Day Five of Bionano's Next-Generation Cytogenomics Symposium: Saphyr Identifies Structural Variants that May Predispose to Severe COVID-19 Illness

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1. *COVID-19 Host Genome Structural Variant (SV) Consortium used Saphyr to identify SVs in severe COVID-19 patients that affect genes involved in immunity, airway mucous, and viral replication*

2. *SVs found by several investigators point to a central role for disease severity of the interferon response pathway*

3. *Consortium has added investigators from Augusta University, Boston Children's Hospital, New York Genome Center, Radboud University, Rockefeller University, UC San Diego, Virginia Commonwealth University, and two dozen other institutes from around the world*

SAN DIEGO, Jan. 18, 2021 (GLOBE NEWSWIRE) -- Bionano Genomics, Inc. (Nasdaq: BNGO) announced that the last day of its five-day Next-Generation Cytogenomics Symposium featured presentations by members of the COVID-19 Host Genome Structural Variant (SV) Consortium using the Saphyr® system for optical genome mapping (OGM) to analyze the genomes of patients with severe COVID-19 disease. The presentations by scientists and clinicians from leading hospitals and research institutions in Europe and the US showed that Saphyr was able to detect structural variants that may predispose to severe or mild COVID-19 disease, which had not been identified previously by large studies using next-generation sequencing (NGS) or array-based methods to analyze genomic variation.

Dr. Alex Hoischen, Radboud University, discussed his published results on genomic variants found in families with severe COVID-19. In two families with severely ill brothers, mutations were found in the Toll Like Receptor 7 gene (*TLR7*), which affects the production of interferons, signaling molecules used to control the immune response. Several other studies have since made similar findings in other genes of the TLR family. Dr. Hoischen discussed how individual patients each may carry individually rare variants, that are collectively common and point to important pathways involved in the disease. His interest in the consortium is based on his understanding that larger SVs have a greater chance to be rare and disruptive, and genome-wide studies have lacked so far in their assessment.

Dr. Erich Jarvis, Howard Hughes Medical Institute investigator, professor at The Rockefeller University and head of the Vertebrate Genome Project (VGP), discussed an interesting difference between hospitalized patients and controls where the severely ill show more variation in a part of the Interferon Alpha and Beta Receptor Subunit 1 gene, a key part of the interferon pathway that regulates immune response. Dr. Jarvis is using Saphyr and the pipeline he developed for the VGP to build reference-quality genomes of patients and controls and will compare them with each other and with animal species that are sensitive to infection with SARS-CoV-2 or not, as previously reported.

Dr. Ravindra Kolhe, Vice-Chairman of Pathology at the Medical College of Georgia at Augusta University and founder of the COVID-19 Host Genome SV Consortium explained that he founded the consortium because COVID-19 shows a split mortality where a very large number of people get infected, but only a small percentage of those get sick or die. Mortalities are associated with diabetes, hypertension and a history of heart failure, yet independent of that a seemingly random group of patients get extremely ill. Since other studies looking at host genetics use NGS or single nucleotide polymorphism (SNP) arrays that are ill suited to analyze SVs, the consortium focuses on the use of OGM to detect the larger genomic variants most likely to make the largest impact.

Dr. Kolhe presented the previously announced finding from the consortium on 37 ICU-admitted, severely ill COVID-19 patients whose genomes were analyzed using Saphyr. In several severely ill patients Saphyr detected structural variants affecting important immune genes. In another patient Saphyr found a duplication of the *STK26* gene, which reduces the production of interferon likely leading to reduced viral clearance and increasing the disease severity. When other severely ill patients were compared with asymptomatic COVID-19 patients, the same *STK26* gene was found to be significantly more active in all the sick patients, making it a possible biomarker for disease severity. OGM identified many more variants in the severely ill patients affecting genes controlling immunity, airway mucous, and viral replication. Dr. Kolhe stated that his team wants to use structural variants identified with Saphyr to design preventative measures for those people whose genomes show them to be the most vulnerable and develop a biomarker panel that can be run at the time of patient admission, to make sure that appropriate measures are taken based on the genetic makeup and patients get the treatment they need as early as possible. In order to do so, the consortium has announced plans to analyze 1000 genomes with Saphyr allowing them to determine with high confidence which SV are involved in disease susceptibility and severity.

Siavash Raisi, Dr. Vineet Bafna's laboratory at UCSD presented on FaNDOM, an algorithm they developed that is used by the consortium to quickly and efficiently verify the structural variants identified by the Saphyr system. It was able to provide an independent confirmation of all of the variants identified by Saphyr using Bionano Access and Solve software and reported in the consortium publication.

Dr. Silviu-Alin Bacanu, Virginia Commonwealth University described how existing resources and other host genome studies can be used to prioritize genes and structural variants identified with Saphyr. He described several studies including the genome-wide association studies on COVID-19 host genetics and the UK Biobank which has collected genomic data on more than 250,000 individuals. Although these large studies are unable to identify important large variants directly, their data can help prioritize variants detected by OGM based on whether they affect genes or pathways which these larger studies have identified as possible correlated with disease severity and outcome.

Dr. Alan Beggs and Dr. Catherine Brownstein, Boston Children's Hospital (BCH) discussed their previously announced study on the genomes of patients with Multisystem Inflammatory Syndrome in Children (MIS-C), a severe inflammatory attack of multiple organs weeks after COVID-19 infection in children with an average age of 8 years old. BCH has reported 67 cases of hospitalized MIS-C, and the Children's Rare Disease Cohort Initiative has banked their specimens. Drs. Beggs and Brownstein are enrolling 50 patients each with MIS-C, severe COVID-19, and asymptomatic or

mildly affected patients and will compare their genomes using OGM with Saphyr and with NGS.

Dr. Michael Zody, New York Genome Center (NYGC) presented on the use of NGS on patients also analyzed with Saphyr. The NYGC has an active research project to sequence both the viral and the patient genomes using NGS. Their study is focused on patients with severe COVID-19 without prior high-risk diseases and on MIS-C cases, and in a collaboration with Dr. Jean-Laurent Casanova has found rare defects in immunity that affect the disease severity by altering the interferon response in patients. By combining the NGS data collected by NYGC with the OGM data from the consortium, smaller events and single nucleotide variants detected by NGS and large variants detected by Saphyr can be analyzed together.

Recordings of all the presentations from the symposium can be found at http://bit.ly/3pLPT28

About Bionano Genomics
Bionano is a genome analysis company providing tools and services based on its Saphyr system to scientists and clinicians conducting genetic research and patient testing and providing diagnostic testing for those with autism spectrum disorder (ASD) and other neurodevelopmental disabilities through its Lineagen business. Bionano's Saphyr system is a research use only 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 is comprised of an instrument, chip consumables, reagents and a suite of data analysis tools, and genome analysis services to provide access to data generated by the Saphyr system for researchers who prefer not to adopt the Saphyr system in their labs. Lineagen has been providing genetic testing services to families and their healthcare providers for over nine years and has performed over 65,000 tests for those with neurodevelopmental concerns. For more information, visit www.bionanogenomics.com or www.lineagen.com.

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 effectiveness and utility of Bionano's technology in basic genetic research and clinical settings, and in the contexts and applications contemplated by the presentations identified in this press release; adoption of Saphyr as a standard platform in research and pathology settings; and the execution of Bionano's strategy. 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 and uncertainties associated with: the impact of the COVID-19 pandemic on our business and the global economy; 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 medical and research institutions to obtain funding to support adoption or continued use of our technologies; 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, 2019 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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