Data Highlighted from 3 Studies Demonstrate Complementarity of BioNano Genomics' Next-Generation Mapping to Sequencing

Over 30 studies presented at PAG XXIV Conference

SAN DIEGO, CA – January 11, 2016 – BioNano Genomics, the leader in physical genome mapping, today announced data from three studies demonstrating how next-generation mapping (NGM) using the Irys® System is a key component to elucidating complex plant and animals genomes. Results from these three studies will be presented in two poster presentations and one workshop at the International Plant & Animal Genome (PAG) XXIV Conference, being held January 9 – 13, 2016 in San Diego, California.

Erik Holmlin, Ph.D., President and Chief Executive Officer of BioNano Genomics, commented, "NGM using the Irys System facilitates better, more complete, affordable and faster genome mapping than traditional methods. Combined with sequencing results, these physical genome maps allow for the construction of better genome assemblies enabling researchers to explore hidden areas of the genome. These findings presented at the PAG conference provide a strong rationale for combining Irys NGM and sequencing information and further demonstrate the versatility of our platform in the genomics community."

Results from three of the studies being presented include:

Poster P0612 / Workshop W144: Progress Toward a Low Budget Reference Grade Genome Assembly

Presenting Author:	Benjamin D. Rosen, ARS, USDA
Poster Session:	Genome Mapping, Tagging & Characterization: Goat
Date, Time:	Monday, January 11; 10:00 – 11:30 am PT
Location:	Exhibit Hall
Workshop Session:	Cattle/Sheep/Goat
Date, Time:	Saturday, January 9; 1:50 – 2:10 pm PT
Location:	San Diego Meeting Room

Findings indicate that *de novo* assembly of the San Clemente goat genome can be conducted at a high degree of completeness and at a relatively modest cost using the combination of NGM with BioNano's Irys System and Pacific BioSciences' next-generation sequencing (NGS) technology to improve the ability to annotate challenging genomic regions, such as highly repetitive immune gene clusters. Starting with 38 million PacBio short-reads, researchers combined results from various instruments to produce an assembly of 3,110 contigs, which was scaffolded using NGM genome maps derived from a single IrysChip. Combining both technologies reduced the contigs to 333 large scaffolds. The sequence scaffolds were then reconstructed using high-throughput chromosome conformation capture sequencing (Hi-C). The study confirms that reference quality *de novo* genome assemblies are not solely the domain of large, well-funded genome projects, but can be completed in the lab cost-effectively using complementary technologies.

Poster P0241: Telomere-to-Telomere Chromosome Assemblies and Identification of Structural Variations in *Arabidopsis thaliana* Ecotypes

Presenting Author:	Florian Jupe, Salk Institute for Biological Studies & Howard Hughes Medical Institute
Poster Session:	Genome Technology: Other Genome Methodology
Date, Time:	Monday, January 11; 3:00 – 4:30 pm PT
Location:	Exhibit Hall

Results demonstrate that the Irys System can be utilized to build physical genome maps for 10 different ecotypes of *Arabidopsis thaliana*. Researchers identified over 300 structural variations (SVs) per ecotype when compared to the reference genome Col-0, which showed similarity in sties and types of SVs mainly around the centromere and evolutionary hotspots. The combination of BioNano's NGM physical maps and Pacific BioSciences' SMRT sequencing allowed the hybrid assembly of all five chromosomes of *A. thaliana* ecotype Landsberg erecta (Ler-0) into single contigs. NGM genome maps obtained from the Irys System were utilized to place PacBio scaffolds in proper order and to provide important revolutionary insights of the centromeric structure, size, and repeat versus non-repeat content. RNA sequencing was further used to identify the centromere specific transcriptome. The study shows that the combination of NGM and NGS technologies allows for the study of SVs on the whole-genome or population level, and can unfold important genomic information.

Workshop W567: Construction of Pseudomonas for the *Aegilops tauschii* Genome, the Wheat D Genome Progenitor

Presenting Author:	Ming-Cheng Luo, Department of Plant Sciences, University of California, Davis
Session # 3122:	IWGSC- Standards and Protocols
Date, Time:	Tuesday, January 12; 3:55 – 4:15 pm PT
Location:	Pacific Salon 3

The workshop discusses results obtained from generating a high quality draft reference sequence of *Aegilops tauschii,* the donor of the D genome of the hexaploid bread wheat, *Triticum aestivum*. Bread wheat is a major pillar of the global food supply, however, its reference map is not available due to its hybrid origin, complexity and enormous genome size. A comprehensive approach integrating BioNano's NGM physical maps, Illumina's whole genome shotgun sequences and Pacific BioSciences' sequencing was used to assemble the genome and ultimately construct pseudomolecules of the seven chromosomes of *Ae. tauschii*.

This work is part of the NSF-funded Project IOS-1238231 to generate a reference sequence for the genome of *Ae. Tauschii,* which can provide significant and fundamental assistance in understanding the grass genome structure, evolution and accelerating progress in genome sequencing of wheat and its relatives. A comprehensive *Ae. tauschii* genome sequence will enable the prediction of the location of genes in wheat and its relatives, enabling gene discovery and manipulation with the objective of integrating these genes into wheat by traditional breeding methods or biotechnology.

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 genomes at the single-molecule level with average single-molecule lengths of about 350,000 base pairs, which leads the industry. The long-range genomic information obtained with the Irys System helps

decipher large, complex DNA 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, 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 Genomics 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, Broad Institute of MIT and Harvard, BGI, Garvan Institute, Salk Institute, and McDonnell Genome Institute of Washington University. Investors in the Company include Battelle Ventures, Domain Associates, Legend Capital, Novartis Venture Fund, Federated Kaufmann, Monashee Investment Management, and Gund Investment Corporation.

For more information, please visit us at www.BioNanoGenomics.com.

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