

**Supplemental Table 4.** Correlation between indices of deconjugation or 7 $\alpha$ -dehydroxylation in serum and gut microbiota in HFD-fed mice

Taxon	Deconjugation			7 $\alpha$ -Dehydroxylation	
	CA/ (CA + Tauro-CA)	$\beta$ -MCA/ ( $\beta$ -MCA + Tauro- $\beta$ -MCA)	DCA/ (DCA + Tauro-DCA)	DCA/ (DCA + CA)	LCA/ (LCA + CDCA)
<i>g__Adlercreutzia</i>	0.81*	0.88*	0.51	-0.52	-0.29
<i>o__Bacteroidales; f__Unclassified</i>	-0.36	-0.71*	0.00	0.19	0.68*
<i>g__Bacteroides</i>	0.37	0.37	-0.35	-0.10	-0.32
<i>g__Parabacteroides</i>	0.73*	0.63*	0.62*	-0.74*	-0.16
<i>f__Rikenellaceae; g__Unclassified</i>	-0.43	-0.79*	-0.14	0.26	0.69*
<i>f__S24-7; g__Unclassified</i>	-0.35	-0.51	0.21	0.17	0.46
<i>g__[Prevotella]</i>	0.48	0.41	0.45	-0.52	-0.04
<i>g__Mucispirillum</i>	-0.37	-0.80*	-0.62*	0.41	0.45
<i>g__Lactobacillus</i>	-0.51	-0.21	0.11	0.40	0.06
<i>g__Lactococcus</i>	-0.56	-0.07	0.05	0.40	-0.24
<i>o__Clostridiales; g__Unclassified</i>	-0.39	-0.62*	-0.12	0.37	0.51
<i>f__Lachnospiraceae; g__Unclassified</i>	-0.88*	-0.62*	-0.41	0.66*	0.03
<i>f__Lachnospiraceae; g__Clostridium</i>	-0.54	-0.29	-0.49	0.57	-0.04
<i>g__[Ruminococcus]</i>	-0.72*	-0.53	-0.11	0.63*	0.27
<i>f__Ruminococcaceae; g__Unclassified</i>	0.45	0.66*	0.37	-0.55	-0.37
<i>g__Anaerotruncus</i>	-0.83*	-0.61*	-0.72*	0.71*	-0.15
<i>g__Oscillospira</i>	-0.54	-0.77*	-0.59*	0.63*	0.46
<i>g__Allobaculum</i>	0.82*	0.70*	0.62*	-0.86*	-0.26
<i>f__Erysipelotrichaceae; g__Clostridium</i>	0.57	0.53	0.35	-0.72*	-0.28
<i>g__Sutterella</i>	0.35	0.50	0.15	-0.37	-0.42
<i>f__Desulfovibrionaceae; g__Unclassified</i>	-0.91*	-0.64*	-0.39	0.76*	0.03
<i>g__Akkermansia</i>	0.94*	0.84*	0.60*	-0.82*	-0.19
Others	0.16	0.41	0.12	-0.14	-0.36

JMP statistical software was used to calculate Pearson's correlation coefficient (*r*). C57BL/6N mice were fed with a high-fat diet (HFD), or the HFD supplemented with 0.32% EGCG (HFD + EGCG) for 8 weeks. Values are expressed six mice in each group; \**p*<0.05.