SEQUENCE WITH CONFIDENCE

Choose the most trusted long-read technology for your core

SMRT® sequencing is smart business

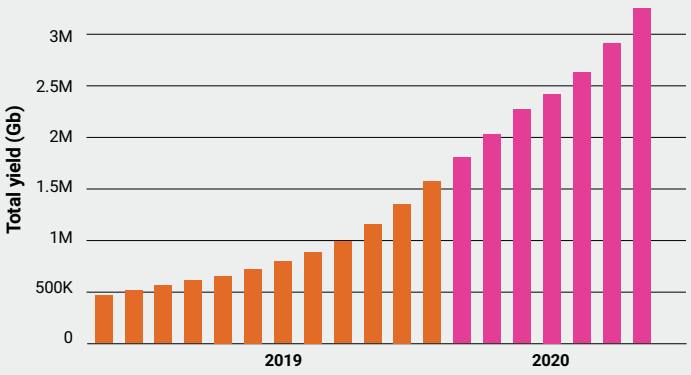
The Sequel® II and IIe systems are powered by Single Molecule, Real-Time (SMRT) sequencing, a technology proven to produce highly accurate long reads, known as HiFi reads, for sequencing data you and your customers can trust. In addition, you can get simultaneous 5-methylcyosine (5mC) calling without additional costs or experiments.

- **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 under three 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.

"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

Outstanding performance and reliability



Sequel II systems provide reliable performance with the total bases produced by the PacBio fleet steadily increasing, and 99% of runs completed successfully.

99%

of runs on the Sequel II system completed successfully

PacBio

SMRT sequencing applications — Efficient and cost-effective

The Sequel II and IIe 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.

		Why choose SMRT sequencing?	Samples/year (mulitplex/SMRT® Cell 8M)*	Reagents cost/ sample†
Whole genome sequencing with methylation	***De novo* assembly (2 Gb)**	Complete, contiguous, and correct assemblies with base-level methylation	Up to 240 genomes at 2 Gb	**$1,300**
	Variant detection (3 Gb)	High precision and recall for all variant types with base-level methylation	Up to 120 samples for 3 Gb genomes	**$2,600**
Iso-Seq® method	**Full-length RNA sequencing**	High-quality comprehensive genome annotation	Up to 2,880 tissues (12)	**$125**
		Novel isoform discovery differential analysis	Up to 240 whole transcriptomes	**$1,300**
Targeted sequencing	**Amplicon (1–20 kb)**	Haplotype phasing while detecting all variant types	Up to 240,000 samples for 1 kb amplicons (1,000)	**$1–2**
	HiFiViral SARS-CoV-2 sequencing	Unique MIPs solution is simple and robust to novel variants	Up to 92,160 samples (384)	**$38**
Microbial sequencing	***De novo* assembly**	Closed genomes and plasmids	Up to 23,040 microbes (96)	**$124**
	Metagenome assembly	Generation of complete or near-complete genome assemblies from microbial populations	Up to 960 samples (4)	**$350**
	Metagenome profiling	Recovery of 8–10 full-length genes per HiFi read, without assembly	Up to 11,520 samples (48)	**$85**
	Full-length 16S rRNA sequencing	Unambiguous species or strain-level resolution	Up to 46,080 samples (192)	**$8**

* 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 IIe 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 IIe 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.

Usage levels		Time to payback (in months)		
Capacity	**SMRT Cells/month**	**3x markup**	**3.5x markup**	**4x markup**
60%	12	26	21	18
80%	16	20	16	13
100%	20	16	13	11

Months of operation required at various capacity levels and consumables markup rates to recoup Sequel II or IIe system cost; 1 FTE for 3 years at $75k/yr, and service contracts.

"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"

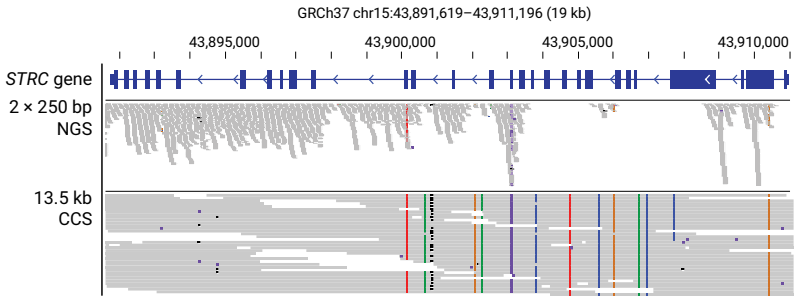
Edward Wilcox, *Manager, DNA Sequencing Center, Brigham Young University*

When accuracy matters, choose HiFi sequencing

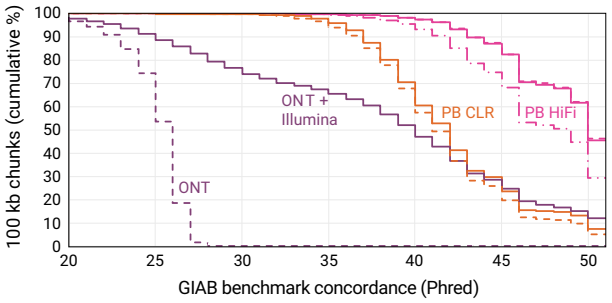
What is the true cost per base if you don't get the answer?

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

% of problem exons mappable	Genes	# of genes
100	*ABCC6, ABCD1, ACAN, ACSM2B, AKR1C2, ALG1, ANKRD11, BCR, CATSPER2, CD177, CEL, CES1, CFH, CFHR1, CFHR3, CFHR4, CGB, CHEK2, CISD2, CLCNKA, CLCNKB, CORO1A, COX10, CRYBB2, CSH1, CYP11B1, CYP11B2, CYP21A2, CYP2A6, CYP2D6, CYP2F1, CYP4A22, DDX11, DHRS4L1, DIS3L2, DND1, DPY19L2, DUOX2, ESRRA, F8, FAM120A, FAM205A, FANCD2, FCGR1A, FCGR2A, FCGR3A, FCGR3B, FLG, FLNC, FOXD4, FOXO3, FUT3, GBA, GFRA2, GON4L, GRM5, GSTM1, GYPA, GYPB, GYPE, HBA1, HBA2, HBG1, HBG2, HP, HS6ST1, IDS, IFT122, IKBKG, IL9R, KIR2DL1, KIR2DL3, KMT2C, KRT17, KRT6A, KRT6B, KRT6C, KRT81, KRT86, LEFTY2, LPA, MST1, MUC5B, MYH6, MYH7, NEB, NLGN4X, NLGN4Y, NOS2, NOTCH2, NXF5, OPN1LW, OR2T5, OR51A2, PCDH11X, PCDHB4, PGAM1, PHC1, PIK3CA, PKD1, PLA2G10, PLEKHM1, PLG, PMS2, PRB1, PRDM9, PROS1, RAB40AL, RALGAPA1, RANBP2, RHCE, RHD, RHPN2, ROCK1, SAA1, SDHA, SDHC, SFTPA1, SFTPA2, SIGLEC14, SLC6A8, SMG1, SPATA31C1, SPTLC1, SRGAP2, SSX7, STAT5B, STK19, STRC, SULT1A1, SUZ12, TBX20, TCEB3C, TLR1, TLR6, TMEM231, TNXB, TRIOBP, TRPA1, TTN, TUBA1A, TUBB2B, UGT1A5, UGT2B15, UGT2B17, UNC93B1, VCY, VWF, WDR72, ZNF419, ZNF592, ZNF674*	**152**
(75, 100)	*ANAPC1, C4A, C4B, CHRNA7, CR1, DUX4, FCGR2B, HYDIN, OTOA, PDPK1, TMLHE*	**11**
(50, 75)	*ADAMTSL2, CDY2A, DAZ1, GTF2I, NAIP, OCLN, RPS17*	**7**
(25, 50)	*DAZ2, DAZ3, KIR3DL1, OPN1MW, PPIP5K1*	**5**
(0, 25)	*NCF1, RBMY1A1*	**2**
0	*BPY2, CCL3L1, CCL4L1, CDY1, CFC1, CFC1B, GTF2IRD2, HSFY1, MRC1, OR4F5, PRY, PRY2, SMN1, SMN2, TSPY1, XKRY 16*	**16**

HiFi reads detect medically relevant genes missed by short reads

Wenger, A. M., et al. (2019) **Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome.** *Nature Biotechnology*, 37, 1155–1162.

> "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*

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As a global company, we have offices in countries around the world. Visit **pacb.com/contact-us** for contact info.

"Although we did not have much prior experience on long-read sequencing on the 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*

Access our training tools
pacb.com/training

Review our complete suite of documentation
pacb.com/documentation

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