

Bionano Genomics' Early-Access Customers to Present Groundbreaking Genome Assembly Data Using Bionano's New Labeling Technology at PAG XXVI Conference

39 Posters and Workshop to feature Bionano Genome Mapping Data

SAN DIEGO, Jan. 12, 2018 (GLOBE NEWSWIRE) -- Bionano Genomics, the genome mapping company, today announced multiple oral and poster presentations featuring genome assembly data generated with its upcoming new labeling technology, to be presented at the International Plant & Animal Genome (PAG) XXVI Conference, January 13 – 17, 2018 in San Diego, California. A total of 23 posters and 16 workshops will discuss genome assemblies and workflows that include Bionano genome mapping data to build the most complete and accurate genome assemblies.

Several presentations will highlight Bionano's new Direct Labeling and Staining (DLS) chemistry, to be released later this quarter. Unlike Bionano's current Nick, Label, Repair and Stain (NLRS) chemistry, which uses nickases to create a single stranded nick at sequence motifs, DLS uses an enzyme that directly labels the sequence motif. The DLS chemistry does not cause the systematic breaks (fragile sites) that were common with nicking and limited the length of genome maps. Instead, samples labeled with DLS chemistry yield intact maps that are up to chromosome-arm length and capture the linear structure, order and orientation of the genome. During an early access period with over a dozen customers, Bionano's DLS chemistry has enabled genome maps with contiguities up to 50 times greater than Bionano's previous labeling method, while maintaining the accuracy of the genome structure Bionano maps have been trusted for. Genomes generated with DLS data have reached scaffold N50s of 100 Mbp, setting a new standard for genome assembly.

Bionano's genome maps can identify structural variation between individuals, cultivars, breeds or species, and be used to build platinum quality genomes by scaffolding sequence contigs. While other scaffolding technologies improve the contiguity of sequence assemblies by adding additional layers of more complex sequence data, Bionano's *de novo* assembled genome maps build a completely sequence-independent, up to chromosome-arm length genome assembly in days for under \$1,000. Because Bionano's assemblies are built *de novo*, without sequence or reference guidance, they can uniquely validate and error correct sequence assemblies while generating genomes of the highest quality and contiguity.

Bionano's blog Bionano.U provides details for each of the 39 posters and workshops that will be presented, which include an oral presentation on DLS chemistry by a Bionano scientist (W025), and presentations by DLS early access customers from the Vertebrate Genome Project lab at Rockefeller University (P0204), and Genoscope (P0176). The Bionano presentation will feature assembly data generated with DLS on a dozen organisms such as fish, birds, wheat, maize, Brassica, mammals and human.

Warren Robinson, Chief Commercial Officer of Bionano, commented, "With the upcoming launch of our Direct Labeling chemistry, Bionano will set a new standard for genome assembly quality. The record number of presentations that include Bionano data at PAG shows that Bionano mapping is an essential tool for genome researchers. With DLS, we will greatly increase the accuracy and contiguity of plant and animal genomes, and 2018 promises to be an exciting year for Bionano and for the genome assembly community as a whole."

Learn more by visiting Bionano's Booth # 523 at the PAG XXVI and visiting <https://bionanogenomics.com/bionano-university/articles/pagxxvi/>

About Bionano Genomics

Bionano Genomics, Inc. offers whole genome analysis tools to better understand the genome and its structure. Its high-throughput system Saphyr builds *de novo* maps of the genome by massively parallel imaging of the longest single DNA molecules in the industry. Bionano genome mapping provides comprehensive structural variation (SV) calls, identifying all types of SVs with sensitivities that far exceed those based on next-generation sequencing. When combined with orthogonal sequencing data, Bionano maps can provide the correct structure, order, and orientation to assemble reference-quality genomes.

For more information, please visit www.BionanoGenomics.com

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