

Cross-Study Analyses of Gut Microbiomes from Healthy and Obese Individuals

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Abstract

Background: With the advent of metagenomics, many large studies have been conducted with the quest of better understanding gut microbiota changes in relation to varying health conditions. Significant findings have been made for diseases such as cirrhosis, colorectal cancers, inflammatory bowel diseases and others, yet one that stands out is obesity for which conflicting results have been reported in the literature.

Methods: Here, we built and analyzed a cross-study dataset of healthy and obese individuals looking for major changes in the the taxonomic and functional composition of their metagenomes.

Results: Our results suggest that the overweight and normal subjects have no strong dissimilarity in their metagenomes composition. Significant differences were observed when comparing the obese and the non-obese individuals in their functional and taxonomic profiles.

Conclusion: In this study, we report the most significant changes that we observed and discuss their potential implication in the obesity condition.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the latest manuscript can be downloaded and [accessed as a PDF](#).

Figures

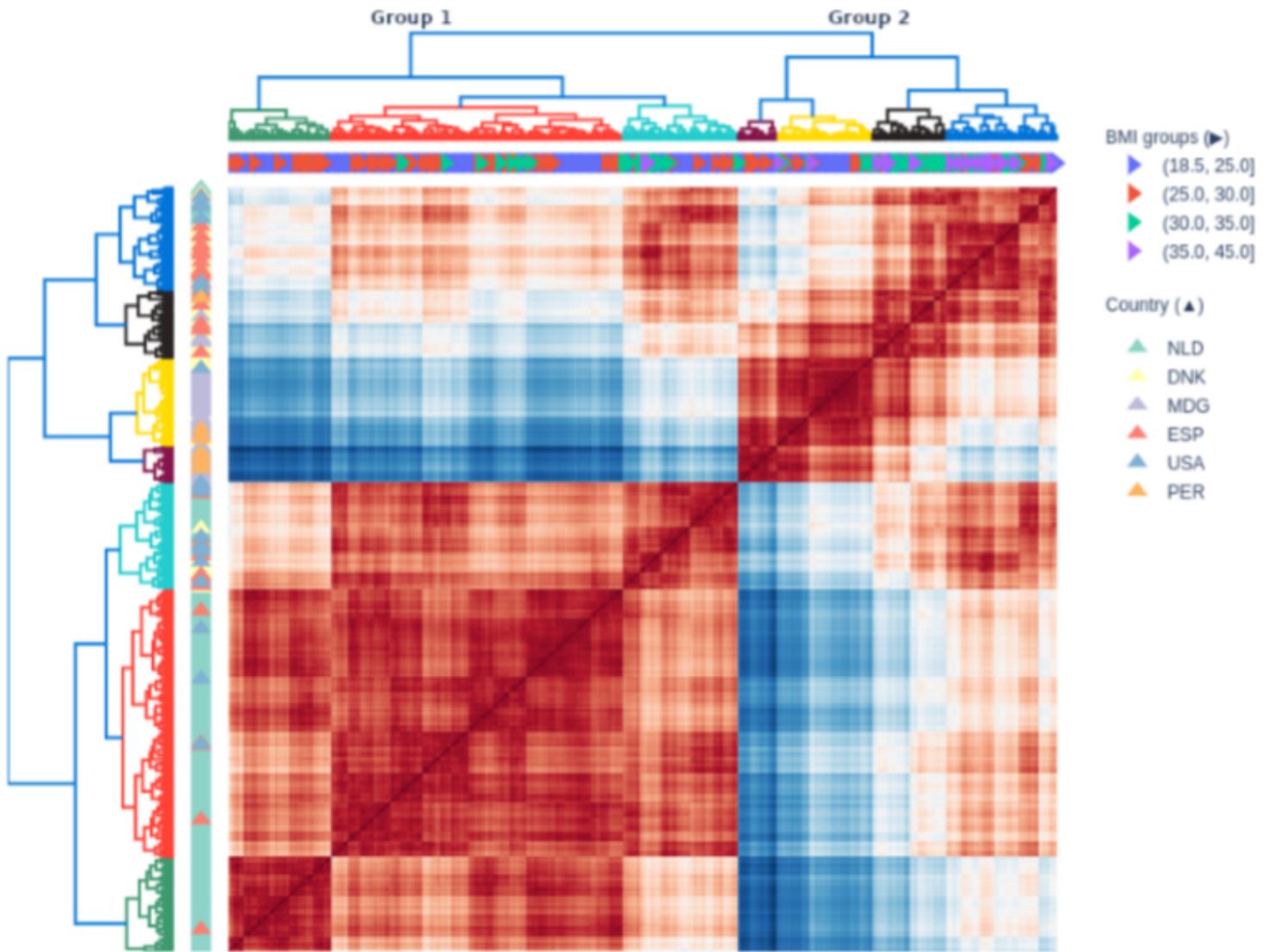


Figure 1

Heatmap and hierarchical clustering of the metagenome based on their shared DNA content (k-mers of length 31). Red color indicate close similarity between metagenome as blue color indicate more dissimilarity. BMI groups are indicated by a right triangle in the upper portion of the figure and country of the individuals on the left side by upper triangles.

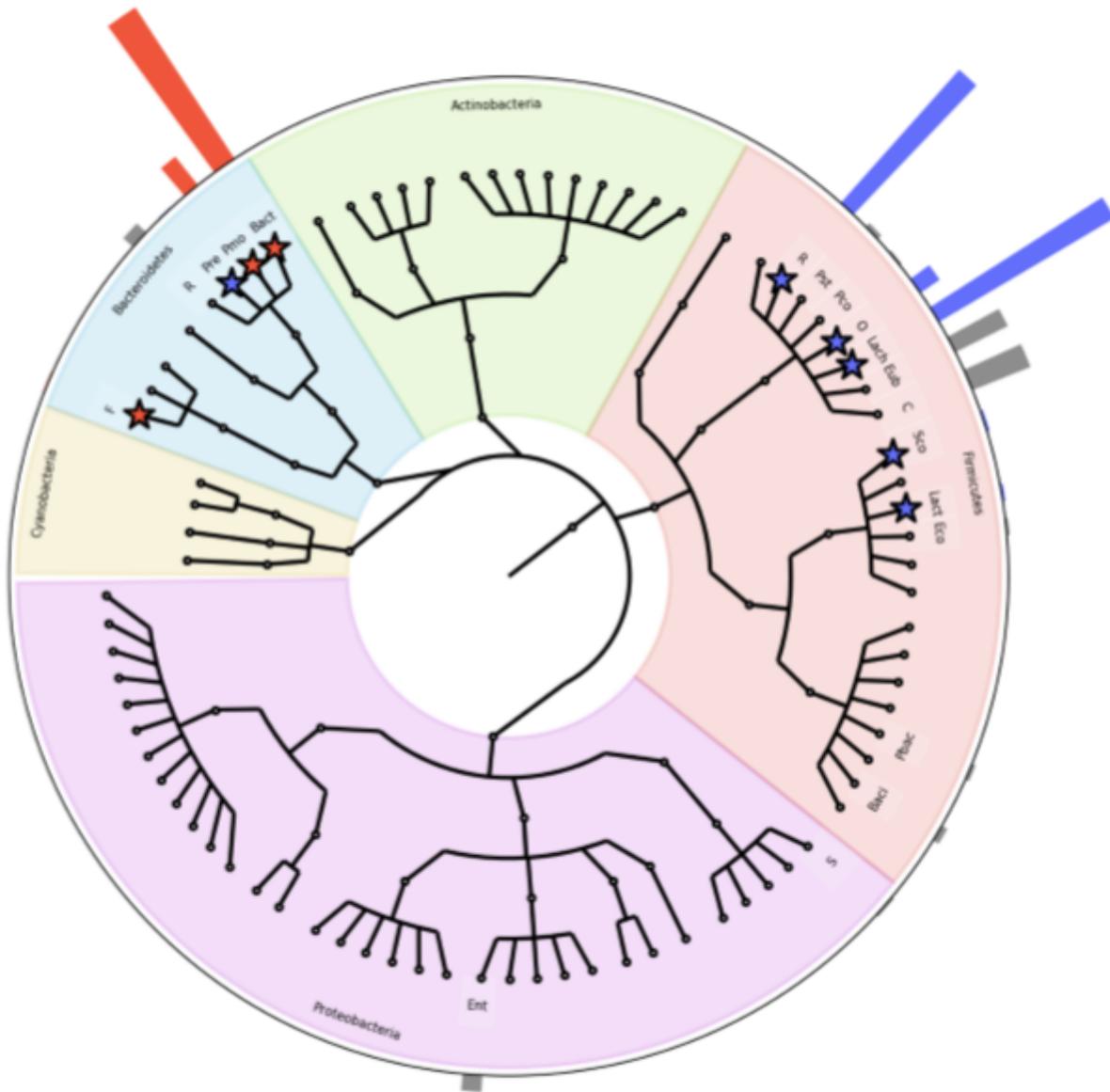


Figure 2

Bacteria cladogram of the gut metagenomics data found in 640 individuals down at the family taxonomic rank. Red bars indicate higher relative abundance of the taxa in obese individuals, while blue bars indicate higher representation in normal individuals. Stars indicate that the relative abundance was significantly different in both cohorts.

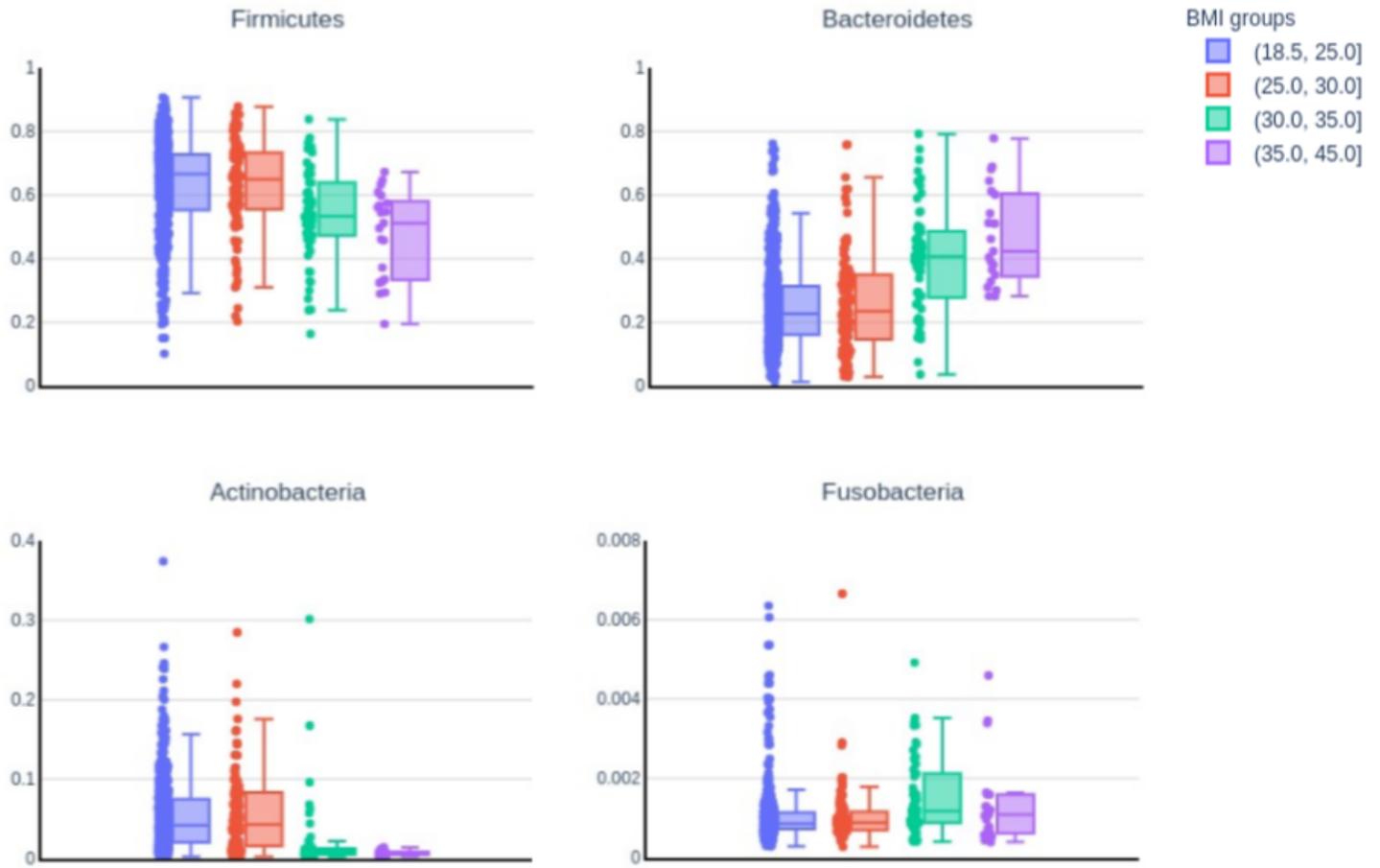


Figure 3

The top 4 most abundant phyla with significant changes in obese and non-obese gut microbiota.

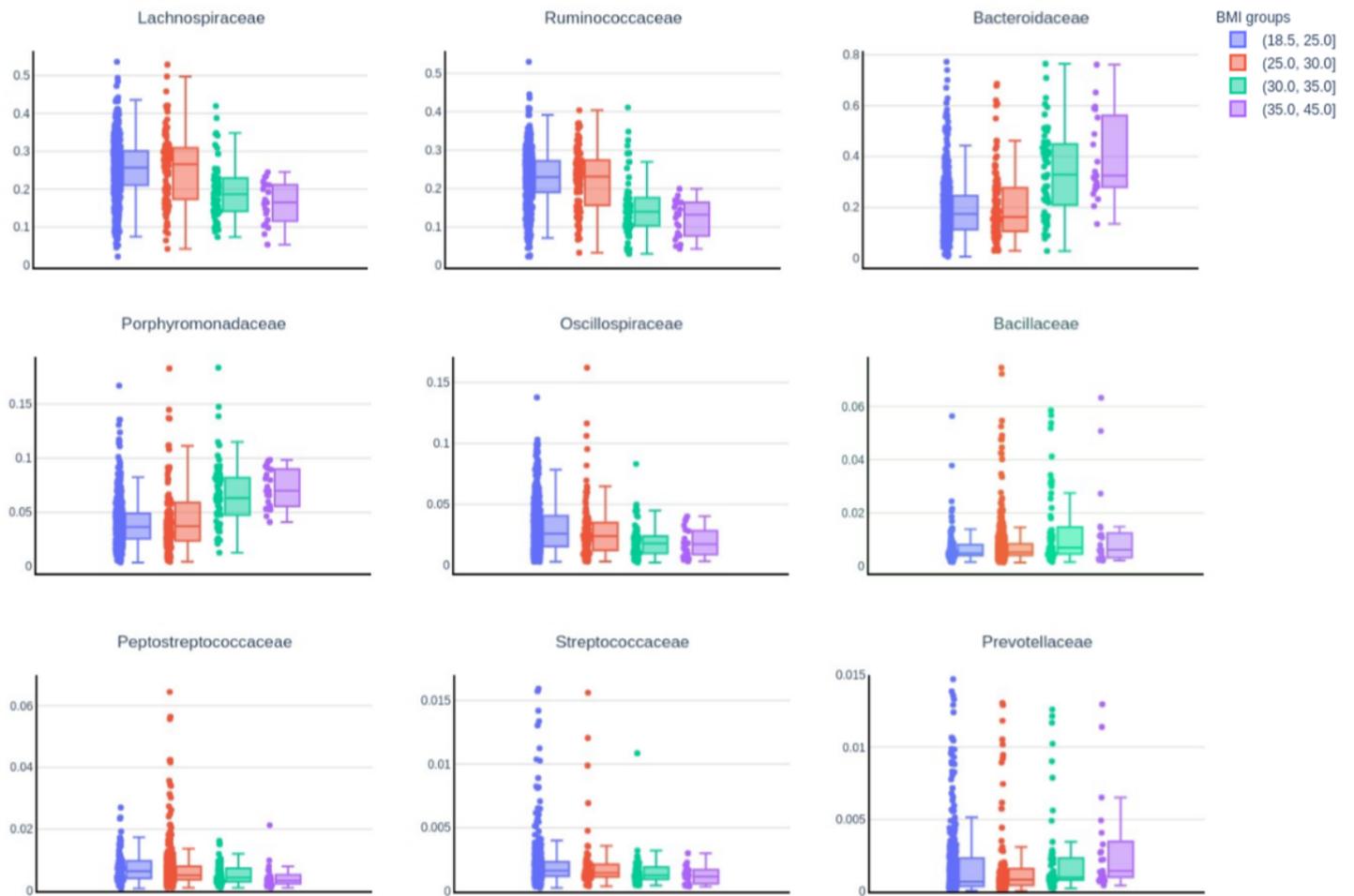


Figure 4

The top 9 most abundant families with significant changes in obese and non-obese gut microbiota.

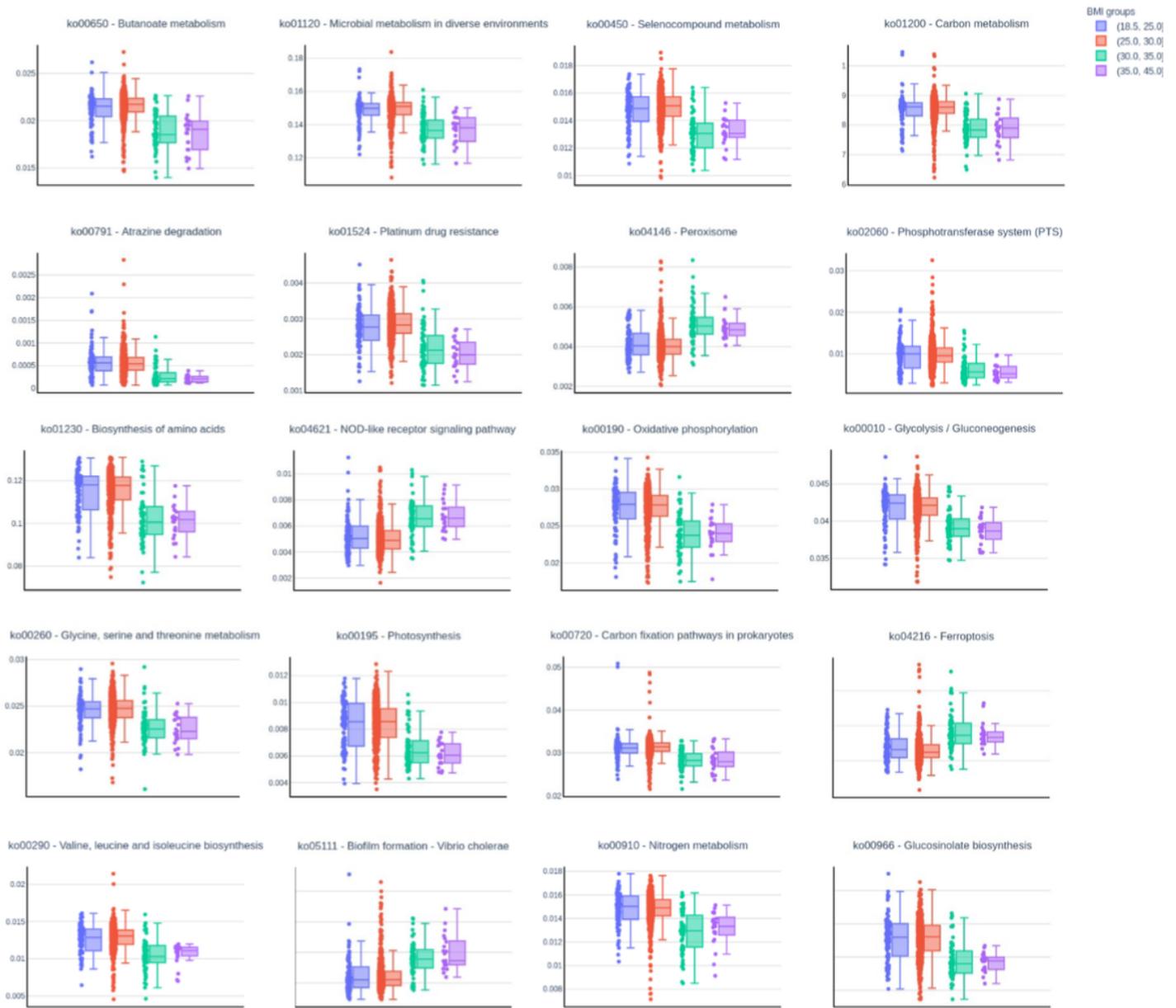


Figure 5

The top 20 KEGG pathways which show the most significant changes in abundances in obese and non-obese gut microbiota.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [metaobesedata.xlsx](#)