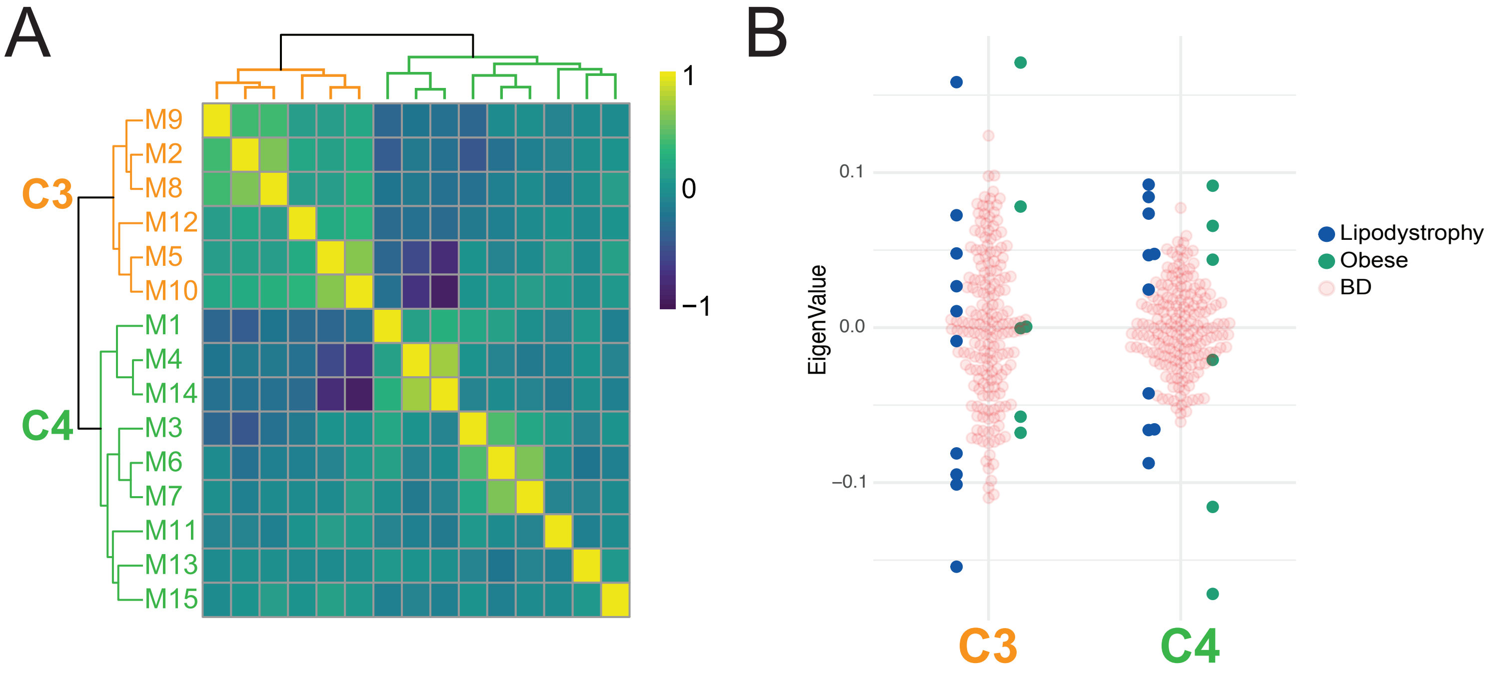

Supplementary figure 2 - Related to Figure 1 - WGCNA analysis with BD individuals metabolite values and cluster functional annotation.
A. Heatmap of BD individuals eigen-metabolites adjacencies in the consensus eigen-metabolites network. Each row and column correspond to one eigen-metabolite (labeled by consensus module color). The heatmap is color-coded by adjacency, yellow indicating high adjacency (positive correlation) and blue low adjacency (negative correlation) as shown by the color legend. B. Beeswarm plot using average eigen-metabolites per cluster. Colors indicate cohorts.