**Sequence with Confidence**

The Sequel II® System is 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 System has high data yields on a robust, highly automated platform 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

The Sequel Systems have reliable performance with 98.8% of the sequencing runs completing successfully, and the Sequel II System provides more than 15-times higher throughput than the Sequel System.
SMRT SEQUENCING APPLICATIONS – EFFICIENT AND COST EFFECTIVE

The Sequel II System supports 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>Do 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 1,920 tissues (6)</td>
<td>Up to 240 whole transcriptomes</td>
<td>Up to 184,320 samples for 1 kb amplicons (768)</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 System and does not include instrument amortization or other reagents.

“We are PacBio service providers since 2012 and are very happy with the product and the support we get from the company. Over the years our users have obtained extremely valuable results on various organisms from bacteria to large plant genomes and we are anxiously awaiting our new Sequel II which will greatly improve throughput and cost effectiveness for large scale projects”
— Alexandre Monpetit, Scientific Director, Centre d’expertise et de services Génome Québec

IMPROVED ECONOMICS WITH THE SEQUEL II SYSTEM

When run at full capacity, the Sequel II System 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.

**Instrument Payback Period**

<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>40%</td>
<td>12</td>
</tr>
<tr>
<td>60%</td>
<td>18</td>
</tr>
<tr>
<td>80%</td>
<td>24</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 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


“HiFi Reads really allow us to call accurate structural variations and other types of variations that you can’t actually see with short-read sequencing”

— Jeremy Schmutz, Faculty Investigator, HudsonAlpha Institute of Biotechnology

pacb.com/HiFi
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

Access Our Training Tools
pacb.com/training

Review Our Complete Suite of Documentation
pacb.com/documentation

Get Support When it Matters – On-Demand Help, Virtually, or Locally
pacb.com/support

Email: support@pacb.com
Phone: 1.877.920.PACB (7222)

Sequencing providers around the world are adding the Sequel II System 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

“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

For Research Use Only. Not for use in diagnostic procedures. © Copyright 2020, Pacific Biosciences of California, Inc. All rights reserved. Information in this document is subject to change without notice. Pacific Biosciences assumes no responsibility for any errors or omissions in this document. Certain notices, terms, conditions and/or use restrictions may pertain to your use of Pacific Biosciences products and/or third party products. Please refer to the applicable Pacific Biosciences Terms and Conditions of Sale and to the applicable license terms at http://www.pacb.com/legal-and-trademarks/terms-and-conditions-of-sale/. Pacific Biosciences, the Pacific Biosciences logo, PacBio, SMRT, SMRTbell, iso-Seq, and Sequel are trademarks of Pacific Biosciences. Pacific Biosciences does not sell a kit for carrying out the overall No-Amp Targeted Sequencing method. Use of the No-Amp method may require rights to third party owned intellectual property. BluePippin and SageELF are trademarks of Sage Science. NGS-go and NGSengine are trademarks of GenDx. Femto Pulse and Fragment Analyzer are trademarks of Agilent Technologies Inc. All other trademarks are the sole property of their respective owners.