

Supplementary material

Fig. S1 Short-chain fatty acids standard chromatograms

Fig. S2 Heatmap of the mice gut microbiota in species level

Fig. S3 Correlation analysis at order classification level

Fig. S4 Correlation analysis at family classification level

Fig. S5 Correlation analysis at genus classification level

Fig. S6 Correlation analysis at species classification level

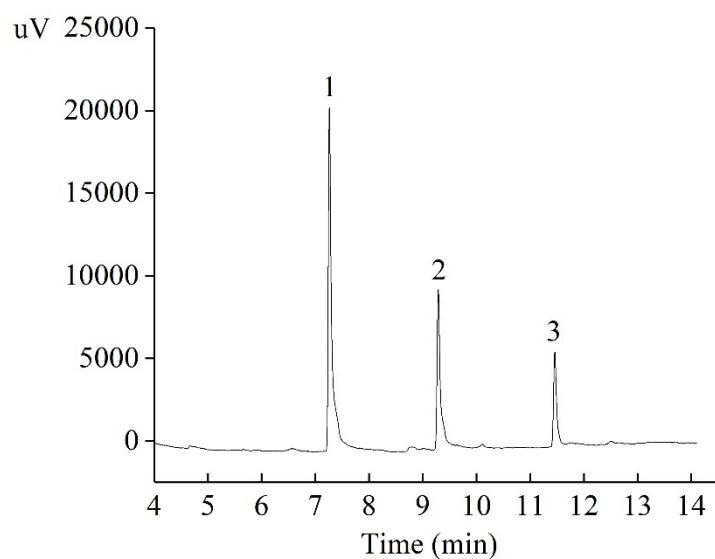


Fig. S1 Short-chain fatty acids standard chromatograms

1: Acetic acid, 7.201 min; 2: Propionic acid, 9.217 min, 3: Butyric acid, 11.392 min. Fecal short-chain fatty acids were measured using 2010 plus gas chromatography equipped with a flame ionization detector (FID) and a Nukol capillaries column (30 m \times 0.32 mm \times 0.25 μ m). The temperature of injection port and detector were 220 $^{\circ}$ C and 250 $^{\circ}$ C. The initial oven temperature was 60 $^{\circ}$ C, then increased to 190 $^{\circ}$ C at a rate of 20 $^{\circ}$ C/min and maintained for 3 min. Split ratio was 20:1. The nitrogen, hydrogen and air were used as carrier gas at a flow rate of 75 mL/min, 70 mL/min and 50 mL/min. The injection volume was 1 μ L.

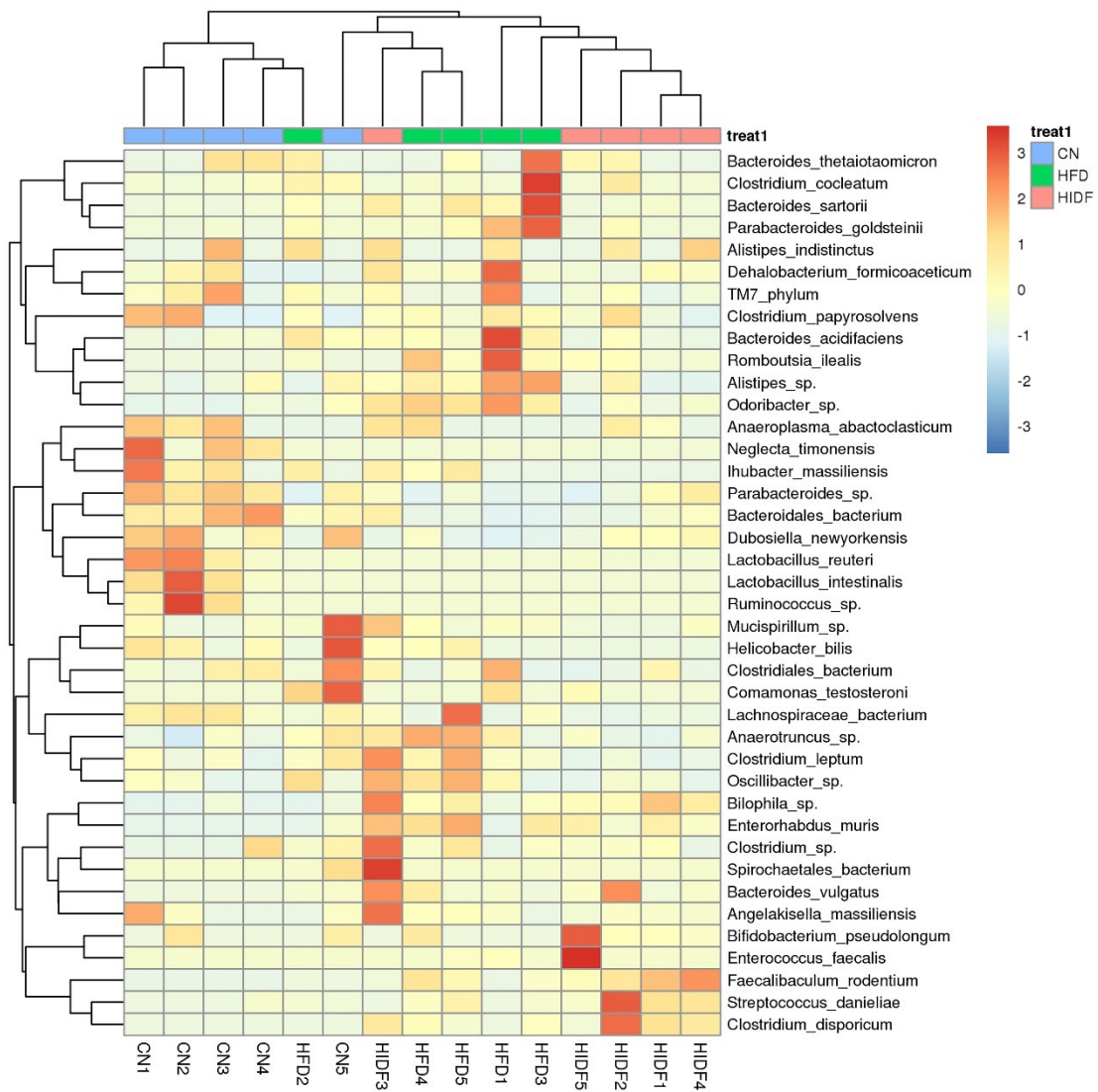


Fig. S2 Heatmap of the mice gut microbiota in species level

CN: Control, HFD: High-fat diet, H1DF: High-does insoluble dietary fiber.

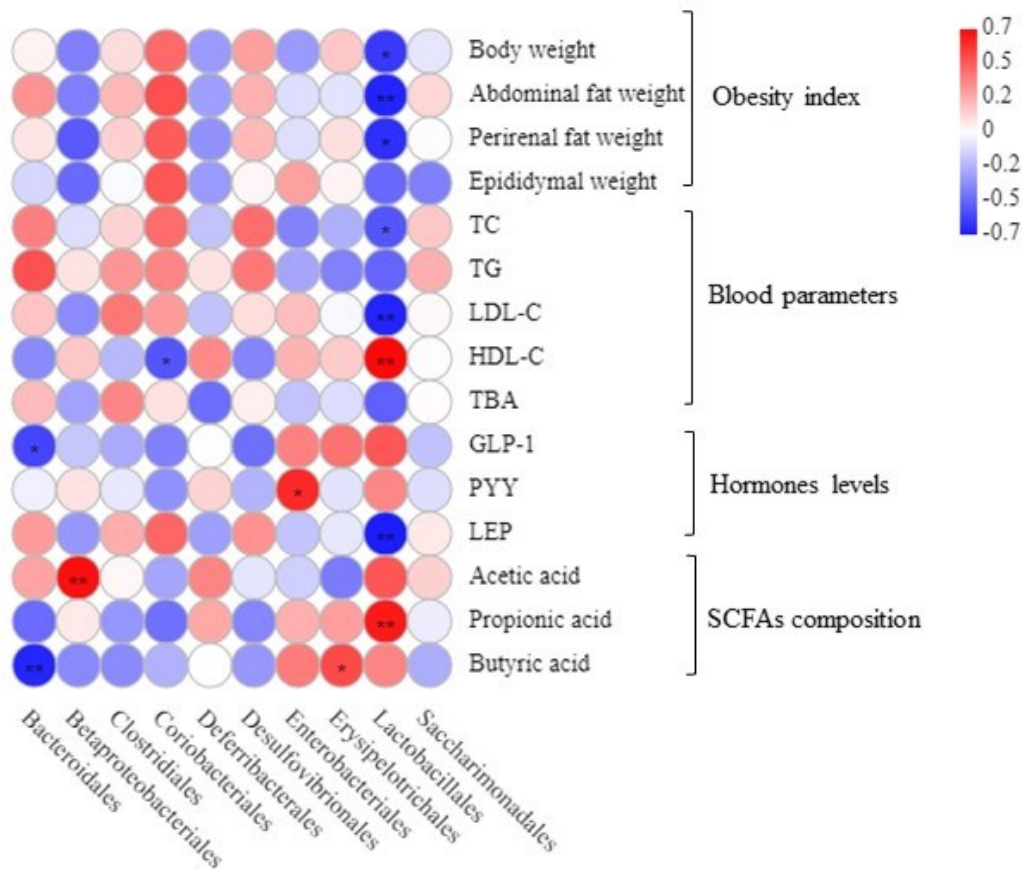


Fig. S3 Correlation analysis at order classification level

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

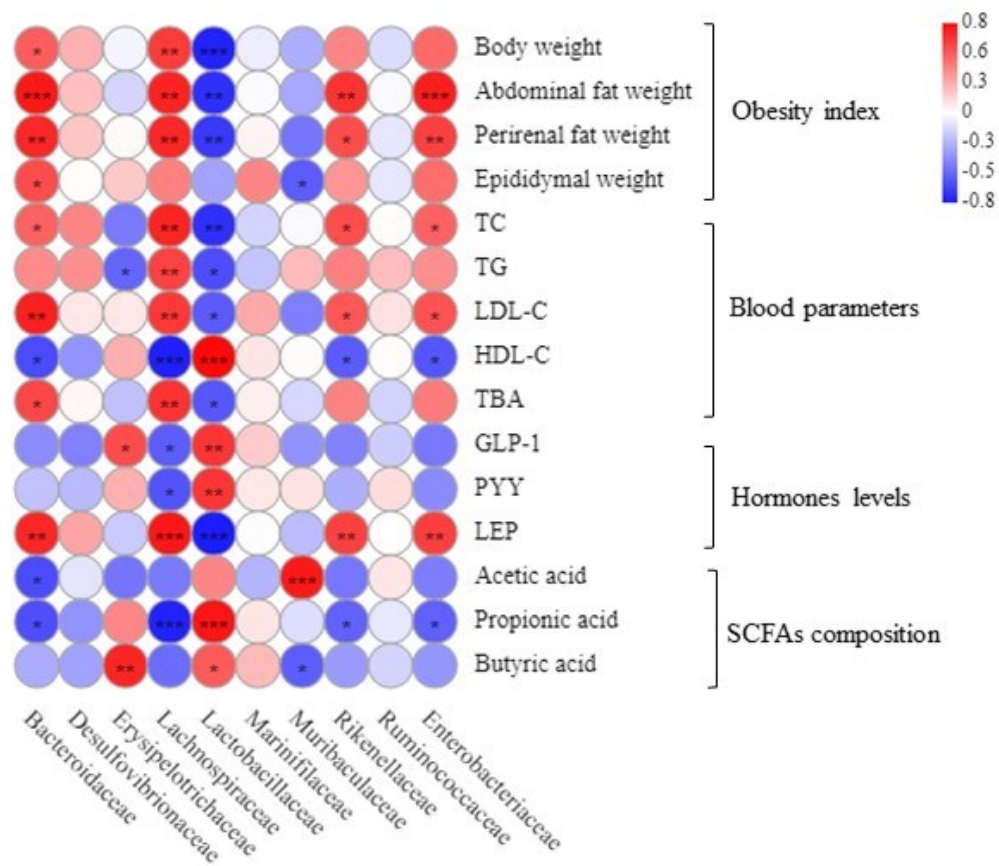


Fig. S4 Correlation analysis at family classification level

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

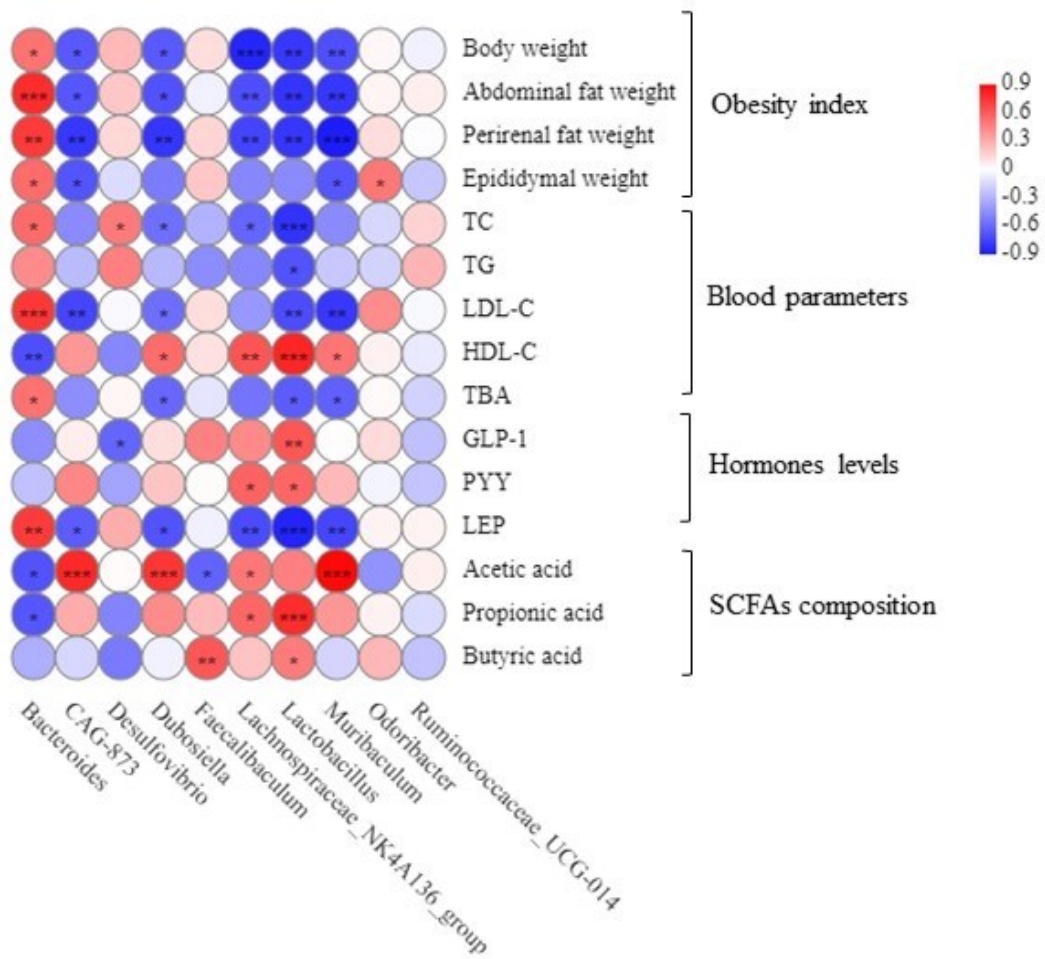


Fig. S5 Correlation analysis at genus classification level

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

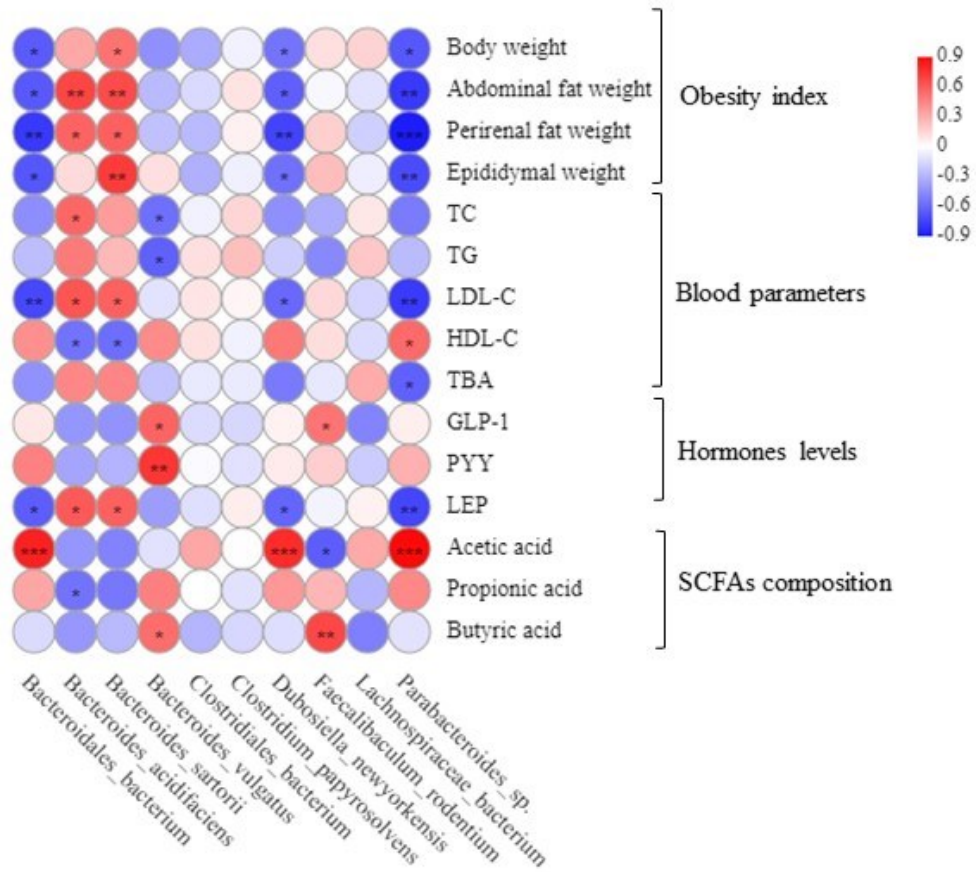


Fig. S6 Correlation analysis at species classification level
 * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.