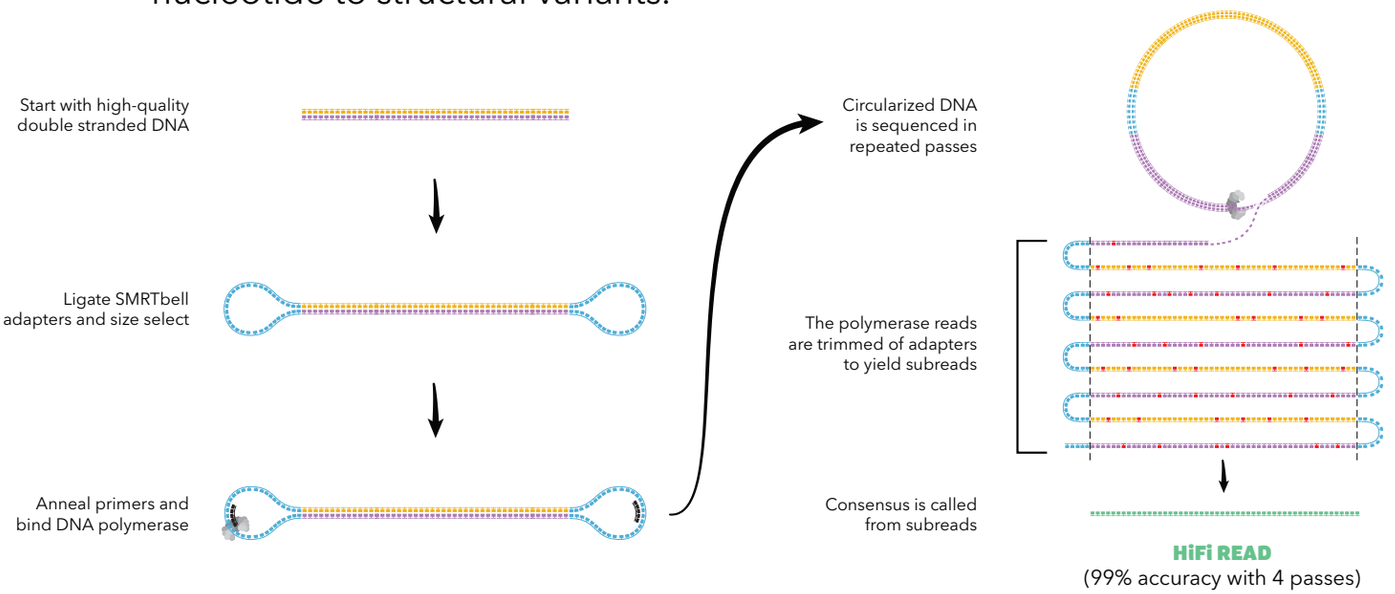
As the foundation for advanced scientific discoveries, sequencing data must be accurate and complete. SMRT Sequencing allows you to optimize your results with two sequencing modes so you no longer have to compromise read length for accuracy.



HiFi READS

Generate Highly Accurate Long Reads

Produce HiFi reads using the circular consensus sequencing (CCS) mode to provide base-level resolution for detection of all variant types from single nucleotide to structural variants.



LONG READS

Optimize Your Run for Even Longer Reads

Sequence read lengths in the tens of kilobases using the continuous long read (CLR) sequencing mode to enable high-quality assembly of even the most complex genomes.

Half of Data in Reads

>50 kb

Longest Reads Up To

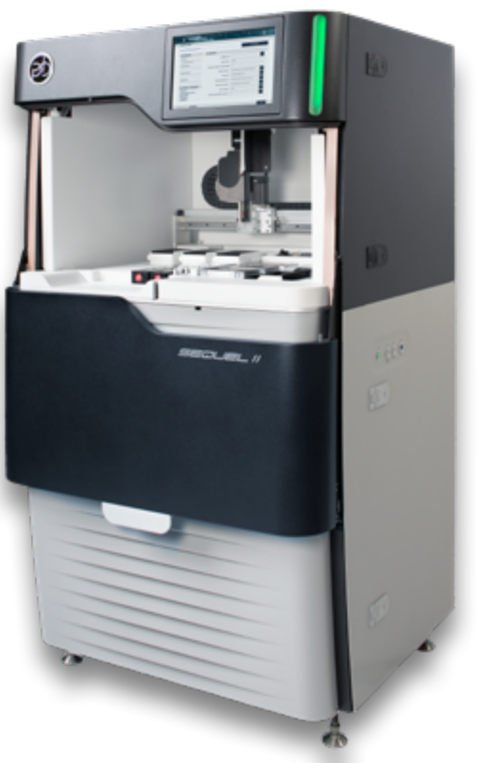
175 kb

Our Solution

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

Sequel II System

- **8X** Generates ~8-times more data than the original Sequel System
- **HiFi** Provides access to even more highly accurate long 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

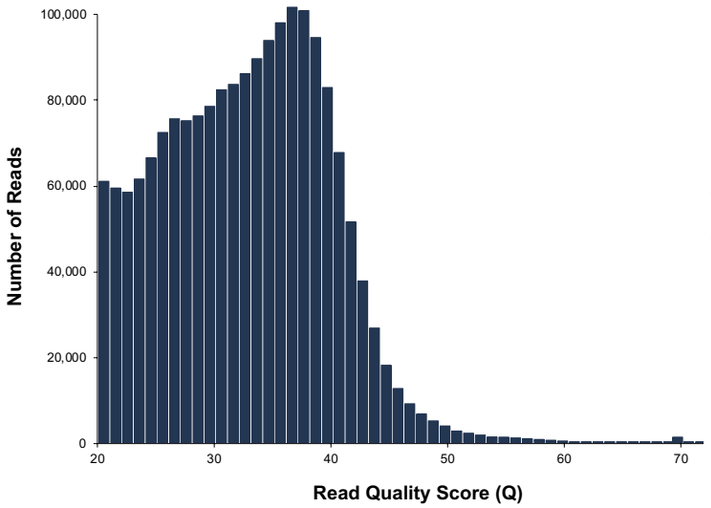
Our analytical software tools support you at every step, from run design through analysis

Sequencing Data You Can Trust

HiFi READS

Highly Accurate Long Reads

Number of >99% (Q20) 9-13 kb
Reads: Up to 2 Million

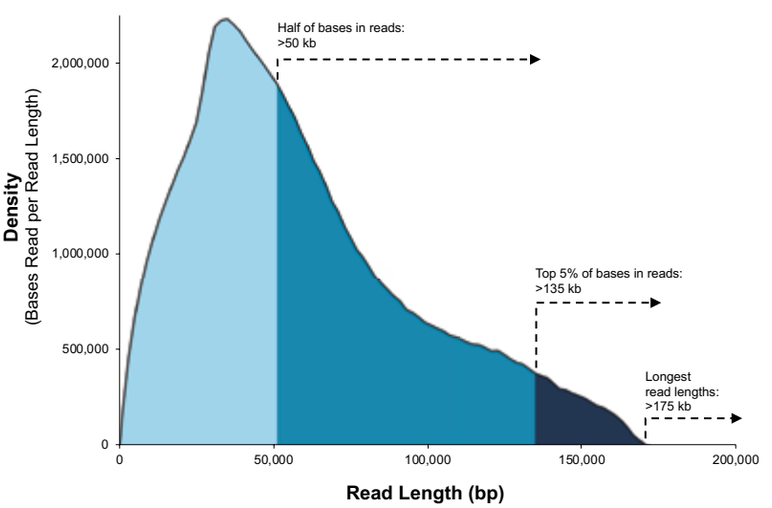


Data from a 11 kb size-selected human library using the SMRTbell Template Prep Kit 1.0 on a Sequel II System (1.0 Chemistry, Sequel II System Software v7.0, 30-hour movie).

LONG READS

Long Read Lengths

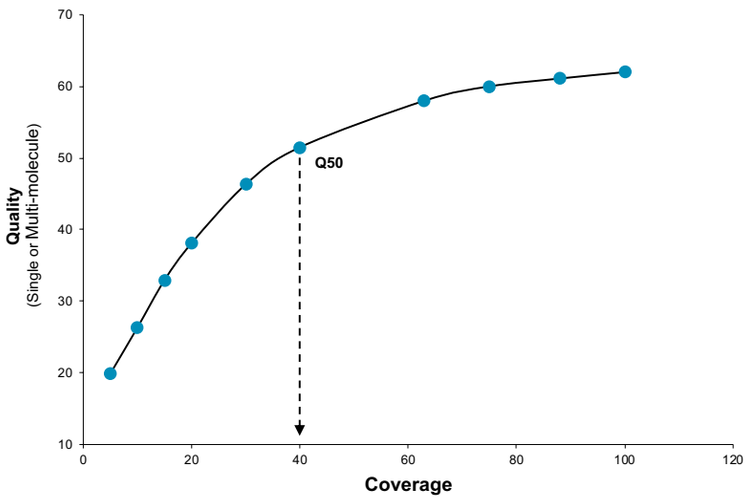
Half the Data in Reads: >50 kb
Data per SMRT Cell: Up to 160 Gb



Data from a 35 kb size-selected *E. coli* library using the SMRTbell Express Template Prep Kit 2.0 on a Sequel II System (1.0 Chemistry, Sequel II System Software v7.0, 15-hour movie).

High Accuracy

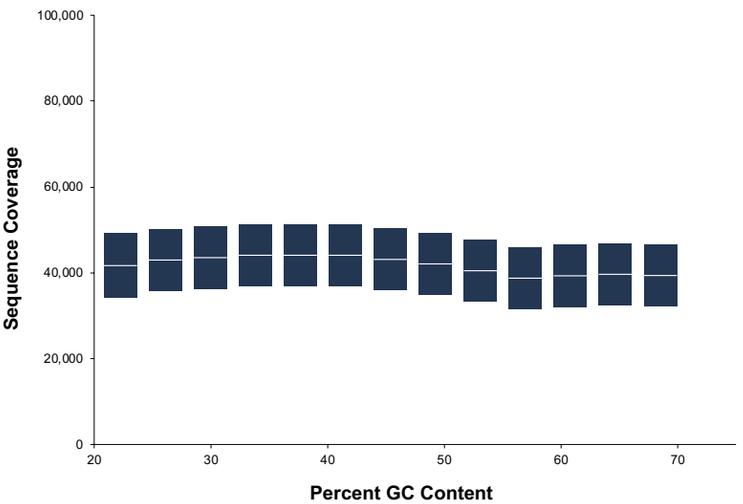
Free of Systematic Errors
Achieves >99.999% Accuracy (Q50)



Consensus accuracy is a function of coverage and chemistry. The data above is based on a bacterial genome run on the Sequel II System (1.0 Chemistry, Sequel II System Software v7.0). Single-molecule accuracy has similar coverage requirements.

Uniform Coverage

No Amplification Required
No Bias Based on GC Content



Mean coverage per GC window across a human sample. Data generated with a 35 kb human library on a Sequel II System (1.0 Chemistry and Sequel II System Software v7.0).

Read lengths, reads/data per SMRT Cell 8M and other sequencing performance results vary based on sample quality/type and insert size.

SMRT Sequencing Applications

Gain comprehensive views of genomes, transcriptomes, and epigenomes.

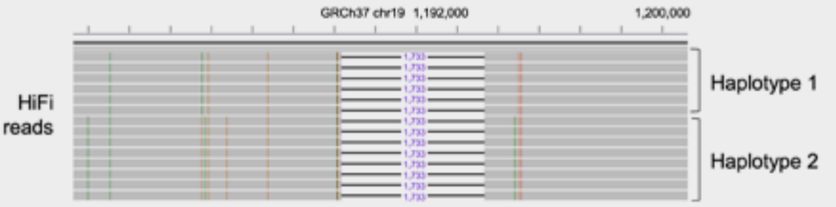
WHOLE GENOME SEQUENCING

Sequence and assemble complete, reference-quality genomes and phase haplotypes

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

VARIANT DETECTION

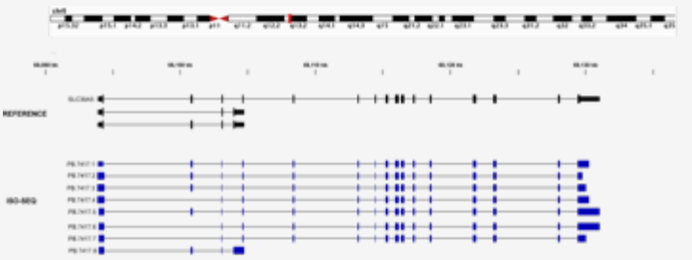
Call all variants – single nucleotide, indel, and structural variants with high precision and recall



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

RNA SEQUENCING

Characterize isoforms with direct sequencing of full-length transcripts, no assembly required



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

TARGETED SEQUENCING

Focus in on variation in even the most difficult regions of the genome

COMPLEX POPULATIONS

Resolve closely related sequences within a heterogenous mixture

EPIGENETICS

Directly detect DNA modifications during sequencing

Flexible Workflows

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

Generate a SMRTbell Library

LIBRARY PREP

- Prepare templates in <3 hours with easy-to-use kits
- Optional size selection for long inserts
- Multiplex and barcode samples to increase throughput

Sequence on the Sequel II System

SMRT SEQUENCING

With **a single SMRT Cell 8M** you can:

- Generate a 2 Gb genome assembly
- Call structural variants in a human genome
- Sequence a whole transcriptome
- Determine the composition of >90 gut microbiome samples

With **2-3 SMRT Cells 8M** you can:

- Detect all variants in a human genome
- Phase a diploid assembly of a human genome

Enable Every User in the Lab with Our Analytical Portfolio

DATA ANALYSIS

- **SMRT Analysis:** Explore intuitive GUI and command-line options
- **PacBio DevNet:** Discover community-developed tools
- **SMRT Compatible Analysis Partners:** Utilize solutions and services offered by trusted partners

Learn More and Get Started with SMRT Sequencing

Products and Services
www.pacb.com/products

Documentation
www.pacb.com/documentation

Application-Specific Workflows
www.pacb.com/applications

Certified Service Providers
www.pacb.com/csp

Publications Using SMRT Sequencing
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