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 treatment. Shedding light on the complete spectrum of sequence variant types with chromosome-level phasing across genomes unique to population, disease or individual may provide a holistic view of human genetics to resolve missing heritability linkages.

Infectious diseases are responsible for more than 23% of global deaths, including 50% of child mortality. Antibiotic drug resistance is a top 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 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.
Single Molecule, Real-Time Sequencing
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.

A New Dimension for Your Research

SMRT Cells containing thousands of ZMWs are processed on a PacBio® RS System which simultaneously monitors each of the waveguides in real time.

» Longest Read Lengths
» Highest Consensus Accuracy
» Least Degree of Bias
» Simultaneous Epigenetic Characterization
SMRT® Sequencing Delivers

**Longest Read Lengths**
Read lengths > 20 kb
Data per SMRT Cell: 500 Mb – 1 Gb

Based on data from a 20 kb size-selected human library using a 4-hour movie with P6-C4 chemistry, analyzed with SMRT Analysis v2.3. Each SMRT Cell generates ~55,000 reads.

- Half of data in reads: > 20 kb
- Top 5% of reads: > 30 kb
- Maximum read length: > 60 kb

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

Consensus Accuracy is a function of coverage and chemistry. The P6-C4 estimates shown here are based on multiple bacterial genomes.

**Least Biased**
No amplification required
Even coverage across GC content

Mean coverage per GC window across GRCh37 for CHM1.

**Simultaneous Epigenetic Characterization**
Directly detect DNA base modifications using polymerase kinetics

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).

See more at www.pacb.com/pubs
Flexible Design and Analytics

- Complete template preparation in as few as 6 hrs
- Accepts inserts from 250 bp to 40 kb for flexible assay design
- Multiplexing and barcoding solutions available
- Rapid sequence time (0.5 to 4 hrs)
- Serially process up to 16 SMRT Cells in a single run with walkaway automation

- Variety of sample types: Genome DNA, Amplicons, cDNA
- Low input sample amounts from 10 ng to 1 µg
- Variety of analysis methods available through SMRT Software Suite and community
- Open source software
- Advanced data visualization and mining

Comprehensive de novo assemblies
Full-length isoform transcripts
Phased SNPs & minor variants
Methylation profiles
Operating Environment

Instrument and environmental cabinet

Power requirements: 208 – 240 VAC. UPS recommended
Operating temperature: 15 °C – 25 °C [59 °F – 77 °F] ± 2 °C per hour
Humidity: 20% – 80%, noncondensing
Ventilation: HVAC capacity of up to 22,720 BTU (6654 Watts)
Nitrogen: 90 – 125 PSI [4,654 – 6,464 torr]
WxDxH: 80 in x 35 in x 63 in [203 cm x 90 cm x 160 cm]
Weight: 1,895 lb [860 kg]

Blade Center

Includes integrated computation and storage for performing single molecule, real-time sequencing, basecalling and quality assessment.
WxDxH: 24.1 in x 35.9 in x 26.2 in [61.3 cm x 91.3 cm x 66.5 cm]
Weight: 220 lb [100 kg]
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