**Metabolomics Approach to Identify Molecules and Pathways Involved in the Development of Atherosclerotic Coronary Artery Disease – a RTI RCMRC Pilot Study**

Metabolomic Analysis: NIH Eastern Regional Comprehensive Metabolomics Resource Core (RTI RCMRC)

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IRB Number(s):

**Abstract:**

Insulin-resistant subjects develop more severe and diffuse coronary artery atherosclerosis than insulin sensitive control but the mechanisms that mediate the atherosclerosis phenotype are unknown. The objective of this study is to investigate whether the severity of atherosclerosis is associated not only with lipoprotein concentrations, weight, blood pressure, biomarkers of inflammation and IR in an animal model but also changes in parameters that measure protein glycation. The experimental approach was to study normocholestrolemic pigs fed a high fat diet that also contained increased NaCl. The choice of pigs was driven by the fact that, like humans, they develop coronary artery and aortic atherosclerosis and insulin resistance. In addition, pigs have been used in many studies to define the mechanisms that mediate increased atherosclerosis in diabetes.

**Sample Description:**

The data obtained for the NMR metabolomics analysis can be found in the accompanying files:

Procedures: 1. Pig Athersclerosis Model Procedures.docx

Study Design Tables: 2. Pig Athersclerosis Model Study Design Table.xls

Metadata: 3. Pig Athersclerosis Model METADATA.xlsm

Processed Data: 4. Pig Athersclerosis Model NMR Normalized Binned Data.xlsx

Raw Data: 5. Pig Athersclerosis Model NMR Raw Data.zip

**Notes:**

Full sample preparation and analysis procedures are available in the accompanying document entitled **1. Pig Athersclerosis Model Procedures**.

Descriptions of abbreviations for factors are available in the Variable Dictionary in the accompanying file no. **2**. **Pig Athersclerosis Model Study Design Table.xls**.

The phenotypic and normalized data are available in the accompanying files: **4. Pig Athersclerosis Model NMR Normalized Binned Data.xlsx** for normalized binned NMR data. Sample ID and factors can be found in the first 5 columns and other columns in the spreadsheet contain sample metadata and the normalized binned data. If the statistical program does not allow variable names to begin with a number then add a prefix to the column names, for example, bin\_8.98 instead of 8.98. The Sample ID serves as the unique identifier (Graphical ID) of the individual samples and is used as the NMR folder name in the raw NMR data file **5. Pig Athersclerosis Model** **RAW NMR Data.zip**.