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 scalable platform for SMRT Sequencing

www.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.

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 Delivers

Long Read Lengths

Read lengths >20 kb
Data per SMRT Cell: 5–8 Gb

[Graph showing read length distribution]

Read length data shown above from a 30 kb size-selected human library on the Sequel System (10-hour movie, 2.0 chemistry) with a total output of 7.6 Gb. Each Sequel System SMRT Cell 1M generates ~365,000 reads.

High Consensus Accuracy

Free of systematic errors
Achieves >99.999% (QV50)

[Graph showing QV vs. coverage]

Consensus accuracy is a function of coverage and chemistry. The data above is based on a bacterial genome run on the Sequel System with 2.0 chemistry.

Uniform Coverage

No amplification required
Even coverage across GC content

[Graph showing uniform coverage across GC content]

Mean coverage per GC window across E. coli

Simultaneous Epigenetic Characterization

Directly detect DNA modifications using polymerase kinetics

[Graph showing polymerase dynamics on forward and reverse strands]

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

**Unobstructed Views**
- Sequence low-complexity regions, like trinucleotide repeats
- Access all variant types, including structural variation
- Allele-specific phasing of haplotypes in targeted regions or between chromosomes

PacBio vs. short-read CHM1 sequencing data aligned to hg19, highlighting the short-read coverage deserts around exon 1 of autism-linked shank3 gene.

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

Novel full-length isoforms identified in Minghui 64 rice cultivar using Iso-Seq™ sequencing.

**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

- Accepts a variety of sample types and insert sizes
- Low template options available from 10 - 100 ng
- Complete template preparation in as few as 6 hrs
- Rapid sequence time (0.5 to 10 hrs)
- Serially process up to 16 SMRT Cells in a single run with walkaway automation
- 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