

Bionano Genomics' Structural Variation Results Presented at ASHG 2018 Provide Insights in Cancer and Genetic Disease

SAN DIEGO, Oct. 16, 2018 (GLOBE NEWSWIRE) -- Bionano Genomics, Inc. (NASDAQ: BNGO), a life sciences instrumentation company that develops and markets Saphyr, a platform for ultra-sensitive and ultra-specific structural variation detection in genome analysis, announces a series of presentations at the upcoming American Society of Human Genetics (ASHG) Annual Meeting, October 16 to 20 in San Diego, California.

Erik Holmlin, Ph.D., CEO of Bionano, commented, "In a record number of presentations this year at ASHG, scientists and clinicians are showing critical structural variants identified with Saphyr. They show complex genome rearrangements that lead to genetic disease, reference genomes assembled with Bionano and tumor variants detected in low allelic fraction. Furthermore, Bionano scientists are presenting improvements to our sample prep, data analysis and visualization, making it easier and faster to get a comprehensive view of all structural variants, even in complex, heterogeneous cancer samples. It is increasingly clear that Bionano genome mapping is an essential tool to call the variants that impact genomes."

Bionano will be hosting a workshop led by prominent clinical genomics researchers, Dr. Mike Friez from Greenwood Genetic Center, Dr. Hayk Barseghyan from Children's National Medical Center, and Dr. Vanessa Hayes from the Garvan Institute. The discovery of structural variations using Bionano mapping in cancer and other genetic diseases will be presented.

Bionano will be onsite at Booth #526 to discuss Bionano mapping, Saphyr, and findings presented during the various sessions.

Over a dozen different scientists are presenting Bionano data:

Bionano Workshop:

- ▮ **Reveal Structural Variation with Bionano: Insights into Cancer and Genetic Disease**
Presenting Authors: Sven Bocklandt, Mike Friez, Hayk Barseghyan, Vanessa Hayes
Date, Time: Thursday, October 18, 12:30 pm – 1:45 pm
Location: Room 29CD - Upper Level/San Diego Convention Center

Platform Presentation:

- ▮ **Structural variation and its impact on 3D genome structure in cancer cells.**
Presenting Author: Jie Xu, Penn State University
Date, Time: Saturday, October 20, 9:15 am – 9:30 am
PgmNR: 298
Location: Room 6B – Upper Level/San Diego Convention Center

Poster Presentations:

- ▮ **Solution-based Isolation of Ultra-High Molecular Weight Genomic DNA from 0.2-0.5 mL of Frozen Human Blood (1.5 million WBCs) in less than 3 Hours.**
Presenting Author: Henry Sadowski, Bionano Genomics
Date, Time: Wednesday, October 17, 2:00 pm – 3:00 pm
PgmNR: 1767/W
- ▮ **Structural complexity at 3q29 locus: Contributions of genomic architecture to genomic disorders.**
Presenting Author: Trenell Mosley, Emory University
Date, Time: Wednesday, October 17, 2:00 pm – 3:00 pm
PgmNR: 433/W
- ▮ **Long-read single-molecule maps of the hydroxymethylome.**
Presenting Author: Yuval Ebenstein, Tel Aviv University
Date, Time: Wednesday, October 17, 3:00 pm – 4:00 pm
PgmNR: 1788/W
- ▮ **Nanobind magnetic disks for rapid high MW DNA extraction and library preparation in long-read sequencing and optical mapping applications.**
Presenting Author: Kelvin Liu, Circulomics
Date, Time: Wednesday, October 17, 3:00 pm – 4:00 pm
PgmNR: 1806/W
- ▮ **Hybrid scaffolding of optical maps provides high contiguity and corrects errors in sequence assemblies.**
Presenting Author: Joyce Lee, Bionano Genomics
Date, Time: Thursday, October 18, 2:00 pm – 3:00 pm
PgmNR: 1447/T
- ▮ **Composite de novo Armenian human genome assembly and haplotyping via optical mapping and ultra-long read sequencing.**

Presenting Author: Hayk Barseghyan, Children's National Medical Center
Date, Time: Thursday, October 18, 2:00 pm – 3:00 pm
PgmNR: 419/T

1 **nanotatoR: An annotation tool for next generation mapping.**

Presenting Author: Surajit Bhattacharya, Children's National Medical Center
Date, Time: Thursday, October 18, 3:00 pm – 4:00 pm
PgmNR: 1408/T

1 **How well can you detect structural variants: Towards a standard framework to benchmark human structural variation.**

Presenting Author: Justin Zook, National Institute of Standards and Technology
Date, Time: Thursday, October 18, 3:00 pm – 4:00 pm
PgmNR: 1648/T

1 **A next-generation mapping approach for the assembly and detection of structural variation within genomic regions containing complex segmental duplications.**

Presenting Author: Feyza Yilmaz, University of Colorado Denver
Date, Time: Thursday, October 18, 3:00 pm – 4:00 pm
PgmNR: 1750/T

1 **Building human reference genomes for Africa.**

Presenting Author: Martin Pollard, Wellcome Sanger Institute
Date, Time: Friday, October 19, 2:00 pm – 3:00 pm
PgmNR: 2771/F

1 **Comprehensive detection of germline and somatic structural mutations in cancer genomes.**

Presenting Author: Andy Pang, Bionano Genomics
Date, Time: Friday, October 19, 2:00 pm – 3:00 pm
PgmNR: 911/F

1 **A novel approach for structural variant calling: Combining data from whole genome next-generation sequencing and optical mapping.**

Presenting Author: Yuval Porat, Genoox
Date, Time: Friday, October 19, 2:00 pm – 3:00 pm
PgmNR: 1643/F

1 **Sensitive detection of low-allele fraction structural variants in clinical cancer samples.**

Presenting Author: Ernest Lam, Bionano Genomics
Date, Time: Friday, October 19, 3:00 pm – 4:00 pm
PgmNR: 1544/F

1 **Amplicon Reconstructor: Optical mapping aids the reconstruction of complex, large cancer genome rearrangements.**

Presenting Author: Jens Luebeck, UC San Diego
Date, Time: Friday, October 19, 3:00 pm – 4:00 pm
PgmNR: 824/F

1 **Detection of gross rearrangements in BRCA1 by next generation mapping and long read technologies.**

Presenting Author: Michael Bonin, IMG M Laboratories GmbH
Date, Time: Friday, October 19, 3:00 pm – 4:00 pm
PgmNR: 902/F

1 **Advancing genetic diagnosis of facioscapulohumeral muscular dystrophy via next generation genome mapping technology.**

Presenting Author: Yi-Wen Chen, Children's National Health System
Date, Time: Friday, October 19, 3:00 pm – 4:00 pm
PgmNR: 2954/F

1 **Latest improvements in the human genome reference assembly (GRCh38).**

Presenting Author: Tayebah Rezaie, NCBI, National Institutes of Health
Date, Time: Friday, October 19, 3:00 pm – 4:00 pm
PgmNR: 444/F

More information about Bionano Genomics is available at www.bionanogenomics.com

About Bionano Genomics

Bionano is a life sciences instrumentation company in the genome analysis space. The Company develops and markets the Saphyr system, a platform for ultra-sensitive and ultra-specific structural variation detection that enables researchers and clinicians to accelerate the search for new diagnostics and therapeutic targets and to streamline the study of changes in chromosomes, which is known as cytogenetics. The Saphyr system comprises an instrument, chip consumables, reagents and a suite of data analysis tools.

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