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Complete Genomics Publishes in Science on Low-Cost Sequencing of Three Human Genomes Using Its Proprietary Sequencing Platform

MOUNTAIN VIEW, Calif. — Nov. 5, 2009 — Complete Genomics, a third-generation human genome sequencing company, today announced publication of a report in the journal *Science* describing its proprietary DNA sequencing platform, including analysis of sequence data from three complete human genomes. The consumables cost for these three genomes sequenced on the proof-of-principle genomic DNA nanoarrays ranged from \$8,005 for 87x coverage to \$1,726 for 45x coverage for the samples described in this report.

“We’ve demonstrated that it’s possible to accurately and affordably sequence and detect variants across entire human genomes,” said Cliff Reid, chairman, president and CEO of Complete Genomics. “This high-quality, cost-effective approach to genome sequencing will allow researchers to study complete genomes from hundreds of patients with a disease to advance the understanding of the genetic causes of that disease, with an end to preventing and treating common human ailments.”

The manuscript, titled, “Human Genome Sequencing Using Unchained Base Reads on Self-Assembling DNA Nanoarrays,” describes the methodology used to sequence cell lines derived from two individuals previously characterized by the International HapMap project. These included a Caucasian male of European descent (NA07022) and a Yoruban female (NA19240). In addition, researchers sequenced lymphoblast DNA from a Caucasian male sample (NA20431) obtained from the Personal Genome Project (PersonalGenomes.org).

Complete Genomics’ proprietary platform enables efficient imaging, while requiring low reagent consumption, through its combinatorial probe anchor ligation (cPAL™) chemistry and its use of patterned genomic DNA nanoarrays. With this approach,

Complete Genomics' scientists generated high-quality diploid base calls in as much as 95 percent of the genomes sequenced, identifying 3.2 million to 4.5 million sequence variants per genome processed.

Detailed validation of one genome dataset demonstrates a sequence accuracy of just one false variant per 100 kilobases, a remarkably low error rate, particularly for such an affordable technology.

Patterned genomic DNA nanoarrays and 70-base, unchained sequence reads are unique technical achievements. The company's new patterned genomic DNA nanoarrays, which achieve a record high density of 2.85 billion spots per slide at 0.7 micron pitch, will enable Complete Genomics to sequence 10,000 human genomes in 2010.

About Complete Genomics

Founded in 2006, Complete Genomics is a California company that has developed a novel approach to sequencing human DNA that is revolutionizing the human genome sequencing industry. Complete Genomics combines its proprietary third-generation DNA sequencing technology with its high-performance computing capabilities to deliver low-cost, high-quality genomic data on an unprecedented scale. The company is currently building the world's largest human genome sequencing center. This development will allow academic and biopharmaceutical researchers, for the first time, to conduct large-scale complete human genome studies that will help identify the genetic underpinnings of complex diseases and drug responses. For additional information about the company, please visit <http://www.completegenomics.com>.

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