



PacBio Transforms Access to the Epigenome and Streamlines Workflows

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Significant Enhancements to the Sequel II/Ile Platform Include Methylation Calling in Native DNA, Greatly Accelerated Sample Preparation, and Support for Gene Therapy Applications

MENLO PARK, Calif., April 21, 2022 (GLOBE NEWSWIRE) -- [PacBio](#) (NASDAQ: PACB), a leading developer of high-quality, highly accurate sequencing solutions, today announced the release of a transformative capability to detect DNA methylation using the [Sequel IIe and Sequel II Systems](#). This extends PacBio's unique and highly capable HiFi sequencing technology to now include access to the epigenome, a second layer of genomic information often left unexplored due to fundamental limitations of common sequencing technologies. PacBio's single-molecule approach provides a much more holistic view of molecular behavior during sequencing. Subtle patterns in this rich information allow detection of modified bases in native DNA during standard HiFi sequencing. As a result, scientists gain access to the epigenome with zero additional cost, effort, or complexity. This advance will unlock important new opportunities across a broad range of applications in fundamental and applied biological science.

This update also includes a wide range of workflow improvements to enhance customer experience, such as simplified, unified, and accelerated library preparation workflows and consumables, live instrument performance monitoring, and on-instrument analysis support for recombinant adeno-associated virus (AAV) genome sequencing, a rapidly growing biopharmaceutical application relevant to gene therapy and vaccine development research.

"With each product release we continue to improve the utility and value of the Sequel II and Ile platform, providing researchers with unique capabilities that differentiate PacBio HiFi sequencing from all other sequencing technologies," said Christian Henry, President and Chief Executive Officer of PacBio. "Our latest enhancements to the Sequel II and Ile platform, including 5-base sequencing and improved workflows are expected to both simplify the ability to generate high quality data and enable deeper insights into the complexity of the genome."

"Multiple tests are currently required to evaluate rare disease cases for sequencing and methylation variation. HiFi sequencing has the potential to change that by measuring both genetic and epigenetic variation across the full genome in a single experiment. We have had success using 5-base HiFi sequencing at Children's Mercy Kansas City to identify abnormal methylation in repeat expansion cases, and we plan to apply it to all the future genomes we sequence. It is exciting to access another aspect of the genome without needing to change sample handling or sequencing procedures," said Emily Farrow, PhD, CGC, Director of Laboratory Operations at Children's Mercy Kansas City and Associate Professor of Pediatrics at University of Missouri Kansas City School of Medicine.

"We found that the CpG methylation patterns detected in tomato and maize genomes using HiFi sequencing are highly concordant to standard bisulfite sequencing but bring power to resolve transposable elements and other sequences that are out of reach with short reads. When combined with the incredible capabilities of HiFi sequencing for genome assembly and variation analysis, this creates an unmatched opportunity for ultra-high-quality genome and epigenome analysis of plant and vertebrate genomes from a single datatype," said Michael Schatz, PhD, Bloomberg Distinguished Professor of Computer Science and Biology at Johns Hopkins University.

PacBio's HiFi sequencing technology offers a comprehensive view of genomes and transcriptomes. But DNA contains much more information subtly encoded as "epigenetic" modifications to DNA bases. This epigenome influences how genes are expressed and plays a major role in determining biological function in both health and disease. Historically, access to the epigenome has been difficult and required sacrifices in read lengths, accuracy, and completeness while adding workflow complexity. By including automatic detection of the key modified base in humans and many other species (5mC in CpG motifs) PacBio sequencing technology provides access to the combined genome and epigenome without sacrificing read lengths, accuracy, or completeness, and without requiring additional workflow steps.

Streamlining workflows is a key focus for PacBio, and this latest update makes it easier to perform HiFi sequencing. The company's new SMRTbell prep kit 3.0 is capable of reducing workflow time for whole-genome sequencing applications by 50 percent or more and reducing required DNA inputs by 40 percent (to three micrograms per human genome). SMRTbell prep kit 3.0 is suitable for a wide range of applications and supports automation and batch processing of samples. PacBio also introduced a new single-reaction sequencing plate and SMRT Cell 8M tray that better enables customers to run samples at their convenience.

For more information about the PacBio Sequel IIe System and new enhancements, visit <https://www.pacb.com/products-and-services/sequel-system/latest-system-release/>

About PacBio

Pacific Biosciences of California, Inc. (NASDAQ: PACB) is empowering life scientists with highly accurate sequencing platforms. The company's innovative instruments are based on Single Molecule, Real-Time (SMRT®) Sequencing technology, which delivers a comprehensive view of genomes, transcriptomes, and epigenomes, enabling access to the full spectrum of genetic variation in any organism. Cited in thousands of peer-reviewed publications, PacBio® sequencing systems are in use by scientists around the world to drive discovery in human biomedical research, plant and animal sciences, and microbiology. For more information, please visit www.pacb.com and follow [@PacBio](https://twitter.com/PacBio).

PacBio products are provided for Research Use Only. Not for use in diagnostic procedures.

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All forward-looking statements speak only as of the date of this press release and are based on current expectations and involve a number of assumptions, risks and uncertainties that could cause the actual results to differ materially from such forward-looking statements. Readers are strongly encouraged to read the full cautionary statements contained in PacBio's filings with the Securities and Exchange Commission, including the risks set forth in the company's Forms 8-K, 10-K, and 10-Q. PacBio disclaims any obligation to update or revise any forward-looking statements.

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