# 1 Supplementary Figures and Tables

## Supplementary Tables

**Supplementary Table S1** Spearman association analysis between gut microbiota and glucolipid metabolism parameters at the genus level

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Bacterial genera |  | Glucolipid metabolism parameters | | | | |
| GLU | TG | TC | LDL | HDL |
| *Bacteroides* | r | -0.200 | -0.203 | -0.314 | 0.232 | -0.928\*\* |
| p | 0.704 | 0.700 | 0.544 | 0.658 | 0.008 |
| *Akkermansia* | r | -0.429 | -0.174 | -0.543 | 0.406 | -0.841\* |
| p | 0.397 | 0.742 | 0.266 | 0.425 | 0.036 |
| *unidentified\_Ruminococcaceae* | r | 0.886\* | 0.348 | 0.771 | 0.058 | 0.638 |
| p | 0.019 | 0.499 | 0.072 | 0.913 | 0.173 |
| *Desulfovibrio* | r | -0.200 | -0.203 | -0.314 | 0.232 | -0.928\*\* |
| p | 0.704 | 0.700 | 0.544 | 0.658 | 0.008 |
| *X.Eubacterium.\_coprostanoligenes\_group* | r | -0.771 | -0.812\* | -1.000\*\* | 0.203 | -0.290 |
| p | 0.072 | 0.049 | 0.000 | 0.700 | 0.577 |
| *Romboutsia* | r | 0.943\*\* | 0.638 | 0.714 | 0.464 | 0.493 |
| p | 0.005 | 0.173 | 0.111 | 0.354 | 0.321 |
| *Coprococcus\_2* | r | 0.371 | 0.812\* | 0.829\* | -0.406 | -0.203 |
| p | 0.468 | 0.049 | 0.042 | 0.425 | 0.700 |
| *Blautia* | r | 0.771 | 0.493 | 0.886\* | -0.232 | 0.580 |
| p | 0.072 | 0.321 | 0.019 | 0.658 | 0.228 |
| *Ruminiclostridium\_6* | r | 0.771 | 0.493 | 0.886\* | -0.232 | 0.580 |
| p | 0.072 | 0.321 | 0.019 | 0.658 | 0.228 |
| *Turicibacter* | r | 0.771 | 0.928\*\* | 0.886\* | 0.029 | 0.232 |
| p | 0.072 | 0.008 | 0.019 | 0.957 | 0.658 |
| *Ruminiclostridium\_5* | r | 0.086 | 0.000 | 0.200 | -0.232 | 0.841\* |
| p | 0.872 | 1.000 | 0.704 | 0.658 | 0.036 |
| *Parabacteroides* | r | -0.829\* | -0.667 | -0.943\*\* | 0.058 | -0.493 |
| p | 0.042 | 0.148 | 0.005 | 0.913 | 0.321 |
| *Oligella* | r | 0.314 | 0.928\*\* | 0.771 | -0.319 | -0.116 |
| p | 0.544 | 0.008 | 0.072 | 0.538 | 0.827 |
| *Clostridium\_sensu\_stricto\_1* | r | 0.600 | 0.551 | 0.714 | -0.232 | 0.841\* |
| p | 0.208 | 0.257 | 0.111 | 0.658 | 0.036 |
| *Bifidobacterium* | r | 0.143 | 0.319 | 0.257 | 0.116 | -0.812\* |
| p | 0.787 | 0.538 | 0.623 | 0.827 | 0.049 |

r: The r value meant correlation coefficient between -1 and 1, r<0 was negative correlation, r> was positive correlation.

p: p-value

\*Correlation was significant at the 0.05 level, \*\*Correlation was significant at the 0.01 level.

**Supplementary Table S2** Spearman association analysis between gut microbiota and serum hormones at the genus level

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Bacterial genera |  | Serum hormone | | | | |
| Ghrelin | T4 | LEP | INS | ADP |
| *X.Eubacterium.\_coprostanoligenes\_group* | r | 0.429 | 0.143 | -0.371 | -0.371 | 0.371 |
| p | 0.397 | 0.787 | 0.468 | 0.468 | 0.468 |
| *Romboutsia* | r | -0.714 | -0.714 | 0.771 | 0.486 | -0.771 |
| p | 0.111 | 0.111 | 0.072 | 0.329 | 0.072 |
| *Roseburia* | r | -0.029 | 0.371 | -0.029 | 0.200 | 0.029 |
| p | 0.957 | 0.468 | 0.957 | 0.704 | 0.957 |
| *Turicibacter* | r | -0.600 | -0.371 | 0.657 | 0.486 | -0.657 |
| p | 0.208 | 0.468 | 0.156 | 0.329 | 0.156 |
| *Lactobacillus* | r | 0.029 | 0.371 | -0.200 | 0.086 | 0.200 |
| p | 0.957 | 0.468 | 0.704 | 0.872 | 0.704 |
| *Oligella* | r | -0.200 | -0.029 | 0.257 | 0.257 | -0.257 |
| p | 0.704 | 0.957 | 0.623 | 0.623 | 0.623 |
| *Anaerotruncus* | r | 0.486 | 0.257 | -0.543 | -0.600 | 0.543 |
| p | 0.329 | 0.623 | 0.266 | 0.208 | 0.266 |
| *Coprococcus\_1* | r | 0.771 | 0.257 | -0.600 | -0.829\* | 0.600 |
| p | 0.072 | 0.623 | 0.208 | 0.042 | 0.208 |

r: The r value meant correlation coefficient between -1 and 1, r<0 was negative correlation, r> was positive correlation.

p: p-value

\*Correlation was significant at the 0.05 level, \*\*Correlation was significant at the 0.01 level.