PacBio® RS
SINGLE MOLECULE, REAL-TIME SEQUENCING

FIND MEANING IN COMPLEXITY

Genome finishing • Epigenetics • Haplotype phasing
Repeat expansions • Full-length transcripts • Minor variants
The PacBio RS is a high-resolution genetic analyzer that observes single molecules in real time, providing high throughput SMRT® sequencing of DNA and base modifications at the same time. Reads are an average of ten times longer than reads from other technologies.

Generate Finished Genomes

The PacBio RS finishes microbial genomes and improves assembly of larger organisms with multi-kilobase reads and unbiased coverage regardless of GC content. No amplification required.

Range of Genome Sizes

Benefits

- Highest N50
- Fewest contigs
- Detect structural variation
- 99.999% accuracy
- Genome finishing at 1/10th the cost

De Novo Assembly Methods

- Hierarchical Assembly
- Hybrid Assembly
- Scaffolding
- Gap Filling

Paper: PloS One: Mind the gap: Upgrading genomes with Pacific Biosciences RS long-read sequencing technology
Paper: Nature Biotechnology: Hybrid error correction and de novo assembly of single-molecule sequencing reads
Paper: Nature Biotechnology: A hybrid approach for the automated finishing of bacterial genomes

www.pacb.com/denovo
Discover the Epigenome

The PacBio® RS detects DNA base modifications using the kinetics of the polymerization reaction during normal sequencing.

Methyltransferases bind specifically to DNA motifs in a genome and methylate bases. PacBio software locates modified sites and motifs.

Methylome of the German E. coli outbreak strain. The inner and outer red circles show the kinetic signals. The colored internal tracks show the different methylation motif distributions.

<table>
<thead>
<tr>
<th>Motif</th>
<th>Occurrence in Genome</th>
<th>Modified in Genome</th>
<th>% Modified</th>
</tr>
</thead>
<tbody>
<tr>
<td>5' - GATC-3' 3' - CTAG-5'</td>
<td>42,992</td>
<td>41,969</td>
<td>97.6%</td>
</tr>
<tr>
<td>5' - ACCAACC-3' 3' - TGGTGG-5'</td>
<td>4,569</td>
<td>4,492</td>
<td>98.3%</td>
</tr>
<tr>
<td>5' - CTGCGG-3' 3' - GACGTC-5'</td>
<td>2,746</td>
<td>2,678</td>
<td>97.5%</td>
</tr>
<tr>
<td>5' - CCAN8TGAY-3' 3' - GCTGNACTR-5'</td>
<td>492</td>
<td>478</td>
<td>97.2%</td>
</tr>
</tbody>
</table>

Genome-wide detection of methylation for the German E. coli outbreak strain.

Paper: Nature Biotechnology: Genome-wide mapping of methylated adenine residues in pathogenic Escherichia coli
Paper: Nucleic Acids Research: The methylomes of six bacteria
Paper: Current Opinion in Structural Biology: Going beyond five bases in DNA sequencing
Characterize Genomic Variation

The PacBio® RS provides exquisite sensitivity and specificity with extraordinarily long reads to fully characterize genetic complexity.

**Compound Mutations and Haplotype Phasing**

Multi-kilobase reads facilitate the study of linked mutations hundreds, even thousands, of bases apart.

Paper: [Nature: Validation of FLT3-ITD as a therapeutic target in human acute myeloid leukemia](#)

**Repeat Expansions**

Long reads and low bias allow accurate sequencing across repeat expansions, even in low complexity regions.

Paper: [Genome Research: Sequencing the unsequenceable: Expanded CGG-repeat alleles of the fragile X gene](#)

**Full-Length Transcripts and Splice Variants**

Single-molecule resolution and long reads span entire cDNAs, allowing full characterization of splicing in the transcriptome.

Poster: [AGBT 2012: Full length cDNA sequencing on the PacBio® RS](#)

**Minor Variants and Quasispecies**

Single molecule sequencing simplifies the analysis of mixed populations of sequences. Exquisitely sensitive and specific.

**Linear variant detection to < 0.1% frequency**

Poster: [ASHG 2012: Sensitive detection of minor variants and viral haplotypes using SMRT® sequencing](#)

**SNP Detection and Validation**

Single molecule sequencing detects and validates SNPs with high accuracy by avoiding mapping errors and systematic error.

**99.999% consensus accuracy.**

Paper: [BMC Genomics: Pacific Biosciences sequencing technology for genotyping and variation discovery in human data](#)

www.pacb.com/target
**PacBio® RS Typical Results**

### Read Length Distribution

- **Average:** 4,575 bp
- **95th Percentile:** 11,660 bp
- **Maximum:** 20,848 bp

Based on data from 11 kb plasmid library using a 120 minute movie

### Throughput per SMRT® Cell

- **One 120 minute movie**
  - 102 Mb
  - 22,375 reads

- **Two 55 minute movies**
  - 252 Mb
  - 59,483 reads

Results from 11 kb plasmidbell (120 min movie) and 2 kb lambda (two 55 min movies)

### Template Preparation

<table>
<thead>
<tr>
<th>Insert Size (bp)</th>
<th>Input DNA per prep (ng)</th>
</tr>
</thead>
<tbody>
<tr>
<td>250 – 500</td>
<td>250</td>
</tr>
<tr>
<td>1,000 – 2,000</td>
<td>500</td>
</tr>
<tr>
<td>5,000 – 10,000</td>
<td>1,000</td>
</tr>
</tbody>
</table>

Each library prep typically supports >35 SMRT Cells.

### Accuracy

Based on data from E. coli with 10 kb libraries using a 90 minute movie
Products and Workflow

The PacBio® RS system, consumables and software provide a simple, fast, end-to-end workflow for SMRT® sequencing.

Library Preparation
- DNA Template Prep Kit
- DNA Polymerase Binding Kit
- MagBead Kit
- No amplification required

Instrument Run
- PacBio RS with touch screen
- RS Remote for run design
- SMRT Cells
- DNA Sequencing Kit
- Sequencing time 30 to 120 min per SMRT Cell

Data Analysis
- SMRT Analysis
- SMRT Portal
- SMRT View
- Open source, open standards

Results in as little as 10 hours

SMRT® Technology

The PacBio RS is a high-resolution genetic analyzer that observes natural DNA synthesis by a DNA polymerase in real time. Single molecule real-time (SMRT) sequencing can produce read lengths an order of magnitude longer than other technologies.

SMRT® Cells

Zero-Mode Waveguides

Phospholinked Nucleotides
Join the SMRT® Community

Our single molecule, real-time sequencing community site is the central resource for life scientists, informatics researchers and independent software vendors to learn about SMRT sequencing technology, share ideas and communicate with each other.

www.smrtcommunity.com

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: 78.9in x 30.3in x 62.2in (200.4cm x 77.0cm x 158.0cm)
- Weight: 2,405lb (1,091kg)

Blade center

Includes integrated computation and storage for performing single molecule, real-time sequencing, kinetic data generation, basecalling and quality assessment.

- WxDxH: 27.5in x 27in x 39.2in (69.9cm x 68.6cm x 99.6cm)
- Weight: 250lb (113kg)