# Experiment 215 data analysis method

Data analysis was performed using Find by Formula algorithm of the Agilent MassHunter Qualitative analysis software. Library for the analysis was constructed partially from the authentic standards and partially by creating “Known Unknowns” from mass spectral features consistently present in a large proportion of the samples. Molecular features were identified by Molecular Feature Extractor (Agilent Mass *Data analysis and normalization:* Data from the three MS platforms were compiled for analysis. Data were normalized by both column (sample) and row (metabolite) prior to analysis.

**Metabolomic Pathway Analysis:** MetaboAnalyst 2.0 was used to generate significant pathways in metabolomics dataset. The raw data was inserted into the software and the phenotype label was set to “discrete” (DMSO vs. CEP). Identified compounds were matched based on KEGG ID. Missing values were replaced by a small value. The data was normalized by creating a pooled average sample from DMSO group. No data transformation or data filtering was applied, while data was scaled by autoscaling (mean-centered and divided by the standard deviation of each variable). Global test was used for pathway enrichment analysis and out-degree centrality was used for pathway topology analysis. The p-value is assigned based on the coverage and change observed in a given metabolic pathway. A pathway impact score was assigned based on the location of the identified metabolites in a given pathway. A significant threshold was assigned at y=1/x for subsequent analysis.