

# Supplementary Materials

Figure S1. Biochemical markers and microbiota composition: Family and Genus.

| Family    |                       |                       | Genus     |                 |                         |
|-----------|-----------------------|-----------------------|-----------|-----------------|-------------------------|
| Variables | Univariant test       | Metagenome Seq        | Variables | Univariant test | Metagenome Seq          |
| AST       | Pasteurellaceae ↑     | Pasteurellaceae ↑     | AST       |                 | Phascolarctobacterium ↑ |
|           | Oscillospiraceae ↓    | Oscillospiraceae ↓    |           |                 | Haemophilus ↑           |
|           |                       | Lactobacillaceae ↓    |           |                 | Lactobacillus ↓         |
|           |                       | Rikenellaceae ↓       |           |                 |                         |
|           |                       | Porphyromonadaceae ↓  |           |                 |                         |
| HDL-c     | Christensenellaceae ↑ | Christensenellaceae ↑ | Insulin   |                 | Phascolarctobacterium ↑ |
|           | Peptococcaceae ↓      | Peptococcaceae ↓      |           |                 | Peptococcus ↑           |
|           |                       |                       |           |                 | Butyricicoccus ↓        |
|           |                       |                       |           |                 |                         |

↑ Represents higher abundance of bacteria compared to the median of the individuals  
↓ Represents lower abundance of bacteria compared to the median of the individuals

Figure S2. Nutritional markers and microbiota composition: Family.

| Family                  |                              |                       |
|-------------------------|------------------------------|-----------------------|
| Variables               | Univariant test              | Metagenome Seq        |
| Protein intake          |                              |                       |
|                         | Unclassified clostridiales ↑ |                       |
| Carbohydrate intake (%) |                              | Enterobacteriaceae ↑  |
| Fibre intake            |                              | Melainabacteriaceae ↓ |
| Fruit intake            |                              | Enterobacteriaceae ↑  |
|                         |                              | Eubacteriaceae ↑      |
|                         |                              | Streptococcaceae ↑    |
| Whole grains            |                              | Melainabacteriaceae ↓ |
| Yogurt                  |                              | Lactobacillaceae ↑    |
| Fermented dairy         |                              | Lactobacillaceae ↑    |
| Soda light              |                              | Clostridiaceae ↓      |
|                         |                              | Methanobacteriaceae ↓ |
|                         |                              | Dehalobacteriaceae ↓  |
| Olive oil               |                              | Verrucomicrobiaceae ↑ |
| Saturated fats          |                              | Acidaminococcaceae ↑  |

↑ Represents higher abundance of bacteria in the group of individuals above the median  
↓ Represents lower abundance of bacterian in the group of individuals above the median

Figure S3. Nutritional markers and microbiota composition: Genus

| Genus               |                 |   |
|---------------------|-----------------|---|
| Variables           | Univariant test | Metagenome Seq                                      |
| Total energy        |                 | Paraprevotella ↑                                    |
| Whole grains        |                 | Melainabacter ↓                                     |
| Soda light          |                 | Ruminococcus ↑<br>Eggerthella ↑                     |
| Olive oil           |                 | Phascolarctobacterium ↑<br>Desulfovibrio ↓          |
| Meat intake         | Oscilospira ↓   | Oscilospira ↓<br>Phascolarctobacterium ↑            |
| Cold meat           | Butyricoccus ↓  |   |
| Trans fat           |                 | Phascolarctobacterium ↑                             |
| Monounsaturated fat |                 | Phascolarctobacterium ↑                             |
| Polyunsaturated fat |                 | Butyricoccus ↑                                      |
| Saturated fat       |                 | Phascolarctobacterium ↑<br>Erysipelatoclostridium ↓ |

↑ Represents higher abundance of bacteria in the group of individuals above the median  
↓ Represents lower abundance of bacterian in the group of individuals above the median