Highly Accurate SMRT Sequencing for Human Genetics to Be Showcased at ASHG 2019 Annual Meeting

October 10, 2019

MENLO PARK, Calif., Oct. 10, 2019 (GLOBE NEWSWIRE) -- Pacific Biosciences of California, Inc. (Nasdaq:PACB), a leading provider of high-quality sequencing of genomes, transcriptomes and epigenomes, today announced that more than 50 presentations will include data from the company's Single Molecule, Real-Time (SMRT®) sequencing platforms at next week's American Society for Human Genetics (ASHG) 2019 annual meeting in Houston. These presentations include conference talks, posters, an educational workshop, and exhibit hall demonstrations.

PacBio will host a workshop titled "Accurate and Affordable Long-Read Sequencing of Human Genomes on the Sequel ® II System," which will take place on Wednesday, October 16, 2019 from 12:45 p.m. to 2:00 p.m. in Lanier Ballroom AB at the Hilton Americas-Houston hotel. The program will be hosted by Chief Scientific Officer Jonas Korlach, PhD, and will update attendees on the latest Sequel II software and chemistry release for highly accurate long-read sequencing. Speakers at the workshop include:

- Shawn Levy, PhD, Faculty Investigator, Genomic Services Laboratory, HudsonAlpha Institute for Biotechnology, who will share information about the Institute's adoption of PacBio human whole-genome sequencing for multiple on-going human genetics projects – including the NIH-funded Clinical Sequencing Exploratory Research (CSER) project.
- Naomichi Matsumoto, MD, PhD, Chair of Human Genetics at Yokohama City University, who will discuss the use of PacBio long-read sequencing for disease genome analysis.
- Emily Hatas, Senior Director of Business Development at PacBio, who will present information about the latest advancements in SMRT Sequencing for human genetics research, including the new Sequel II Consumables 2.0 and SMRT Link v8.0 release, and ways users can now detect structural variants for up to two ~3Gb genomes, or characterize alternative splicing across a whole transcriptome, with just one SMRT Cell 8M.

Interested attendees can pre-register for the workshop.

"We are looking forward to sharing our latest product updates and scientific advances with the human genetics community, which will allow them to sequence human genomes and transcriptomes with confidence," said Dr. Korlach. "Through our workshop and other presentations, attendees will be able to see the power of SMRT Sequencing for *de novo* genome assembly, targeted sequencing, isoform sequencing and variant detection, including finding important structural variants."

The following podium and poster presentations represent a selection of the more than 50 presentations that will include SMRT Sequencing data, which represents a doubling over the number last year.

Platform Presentations:

- #57 on Wednesday, 10/16 at 5:30 p.m.: "Single-cell isoform RNA sequencing characterizes isoforms in thousands of cerebellar cells," by Hagen Tilgner, PhD, from Weill Cornell Medicine.
- #221 on Thursday, 10/17 at 4:15 p.m.: "A robust and production-level approach to haplotype-resolved assembly of single individuals," moderated by Avery Davis Bell from Harvard Medical School and Joanna Kaplanis, from the Wellcome Sanger Inst, Hinxton, UK.
- #223 on Thursday, 10/17 at 4:15 p.m.: "Long-read single molecule, real-time (SMRT) sequencing of NUDT15: Phased full gene haplotyping and pharmacogenomic allele discovery," with Yao Yang, PhD, from the Icahn School of Medicine at Mount Sinai.
- #313 on Saturday, 10/19 at 9 a.m.: "Incorporating long transcriptomic data into GENCODE," with Jane Loveland, PhD, from European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, United Kingdom.

Poster Presentations:

- Poster #1068: "Comprehensive structural and copy-number variant detection with long reads," by Aaron Wenger, PhD, of PacBio.

- Poster #1455: “Full-length RNA-seq of Alzheimer brain sample on the PacBio Sequel II platform,” by Elizabeth Tseng, PhD, of PacBio.

- Poster #1692: “High-quality human genomes achieved through HiFi sequence data and FALCON-Unzip Assembly,” by Zev Kronenberg, PhD, of PacBio.

- Poster #1866: “Detection and phasing of small variants in Genome in a Bottle samples with highly accurate long reads,” by William Rowell of PacBio.

Other scientific program highlights featuring SMRT Sequencing include the CoLab Session on Friday, October 18 at 10:00 a.m. in Theater 3, where ASHG meeting attendees will have the opportunity to hear from PacBio scientists on the exhibit hall floor in the session “PacBio Sequel II System: Structural Variants and Whole Transcriptome in 1 SMRT Cell Each.” The session will include talks on whole genome sequencing for structural variation discovery and Iso-Seq® Analysis. Attendees can also visit PacBio at booth #1020.

PacBio will be sponsoring a grant program for scientists interested in a chance to win free SMRT Sequencing for their human genetics sequencing projects, including scientists who are not attending this year’s ASHG annual meeting. For more information visit www.pacb.com/smrtgrant.

About Pacific Biosciences

Pacific Biosciences of California, Inc. (NASDAQ:PACB) offers sequencing systems to help scientists resolve genetically complex problems. Based on its novel Single Molecule, Real-Time (SMRT®) technology, Pacific Biosciences’ products enable: de novo genome assembly to finish genomes in order to more fully identify, annotate and decipher genomic structures; full-length transcript analysis to improve annotations in reference genomes, characterize alternatively spliced isoforms in important gene families, and find novel genes; targeted sequencing to more comprehensively characterize genetic variations; and real-time kinetic information for epigenome characterization. Pacific Biosciences’ technology provides high accuracy, ultra-long reads, uniform coverage, and the ability to simultaneously detect epigenetic changes. PacBio® sequencing systems, including consumables and software, provide a simple, fast, end-to-end workflow for SMRT Sequencing. 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 product updates or enhancements, upcoming conference presentations, the attributes of the Sequel II System, the future availability, uses, accuracy, quality or performance of, or benefits of using, products or technologies, the suitability or utility of methods, products or technologies for particular applications, studies or projects, the importance of long-read sequencing data, and other future events. You should not place undue reliance on forward-looking statements because they involve known and unknown risks, uncertainties, changes in circumstances and other factors that are, in some cases, beyond Pacific Biosciences’ control and could cause actual results to differ materially from the information expressed or implied by forward-looking statements made in this press release. Factors that could materially affect actual results can be found in Pacific Biosciences’ most recent filings with the Securities and Exchange Commission, including Pacific Biosciences’ most recent reports on Forms 8-K, 10-K and 10-Q, and include those listed under the caption “Risk Factors.” Pacific Biosciences undertakes no obligation to revise or update information in this press release to reflect events or circumstances in the future, even if new information becomes available.

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