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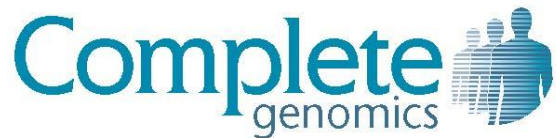
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**Genentech Uses Complete Genomics' Human Genome Sequencing Service to Compare Tumor and Normal Genome in Patient with Non-small Cell Lung Cancer; Results Published in Nature**

**MOUNTAIN VIEW, Calif. – May 26, 2010** – Complete Genomics Inc., a third-generation human genome sequencing company, today announced that Genentech Inc., a wholly owned member of the Roche Group (SIX: RO, ROG; OTCQX: RHHBY), used the company's sequencing, bioinformatics and analytics services to sequence and compare a patient's primary lung tumor and adjacent normal tissue. Tumor-normal pairs like this allow researchers to compare the patient's genome before and after it was altered by the cancer; the patient's normal genome serves as the ideal control. This is the first time that such a comparison has been made across the whole genome for a lung cancer patient. Genentech's findings will be published online in Nature later today in a paper titled "The mutation spectrum revealed by paired genome sequences from a lung cancer patient."

Complete Genomics sequenced the patient's cancer and normal genome to a depth of 60x and 46x, respectively, providing high-resolution results and allowing somatic variations to be called with high confidence. This depth of sequencing enabled the Genentech researchers to identify a large number of somatic mutations and structural variations in the non-small cell lung cancer genome.

Using Complete Genomics' sequencing service, the Genentech team, led by Dr. Zemin Zhang, senior scientist, was able to detect significantly more somatic variations than have been discovered in other cancer studies (leukemia and breast cancer) conducted on a genome-wide basis. Genentech identified more than 50,000 high-confidence somatic single nucleotide variations (SNVs), which yielded an estimated genome-wide somatic mutation rate of 17.7 per Mb.



The Genentech researchers validated 392 somatic SNVs in coding regions, including one in the KRAS proto-oncogene. They also validated 43 large-scale structural variations in the tumor.

In addition, the researchers observed a distinct pattern of selection against mutations within expressed genes compared to non-expressed genes and in promoter regions up to 5 kb upstream of all protein-coding genes. This is the first time that such selection pressures within a tumor environment have been clearly identified.

### **About Complete Genomics**

Founded in 2006, Complete Genomics is a California company that has developed a novel approach to sequencing human DNA. Complete Genomics combines its proprietary third-generation DNA sequencing technology with its high-performance computing capabilities to deliver low-cost, high-quality genomic data. The company is currently building a high-throughput human genome sequencing center. This development will allow academic and biopharmaceutical researchers 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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