



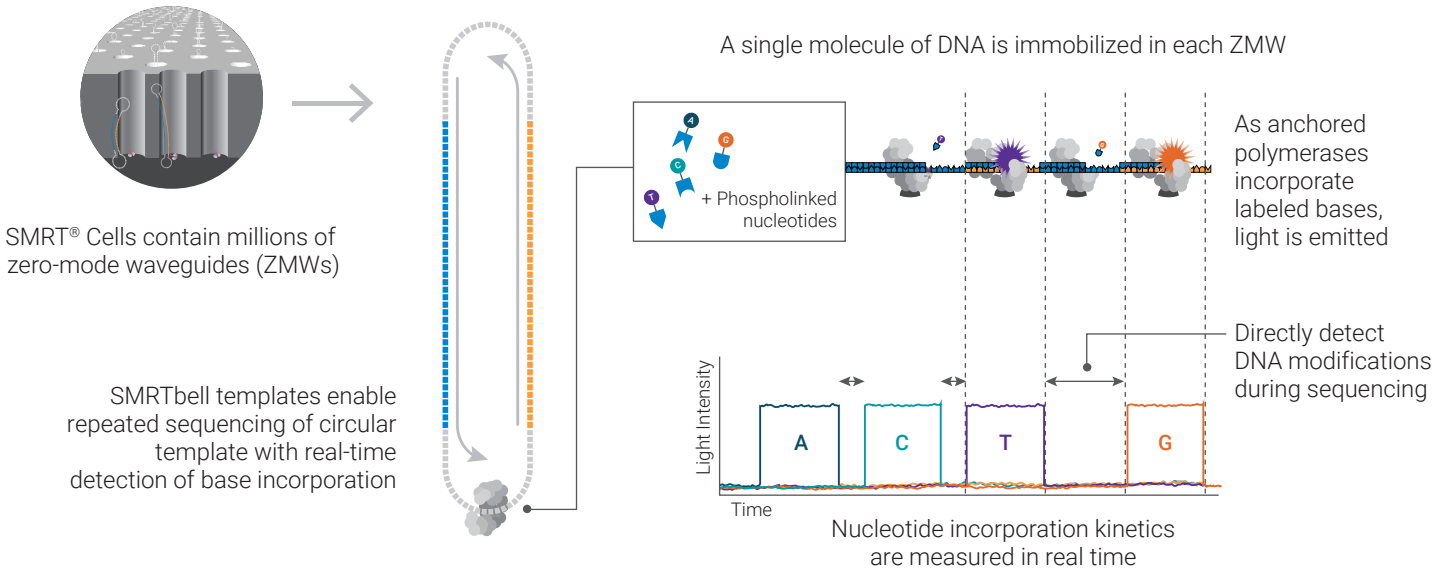
# SEQUENCE WITH CONFIDENCE

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 errors 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

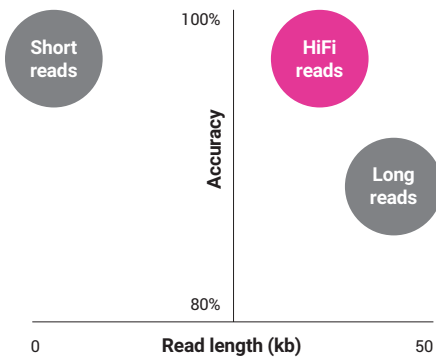


### Epigenetics

With no PCR amplification step, base modifications are directly detected during sequencing

# Better data for better biology with highly accurate long reads

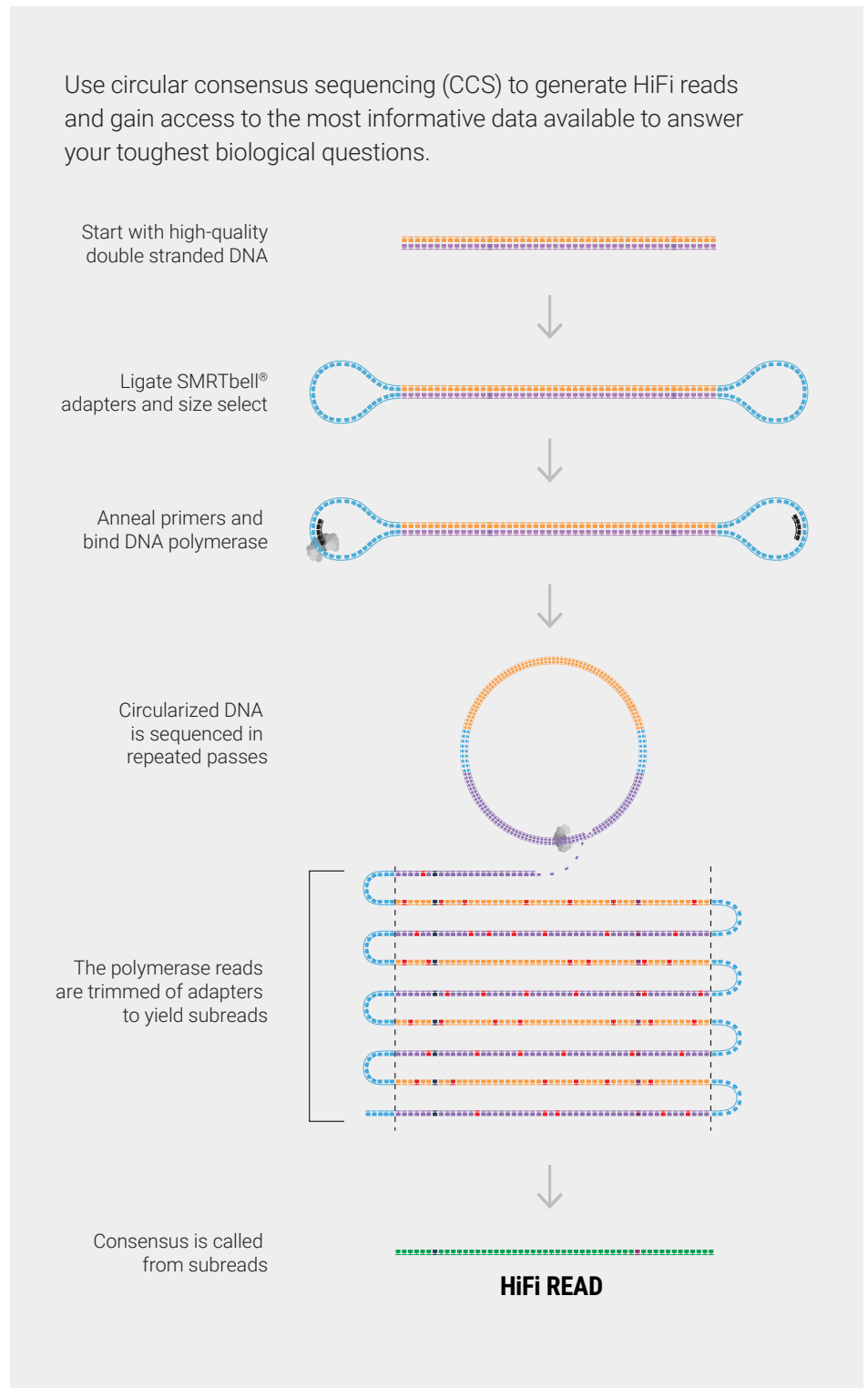
As the foundation for advanced scientific discoveries, sequencing data must be accurate and complete. With highly accurate long reads – HiFi reads – you no longer need to compromise between long read lengths and high-accuracy sequencing.



**PacBio is the only sequencing technology to offer HiFi reads**

## 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

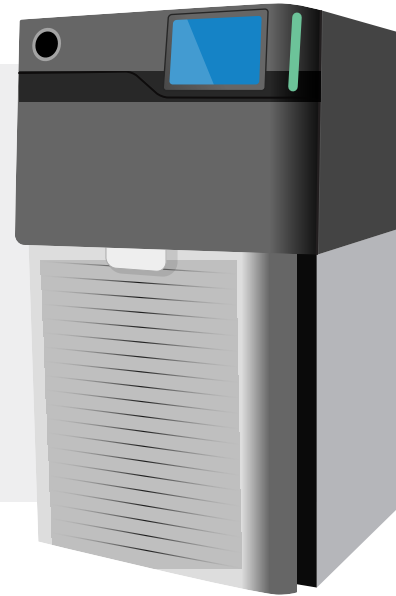


# Our solution

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

## Sequel<sup>®</sup> IIe system

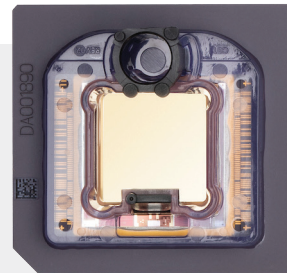
- Generates reliable high-throughput sequencing data
- Provides direct access to HiFi reads
- Reduces project time for faster results
- Makes sequencing more affordable
- Supports the range of SMRT sequencing applications



## 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

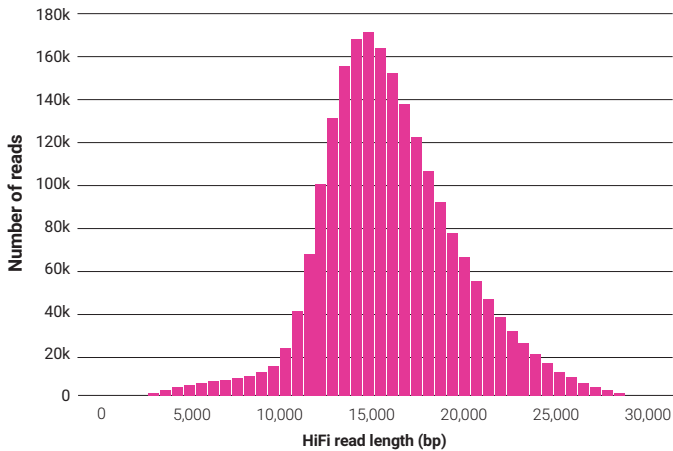
Our analytical software tools support you at every step, from run design through analysis



# Sequencing data you can trust

## Long read lengths

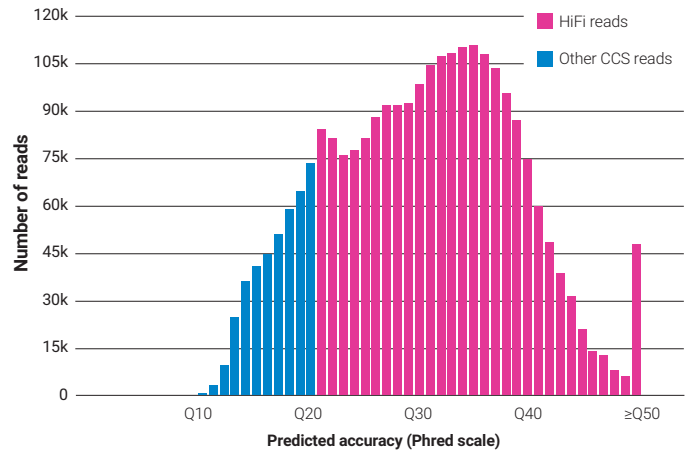
HiFi reads provide long read lengths up to 25 kb



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

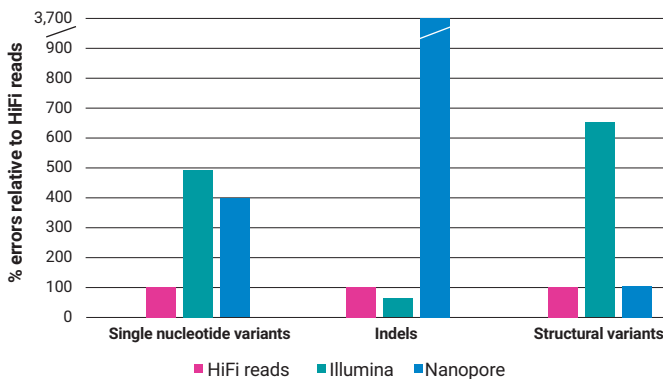
HiFi reads are highly accurate with median accuracy of >99.9% (Q30)



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

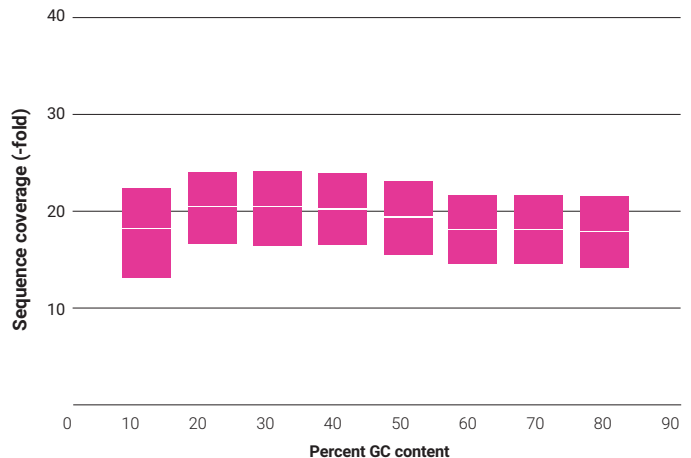
Only HiFi reads offer low error rates for detecting all variant types



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



## Variant detection

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



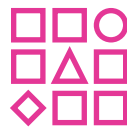
## RNA sequencing

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



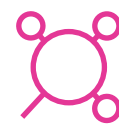
## Targeted sequencing

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



## Complex populations

Resolve closely related sequences within a heterogeneous mixture

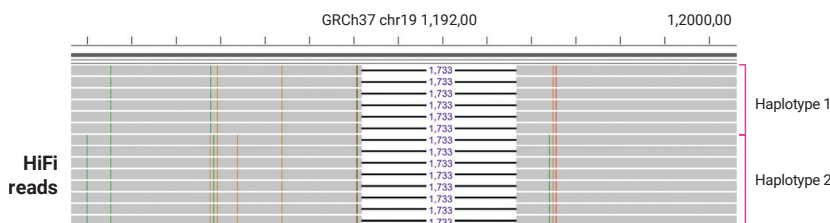


## Epigenetics

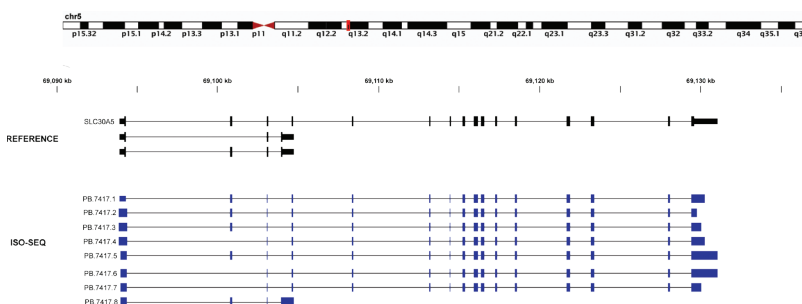
Directly detect DNA modifications during sequencing



Megabase sized contigs assembled into a nearly complete human *chromosome one*



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.



## Library prep

### Generate a SMRTbell library

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



## SMRT sequencing

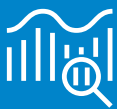
### Sequence on the Sequel IIe system

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 96 microbial isolates
- Determine the composition of up to 192 microbiome samples

With two 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



## Data analysis

### Enable every user in the lab with our analytical portfolio

- **SMRT analysis**  
Explore intuitive GUI and command-line options
- **PacBio DevNet**  
Discover community-developed tools
- **SMRT compatible analysis partners**  
Use solutions and services offered by trusted partners





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## READY TO GET STARTED WITH HIFI SEQUENCING?



Products and services  
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Documentation  
**pacb.com/documentation**

Application-specific workflows  
**pacb.com/applications**

Publications using SMRT® sequencing  
**pacb.com/pubs**



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