

**Table. S2**

Partial correlations between human parameters and gut microbiota at genus level in OG

<b>Parameters</b>	<b>Genus in OG</b>	<b>r</b>	<b>p value</b>
LH	<i>Dialister</i>	-0.407	0.025
	<i>Romboutsia</i>	-0.385	0.036
FSH	<i>Ruminococcaceae_UCG-014</i>	0.470	0.009
DHEA	<i>Ruminococcus_torques_group</i>	0.553	0.002
	<i>Sutterella</i>	-0.370	0.044
PRL	<i>Lachnospirillum</i>	0.587	0.001
	<i>Ruminococcaceae_UCG-014</i>	-0.434	0.017
	<i>Ruminococcus_gnavus_group</i>	0.366	0.047
E2	<i>Escherichia-Shigella</i>	-0.530	0.003
	<i>Subdoligranulum</i>	0.512	0.004
	<i>Collinsella</i>	0.436	0.016
	<i>Ruminococcus_gnavus_group</i>	-0.428	0.018
	<i>Sutterella</i>	0.398	0.030
	<i>Agathobacter</i>	0.392	0.032
T	<i>Ruminococcus_2</i>	0.529	0.003
	<i>Collinsella</i>	0.371	0.043
FBG	<i>Haemophilus</i>	-0.393	0.032
	<i>Megasphaera</i>	-0.382	0.037
Insulin_0min	<i>Streptococcus</i>	-0.521	0.003
	<i>Roseburia</i>	-0.475	0.008
	<i>Paraprevotella</i>	0.366	0.047
	<i>Agathobacter</i>	-0.362	0.049
Insulin_30min	<i>Lachnospiraceae_UCG-004</i>	-0.440	0.015
	<i>Streptococcus</i>	-0.437	0.016
Insulin_60min	<i>Faecalibacterium</i>	-0.467	0.010
	<i>Dorea</i>	0.394	0.031
Insulin_90min	<i>Lachnospiraceae_UCG-004</i>	-0.551	0.002
Insulin_180min	<i>Butyricicoccus</i>	-0.451	0.012

r, the correlation coefficient used to measure the linear relationship between two variables.