PACBIO®

Revolutionize Genomics with SMRT® Sequencing

Single Molecule, Real-Time Technology

Resolve to **Master Complexity**

HUMAN BIOMEDICAL RESEARCH

Despite large investments in population studies, the heritability of the majority of Mendelian and complex diseases remains unclear, limiting development of diagnostics and treatments. Shedding light on the **complete spectrum of sequence variant types** with chromosome-level phasing across genomes unique to a population, disease or individual may provide a holistic view of human genetics to resolve missing heritability linkages.

PLANT AND ANIMAL SCIENCES

The complex genomes of plants and animals, with their multi-gigabase sizes, polyploidy, and difficult-to-sequence repetitive regions, hold the key to resolving agricultural and environmental challenges like drought and disease. With a **complete view of genomes and transcriptomes** of crops, livestock, and associated microbes, scientists can finally unlock the genetic diversity required to advance breeding, precision engineer genes, develop novel treatments and natural growth enhancers, and secure a global food supply.

MICROBIOLOGY AND INFECTIOUS DISEASE

Infectious diseases are responsible for more than 23% of global deaths, including 50% of child mortality. Antibiotic drug resistance is a major threat to global health security, extending far beyond the human health sector, and globalization has created vast opportunities for novel diseases to emerge, spread, and kill. Only **comprehensive characterization of these pathogens including their mobile elements** will lead to the discovery and design of better vaccines, treatments, and outcomes.

The most comprehensive view of genomes, transcriptomes, and epigenomes

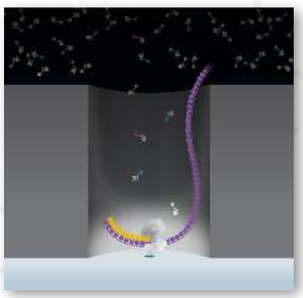
Sequel® System

Accelerate Your Science

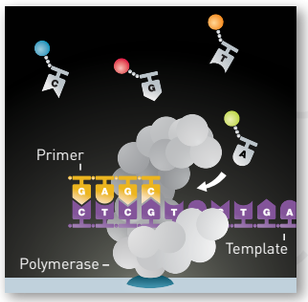
pacb.com/sequel

A SMRT Foundation

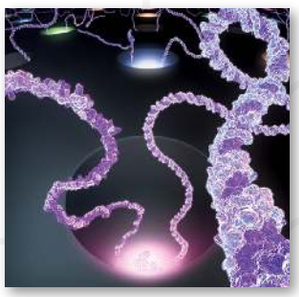
Single Molecule, Real-Time (SMRT®) technology is built upon two key innovations that overcome major challenges in the field of sequencing. Zero-Mode Waveguides (ZMWs) allow light to illuminate only the bottom of a well in which a DNA polymerase/template complex is immobilized. Phospholinked nucleotides allow observation of the immobilized complex as the DNA polymerase produces a completely natural DNA strand.



Zero-Mode Waveguides



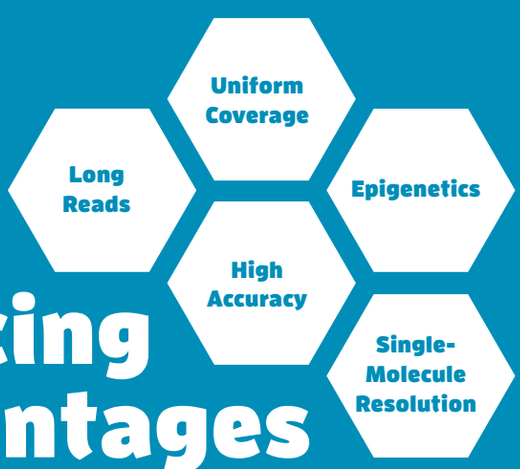
Phospholinked Nucleotides



Up to a million ZMWs per SMRT Cell

SMRT Cells containing up to a million ZMWs are processed on PacBio® Systems which simultaneously monitor each of the waveguides in real time.

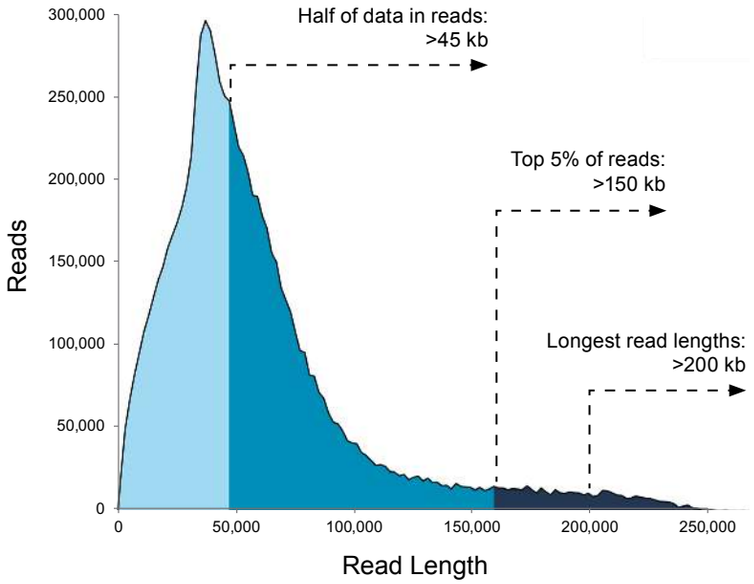
SMRT Sequencing Advantages



SMRT Sequencing Achieves

Long Read Lengths

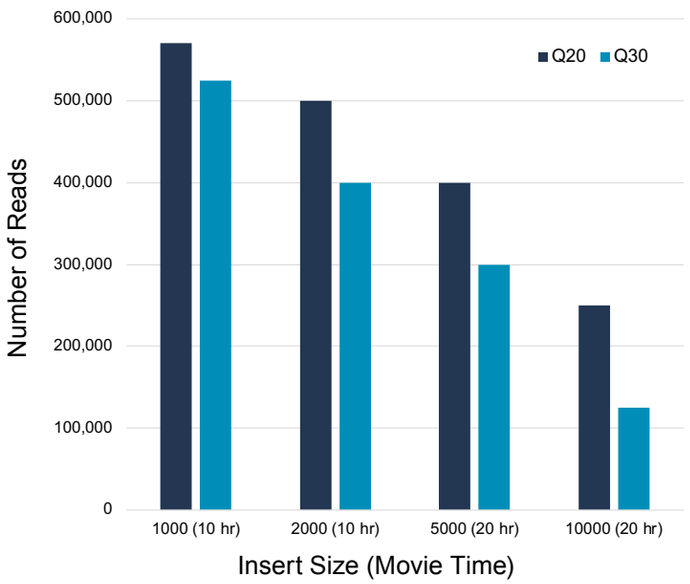
Half of data in reads: >45 kb
Data per SMRT Cell: Up to 20 Gb



Read length data shown above from a 35 kb size-selected human library using the SMRTbell® Express Template Prep Kit on a Sequel System (3.0 Chemistry, Sequel System Software v6.0, 20-hour movie). Read lengths, reads/data per SMRT Cell and other sequencing performance results vary based on sample quality/type and insert size among other factors.

High-Fidelity, Long Reads

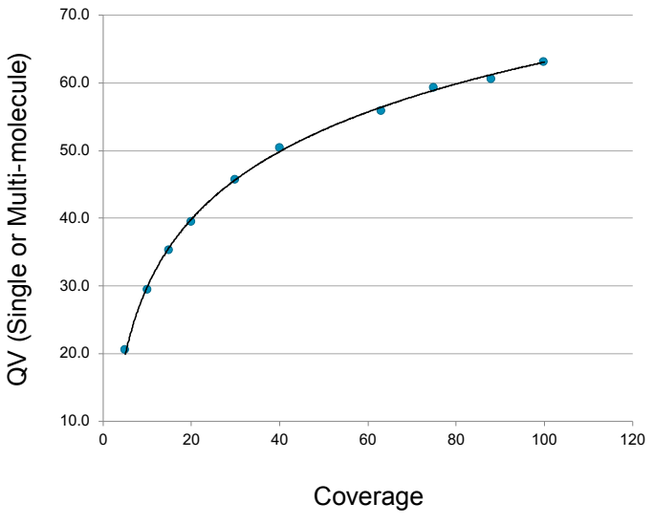
Long reads with Q20 single-molecule accuracy



Estimated number of high-fidelity, long reads (Q20 or Q30) per Sequel SMRT Cell (Chemistry 3.0. Sequel System Software v6.0) based on insert size and movie collection time.

High Consensus Accuracy

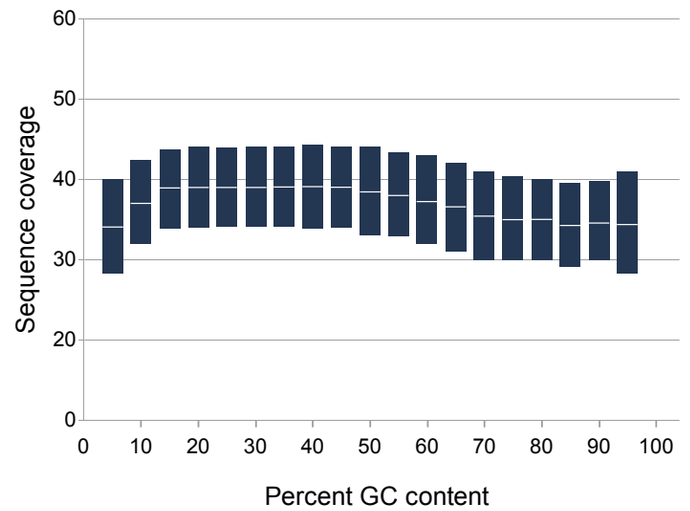
Free of systematic errors
Achieves >99.999% (QV50)



Consensus accuracy is a function of coverage and chemistry. The data above is based on a bacterial genome run on the Sequel System (3.0 Chemistry, Sequel System Software v6.0) Single-molecule accuracy has similar coverage requirements.

Uniform Coverage

No amplification required
Even coverage across GC content

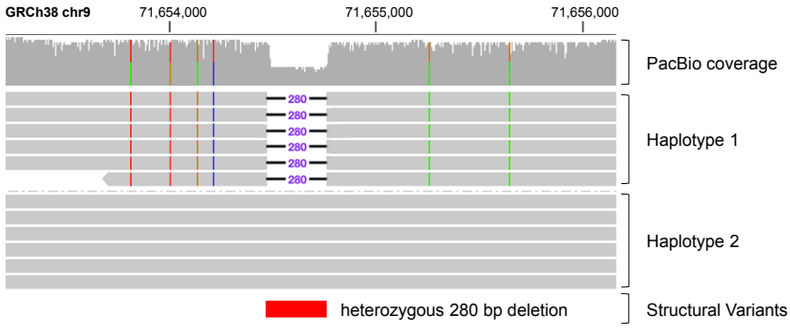


Mean coverage per GC window across a human sample.

Comprehensive Genomics

Unobstructed Views

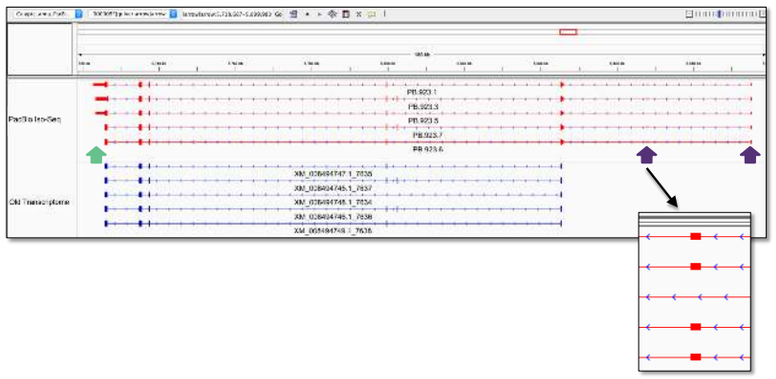
- Sequence low-complexity regions, like trinucleotide repeats
- Access all variant types, including structural variants, Indels and SNVs
- Allele-specific phasing of haplotypes in targeted regions or between chromosomes



A heterozygous deletion structural variant downstream of the gene *TMEM2* is supported by half of the PacBio reads that map to the locus. Sequence data is from the human sample HG002.

Confident Discoveries

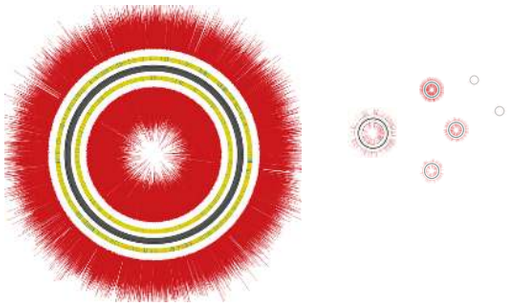
- Directly detect full-length transcripts without assembly
- Characterize gene-isoform expression within targeted genes, or across an entire transcriptome



Full length isoform sequences from brain tissue of Anna's hummingbird (red transcript models) identify two additional non-coding 5′ exons (purple arrows and inset) and extend 3′ UTRs (green arrow) while also capturing all five known splice variants (blue transcript models).

Complete Knowledge

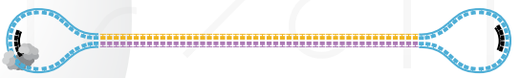
- Affordably generate gold-standard microbial genomes
- Detect and resolve plasmids, mobile elements, and structural variation including gene duplication and inversion
- Simultaneously analyze genome-wide methylation with single-base resolution



Complete genome assembly and methylome (red spikes) of an *E. coli* strain with six plasmids (not to scale).

Flexible Design and Analytics

- Express template preparation in as few as 3 hrs
- Accepts a variety of sample types and insert sizes



- Size-selection options to enrich for longest inserts
- Multiplexing and barcoding solutions available

Sequel System

- Flexible run time less than a day
- Serially process up to 12 SMRT Cells in a single run
- Walk away time up to 4 days

- Variety of analysis methods available through SMRT Link and PacBio DevNet community
- Open source software
- Advanced data visualization and mining

Comprehensive *de novo* assemblies

Target all types of variants across relevant genomic regions

Full-length isoform transcripts

Resolution of complex populations

Methylation profiles

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