Users of Bionano Genomics' Saphyr System to Present Reference Genome Assembly and SV Discovery for Plant and Animal Genomes at the PAG XXVIII Conference

January 10, 2020

Presenters are scheduled to discuss Saphyr's impact for applications in plant and animal research

SAN DIEGO, Jan. 10, 2020 (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, today announced multiple oral and poster presentations at the upcoming International Plant & Animal Genome (PAG) XXVIII Conference, to be held January 11 – 15, 2020 in San Diego, California. A total of 21 posters and 13 oral presentations will discuss genome assemblies and workflows that include Bionano genome imaging data to build the most complete and accurate genome assemblies and to analyze variations of genome structure.

Data from the Saphyr system can be used to identify structural variation between cultivars, breeds or species, and 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. Because Bionano's assemblies are built *de novo*, without sequence or reference guidance, they are independent of the common sequence biases and therefore can uniquely validate sequence assemblies and correct assembly errors, while generating genomes of the highest quality and contiguity.

Erik Holmlin, Ph.D., CEO of Bionano, commented, "With record participation this year at PAG XXVIII, scientists are showing how data from the Saphyr system drives the assembly of reference-quality genomes and enables the sensitive detection of structural variations. Scientists from Bionano are further presenting improvements to almost every step of our workflow including sample prep, data analysis and visualization, making it easier and faster to get a comprehensive view of structure and structural variants, even in large complex genomes common with plants and animals. It is increasingly clear that genome imaging data are essential for having the most contiguous and accurate genome assemblies."

Bionano will be hosting a workshop entitled, "Generating Accurate *De Novo* Assemblies with Bionano Optical Mapping," led by prominent genomics researchers, Dr. Michael Hiller from Max Planck Institute, Dr. Victor Llaca from Corteva Agriscience and Geoff Waldbieser from USDA. Examples will be presented on how the Bionano Saphyr platform is helping to build the most complete and accurate genome assemblies.

Bionano will be onsite at Booth #325 to discuss the Saphyr system and answer questions regarding genome imaging and the summarized findings presented during the various sessions.

Multiple scientists from around the world are scheduled to present Bionano data, including in the workshop, oral and poster presentations below:

Bionano Workshop:

Generating Accurate *De Novo* Assemblies with Bionano Optical Mapping
Presenting Authors: Chad Collier, Dr. Michael Hiller, Dr. Victor Llaca, Geoff Waldbieser
Date, Time: Monday, January 13, 4:00 pm – 6:10 pm
Location: Room East 2

Oral Presentations:

- **A Long Reads-Based De-Novo Assembly of the Rainbow Trout Arlee-Line Genome**
  Gao *et al.*, Saturday, Jan 11, 8:20am, Royal Palm Salon 3-2

- **New Genomic Resource in Watercress (Nasturtium officinale, R.) Enabling Molecular Breeding for Improved Anti-Cancer Properties, Flavour and Nutrient Density**, Taylor *et al.*, Saturday, Jan 11, 11:30am, San Diego

- **Insights into Rye Biology and Triticeae Relationships based on a Chromosome-Scale Genome Assembly,** Nils Stein, Saturday, Jan 11, 1:30pm, Golden Ballroom

- **Long-Read A188 Maize Genome Assembly and Short-Mer Guided Error Estimation**, Sanzhen Liu, Saturday, Jan 11, 1:30pm, Pacific Salon 3

- **Pangenome of the Maize NAM Founder Inbreds**, Dawe *et al.*, Saturday, Jan 11, 2:10pm, Pacific Salon 3

- **The Sweet Corn Genome Assembly and Comparative Analysis with Other Field Corn Genomes**, Hu *et al.*, Saturday, Jan 11, 7:20pm, Pacific Salon 3

- **An Improved Genome Assembly for the Highland Ecotype of Quinoa**, Zhang Heng, Sunday, Jan 12, 10:30am, Garden 1, Handlery Hotel

- **Haplotype-Resolved Cattle Genomes**, Williams *et al.*, Sunday, Jan 12, 11:20am, Sunday, Jan 12, 11:20am, San Diego

- **Chromosome-Level Genome and Comparative Analyses of Duck Uncover Genome and Chromatin Architecture Evolution of Birds**, Li *et al.*, Sunday, Jan 12, 1:20pm, East 1

- **Whole Genome Assembly and Structure Analysis in Japanese Strawberry**, Isobe *et al.*, Monday, Jan 13, 4:10pm, California

- **Advancements Toward Molecular Breeding and Genomics in the 'Breeding Better Bananas' Project in East Africa**, Brown *et al.*, Tuesday, Jan 14, 1:55pm, Pacific Salon 6-7

- **Annotation of the Wheat Prolamins**, Gu *et al*., Tuesday, Jan 14, 2:10pm, Pacific Salon 2

- **Maize Reference Genome Assembly in a Day**, Canaguier *et al.*, Tuesday, Jan 14, 2:12pm, Pacific Salon 3

Poster Presentations:

- **Bionano Hybrid Scaffold Assemblies Provide High Contiguity and Accuracy**
  Presenting Authors: Andy Wing Chun Pang, Joyce Lee, Jian Wang, Karl Hong, Ernest Lam, Thomas Anantharaman, Mark Oldakowski, Alex R. Hastie, Bionano Genomics
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0090

- **Isolating High-Quality Ultra-High Molecular Weight (UHMW) Genomic DNA (gDNA) from 5-10mg of Fresh or Freshly Frozen Animal Tissue**
  Presenting Authors: Yang Zhang, Khoa Pham, Henry B. Sadowski, Hannah Way, Mark Oldakowski, Bionano Genomics
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0130

- **MOMS: A Chromosome-Level Genome Scaffolder Using Multi-Channel Optical Maps**
  Presenting Authors: Jiang Xu, Baosheng Liao, Shuiming Xiao, Shuai Guo, Xiaofeng Shen, Yang Chu, Wenguang Wu, Qiushi Li, Shilin Chen
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0172

- **Identifying Parental Alleles with Bionano Genomics' Ultra-High Molecular Weight DNA**
  Presenting Authors: Joyce Lee, Andy Wing Chun Pang, Thomas Anantharaman, Alex R. Hastie, Mark Oldakowski, Bionano Genomics
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0174

- **Chromosome-Level Assembly for an American Shorthair Cat Genome**
  Presenting Authors: Yuki Matsumoto, Kei Watanabe, Genki Ishihara, Hideki Hirakawa, Sachiko Isobe, Ting-Fung Chan, Hon-Ming Lam, Yasuhiro Tanizawa, Yasukazu Nakamura
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0280

- **A Long Reads-Based De-Novo Assembly of the Rainbow Trout Arlee-Line Genome**
  Presenting Authors: Guangtu Gao, Geoff Waldbieser, Ramey C. Youngblood, Paul A. Wheeler, Brian E. Scheffler, Gary H. Thorgaard, Yniv Palti
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0432

- **A New, Chromosome-Level Aspergillus Flavus Reference Genome Reveals Large Insertions Potentially Contributing to Isolate Stress Tolerance and Aflatoxin Production**
  Presenting Authors: Jake Fountain, Josh Clevenger, Brian Nadon, Justin N. Vaughn, Ramey C. Youngblood, Walid Korani, Perng-Kuang Chang, Gaurav Agarwal, Bob Kemerait, Manish K. Pandey, Deepak Bhatnagar, Peggy Ozias-Akins, Rajeev K. Varshney, Brian E. Scheffler, Baozhu Guo
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0488

- **The Chromosome-Scale Reference Genome of Black Pepper Provides Insight into Piperine Biosynthesis**
  Presenting Authors: Zhongping Xu, Shuangxia Jin
  Date, Time: Monday, January 13, 10:00 am – 11:30 am

PgmNR: PE0534

- **Construction of Reference Genome Sequences of Cultivated-Type 'SBA' and Citron-Type PI189225 Accession in Watermelon**
  Presenting Authors: Yoon Jeong Jang, Minseok Seo, Bal-Kum Han, Gung-Pyo Lee
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0690

- **Genetic and Genomic Resources for Maize Transformation**
  Presenting Authors: Guifang Lin, Yan Liu, Tej Man Tamang, Jun Zheng, Mingxia Zhao, Ha Le, Cheng He, Junjie Fu, Myeong-Je Cho, Sunghun Park, Hairong Wei, Frank F. White, Yunjun Liu, Guoying Wang, Sanzhen Liu
  Date, Time: Monday, January 13, 10:00 am – 11:30 am
  PgmNR: PE0782

- **Combining Various Genomic Strategies With New Technologies to Decipher the Complex Structure of Plant Genomes**
  Presenting Authors: Stephane Cauet, Nathalie Rodde, Carine Satgé, Margaux-Alison Fustier, Caroline Callot, William Marande, Sandrine Arribat, Arnaud Bellec, Sonia Vautrin
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0095

- **High MW DNA Extraction From Diverse Animal and Plant Species**
  Presenting Authors: Michelle Kim, Renee Fedak, Duncan Kilburn, Jeffrey Burke, Kelvin Liu
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0113

- **De novo Haplotype Phased Genome Assembly and Genomic Selection of Buffaloes in India**
  Presenting Authors: Ananthasayanam Sudhakar, Harish Kothandaraman, Nilesh Nayee, Sujit Saha, Dushyant Singh Baghel, Swapnil Gajjar, Benjamin D. Rosen, Curtis P. Van Tassell, Michael C. Schatz
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0373

- **A Long Reads-Based Trio-Binning De-Novo Assembly of the North American Atlantic Salmon Genome**
  Presenting Authors: Ananthasayanam Sudhakar, Harish Kothandaraman, Nilesh Nayee, Sujit Saha, Dushyant Singh Baghel, Swapnil Gajjar, Benjamin D. Rosen, Curtis P. Van Tassell, Michael C. Schatz
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0425

- **A Multiomics Toolbox to Advance Avian Research**
  Presenting Authors: Ashley E. Meyer, LaDeana Hillier, Erich D. Jarvis, Giulio Formenti, Olivier Fedrigo, Bettina Haase, Jacquelyn Mountcastle, Jennifer Balacco, Christine G. Elsik, Yvonne Drechsler, Nicholas Anthony, Ron Okimoto, Arang Rhie, Adam M. Phillippy, Hans H. Cheng, Wesley Warren
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0449

- **Chromosome-Level Genome and Comparative Analyses of Duck Uncover Genome and Chromatin Architecture Evolution of Birds**
  Presenting Authors: Jing Li, Jilin Zhang, Zhengkui Zhou, Qi Zhou
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0459

- **Efforts to Create Reference Quality Rat Genomes**
  Presenting Authors: Yanchao Pan, Bilge Ozel, Tristan Jong, David Ashbrook, Clifton Dalgard, Leah Catherine Solberg Woods, Hao Chen, Robert Williams, Abraham Palmer, Huda Akil, Jun Li
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0477

- **Genome Assembly of Five Different Brassica oleracea Morphotypes**
  Presenting Authors: Chengcheng Cai, Johan Bucher, Fernanda A. de F. Guedes, Richard Finkers, Guusje Bonnema
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0587

- **Discovery of Structural Variation with Whole Genome Sequences and Bionano Genome Maps in Maize**
  Presenting Authors: Ha Le, Guifang Lin, Pierre A. Migeon, Jie Ren, Sanzhen Liu
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0775

- **Improved Genome Assembly for Aegilops tauschii with the Aid of Optical Maps and Whole Genome SMRT Sequencing**
  Presenting Authors: Le Wang, Tingting Zhu, Karin R. Deal, Jan Dvorak, Ming-Cheng
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0915

- **Insights into Rye Biology and Triticea Relationships Based on a Chromosome-Scale Genome Assembly**
  Presenting Author:
  Date, Time: Monday, January 13, 3:00 pm – 4:30 pm
  PgmNR: PO0984

Learn more by visiting Bionano's Booth # 325 at the PAG XXVIII and visiting https://bionanogenomics.com/

About Bionano Genomics

Bionano is a life sciences instrumentation company in the genome analysis space. Bionano 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 drive the adoption of digital cytogenetics, which is designed to be a more systematic, streamlined and industrialized form of traditional cytogenetics. The Saphyr system comprises an instrument, chip consumables, reagents and a suite of data analysis tools.

Forward-Looking Statements

This press release contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995. Words such as "may," "will," "expect," "plan," "anticipate," "estimate," "intend" and similar expressions (as well as other words or expressions referencing future events, conditions or circumstances) convey uncertainty of future events or outcomes and are intended to identify these forward-looking statements. Forward-looking statements include statements regarding our intentions, beliefs, projections, outlook, analyses or current expectations concerning, among other things, the timing and content of the presentations identified in this press release, the use or adoption of Saphyr as a routine tool in plant or animal research settings and the effectiveness and utility of the Saphyr system in such settings. Each of these forward-looking statements involves risks and uncertainties. Actual results or developments may differ materially from those projected or implied in these forward-looking statements. Factors that may cause such a difference include the risks that our sales, revenue, expense and other financial guidance may not be as expected, as well as risks and uncertainties associated with general market conditions; changes in the competitive landscape and the introduction of competitive products; changes in our strategic and commercial plans; our ability to obtain sufficient financing to fund our strategic plans and commercialization efforts; the ability of key clinical studies to demonstrate the effectiveness of our products; the loss of key members of management and our commercial team; and the risks and uncertainties associated with our business and financial condition in general, including the risks and uncertainties described in our filings with the Securities and Exchange Commission, including, without limitation, our Annual Report on Form 10-K for the year ended December 31, 2018 and in other filings subsequently made by us with the Securities and Exchange Commission. All forward-looking statements contained in this press release speak only as of the date on which they were made and are based on management's assumptions and estimates as of such date. We do not undertake any obligation to publicly update any forward-looking statements, whether as a result of the receipt of new information, the occurrence of future events or otherwise.

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