

BIONANO GENOMICS TO MAP HUMAN GENOME AT AGBT 2014

Irys System to Create a High Resolution Genome Map for Genome in a Bottle Consortium

SAN DIEGO and MARCO ISLAND, Fla. — Feb. 10, 2014—BioNano Genomics announced today that they will map a human genome *de novo* during the 15th Annual Advances in Genome Biology and Technology (AGBT) meeting, which will be held February 12 to 15 in Marco Island, Florida. During the four days of the conference, BioNano will use the Company's IrysTM System to produce a high-resolution genome map for the Genome in a Bottle Consortium. High-resolution genome maps are essential for the precise assembly of DNA sequences, completion of large genomes and understanding of genomic variation. As DNA sequencing methods move into clinical applications, comprehensive detection of all genome variation will be essential to reach the sensitivity and specificity required for diagnostics.

BioNano will hold a limited number of private viewings during the conference as well as open house sessions during conference breaks in Lanai Suite 183 of the Marco Island Marriott Resort. To inquire about availability of private viewings and schedule a session, email info@bionanogenomics.com.

"Large structural variations account for significantly more base pair differences than SNPs and small indels in the population and thus contribute meaningfully to genetic diversity and complex trait diseases. Methods in widespread use today, however, cannot comprehensively and effectively detect them and thus fail to provide sufficient, unambiguous information in complex large genomes," said Han Cao, Ph.D., founder and chief scientific officer of BioNano Genomics.

Dr. Cao continued, "While the price to generate short read sequences have decreased, the bottleneck has been in the labor-intensive approaches to genome assembly, annotation, and structural variation analysis. BioNano's Irys System streamlines the process by providing a high-quality genome map, upon which DNA sequences can quickly and accurately be organized, and provides a single platform to perform large, comprehensive structural variation studies."

Genome maps built with the Irys System reveal the biologically and clinically significant order and orientation of functionally relevant components of complex genomes, including genes, promoters, regulatory elements as well as the length and location of long areas of repeats across the entire genome. Assembling such a comprehensive view of a genome has previously been a major hurdle because information about repetitive elements and structural variations are lost with next generation sequencing (NGS) methods.

"The Genome in a Bottle Consortium was started because comparing the outputs of different sequencing and bioinformatics analysis methods have shown confusing variant information at up to hundreds of thousands of positions across the human genome, which makes it impossible to determine how variants are relevant to disease," said Todd Dickinson, Ph.D., vice president, Global Commercial Operations of BioNano Genomics.

Dr. Dickinson continued, "By using the Irys System to generate a high resolution genome map for Genome in a Bottle, we can resolve the variant information generated by next generation sequencing



platforms, as well as reveal new, previously undetected variants, to enable clinically useful genomic information."

The National Institute of Standards and Technology (NIST) organized the Genome in a Bottle Consortium to develop the reference materials, reference data, and reference methods needed to assess performance of human genome sequencing.

About Irys

Irys makes it possible to routinely and accurately detect genomic structural variation and to finish genome assemblies. The fully automated Irys benchtop instrument uses the IrysChip to uncoil and confine long DNA molecules in proprietary Nanochannel Arrays™ where they are uniformly linearized in a highly parallel display for high-resolution, single-molecule imaging. Irys does not employ DNA fragmentation or amplification, which are typical with next-generation sequencing. The result is sequence information over extremely long "reads" ranging from hundreds of kilobases to a megabase, where the sample's valuable structural information is preserved. Irys makes it possible for researchers to directly observe structural variants including replications, deletions, translocations and inversions.

About BioNano Genomics

Headquartered in San Diego, BioNano Genomics is delivering an altogether better way of gaining a fully informed understanding of genomes. The Company's platform provides researchers and clinicians the most comprehensive, organized and actionable picture of a genome with unprecedented insights into how the individual components of genomes are ordered, arranged, and interact with each other. BioNano Genomics works with institutions in life science, translational research, molecular diagnostics and personalized medicine. The Company is supported by private investors and grant funding from genomics programs at federal agencies, including the NIH and NIST-ATP.

www.BioNanoGenomics.com

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