Bionano Genomics' Structural Variation Data Featured In Many Scientific Presentations at the ASHG 2017 Annual Meeting

Scientists will present Bionano genome mapping studies across large populations that identify structural variations in genetic disease and cancer

SAN DIEGO, Oct. 09, 2017 (GLOBE NEWSWIRE) -- Bionano Genomics, the structural variation company, announces a series of presentations at the upcoming American Society of Human Genetics (ASHG) Annual Meeting, October 17 to 21 in Orlando, Florida. Bionano will present Saphyr™, its most advanced system for genome mapping. Saphyr has roughly 10 times the throughput of its predecessor, allowing the system to generate sufficient data in one day to map up to two human genomes. This increase in throughput enables larger scale studies like the ones presented at this conference.

Erik Holmlin, Ph.D., CEO of Bionano, commented, "The last year saw a significant increase in the uptake of Bionano mapping in human genetic disease and cancer research. Scientists are understanding the importance of structural variation and realizing the inherent limitations of sequencing to find these large variants. We are thrilled to see Saphyr enabling the adoption of our technology for translational studies across populations and to see that Bionano mapping was able to identify disease causing variants for patients with genetic diseases for whom whole genome sequence wasn't able to do so."

Bionano will be hosting an Exhibitor Event led by prominent genomics researchers, Dr. Jim Broach from Penn State University, Dr. Vanessa Hayes from the Garvan Institute, and Dr. Hayk Barseghyan from Children's National Medical Center. The discovery of structural variations using Bionano mapping in cancer and other genetic diseases will be presented.

Bionano will be onsite at Booth #555 to further discuss Bionano mapping, Saphyr, and findings presented during the various sessions.

Over a dozen different scientists are presenting Bionano data including:

Bionano Workshop:

Solved with Bionano: How Order and Orientation Help Understand Genetic Disease.

Presenting Authors:	Jim Broach, Vanessa Hayes and Hayk Barseghyan
Date, Time:	Friday, October 20, 1:00 pm – 2:15 pm
Location:	Hilton Orlando, Lake Mizell, Lobby Level

Oral Presentations:

Oral Session 80: Next-Generation Mapping (NGM): A novel approach for genetic diagnosis of structural variants.

Presenting Author:	Hayk Barseghyan
Session:	#18: Strategies for Variant Interpretation
Date, Time:	Wednesday, October 18, 1:45 am – 12:00 pm
Location:	Room 230G – Level 2/Convention Center

Oral Session 26: Single-molecule mapping of complex genomic regions across 26 human populations reveals population specific variation patterns.

Presenting Author: Pui-Yan Kwok
Session: #9: Genome Structure and Function: The Contribution of M
Date, Time: Wednesday, October 18, 9:45 am – 10 am
Location: Room 230G - Level 2/Convention Center

Poster Presentations:

Poster #808/W: Optical mapping reveals a higher level of chained fusion events in human cancer.
Presenting Author: Vanessa Hayes, Ph.D., Lab Head of Human Comparative and Prostate Cancer Genomics, Garvan Institute of Medical Research
Session: Cancer Genetics
Date/Time: Wednesday, October 18, 3 pm – 4 pm

Poster #1032/F: Combining Bionano and exome sequencing identifies a homozygous structural variation in the novel AGBL3 gene underlying microcephaly.
Presenting Author: Denice Belandres
Session: Mendelian Phenotypes
Date/Time: Friday, October 20, 12:30 pm – 1:30 pm

Poster #946/W: Characterization of a complex translocation causing 3q28ter duplication and 10q26.2ter deletion in a child with self-injurious behavior.
Presenting Author: Ikeoluwa Adeshina
Session: Mendelian Phenotypes
Date/Time: Wednesday, October 18, 3 pm – 4 pm.

Poster #1332/F: An alignment-based approach for sensitively detecting SVs using optical maps data.
Presenting Author: Xian Fan
Session: Bioinformatics and Computational Approaches
Date/Time: Friday, October 20, 12:30 pm – 1:30 pm

Poster #1487/T: Disease Relevant Structural Variation Analysis by Bionano Mapping.
Presenting Author: Alex Hastie
Session: Omics Technologies
Date/Time: Thursday, October 19, 2:00 pm – 3:00 pm

Poster # 1520/T: Automation of Ultra-High Molecular Weight DNA Isolation and Labeling for Genome Mapping.
Presenting Author: Pat Lynch
Session: Omics Technologies
Date/Time: Thursday, October 19, 3:00 pm – 4:00 pm

Poster #2582/T: Structural variant detection with optical mapping and microfluidic partitioning: A t(9;13) case report.
Presenting Author: Dustin Baldridge
Session: Molecular and Cytogenetic Diagnostics
Date/Time: Thursday, October 19, 3:00 pm – 4:00 pm

Poster # 788/T: Use of Bionano Genome Maps to Identify Medically-Relevant Genomic Variation.
Presenting Author: Andy Pang
Session: Cancer Genetics
Date/Time: Thursday, October 19, 3:00 pm – 4:00 pm

More information about Bionano Genomics is available at www.bionanogenomics.com and in our newly released blog **Bionano U** at www.bionanogenomics.com/bionano-university/.

About Bionano Genomics

Bionano Genomics, Inc. provides the Irys® and Saphyr™ systems for Bionano Genome Mapping, which is the leading solution in physical genome mapping. Bionano mapping offers customers whole genome analysis tools that reveal true genome structure and enable researchers to capture what's missing in their data to advance human, plant and animal genomic research. Bionano genome mapping uses NanoChannel arrays to image DNA at the single-molecule level with average single-molecule lengths of about 350,000 base pairs, which leads the genomics industry. The long-range genomic information obtained with Bionano mapping detects and deciphers structural variations (SVs), which are large, complex DNA segments involving repeats that are often missed by sequencing technologies and which are a leading cause of inaccurate and incomplete genome assembly. As a stand-alone tool, Bionano mapping enables the accurate detection of SVs, many of which have been shown to be associated with human disease as well as complex traits in plants and animals. As a complementary tool to next-generation sequencing (NGS), Bionano mapping integrates with sequence assemblies to create contiguous hybrid scaffolds for reference-quality genome assemblies that reveal the highly informative native structure of the chromosome. Bionano mapping also provides the additional ability to verify, correct and improve a NGS-generated genome assembly.

Only Bionano provides long-range genomic information with the cost-efficiency and high throughput to keep up with advances in NGS.

Bionano mapping has been adopted by a growing number of leading institutions around the world, including: National Cancer Institute (NCI), National Institutes of Health (NIH), Wellcome Trust Sanger Institute, BGI, Garvan Institute, Salk Institute, Mount Sinai and Washington University. Investors in the Company include Domain Associates, Legend Capital, Novartis Venture Fund and Monashee Investment Management.

For more information, please visit www.BionanoGenomics.com. Notes: Bionano Genomics is a trademark of Bionano Genomics, Inc. Any other names of actual companies, organizations, entities, products or services may be the trademarks of their respective owners.

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