**Metabolomics of Mice Cohousing and Microbiota Transfer**

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

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**Abstract:**

For this metabolomics study, we received twelve mice serum samples from Dr. Martin Blaser's laboratory at NYU School of medicine. Serum from week 15 mice were analyzed: (a) mice received low-dose antibiotics until week 4 (STAT), (b) mice received no antibiotics (control), (c) mice received low dose antibiotics (STAT) and then cohoused with control animals (STAT-coho), (d) mice received no antibiotics and then were cohoused with STAT animals (Control-coho). In this collaboration, we are interested in the metabolic differences among these groups.

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

Procedures: 1. Mouse Serum GCMS Procedures.docx

1a. GCMS Procedures Flowchart.pdf

1b. GCMS Preparation of fatty acid methyl esters mixture.pdf

Study Design Table: 2. Mouse Serum GCMS Study Design Table.xlsx

Metadata: 3. Mouse Serum METADATA.xlsx

Raw Data: 4. Mouse Serum Raw GCMS data.zip

Processed Data: 5. Mouse Serum Processed Data.xlsx

**Notes:**

Full sample preparation and instrumentation parameters are detailed in accompanying file **1. Mouse Serum GCMS Procedures.docx**. A flowchart detailing the sample preparation steps is located in accompanying file **1a. GCMS Procedures Flowchart.pdf**. The preparation of the fatty acid methyl esters (FAME) mixture is located in accompanying file **1b. GCMS Preparation of fatty acid methyl esters mixture.pdf**.

Factors listed in the study design are defined in the Variable Dictionary located in the accompanying file entitled **2. Mouse Serum GCMS Study Design Table.xlsx**. Available in the same file is information linking the Data File names to the Sample IDs.

Data files for each sample are generated by Leco’s ChromaTOF software and are exported in netCDF format. These files are located in the accompanying file entitled **4. Mouse Serum Raw GCMS data.zip**.

The spreadsheet in accompanying file **5. Mouse Serum Processed Data.xlsx** has one data tab entitled BinBase Processed Data. The BinBase Processed Data shows raw output from BinBase. The height values have not been normalized.

**Reference:**

O Fiehn, G. Wohlgemuth, M Scholz, T Kind, DY Lee, Y Lu, S Moon and B Nikolau: Quality control for plant metabolomics: reporting MSI-compliant studies. The Plant Journal 2008; 53:691-704.