

Bionano Genomics Highlights Five Studies at PAG XXV Demonstrating How Next-Generation Mapping Improves Assembly of and Structural Variation Detection in Complex Plant and Animal Genomes

SAN DIEGO, CA – January 16, 2017 – Bionano Genomics, the leader in physical genome mapping, highlighted results from five studies demonstrating how using next-generation mapping (NGM) reveals true genome structure as well as improves the assembly of complex plant and animal genomes. The results are being presented this week in posters and workshops at the International Plant & Animal Genome (PAG) XXV Conference in San Diego, California.

Erik Holmlin, Ph.D., CEO of Bionano, commented, “Collectively, results from these five studies demonstrate how NGM overcomes challenges of sequencing technologies to facilitate actionable breakthroughs for researchers of complex plant and animal genomes. Large-scale structural variations detected by NGM accelerate research to solve significant challenges in the agricultural field related to pest resistance, climate change, population growth and decreasing energy resources. We look forward to discussing with researchers at PAG XXV how NGM is an essential tool to find what’s missing in their research.”

Results from five of the studies being presented include:

Poster [P0837](#): Structural Variation of a Wheat Chromosome Arm Revealed By Optical Mapping

Presenting Author:	Zuzana Tulpova, Institute of Experimental Botany
Poster Category:	29. Genome Mapping, Tagging & Characterization: Wheat, Barley, Oat, and related
Date, Time:	Monday, January 16 th ; 3:00 – 4:30 p.m. PST

The study shows that Bionano’s NGM provides an affordable approach to validate and improve DNA sequence assemblies and to study structural variations (SVs) among individuals, cultivars or species. Researchers used NGM to generate genome maps with N50 of 1.3 Mb for lines of two bread wheat accessions, Chinese Spring (CS) and CI2401. Alignment of the optical maps to a reference genome (‘Chinese Spring’ by IWGSC) revealed significant variability in various regions. Comparison of Bionano’s maps spanning the region disclosed an 8-kb insertion in the proximity of a candidate gene in the susceptible reference genome, and the variable regions will next be scrutinized on the sequence level.

Poster [P1107](#): Comparative Genomics of *Drosophila melanogaster* using Bionano Optical Maps

Presenting Author:	Carrie R. Evans, Brigham Young University
Poster Category:	38. Genome Mapping, Tagging & Characterization: Insects
Date, Time:	Monday, January 16 th ; 3:00 – 4:30 p.m. PST

Using NGM, researchers constructed a genome map of multiple strains of the model organism *Drosophila melanogaster*, the common fruit fly typically difficult to sequence due to the complexity of its genome structure. Researchers compared the NGM maps to sequence-based maps to verify chromosome integrity and to identify SVs and regions of the genomes that may have been previously assembled incorrectly.

Ultimately, these NGM-identified SVs will be used to enhance understanding of the evolutionary history of *Drosophila melanogaster*.

Poster [P0718](#): Comparative Structural Genomics of Maize Inbred Lines B73 and Mo17

Presenting Author: Pierre A Migeon, Kansas State University Department of Plant Pathology and Interdepartmental Genetics
Poster Category: 25. Genome Mapping, Tagging & Characterization: Maize, Sorghum, Millet, Sugar Cane, and related
Date, Time: Monday, January 16th; 10:00 – 11:30 a.m. PST

The study used Bionano's NGM to detect and quantify large SVs – which cannot be reliably detected with other technologies – by generating highly contiguous optical maps for maize inbred lines B73 and Mo17. Researchers concurrently analyzed fixed-length substrings of size k (k-mers) derived from near-raw sequencing data for both lines in order to generate a base-pair resolution snapshot of highly repetitive and variable elements.

Poster [P0041](#): Toward a Better Understanding of Plant Genomes Structure: Combining NGS and Optical Mapping Technology to Improve the Sunflower Assembly

Presenting Author: Celine Chantry Darmon, French Plant Genomic Resources Center (CNRGV)
Poster Category: 3. Genome Technology: Other Genome Methodology
Date, Time: Monday, January 16th; 3:00 – 4:30 p.m. PST

The study demonstrates how Bionano's NGM enables the rapid construction of physical whole genome maps for assembly of complex plant genomes – which have remained challenging despite advances in NGS technologies – and for comparison of SVs in different genotypes. Researchers will present the improvement of the sunflower genome assembly using hybrid scaffolding, which combined BioNano's NGM and PacBio's sequencing.

Poster [P0506](#): Multiple Alignment of Optical Mapping Facilitates Typing in Complex Regions

Presenting Author: Claire Yik-Lok Chung, The Chinese University of Hong Kong
Poster Category: 18. Bioinformatics: Algorithms
Date, Time: Monday, January 16th; 10:00 – 11:30 a.m. PST

Systematic analysis demonstrates how NGM is useful in improving genome assembly and large SV detection through a reference-free method based on hierarchical alignment of multiple optical map contigs. Researchers demonstrate that the method illustrated in this poster is useful in typing samples with high degree of genomic rearrangement, and that the method has a high resolving power in sample clustering, concluding that this method will facilitate comparative genomics work on animal and plants for which there is no genome reference model.

The full list of Bionano's poster presentations and workshops is available online in the downloadable [2017 Brochure on PAG Activities](#).

Learn more by visiting **Bionano's Booth # 331** at PAG XXV and visiting www.bionanogenomics.com.

About Bionano Genomics

Bionano Genomics, Inc., the leader in next-generation mapping (NGM), provides customers with genome analysis tools that advance human, plant and animal genomics and accelerate the development of clinical diagnostics. The Company's Irys® System uses NanoChannel arrays integrated within the IrysChip® 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 the Irys System helps decipher complex DNA involving repeats, which are the primary cause of inaccurate and incomplete genome assembly.

On its own, next-generation mapping with the Irys System enables detection of structural variants, many of which have been shown to be associated with human disease as well as complex traits in plants and animals. As a companion to next-generation sequencing (NGS), next-generation mapping with the Irys System integrates with sequence assemblies to create contiguous hybrid scaffolds that reveal the highly informative native structure of the chromosome.

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

The Irys System 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.

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