10x Genomics Launches Comprehensive Software Suite for Single-Cell RNA-seq Data Analysis and Visualization

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– Complete software suite provides a comprehensive, scalable solution for cell characterization and gene expression profiling of hundreds to millions of individual cells –

PLEASANTON, Calif. – February 13, 2017 – 10x Genomics, a company focused on enabling the mastery of biology by accelerating genomic discovery, today announced the launch of a new software suite for analyzing and visualizing single-cell RNA sequencing (scRNA-seq) data generated by the company's Chromium Single Cell 3' Solution. The new software suite, announced at the 17th Annual Advances in Genome Biology and Technology (AGBT) Meeting, includes the Loupe Cell Browser and an updated version of Cell Ranger pipelines, which together provide a complete and seamless analysis workflow for detailed gene expression profiling information on a cell-by-cell basis.

"Advances in single-cell RNA quantification techniques have enabled the comprehensive study of gene expression dynamics within single cells but scalable software solutions have been a barrier to expanding their application," said Alexander Wong, vice president of software and infrastructure for 10x Genomics, who will present the new software during the company's pre-conference symposium at the AGBT meeting. "With this in mind, we designed our new software as part of a comprehensive solution to make scalable single-cell gene expression analysis possible for every lab, from sample to discovery."

The Loupe Cell Browser is an easy-to-use, interactive visualization tool that delivers insights into single-cell gene expression. With the Loupe Cell Browser, researchers can easily identify distinct cellular sub-populations, isolate significant genes, measure expression levels, and export findings for further analysis and collaborative sharing.

The updated Cell Ranger, a set of analysis pipelines that combine robust transcriptome alignment with cellular barcoding to rapidly generate expression profiles across tens of thousands of cells at once, now automatically generates Loupe Cell Browser-ready files for both single-sample and multi-sample experiments. Cell Ranger pipelines also feature a powerful new graph-based clustering method with the ability to identify and resolve more cellular sub-populations within single-cell experiments. The new release also increases transcriptome mapping rate and optimizes computational performance to enable the analysis of large-scale datasets of over one million cells.

"The Chromium Single-Cell 3' Solution was announced last year at AGBT as the first comprehensive and commercially available droplet-based NGS solution for scRNA-seq, and has quickly become the industry leader for its scalability and cost," said Serge Saxonov, co-founder and chief executive officer of 10x Genomics. "The system enables massively parallel RNA-seq analysis of single cells from a hundred to a million cells, a revolutionary change in how gene expression experiments can be performed at the massive scale and throughput needed to accomplish tissue and cell atlas studies."

The company will feature the new software suite and data during their pre-conference symposium at the annual AGBT meeting, Monday, February 13. The single-cell session will feature presentations by researchers using the Chromium System for single-cell gene expression profiling in stem cells and tumors, as well as Perturb-seq, a novel method for massively-parallel functional genomics with CRISPR.

Single-cell datasets, including the 1.3 Million Neuron Dataset, are available for download on the 10x Support website at:

https://support.10xgenomics.com/single-cell/software/downloads/latesthttps://support.10xgenomics.com/single-cell/datasets/1M_neurons

Researchers can join the 10x Data Sharing Community and Developer Network at:

https://community.10xgenomics.com/t5/Single-Cell-Community/ct-p/single-cell

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, Exome and *de novo* Assembly applications that incorporate their pre-existing sequencing technologies.

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