

Broad Metabolomics Platform (see S1 Text)

LC-MS profiling

Signal peak detection and alignment
(using Progenesis Q1)

Targeted metabolite identification
(using TraceFinder)

PAIRUP-MS Data Processing (see S2-S3 Text)

Normalization using internal standards
and pooled samples

Removal of outlier data points and
signals with noisy trends

Removal of samples and signals
based on % missingness

Missing value imputation
(using MICE)

Covariate adjustment
(when appropriate)

Rank-based inverse normal
transformation

Performed on each
metabolite signal in each
profiling method

Performed on merged
dataset containing data
from all methods

**PAIRUP-MS Imputation-based
Matching Method**

**PAIRUP-MS Pathway Annotation
and Analysis Method**