

Revolutionize Genomics with SMRT® Sequencing

Single Molecule, Real-Time Technology

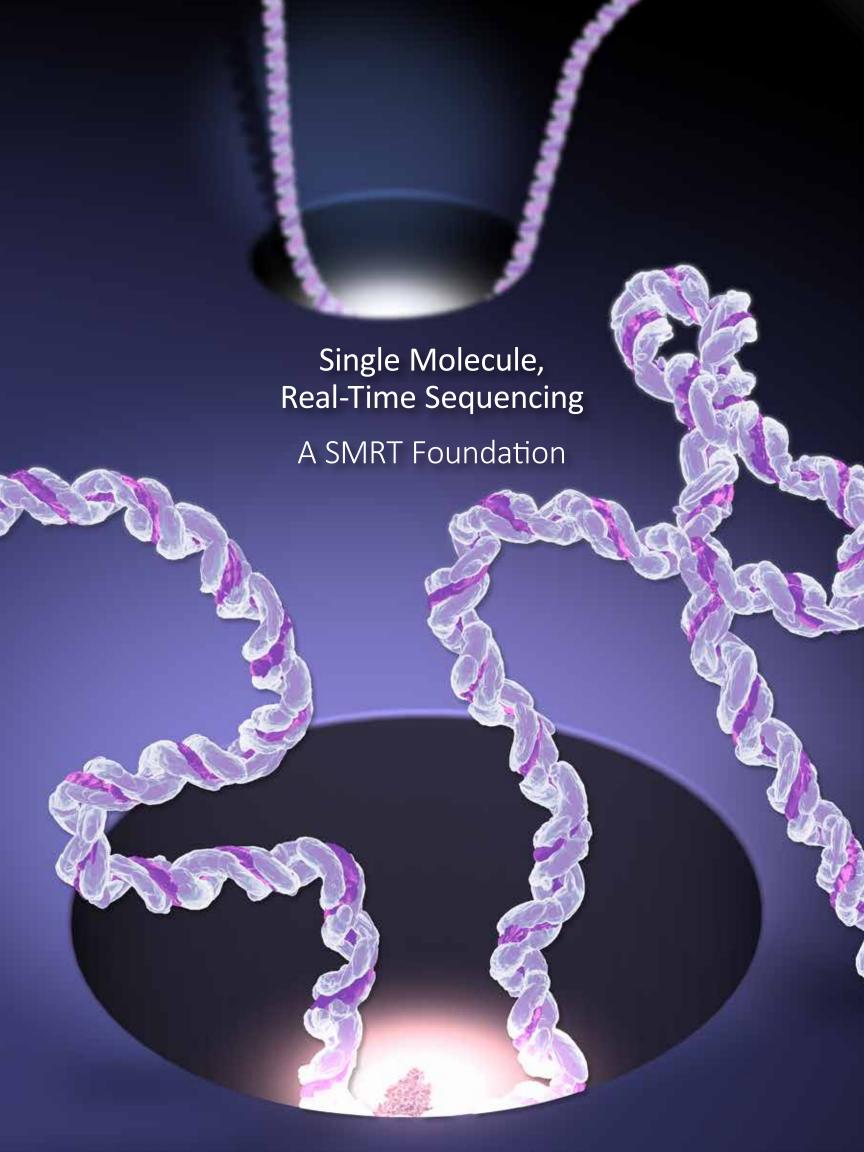


Resolve to Master Complexity

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 multigigabase 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.

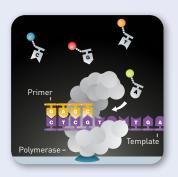


A New Dimension for Your Research

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

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



SMRT Cells



PacBio RS II System

- » Longest Read Lengths
- » Highest Consensus Accuracy
- » Least Degree of Bias
- » Simultaneous Epigenetic Characterization

SMRT® Sequencing Delivers

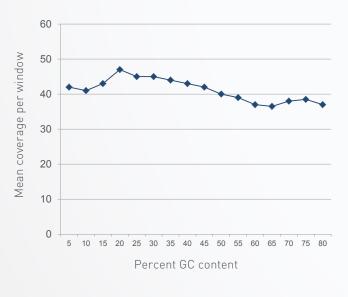
Read lengths > 20 kb Data per SMRT Cell: 500 Mb – 1 Gb Half of data in reads: > 20 kb Top 5% of reads: > 30 kb Maximum read length: > 60 kb Read Length Based on data from a 20 kb size-selected human library using a 4-hour movie with P6-C4 chemistry, analyzed with SMRT Analysis v2.3. Each SMRT Cell generates ~55,000 reads.

Highest Consensus Accuracy Free of systematic errors Achieves >99.999% (QV50) 70.0 Perfect consensus 60.0 50.0 \mathbb{Q}^{\vee} 40.0 30.0 20.0 10.0 20 40 60 80 100 Coverage Aligned to Reference

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

Least Biased

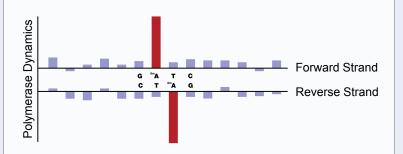
No amplification required Even coverage across GC content



Mean coverage per GC window across GRCh37 for CHM1.

Simulateneous Epigenetic Characterization

Directly detect DNA base modifications using polymerase kinetics

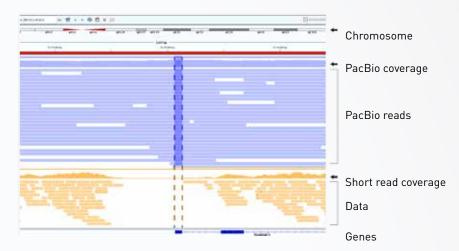


Kinetic analysis of DNA base incorporation during sequencing can distinguish modified versus unmodified bases. This information is automatically generated and processed during every run.

Comprehensive Genomics

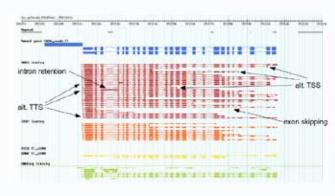
Unobstructed Views

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



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

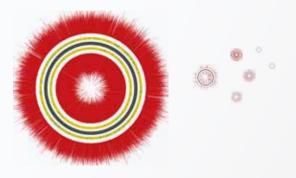


Novel full-length isoforms identified in Minghui 64 rice cultivar using Iso-Seq™ sequencing.

- 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



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

Flexible Design and Analytics



- Variety of sample types:
 Genome DNA, Amplicons, cDNA
- Low input sample amounts from 10 ng to 1 μg





- 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 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: $15 \,^{\circ}\text{C} - 25 \,^{\circ}\text{C} \, (59 \,^{\circ}\text{F} - 77 \,^{\circ}\text{F}) \pm 2 \,^{\circ}\text{C} \, per hour}$

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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