Supporting Information

Current Understanding of Human Metaproteome Association and Modulation

Shahd Ezzeldin[1], Aya El-Wazir[2,3], Shymaa Enany[4], Abdelrahman Muhammad[5], Dina Johar[6], Aya Osama[1], Eman Ahmed[1,7], Hassan Shikshaky[1], Sameh Magdeldin[1,8*]

[1]*Proteomics and Metabolomics Unit, Department of Basic Research, Children's Cancer Hospital Egypt 57357, 11441, Cairo, Egypt*

[2]*Genetics Unit, Department of Histology and Cell Biology, Faculty of Medicine, Suez Canal University, 41522, Ismailia, Egypt*

[3]*Center of Excellence of Molecular and Cellular Medicine, Suez Canal University, 41522, Ismailia, Egypt*

[4]*Department of Microbiology and Immunology, Faculty of Pharmacy, Suez Canal University, 41522, Ismailia, Egypt*

[5]*Department of Biomedical Engineering, Higher Technological Institute, 44634, Sharqia, Egypt*

[6]*Biomedical Sciences Program, University of Science and Technology, Zewail City of Science and Technology, 12588, Giza, Egypt*

[7]*Department of Pharmacology, Faculty of Veterinary Medicine, Suez Canal University, Ismailia, 41522, Egypt*

[8]*Department of Physiology, Faculty of Veterinary Medicine, Suez Canal University, Ismailia 41522, Egypt*

Sameh Magdeldin, Ph.D* (Corresponding address)
Proteomics and Metabolomics Unit, Department of Basic Research,
Children's Cancer Hospital Egypt 57357, Cairo, Egypt
Email: Sameh.Magdeldin@57357.org

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Supplementary 1. Nodes annotation and interactions score for network analyses of gut metaproteome from different metaproteomics studies representing healthy and diseased cohorts; type-1 diabetes (T1D), obesity, and crohn's disease (CD) patients. All networks are generated by STRING version 10.5 (https://string-db.org)   (provided as separate excel file)

Supplementary 2. Supplementary information for figure 3 providing details on the analysis done to generate the heatmaps.

Supplementary 2.

Figure 3, entitled "Metaproteome functional enzymes in the healthy human gut" represents a descriptive overview on the functional profile of microbial metaproteins in healthy human gut, with an ultimate goal to highlight that the gut metaproteome is conserved across healthy individuals with limited variability reflecting a personalized microbiome through metaproteomics analysis. To achieve this, supplementary datasets containing the list of identified microbial KEGG Orthologies (KOs) and their corresponding abundance were used from two recently published metaproteomics-based studies, entitled "Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults", and "Potential and active functions in the gut microbiota of a healthy human cohort". The used datasets were re-analyzed to generate the heatmaps of figure 3 as follows;

KOs identified in the healthy subjects and through a metaproteomics approach were only included in the analysis. An average value was calculated for each KOs across the study subjects and was used to sort the top 25 KOs. The maximum of each set of the top 25 KOs was then calculated, followed by data normalization. To normalize the data, each value was divided by the corresponding maximum. This was added to the division of (log10 of the value multiplied by 100) by (log10 of the corresponding maximum multiplied by 100). In other words, the following calculations were done for data normalization;

$$\text{Normalized value} = \left[\frac{\log 10\ (\text{value} \times 100)}{\log 10\ (\text{maximum} \times 100)}\right] + \left[\frac{\text{value}}{\text{maximum}}\right]$$

Where "value" represents each abundance of the top 25 in each study, and "maximum" represents the maximum of each corresponding 25 set.

The generated heatmaps from the reprocessed supplementary published data following the above mentioned steps pinpoint the stability of gut microbiome and further highlight that the gut metaproteome is conserved across healthy individuals and there is core microbial functions as shown by the great similarity between the top 25 KOs results from two different studies.