PACBIO®

Cultek

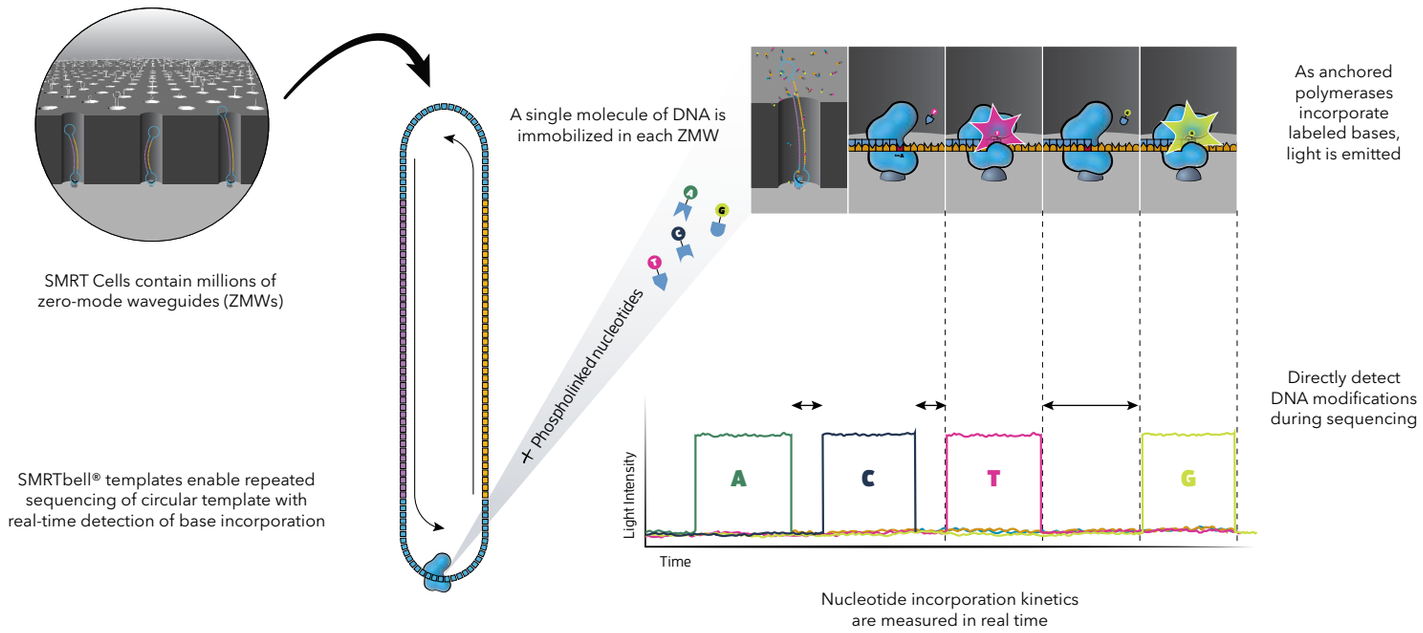
SEQUENCE WITH CONFIDENCE

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

Our Core Technology

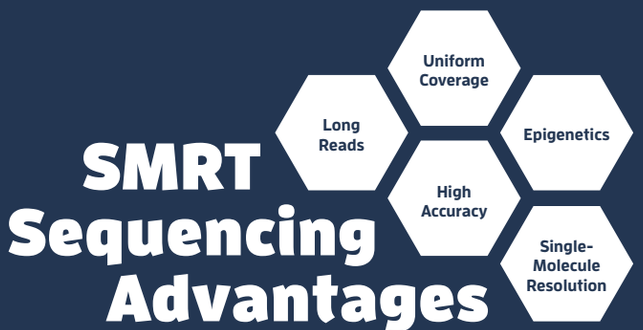
PacBio® Systems are powered by Single Molecule, Real-Time (SMRT®) Sequencing technology. This innovative approach enables simultaneous collection of data from millions of wells using the natural process of DNA replication to sequence long fragments of native DNA.

How SMRT Sequencing Works



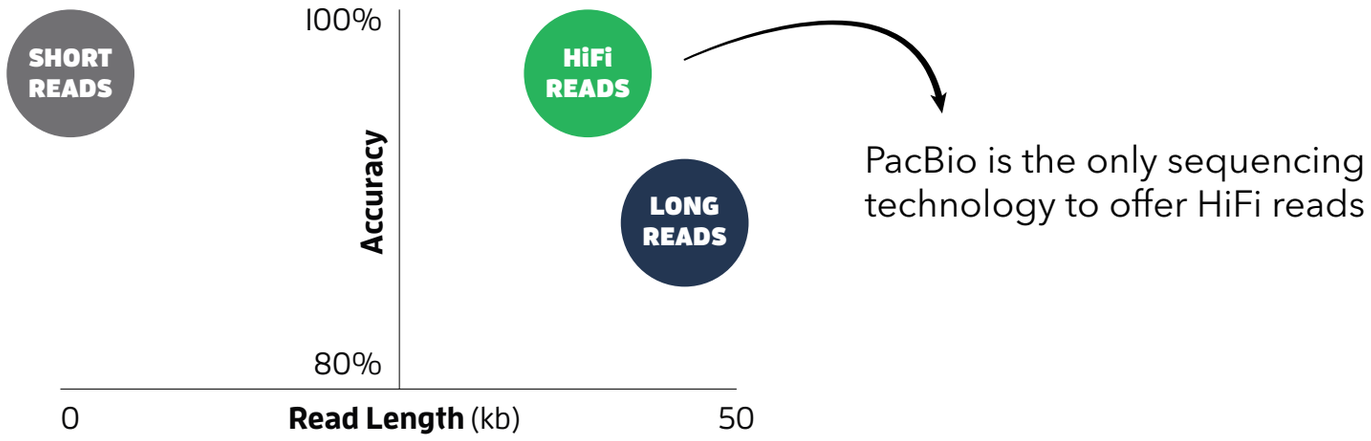
Explore the SMRT Sequencing Advantages

- **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% 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

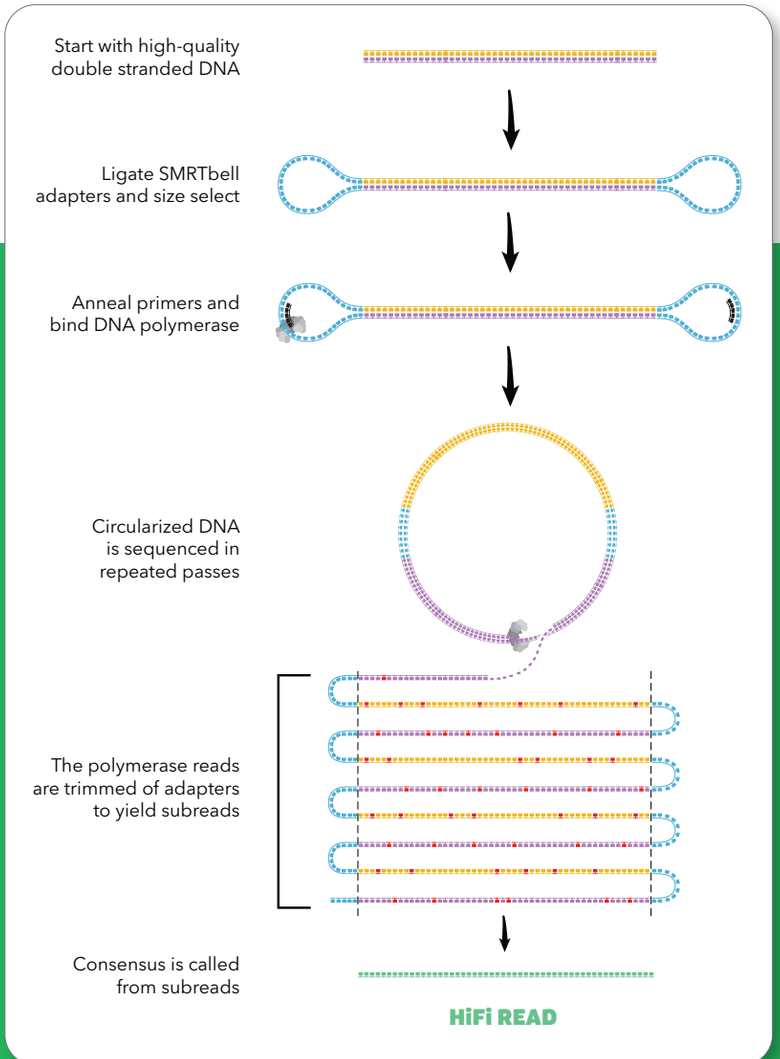


Better Data for Better Biology with Highly Accurate Long Reads

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® IIe System

- Generates reliable high-throughput sequencing data
- 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

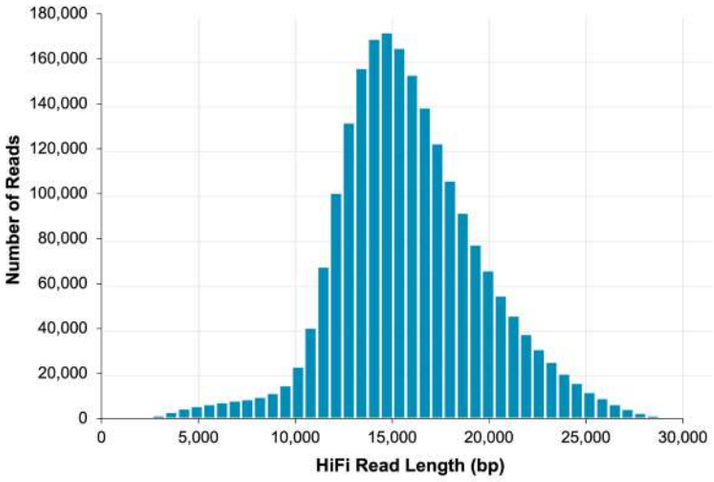
SMRT Software

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

Sequencing Data You Can Trust

Long Read Lengths

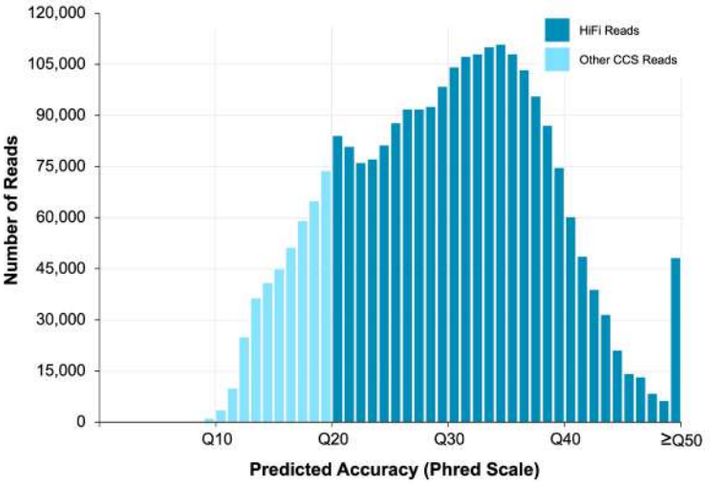
HiFi reads provide long read lengths up to 25 kb



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

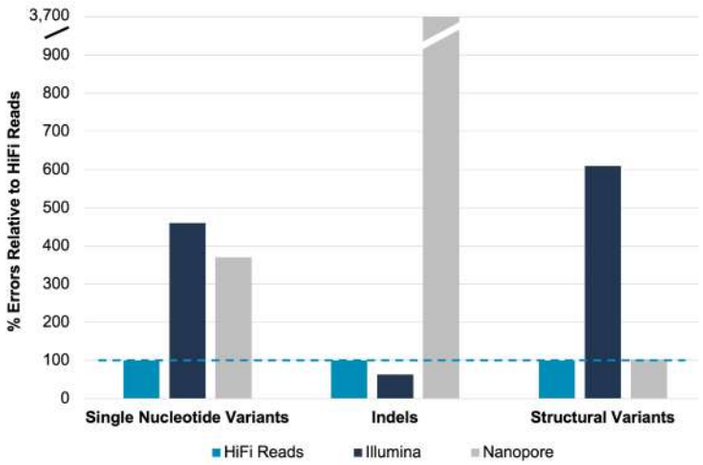
HiFi reads are highly accurate with median accuracy of >99.9% (Q30)



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

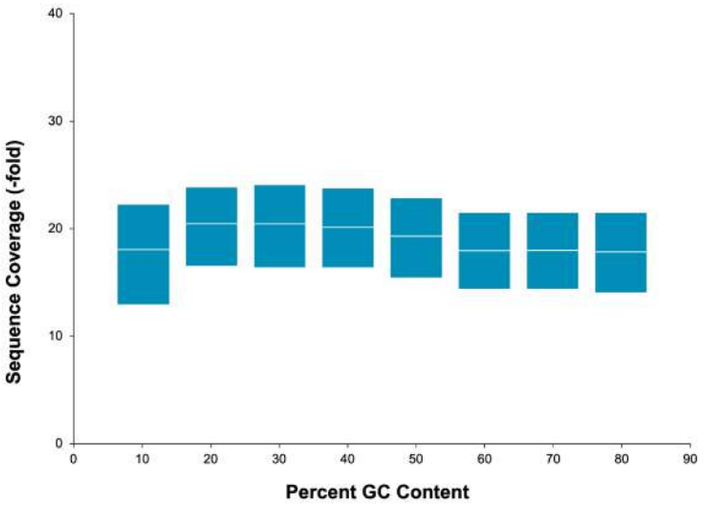
Only HiFi reads offer low error rates for detecting all variant types



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.

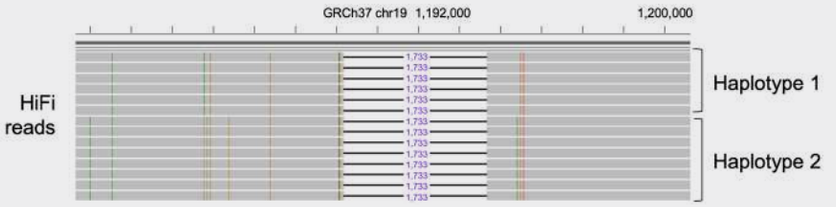
WHOLE GENOME SEQUENCING

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

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

VARIANT DETECTION

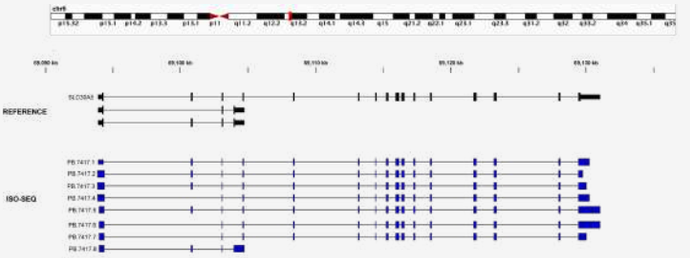
Call all variants – single nucleotide, indel, and structural variants with high precision and recall



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 IIe System

SMRT SEQUENCING

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

- Produce reference-quality assemblies for genomes up to 2 Gb
- Detect structural variants for up to 2 samples with ~3 Gb genomes
- Characterize a whole transcriptome and identify alternative splicing
- Generate reference-quality assemblies for up to 48 microbial isolates
- Determine the composition of up to 96 microbiome samples

With 2 SMRT Cells 8M you can run experiments that:

- Call single nucleotide, indel, and structural variants in a ~3 Gb genome
- Phase a diploid assembly of a ~3 Gb 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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