**Sequence with Confidence**

The Sequel® II and IIe Systems are powered by Single Molecule, Real-Time (SMRT®) Sequencing, a technology proven to produce highly accurate long reads, known as HiFi reads, for sequencing data you and your customers can trust.

**SMRT SEQUENCING IS SMART BUSINESS**

**HiFi Reads:** PacBio is the only sequencing technology to offer highly accurate long reads. Because HiFi reads are extremely accurate, downstream analysis is simplified and streamlined, requiring less compute time than the error-prone long reads of other technologies.

**High Throughput:** The Sequel II and IIe Systems have high data yields on robust, highly automated platforms to increase productivity and reduce project costs.

**Efficient and Easy-To-Use Workflows:** Our end-to-end solutions feature library preparation in <3 hours and many push-button analysis workflows, so you can run projects quickly and easily.

**Support:** All of our products are backed by a global team of scientists, bioinformaticians, and engineers who stand ready to provide you with outstanding service.

**OUTSTANDING PERFORMANCE AND RELIABILITY**

"In our experience, the Sequel II System was essentially production-ready right out of the box. We have used it for a range of applications and sample types — from human genome sequencing to metagenome and microbiome profiling to non-model plant and animal genomes — and results have been very good."

— **Luke Tallon**, Director of the Genomics Resource Center at Maryland Genomics

[Graph showing total yield over time with 99% of runs completed successfully]
SMRT SEQUENCING APPLICATIONS – EFFICIENT AND COST EFFECTIVE

The Sequel II and Ile Systems support a wide range of applications, each adding unique value to a sequencing study. The price per sample depends on multiplex level and the service provider’s fee-for-service rate. A typical service provider fee-for-service rate is a 2- to 4-fold increase.

<table>
<thead>
<tr>
<th>Applications</th>
<th>Whole Genome Sequencing</th>
<th>RNA Sequencing</th>
<th>Targeted Sequencing</th>
<th>Microbial Sequencing</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>De novo assembly (2 Gb)</td>
<td>Variant detection (3 Gb)</td>
<td>Transcriptome sequencing</td>
<td>Amplicon (1-20 kb)</td>
</tr>
<tr>
<td>Why Choose SMRT Sequencing?</td>
<td>Complete, contiguous, and correct assemblies</td>
<td>High precision and recall for all variant types</td>
<td>Assembly-free comprehensive genome annotation</td>
<td>Exhaustive uniform characterization with no assembly required</td>
</tr>
<tr>
<td>Samples/Year (Multiplex/SMRT Cell 8M)*</td>
<td>Up to 240 genomes at 2 Gb</td>
<td>Up to 120 samples for 3 Gb genomes</td>
<td>Up to 1,920 tissues (8)</td>
<td>Up to 240 whole transcriptomes</td>
</tr>
<tr>
<td>Reagents Cost/ Sample†</td>
<td>$1,300</td>
<td>$2,600</td>
<td>$185</td>
<td>$1,300</td>
</tr>
</tbody>
</table>

*Study design, sample type, and level of multiplexing may affect the number of SMRT® Cells 8M required.
†All prices are listed in USD and cost may vary by region. Pricing includes library and sequencing reagents run on your Sequel II or Ile System and does not include instrument amortization or other reagents.

“My sequencing center has seen the level of interest in projects to be run on our Sequel II System increase by over 100% this year, as compared to the previous year. Many of these projects are coming from investigators/collaborators that are new to my center, they are interested in using HiFi sequencing in their research.”

— Bruce Kingham, Director, Sequencing and Genotyping, University of Delaware

IMPROVED ECONOMICS WITH THE SEQUEL II SYSTEM

When run at full capacity, the Sequel II and Ile Systems can sequence 240 SMRT Cells 8M per year. And the total instrument cost can be recovered in less than three years by running only 12 SMRT Cells 8M per month.

<table>
<thead>
<tr>
<th>Usage Levels</th>
<th>Time to Payback (in months)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SMRT Cells/ Month</td>
</tr>
<tr>
<td>60%</td>
<td>12</td>
</tr>
<tr>
<td>80%</td>
<td>16</td>
</tr>
<tr>
<td>100%</td>
<td>20</td>
</tr>
</tbody>
</table>

“As a PacBio service provider we see high demand for our Sequel II services. On average we run at 100% capacity with an average project queue of 1.5 months or greater”

— Edward Wilcox, Manager, DNA Sequencing Center, Brigham Young University

Months of operation required at various capacity levels and consumables markup rates to recoup Sequel II or Ile System cost, 1 FTE for 3 years at $75k/yr, and service contracts.
When Accuracy Matters — Choose HiFi Sequencing

WHAT IS THE TRUE COST PER BASE IF YOU DON’T GET THE ANSWER?

HiFi reads achieve a higher quality assembly of the human genome compared to other technology platforms. With fewer sequencing gaps, HiFi reads capture 5% more variants in the medical exome, including 193 medically-relevant genes that are not fully captured with other sequencing methods. When gaps are present and genes are missed, the cost and time to obtain biological conclusions increase greatly and limit scientific progress.

“PacBio Sequel II has been generating amazing data both in size and quality. All the customers have been very pleased with the data they are getting off of PacBio Sequel II”
— Nasun Hah, Director, Genomics Sequencing Core, Salk Institute

HiFi reads let you map, and call variants missed by short reads

HiFi reads are more concordant with GIAB benchmark

HiFi reads detect medically-relevant genes missed by short reads

PacBio — A Trusted Partner

With a dedicated global team of scientists, engineers, and bioinformaticians, we are proud to offer end-to-end support to our customers and end users.

Explore How Scientists Use SMRT Sequencing in Their Research, Including More Than 7000 Publications
pacb.com/smrt-resources

Learn More About Application-Specific End-To-End Workflows
pacb.com/applications

Whole Genome Sequencing
VARIANT DETECTION
RNA Sequencing
TARGETED SEQUENCING
COMPLEX POPULATIONS
EPIGENETICS

“Although we did not have much prior experience on long read sequencing on PacBio platform, every aspect of PacBio operations (starting from instrument installation, training, library, instrument operation and SMRT Link) has been easy and smooth thanks to the amazing PacBio team that we have.”
— Nasun Hah, Director Genomics Sequencing Core, Salk Institute

“Our Field Application Scientist has always been very straightforward, helpful, and easy to get on the phone when we needed “right-now support”.
— Dan New, IBEST Genomics Resources Core

Sequencing providers around the world are adding the PacBio Systems to their portfolios to meet the demand for highly accurate long-read sequencing.

Are you ready to join them?

Contact Your Local Sales Team:

North America: nasales@pacb.com
South America: sasales@pacb.com

Europe/Middle East/Africa: emea@pacb.com
Asia Pacific: apsales@pacb.com