Supplementary Information

Combining proteogenomics and metaproteomics for deep taxonomic and functional characterization of microbiomes from non-sequenced hosts

Duarte Gouveia[1], Olivier Pible[1], Karen Culotta[1], Virginie Jouffret[1], Olivier Geffard[2], Arnaud Chaumot[2], Davide Degli-Esposti[2], Jean Armengaud[1]*

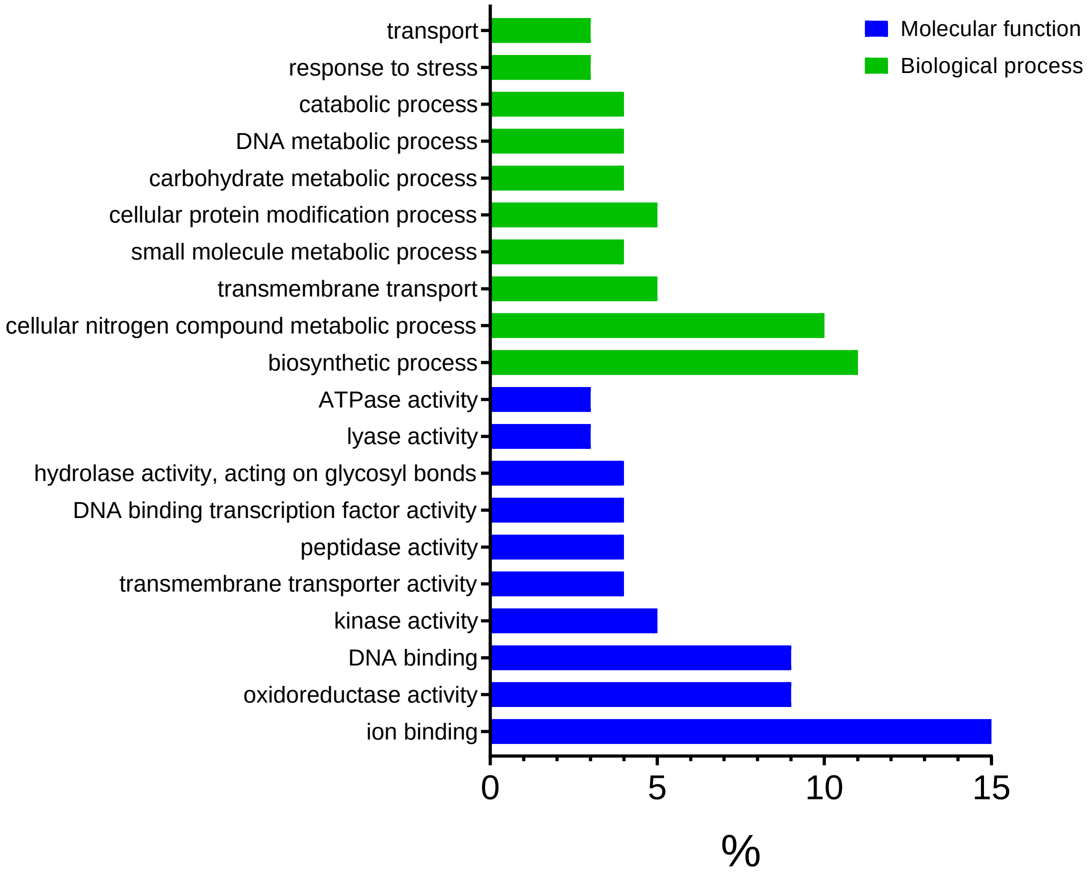
[1] Laboratoire Innovations technologiques pour la Détection et le Diagnostic (Li2D), Service de Pharmacologie et Immunoanalyse (SPI), CEA, INRA, F-30207 Bagnols-sur-Cèze, France.

[2] Irstea, UR Riverly Laboratoire d'écotoxicologie, centre de Lyon-Villeurbanne, F-69625 Villeurbanne, France.

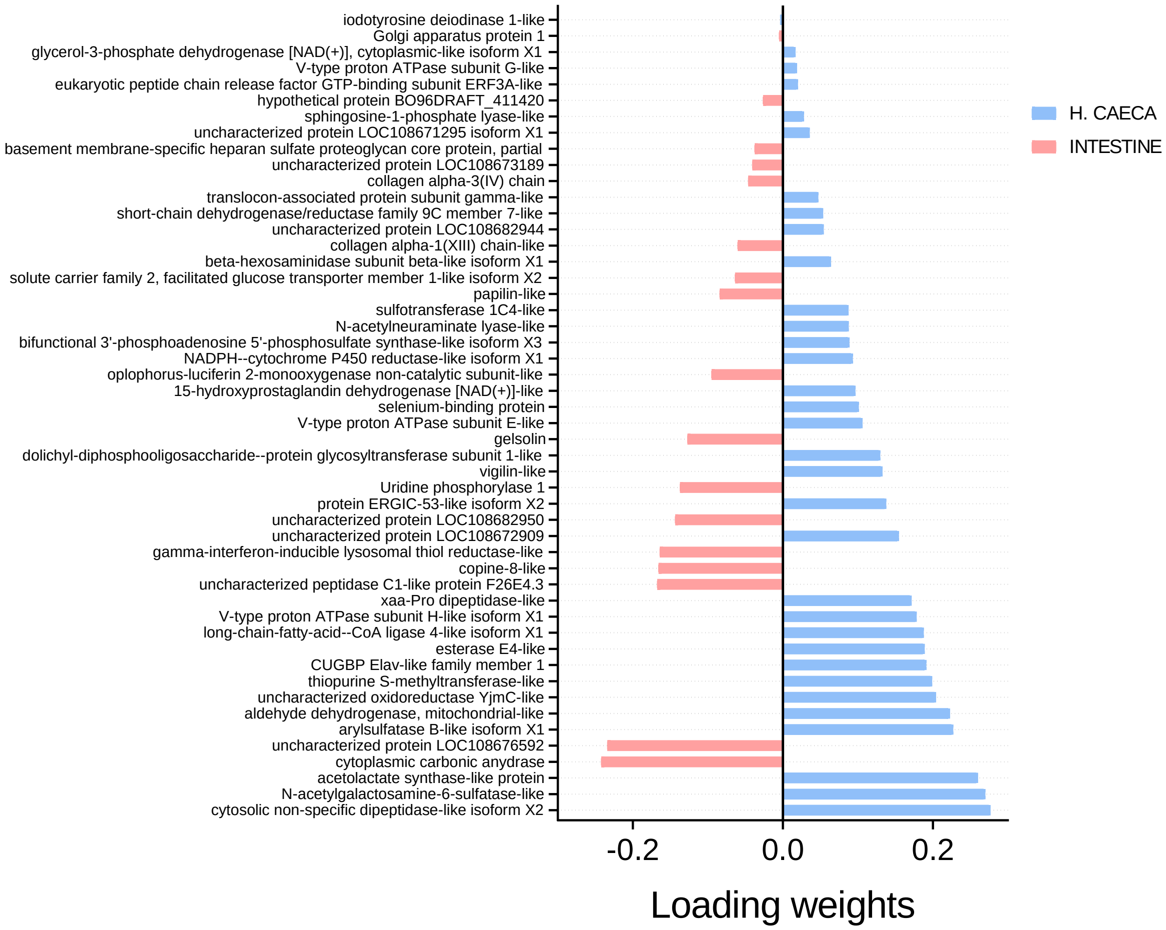
*** Corresponding author**

Jean Armengaud, CEA-Marcoule, DRF-Li2D, Laboratory "Innovative technologies for Detection and Diagnostics", BP 17171, F-30200 Bagnols-sur-Cèze, France;

jean.armengaud@cea.fr; Tel: +00 33 4 66 79 68 02; Fax: +00 33 4 66 79 19 05.



Supplementary Figure 1 - The ten most abundant GOslim terms for the categories "Molecular Function" and "Biological Process", obtained through annotation of proteins from the microbiota.



Supplementary Figure 2 - Loadings from the sPLS-DA analysis comprising the fifty host protein groups that best discriminate HC from INT.

Captions for the Supplementary Data Sets

Supplementary Data 1: Taxa selected in step 1 for the construction of the sub-databases.

Supplementary Data 2: Results of database searches for each step of the pipeline.

Supplementary Data 3: List of identified genus and their relative abundances based on the number of total and specific TSMs, and number of specific peptides.

Supplementary Data 4: List of protein groups identified in Step 3.

Supplementary Data 5: List of GOslim annotations and their relative abundances.

Supplementary Data 6: List of genus associated with biosynthetic process and cellular nitrogen compound metabolic process

Supplementary Data 7: Univariate non-parametric statistics performed on the discriminant features from sPLS-DA.