Revolutionize Genomics with SMRT® Sequencing

Single Molecule, Real-Time Technology
Resolve to **Master Complexity**

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.

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.

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.
Accelerate your research with the most comprehensive view of genomes, transcriptomes and epigenomes

Sequel® System
The Leader in Long-Read Sequencing

pacb.com/sequel
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.

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

The SMRT Sequencing advantage:

- Long Read Lengths
- High Consensus Accuracy
- Uniform Coverage
- Simultaneous Epigenetic Characterization
SMRT Sequencing Achieves

Long Read Lengths
Half of data in reads: >30 kb
Data per SMRT Cell: Up to 10 Gb

High Consensus Accuracy
Free of systematic errors
Achieves >99.999% (QV50)

Uniform Coverage
No amplification required
Even coverage across GC content

Simultaneous Epigenetic Characterization
Directly detect DNA modifications using polymerase kinetics

Read length data shown above from a 35 kb size-selected E. coli library using the SMRTbell® Express Template Prep Kit on a Sequel System (2.1 Chemistry, Sequel System Software v5.1, 10-hour movie). Sequel System SMRT Cells typically generate ~400,000 reads each. Read lengths, reads/data per SMRT Cell and other sequencing performance results vary based on sample quality/type and insert size among other factors.

Consensus accuracy is a function of coverage and chemistry. The data above is based on a bacterial genome run on the Sequel System with 2.1 chemistry and 5.1 Sequel Software. Single-molecule accuracy has similar coverage requirements.

Mean coverage per GC window across a human sample.

Kinetic analysis of DNA base incorporation during sequencing can distinguish modified versus unmodified bases. This information is automatically generated and processed during every run.
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

Confident Discoveries

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

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

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.

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