Supplementary Information for:

Diet influences the functions of the human intestinal microbiome

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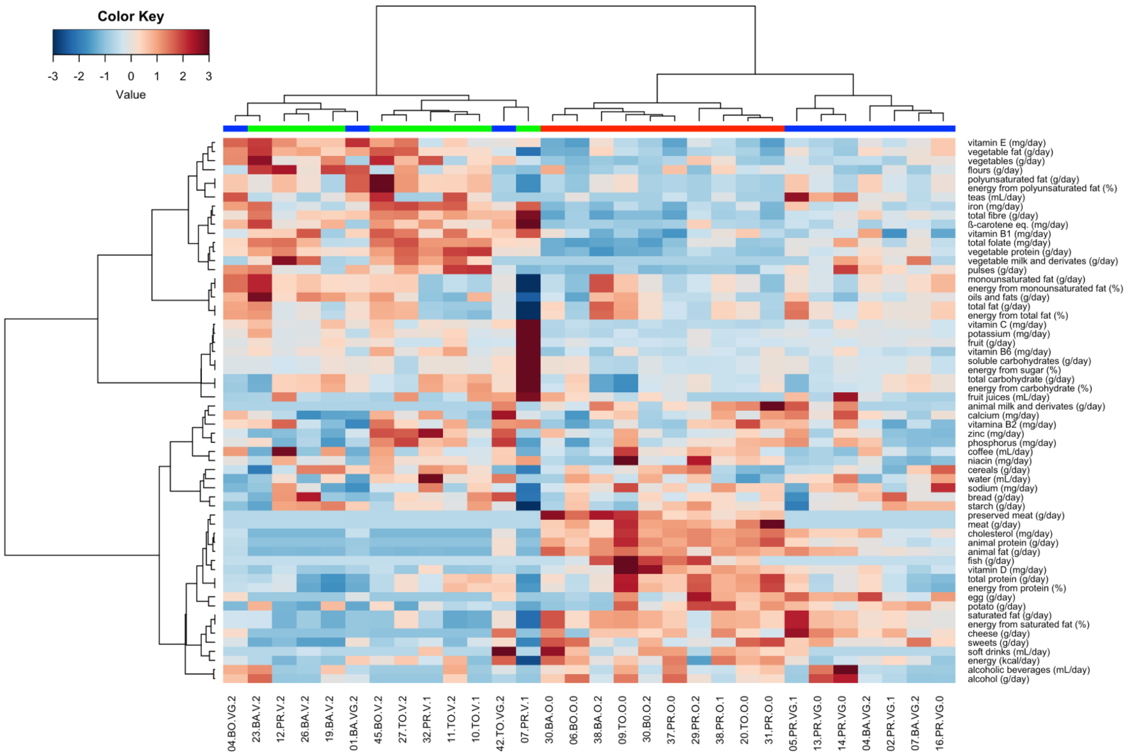
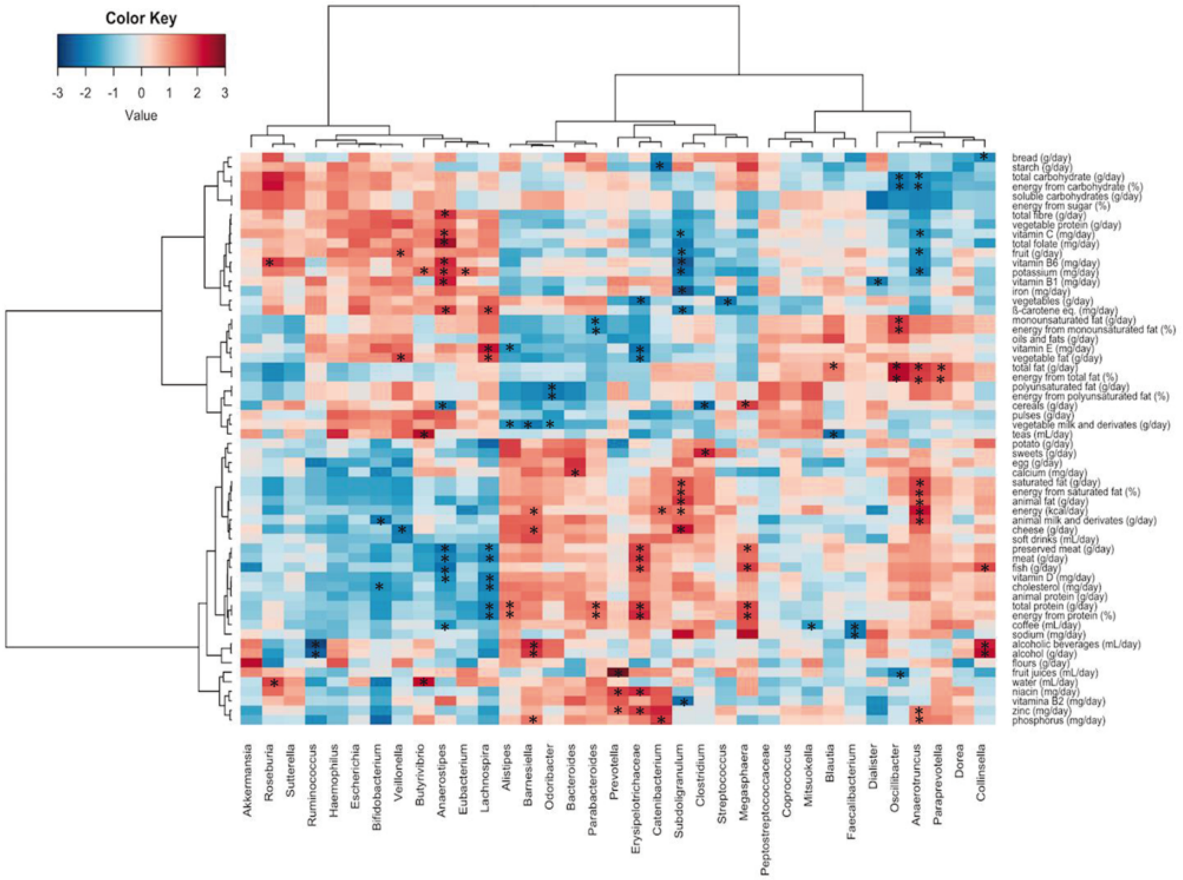
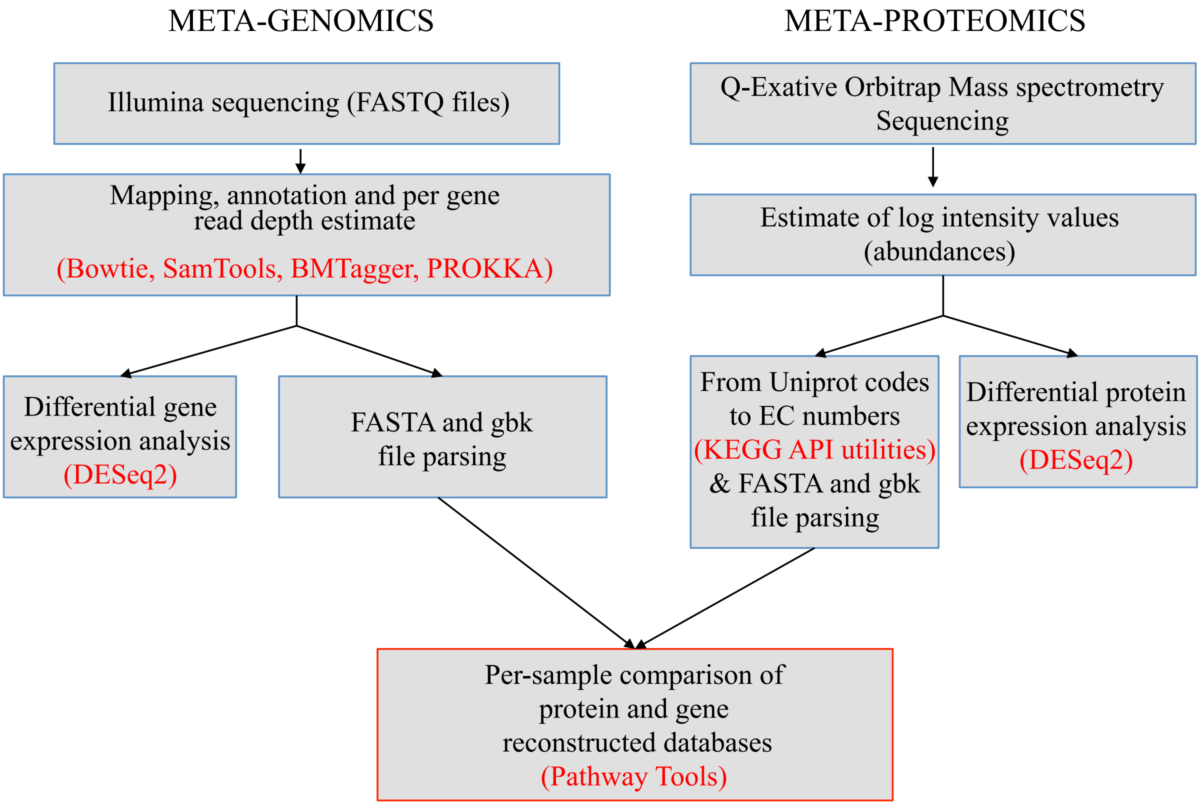


Supplementary Figure S1. Average-linkage clustering based on the Spearman distance of omnivores (O), vegans (V) and vegetarians (VG) and dietary information. The columns are color-coded as follows: red, O; green, V; and blue, VG. Rows and columns are clustered by Ward linkage hierarchical clustering. The intensity of the colors, denoted as the Z-score, represents the degree of correlation between samples and dietary information, as measured by Spearman's correlations; red indicates a high correlation, and blue indicates a low correlation. Sample codes include (i) the type of diet as O, omnivorous; V, vegan; or VG, vegetarian; and (ii) Mediterranean diet adherence as low, 0; medium, 1; or high, 2.



Supplementary Figure S2. Correlation between dietary information and fecal microbiome composition. Heatplot showing Spearman's correlations between microbial genera and dietary information. Rows and columns are clustered by Euclidean distance and Ward linkage hierarchical clustering. The intensity of colors represents the degree of association between genera and nutrients, as measured by Spearman's correlations. Asterisks indicate significant correlations (FDR < 0.05).



Supplementary Figure S3. Display of features of followed analysis workflow for meta-genomic and meta-proteomic data. Illumina and Mass spectrometry sequencing raw data files were analysed thanks to the software reported in red. Gene and protein annotation files converged in the Pathway Tools metabolic map reconstruction.