# 10x Genomics Announces Automated Workflow for Dried Blood Spot and Saliva for Linked-Read Sequencing.

October 12, 2017

*–Automated workflow will enable population and genetic health studies–*

PLEASANTON, Calif.—October 12, 2017—10x Genomics, a company focused on enabling the mastery of biology by accelerating genomic discovery, today announced a new automation solution for whole genome and exome sequencing developed in collaboration with PerkinElmer, Inc. The new workflow allows Linked-Read sequencing to be performed on saliva as well as dried blood spots (DBS), an important archival sample type stored by blood banks and used in population and genetic health research studies.

DBS sample collection offers a powerful tool in screening programs and in large population-based surveys, but has been a difficult sample type for long-range sequencing due to poor DNA quality after extraction. The method has the advantage of being more economical, less invasive, relatively painless and is particularly suitable for collection in neonates and the elderly. However, if extracted incorrectly, DNA from DBS samples tends to result in poor yields and excessive fragmentation, making these archival samples inaccessible to long-range sequencing.

"Long-range information is necessary to get a comprehensive view of variants in the genome, and our collaboration with 10x provides contextual genomic and haplotype information from DBS samples, thereby providing increased resolution to variant calling, especially in regions of the genome inaccessible by short-reads," said Madhuri Hegde, Vice President and Chief Scientific Officer, PerkinElmer Laboratory Services. "This further maximizes the probability of detecting variants previously refractory or undetectable by standard NGS assays. Therefore, we are planning to use this combined workflow in our whole genome and exome sequencing services."

The combination of PerkinElmer's chemagic nucleic acid extraction technology and Sciclone® automation platform, and the 10x Genomics' Chromium Genome and Exome Solutions, enable an end-to-end workflow that yields high throughput, Linked-Reads with long phase blocks from as little as 1ng of input material. PerkinElmer's automated magnetic separation procedure uses chemagen M-PVA Magnetic Beads to isolate and purify nucleic acid from the DBS & saliva. These beads have a high affinity for nucleic acids and low protein binding, resulting in very pure, high molecular weight DNA/RNA.

This unique approach provides haplotype information from Linked-Reads which reveals the diploid nature of each personalized human genome, revealing parental lineage in population based studies. Additionally, Linked-Read technology can provide insight into large structural variants, including inversions and translocations, where short-read methods have traditionally struggled. This allows interrogation of entire regions of the genome which have remained inaccessible to most short-read analytical methods due to widespread high identity repeats and paralogs.

"The collaboration between 10x Genomics and PerkinElmer will allow clinical researchers working with dry blood spots the ability to resolve phasing and variants using an efficient sample-to-solution sequencing workflow," said Masoud Toloue, Vice President and General Manager, Applied Genomics, PerkinElmer. "This combination will help scale the detection of genetic information in difficult to reach genomic regions."

"The collaboration with PerkinElmer uniquely enables population genetics studies with a cost-effective, high throughput method to interrogate archival specimens that are otherwise inaccessible," said Anjana Narayanan, product manager at 10x Genomics. "PerkinElmer's extraction solutions and 10x Genomics technology provides an end-to-end workflow solution that enables researchers to gain insight into genetic abnormalities with unprecedented accuracy and throughput, even with 1ng of starting material. In addition to providing high throughput workflows that will facilitate a more comprehensive understanding of disease, 10x can better serve our customers and meet the clinical research community's critical need for long-range information from difficult but standard samples types like dried blood spots."

The new workflow will be presented by Dr. Madhuri Hegde during two workshops at the 67th Annual Meeting of the American Society of Human Genetics (ASHG) in Orlando, Florida:

- "Advancing Genomic and Single-Cell Sequencing Drop-by-Drop with the 10x Chromium System" on Wednesday, October 18th, from 12:30 PM – 1:45 PM
- "Automation Compatible Linked Read Analysis of Dried Blood Spots" on Thursday, October 19th, from 7:15am – 8:45am

**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, V(D)J, Genome, Exome and *de novo* Assembly applications that incorporate their pre-existing sequencing technologies.

www.10xGenomics.com

**Media Contact**

Ryan Ferrell
HDMZ
(312) 506-5202
ryan.ferrell@hdmz.com

**Investor Contact**

Matt Clawson
Pure Communications
(949) 370-8500
mclawson@purecommunications.com