

“Proteomic Analysis of Proximal Pulmonary Venous Blood Identifies Biomarkers for Non-Small Cell Lung Cancer”

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Abstract: As in the case of prostate specific antigen (PSA) for prostate cancer, a reliable and easily accessible biomarker would prove invaluable in the early identification of patients with non-small cell lung cancer (NSCLC). To this end, in the current application, we suggest a new and innovative strategy to identify biomarkers from the serum of NSCLC patients by mass spectroscopy (MS) using iTRAQ (isobaric tagging for relative and absolute quantitation) technology. Unlike previous efforts aimed at identifying serum biomarkers using peripheral blood from NSCLC patients, in our studies the peripheral blood will be used only as reference while blood draining directly from the tumor (pulmonary vein) will instead be used for biomarker identification. Because of its proximity to the cancer, the pulmonary venous blood (PVB) is highly enriched for tumor proteins, allowing for greater sensitivity of detection of relevant proteins. In addition, each patient will serve as his/her own control, eliminating many of the sources of heterogeneity that have plagued the serum proteomic field and hampered biomarker discovery. The proteomic signature elaborated from the PVB, will then be validated in the peripheral blood using more sensitive techniques and the clinical applicability of the signature with respect to detection of lung cancer will be tested in an independent set of blood from patients screened for lung cancer. In summary these studies will lead to the identification of new blood-based biomarkers that by allowing for early lung cancer detection have the potential to make a profound clinical impact by reducing lung cancer mortality.