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NIH Announces Two Integral Components of The Cancer Genome Atlas Pilot Project

The National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI), both parts of the National Institutes of Health (NIH), today announced another two of the components of The Cancer Genome Atlas (TCGA) Pilot Project, a three-year, $100 million collaboration to test the feasibility of using large-scale genome analysis technologies to identify important genetic changes involved in cancer. Lung, brain (glioblastoma), and ovarian cancers have been chosen as the tumors for study by TCGA Pilot Project.

Awards have been made to seven institutions in five states to establish Cancer Genome Characterization Centers (CGCCs). The Cancer Genome Characterization Centers will work as a network, with each center using advanced genome analysis technologies to identify major changes in the genomes of the cancers chosen for TCGA pilot program. NCI awarded a total of $11.7 million per year to support the CGCCs. The institutions receiving CGCC awards are:

- **Broad Institute of MIT and Harvard, Cambridge, Mass.** Using the Affymetrix platform, this center will identify changes in expression and copy number alterations that occur in cancer.
- **Harvard Medical School and Brigham and Women's Hospital, Boston, Mass.** Using the Agilent platform, this center will characterize tumor samples for alterations in

chromosome segments copy number. This center will also develop new technologies to analyze expression profiles.

- **Lawrence Berkeley National Laboratory, Berkeley, Calif.** Using an Affymetrix Exon 1.0 array platform, this center will identify changes in the transcription profiles that occur in cancer.
- **Memorial Sloan-Kettering Cancer Center, New York, N.Y.** Using Agilent arrays, this center will provide characterization of chromosome segment gains and losses. This center will also develop new approaches to detect novel genetic rearrangements.
- **The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University, Baltimore, Md.** This is a joint project with the University of Southern California/Norris Comprehensive Cancer Center, which will use Illumina's GoldenGate® Genotyping platform, to detect changes in methylation profiles associated with transcribed genes in cancer samples.
- **Stanford University School of Medicine, Palo Alto, Calif.** Using Illumina's HumanHap550 Genotyping BeadChip, this project will identify chromosome segments copy number variation found in cancer.
- **University of North Carolina Lineberger Comprehensive Cancer Center, Chapel Hill, N.C.** Using an Agilent array platform, this center will identify changes in the transcription profiles that occur in cancer.

Additionally, SRA International Inc. of Fairfax, Va., has been selected to develop the Data Coordinating Center (DCC) for the TCGA Pilot Project. The DCC will track data produced by components of TCGA, ensuring that this data meets quality standards set for the project, and make TCGA data publicly accessible through databases supported by NCI's Cancer Biomedical Informatics Grid (caBIG™) and the National Library of Medicine's National Center for Biotechnology Information (NCBI). The DCC will establish public data resources that scientists can use in their research to generate new insights into the causes and potential targets for interventions in cancer. Access to all TCGA data will be provided in a manner that meets the highest standards for protection and respect of the research participants.

TCGA was launched in December 2005. When fully operational, it will consist of four integrated components: the CGCCs and DCC announced today, as well as the Biospecimen Core Resource (BCR) announced last month, and the Genome Sequencing Centers, which will be selected in the coming months.

"We are, today, gaining new insights into the genetic changes that accumulate over a lifetime and are associated with malignancy," said NCI Director John E. Niederhuber, M.D. "TCGA holds the potential to help turn what we know into what we can harness -- to be able to study

changes in a patient's genetic sequence over time and then use that information to design highly targeted, individually based interventions."

"TCGA will analyze genomic changes in lung, brain, and ovarian cancers with a goal of identifying all alterations in genes for these three tumors -- especially those that can serve to differentiate cancer subtypes. The Cancer Genome Characterization Centers will identify genomic aberrations, such as copy number changes and/or chromosomal translocations that will enable the development of targeted diagnostics and therapies for cancer patients, and provide a path to more personalized cancer medicine," said NCI Deputy Director for Advanced Technologies and Strategic Partnerships, Anna D. Barker, Ph.D.

"The Cancer Genome Atlas Pilot Project will generate large quantities of data that will require an immense amount of expertise and coordination," said NHGRI Director Francis S. Collins, M.D., Ph.D. "The Data Coordinating Center is an essential component of The Cancer Genome Atlas Pilot Project and will help researchers take advantage of the molecular information describing the genomic changes in the cancers studied. The integration of these data will enable individual researchers throughout the world to discover new cancer targets and inform the design of a new generation of cancer drugs."

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NCI and NHGRI are two of the 27 institutes and centers at NIH, an agency of the U.S. Department of Health and Human Services.

For more details about The Cancer Genome Atlas, please visit http://cancergenome.nih.gov.

For more information about cancer and the National Cancer Institute, please visit the NCI Web site at http://www.cancer.gov or call NCI's Cancer Information Service at 1-800-4-CANCER (1-800-422-6237).

For more information about the National Human Genome Research Institute, please visit the NHGRI Web site at http://www.genome.gov.

For information about caBIG™, please visit http://cabig.cancer.gov.