Next-Generation Mapping from Bionano Genomics Uncovers 10 Times More Large Structural Variations in Prostate Cancer than Next-Generation Sequencing

Study published in Oncotarget *validates value of Bionano's NGM for identification of relevant oncogenes and potentially pathogenic driver mutations*

SAN DIEGO, CA – March 8, 2017 – Bionano Genomics®, Inc., a company focused on genome structure analysis, today announced results from a first-of-its-kind study demonstrating that next-generation mapping (NGM) accurately identified potentially clinically-relevant oncogenes and pathogenic driver mutations never before detected by next-generation sequencing (NGS). The study, "Next-generation mapping reveals novel large genomic rearrangements in prostate cancer," was published in the March 1, 2017 online issue of the peer-reviewed journal *Oncotarget* (DOI: 10.18632/oncotarget.15802).

The study was led by Dr. Vanessa Hayes, Lab Head of Human Comparative and Prostate Cancer Genomics at the Garvan Institute of Medical Research in Sydney, Australia. Dr. Hayes and her team demonstrate the significance of physical genome mapping as an essential tool to identify large structural variations (SVs) implicated in the progression of prostate cancer. The study found that NGM using Bionano's Irys® System at 35x genome coverage identified 10 times more SVs larger than 1,000 base pairs than the Illumina X10 platform at 60x genome coverage. Of those novel SV calls otherwise missed by NGS, 94% were validated using a combination of analysis tools. Importantly, of the large SVs detected on the Bionano system, half were in or near genes with oncogenic potential. Of the sequence variants detected with NGS, only 0.5 percent were in or near such genes.

Dr. Vanessa Hayes commented, "These findings validate the importance of Bionano's NGM and demonstrate that NGS is not enough to identify all genome variations that may cause disease in patients. This study has generated promising results that help in understanding previously undetected prostate cancer genomic driver events and progression. We expect next-generation mapping to be critical in obtaining a more complete clinical picture of cancer patients at the Garvan Institute. This NGM technique is highly complementary to NGS platforms and other long-range platforms, such as PacBio and 10x Genomics, capturing a unique size range of SVs. In this study, we found 10 times more SVs using NGM compared to short-read NGS, which further strengthens our confidence in our search for funds to open a first-in-the-world Cancer Genome Mapping Facility based around the Bionano Genomics technology."

Erik Holmlin, Ph.D., CEO of Bionano Genomics, added, "We are excited by these data obtained for complex human genomic rearrangements in prostate cancer. Cancer is one of the most studied diseases, yet there is an urgent need to find more relevant genomic information that can aid in the development of effective therapies and strategies for precise patient management. With the use of our NGM technique in cancer and other clinical translational studies, researchers can discover the large SVs that would be missed with NGS alone. This validation comes at a perfect time since we have just launched Saphyr™, our newest system for NGM, which brings substantial improvements in speed and throughput making it the ideal solution for applying NGM to human genome research."

About the Garvan Institute of Medical Research

The Garvan Institute of Medical Research is one of Australia's leading medical research institutes. Garvan's researchers pioneer studies into some of the most widespread diseases affecting the community today. Research at Garvan is focused upon understanding the role of molecular and cellular processes in health and disease as the basis for developing future preventions, treatments and cures, and Garvan is at the forefront of next-generation genomic sequencing in Australia.

Garvan's scientists work across six major research divisions: Bone Biology, Cancer, Diabetes and Metabolism, Genomics and Epigenetics, Immunology, and Neuroscience.

About Bionano Genomics®

Bionano Genomics, Inc. provides the Irys and Saphyr systems for next-generation mapping (NGM), which is the leading solution in physical genome mapping. NGM offers customers whole genome analysis tools that reveal true genome structure and enabling researchers to capture what's missing in their data to advance human, plant and animal genomic research. NGM uses NanoChannel arrays 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 NGM detects and deciphers structural variations (SVs), which are large, complex DNA segments involving repeats that are often missed by sequencing technologies and which are a leading cause of inaccurate and incomplete genome assembly.

As a stand-alone tool, NGM enables the accurate detection of SVs, many of which have been shown to be associated with human disease as well as complex traits in plants and animals. As a complementary tool to next-generation sequencing (NGS), NGM integrates with sequence assemblies to create contiguous hybrid scaffolds for reference-quality genome assemblies that reveal the highly informative native structure of the chromosome. NGM also provides the additional ability to verify, correct and improve a NGS-generated genome assembly.

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

NGM 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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