# 10x Genomics Announces Commercial Availability of Chromium de novo Assembly Solution and Supernova Assembler for Low-Cost Diploid de novo Genome Assembly

October 12, 2016

*– New technology selected for use by multiple human and non-human genome projects*

*– Company to feature presentations on human and non-human projects at American Society of Human Genetics Meeting*

PLEASANTON, Calif. — [October 12, 2016] – 10x Genomics, a company focused on improving and broadening the application of genomic information, today announced the commercial availability of their new Chromium *de novo* Assembly Solution and the Supernova Assembler, making low-cost, true diploid *de novo* assemblies readily accessible and at scale for human and non-human applications. This method has been adopted by investigators at leading genome centers, for human and non-human genomes for agricultural and environmental applications, including the chili pepper, monk seal, spotted owl, hummingbird, komodo dragon and other genomes.

While *de novo* assemblies are considered the gold standard for determining an organism's genome sequence, the cost and computational requirements necessary to undertake them have precluded their widespread use. Moreover nearly all assemblies of diploid genomes have been haploid, thus fundamentally misrepresenting their biology. Now for the first time, true diploid assemblies can be generated straightforwardly at low cost.

"While thousands of individual whole genomes have been analyzed since the completion of the Human Genome Project, the majority of these have been analyzed by alignment of sequence reads to the reference assembly," says Deanna Church, senior director of applications at 10x Genomics. "This approach is plagued by bias and leads to an incomplete understanding of that individual genome. By contrast *de novo* assembly is unbiased, but methods for it have been cumbersome and expensive to execute in the lab and computationally. Our goal in developing the Chromium *de novo* Assembly Solution and the Supernova Assembler was to be able to offer our customers a solution to address two of the main issues that plague the research community—scalability and cost."

The Chromium *de novo* Assembly Solution provides reagents, instrumentation and software for a fast and simple workflow from sample to diploid assembly in less than two weeks. Starting with approximately 1 ng of high molecular weight DNA, far less than other approaches, researchers can quickly and easily generate libraries that can be sequenced on high-throughput Illumina HiSeq X Ten instruments at a cost that is orders of magnitude lower than alternative diploid assembly methods. The Supernova Assembler then uses the "Linked-Reads" data output from the Chromium *de novo* Assembly Solution to build comprehensive diploid genome assemblies with >10 Mb scaffold size and long-range accuracy not normally seen using short-read sequencing methods.

"We designed Supernova to be a 'pushbutton' solution, meaning there are no parameters to set, and thus no specialized expertise is required to run it. Moreover, the computational cost and burden is an order of magnitude lower than existing methods," said David Jaffe, Ph.D. and computational fellow at 10x Genomics. "For example, a human genome can be assembled by the Supernova Assembler for less than $500 using widely available cloud-based servers, like those offered by Amazon Web Services (AWS), using a single server for only two days."

In addition to the commercial availability of the Chromium *de novo* Assembly Solution and the Supernova Assembler, data on the human NA12878 and the monk seal assemblies will be presented at the 2016 American Society of Human Genetics (ASHG) Annual Meeting being held October 18 – 22 in Vancouver, Canada:

**Oral Presentation #314:**

**"A hybrid approach for *de novo* human genome sequence assembly, phasing and detection of complex structural variation"**

**Presenting Author:** Yulia Mostovoy, Ph.D., Department of Dermatology, University of California, San Francisco, San Francisco, CA

**Date, Time:** Saturday, October 22 from 10:30 a.m. – 10:45 a.m. PT

**Location:** Room 211, West Building

**Oral Presentation #316:**

**"*de novo* assembly of individual human haplotypes from diploid samples"**

**Presenting Author:** Deanna Church, Ph.D., senior director of applications, 10x Genomics

**Date, Time:** Saturday, October 22 from 11:00 a.m. – 11:15 a.m. PT

**Location:** Room 211, West Building

**Poster Presentation #3188T:**

**“Comparison of synthetic long read sequencing methods and optical mapping for *de novo* genome assembly”**

**Presenting Author:** David Mohr, director of the GRCF High Throughput Sequencing Laboratory at Johns Hopkins School of Medicine, Institute of Genetic Medicine

**Date, Time:** Thursday, October 20 from 3:00 p.m. – 4:00 p.m. PT

**Location:** Exhibit Hall B, West Building

More information on the Chromium *de novo* Assembly Solution and the new Supernova Assembler can be found at https://www.10xgenomics.com/assembly and at http://support.10xgenomics.com/de-novo-assembly.

Chromium *de novo* Assembly Solution datasets for seven human assemblies are available for download at: http://support.10xgenomics.com/de-novo-assembly/datasets

**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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