

**Table. S1**

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

<b>Parameters</b>	<b>Genus in NG</b>	<b>r</b>	<b>p value</b>
LH	<i>Ruminococcaceae_UCG-002</i>	0.395	0.034
FSH	<i>Dialister</i>	0.426	0.021
	<i>Veillonella</i>	0.399	0.032
DHEA	<i>Roseburia</i>	0.085	0.023
	<i>Agathobacter</i>	-0.378	0.043
PRL	<i>Lachnoclostridium</i>	-0.456	0.013
E2	<i>Parasutterella</i>	0.466	0.011
	<i>Dialister</i>	0.439	0.017
T	<i>Prevotella_2</i>	0.410	0.027
	<i>Megasphaera</i>	0.381	0.041
FBG	<i>Megamonas</i>	-0.409	0.028
Insulin_0min	<i>Bifidobacterium</i>	-0.433	0.019
	<i>Collinsella</i>	-0.368	0.049
Insulin_60min	<i>Lachnospiraceae_unclassified</i>	-0.609	0.0004
	<i>Ruminococcaceae_UCG-002</i>	0.475	0.009
	<i>Lachnoclostridium</i>	-0.473	0.010
	<i>Prevotella_2</i>	0.434	0.019
	<i>Lachnospiraceae_NK4A136_group</i>	0.419	0.024
	<i>Coprococcus_2</i>	0.410	0.027
	<i>Ruminococcaceae_UCG-005</i>	0.407	0.028
	<i>Ruminococcus_gnavus_group</i>	-0.407	0.028
	<i>Eubacterium_coprostanoligenes_group</i>	0.371	0.047
	Insulin_90min	<i>Lachnospiraceae_unclassified</i>	-0.473
<i>Streptococcus</i>		-0.445	0.015
<i>Klebsiella</i>		-0.423	0.022
<i>Ruminococcaceae_UCG-014</i>		0.406	0.029
<i>Parabacteroides</i>		-0.406	0.029
<i>Coprococcus_2</i>		0.403	0.030
<i>Lachnospiraceae_UCG-004</i>		0.398	0.032
Insulin_120min	<i>Ruminococcaceae_UCG-014</i>	0.414	0.026
	<i>Lachnospiraceae_unclassified</i>	-0.408	0.028
	<i>Lachnospiraceae_UCG-004</i>	0.407	0.028
	<i>Coprococcus_2</i>	0.398	0.033
Insulin_180min	<i>Klebsiella</i>	-0.509	0.005
	<i>Lachnospiraceae_unclassified</i>	-0.508	0.005
	<i>Lachnospiraceae_uncultured</i>	-0.444	0.016
	<i>Bifidobacterium</i>	-0.373	0.046

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