Stanford Researchers Publish Seminal Paper on Use of 10x Genomics' GemCode Technology for Genomic Analysis

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10x Genomics today announced the publication of a study in Nature Biotechnology on the GemCode technology platform, a powerful approach that enables researchers to discover previously inaccessible genomic information, providing key insights into heritable disease and cancer genetics.

"The Linked-Read approach allows precise resolution of phased structural and single nucleotide variants. This comprehensive genome-scale view can be used to identify causative germline variants in heritable disorders, and provide a deeper understanding of the genomic alterations underlying tumor development and maintenance in cancer patients," said Hanlee Ji, M.D., Associate Professor of Medicine, Stanford University, a director at the Stanford Genome Technology Center and senior author of the study.

The microfluidics-based, Linked-Read sequencing technology, built on the proprietary GemCode platform, can phase and haplotype germline and cancer genomes using only nanograms of input DNA. This droplet-based system prepares barcoded libraries for short-read sequencing and computationally reconstructs long-range haplotype and structural variant information. This report demonstrates the utility of the GemCode platform for generating haplotype blocks and phasing a set of structural variants, as well as resolving the structure of a gene fusion in a cancer cell line using phased exome sequencing. The article describes the first genome-scale haplotype analysis of a primary tumor derived from a clinical sample, thus revealing a series of novel features not apparent with standard whole genome sequencing approaches.

"Our GemCode technology has been adopted for use in multiple applications, including whole-genome phasing and structural variant analysis, *de novo* genome assembly, remapping of difficult regions of the genome, and dynamic gene expression of single cells," said Serge Saxonov, Ph.D., Chief Executive Officer of 10x Genomics. "We are providing tools for researchers to understand the genetic basis of disease at unprecedented levels, which will ultimately lead to transformative advancements in patient care."

The study, "Haplotyping germline and cancer genomes with high-throughput Linked-Read sequencing" by Zheng, et al. was published online today in Nature Biotechnology.

About 10x Genomics

10x Genomics meets the critical need for long range, structural and cellular information, with an innovative system that transforms the capability of existing short-read sequencers. Our GemCode platform supports comprehensive genomics and high-throughput single-cell transcriptomics. It enables researchers to discover previously inaccessible genomic information at massive rate and scale, including phased structural variants, phased single nucleotide variants, and dynamic gene expression of individual cells—while leveraging their existing sequencing systems and workflows. For more information, please visit www.10xGenomics.com.

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