April 30, 2013

Study Published in *Journal of Clinical Oncology* Finds High Concordance of Genomic Alterations in NSCLC Primary and Matched Metastatic Tumor Pairs

Foundation Medicine and Institut Gustave Roussy Research Reveals 94% Concordance of Driver Alterations

CAMBRIDGE, Mass., and PARIS, France. - April 30, 2013 - Foundation Medicine, Inc. and the Institut Gustave Roussy today announced the results of a next-generation sequencing study of primary and matched metastatic tumor pairs from 15 patients with non-small cell lung cancer (NSCLC) in the May 2013 edition of the *Journal of Clinical Oncology (JCO)*[1] . The study found 94% concordance between cancer-driving alterations in formalin-fixed, paraffin-embedded (FFPE) archived primary tumor samples and matched metastasis. High concordance in driver alterations suggests genomic profiling of FFPE primary tumor samples can often identify the key driver alterations present in matched NSCLC metastases and that this genomic information may be used to guide treatment upon recurrence.

"This study suggests that cancer-driving alterations in NSCLC are largely homogeneous between the examined primary and matched metastasis, thus FFPE primary tumor samples may be sufficient for clinical genomic profiling in some settings," said Vincent Miller, senior vice president of clinical development at Foundation Medicine, and co-author of the study. "While additional research is needed and these results cannot be generalized to other settings, this is a promising result for patients as these samples are often available for analysis without the need for an invasive re-biopsy solely for genotyping."

"In treating NSLC patients, physicians are often faced with limited tissue and must make choices in selecting an appropriate tumor sample for molecular analysis, which raises questions about sample type and the necessity of re-biopsy," said Pr Jean-Charles Soria, Early Innovative Therapies Unit Director, Medical Oncology Department, Institute Gustave Roussy. "We chose to study one aspect of this issue to provide physicians with data to understand the genomic similarities and differences between primary and metastatic tumors. The results demonstrated a high level of concordance between key alterations in the matched samples for this cohort of patients with NSCLC."

Primary and matched metastatic tumor pairs from 15 patients were analyzed using a targeted next-generation sequencing assay in Foundation Medicine's CLIA-certified laboratory. Genomic libraries were captured for 3,230 exons in 182 cancer-related genes plus 37 introns from 14 genes often rearranged in cancer and sequenced to high coverage.

Among the 30 tumors analyzed (primary and metastatic for each of 15 patients), 311 genomic alterations were identified in total. Of these, 20.3% (63) were suspected drivers of tumor growth while the rest are believed to be passenger alterations. Ten of the 15 patients (66.7%) harbored two or more likely driver alterations.

The study by Vignot S, et al, *"Next Generation Sequencing Reveals High Concordance of Recurrent Somatic Alterations between Primary Tumor and Metastases from Non-Small Cell Lung Cancer Patients"* was conducted by researchers from Foundation Medicine, Inc. in collaboration with a team from the Institut Gustave Roussy in Paris and the University Hospital of Grenoble (CHU of Grenoble), France.

About Institut Gustave Roussy
Europe's leading oncology centre, Institut Gustave Roussy is an international institute with expertise in oncology entirely dedicated to its patients. Its single venue contains 2,600 health professionals whose three main missions are care-giving, research and education. By devoting 20% of its budget to research, Institut Gustave Roussy proudly declares its determination to promote research as an innovative engine for the benefit of its patients. Institut Gustave Roussy is a private health facility working within the French public health system and is authorised to receive donations and bequests.

About FoundationOne™
FoundationOne is a fully informative genomic profile that complements traditional cancer decision tools and often expands treatment options by matching each patient with targeted therapies that may be relevant to the molecular changes in their tumor. Using next-generation sequencing, FoundationOne interrogates all genes somatically altered in human cancers that are validated targets for therapy or unambiguous drivers of oncogenesis based on current knowledge. It reveals all classes of genomic alterations including base substitutions, insertions, deletions, copy number alterations and select rearrangements. Each patient's genomic profile is reported to the physician matched with targeted therapies and clinical trials that may be relevant based on the molecular blueprint of their tumor. Results are supported by a comprehensive review of published literature. FoundationOne has been optimized to fit easily into the clinical workflow of a practicing oncologist. It is available for

all solid tumors and clinical grade results can be obtained from as little as 50ng of DNA obtained from formalin-fixed, paraffin-embedded tumor tissue samples. FoundationOne is a laboratory-developed test performed at Foundation Medicine's CLIA-certified facility and is currently available for all solid tumor types. Please visit www.FoundationOne.com for more information.

About Foundation Medicine
Foundation Medicine is a molecular information company dedicated to a transformation in cancer care in which treatment is informed by a deep understanding of the genomic changes that contribute to each patient's unique cancer. The company's initial clinical assay, FoundationOne™, is a fully informative genomic profile to identify a patient's individual molecular alterations and match them with relevant targeted therapies and clinical trials. Foundation Medicine's molecular information platform aims to improve day-to-day care for patients by serving the needs of clinicians, academic researchers and drug developers to help advance the science of molecular medicine in cancer. For more information, please visit www.foundationmedicine.com or follow Foundation Medicine on Twitter (@FoundationATCG).

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[1]Vignot S, et al "Next-generation sequencing reveals high concordance of recurrent somatic alterations between primary tumor and metastases from patients with non-small cell lung cancer" J Clin Oncol 2013; DOI: 10.1200/JCO.2012.47.7737. Available online: http://jco.ascopubs.org/content/early/2013/04/29/JCO.2012.47.7737.abstract

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