

Pacific Biosciences Releases New DNA Sequencing Chemistry to Enhance Read Length and Accuracy for the Study of Human and Other Complex Genomes

New Chemistry Boosts Accuracy and Increases Average Read Length to 10,000 to 15,000 Bases Accelerating Innovative Genomic Research

MENLO PARK, Calif., Oct. 15, 2014 (GLOBE NEWSWIRE) -- Pacific Biosciences of California, Inc., (Nasdaq:PACB) provider of the PacBio[®] RS II DNA Sequencing System, today announced the release of new chemistry and software designed to enhance the performance and output of the platform by 45%. The latest release increases read length and improves accuracy to further accelerate innovative genomic research in complex organisms such as humans, plants, and animals.

The new release, P6-C4, which represents the company's 6th generation of polymerase and 4th generation chemistry, further extends the industry's leading average read length to 10,000 - 15,000 bases, with the longest reads exceeding 40,000 bases.

The throughput with the new chemistry is expected to be between 500 million to 1 billion bases per SMRT[®] Cell, depending on the sample being sequenced. By providing an increasing number of longer reads per instrument run, the new chemistry enables users to assemble genomes to a higher quality.

A complete genome is an extremely valuable tool in many types of scientific research, yet most organisms do not have their complete genome assembled — including humans. Instead, complex genomes are only partially completed with difficult repetitive regions and longer structural variants excluded from the assembly, resulting in highly fragmented, incomplete genomes. To sequence the complete genome of an organism, very long sequencing reads are required to span these regions, which can be critical in understanding gene function. This missing information is becoming increasingly recognized as important to a full understanding of any organism. The ability of Single Molecule, Real-Time (SMRT) Sequencing to generate ultra-long reads with unbiased coverage allows researchers to characterize previously undetected structural variants, highly repetitive regions, and distant genetic elements.

Among users with early access to the chemistry are researchers sequencing large genomes including Macrogen, who recently purchased multiple PacBio instruments to *de novo* assemble a Korean human genome to establish a better reference and expand their service offering.

The P6-C4 chemistry will replace the P5-C3 chemistry and is recommended for all SMRT Sequencing applications, including *de novo* assembly, targeted sequencing, isoform sequencing, minor variant detection, scaffolding, long-repeat spanning, SNP phasing, and structural variant analysis.

This new release also includes improvements to the SMRT Analysis software suite for long amplicon analysis and the Iso-S e q¹ method. Together with chemistry enhancements, these advances boost accuracy, speed up analysis, and support sequencing of multiplexed amplicons of different sizes.

"The performance of this new chemistry reflects our commitment to consistently deliver significant improvements in throughput and accuracy to our expanding user base," said Kevin Corcoran, Senior Vice President of Market Development at Pacific Biosciences. "With the longest reads now exceeding 40,000 bases, SMRT Sequencing is rapidly becoming the go-to platform for phasing complex genomic regions like full-length HLA genes, and generating gold-standard genome assemblies."

Researchers attending the 2014 American Society of Human Genetics annual meeting in San Diego can attend a workshop on October 21 from 12:30-2:00 p.m. titled "A New Look at the Human Genome - Novel Insights with Long-read PacBio[®] Sequencing" to learn more about the PacBio RS II and hear from customers who are using the system.

More information about the PacBio RS II and the latest product enhancements is available at: <u>www.pacb.com</u>.

About Pacific Biosciences

Pacific Biosciences of California, Inc. (Nasdaq:PACB) offers the PacBio RS II DNA Sequencing System to help scientists solve genetically complex problems. Based on its novel Single Molecule, Real-Time (SMRT) technology, the company's products enable: targeted sequencing to more comprehensively characterize genetic variations; de novo genome assembly to more fully identify, annotate and decipher genomic structures; and DNA base modification identification to help characterize epigenetic regulation and DNA damage. By providing access to information that was previously inaccessible, Pacific Biosciences enables

scientists to increase their understanding of biological systems. More information is available at www.pacb.com

Forward Looking Statements

All statements in this press release that are not historical are forward-looking statements, including, among other things, statements relating to the current or future performance of products and product enhancements, future uses of the Company's products and other future events. You should not place undue reliance on forward-looking statements because they involve known and unknown risks, uncertainties and other factors that are, in some cases, beyond the Company's control and could materially affect actual results. Factors that could materially affect actual results can be found in our filings with the Securities and Exchange Commission, including our most recent reports on Forms 10-K and 10-Q, and include those listed under the caption "Risk Factors." The Company undertakes no obligation to update forward-looking statements.

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