Research Published in Nature Methods with Kwok Lab, UCSF

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New research shows 10x Genomics Technology Provides Faster, More Cost-Effective, High-Quality Genome Assemblies

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10x Genomics, a company focused on improving and broadening the application of genomic information, today announced the publication of a study in *Nature Methods* highlighting the benefits of their GemCode Technology to generate high-quality assemblies of complex genomes with their proprietary Linked-Read approach. The article demonstrates a new strategy for performing rapid, accurate and cost-effective *de novo* genome assembly using 10x Genomics' Linked-Reads in combination with other technologies.

"After working in this field for many years, we are very excited to find a clear path to *de novo* sequence assembly of complex genomes," said Pui-Yan Kwok, M.D., Ph.D., Henry Bachrach Distinguished Professor at the University of California, San Francisco. "The 10X Genomics' Linked-Read data is the critical component that allows us to build long-range phased assemblies and map breakpoints of structural variations to single basepair resolution. Our approach makes high quality *de novo* genome sequence assemblies readily accessible to any researcher interested in genome analysis."

The study evaluated the combination of 10x Genomics' Linked-Reads with Illumina short reads and BioNano's genome map data to achieve *de novo* genome assembly. For proof-of-concept, *de novo* assembly of human genome NA12878 was conducted. As a result, the 10x-BioNano assembly showed higher contiguity than and comparable accuracy with previous high-quality NA12878 assemblies performed with PacBio and Illumina-based systems with mate-pair libraries. The assembly also spanned repetitive and other complex regions. As a result of the assembly, approximately 14.3 Mb of novel genome sequences were obtained.

"To be featured in a second *Nature* journal publication this year is very exciting. It highlights the clinical utility of our GemCode Technology, and how we enable researchers to see previously inaccessible genomic information," said Serge Saxonov, co-founder and chief executive officer of 10x Genomics. "The results of this study clearly show the unique value of using Linked-Reads to provide long-range information for a better understanding of genome structure, phasing and *de novo* assembly."

In addition to scientists from 10x Genomics and BioNano Genomics, the study included researchers from The Cardiovascular Research Institute; the Institute for Human Genetics; the Department of Dermatology, University of California San Francisco and the Department of Molecular and Cell Biology, University of Cape Town.

The paper titled, "A hybrid approach for phased genome sequence assembly" was published online today, May 9, in Nature Methods and can be viewed online at http://www.nature.com/nmeth/index.html.

About 10x Genomics

10x Genomics is changing the definition of sequencing by providing an innovative genomics platform that dramatically upgrades the capabilities of existing sequencing technologies. This is achieved through a combination of new microfluidic science, chemistry and bioinformatics. By implementing GemCode™ Technology within the Chromium System, researchers can now, for the first time, find new structural variants, haplotypes, and other valuable genomic information with comprehensive workflows for Single Cell, Genome and Exome applications that incorporate their pre-existing sequencing technologies.

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