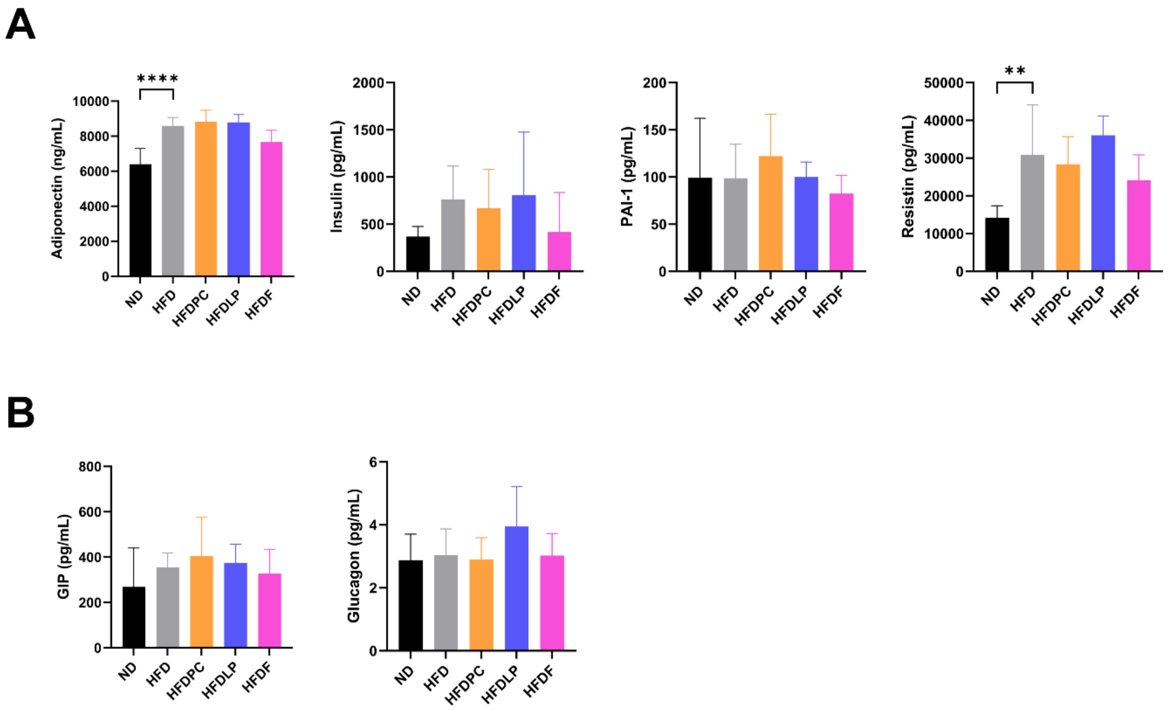
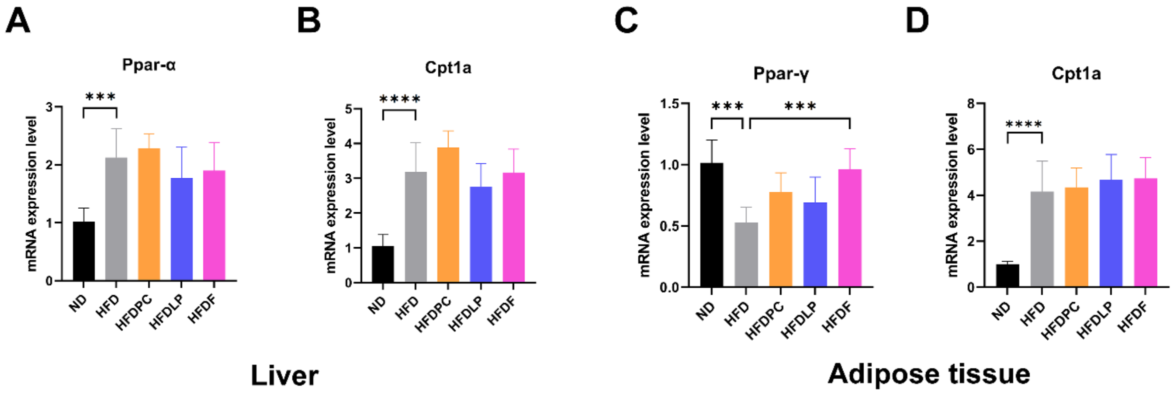
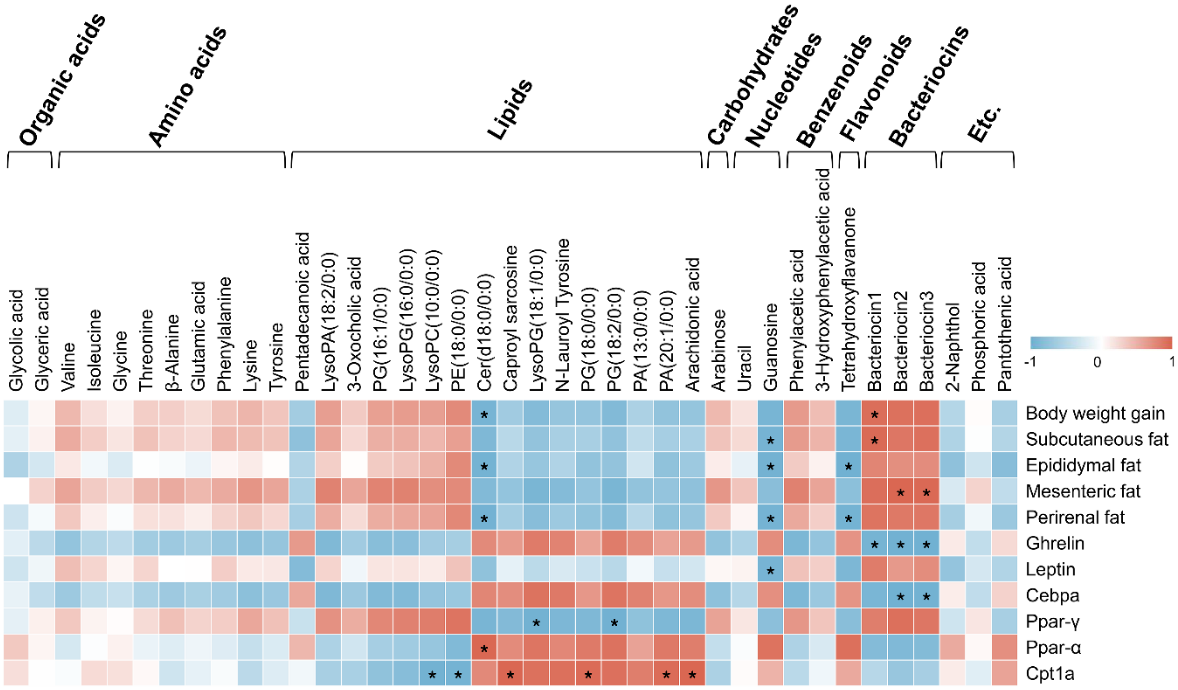
Supplementary Figures



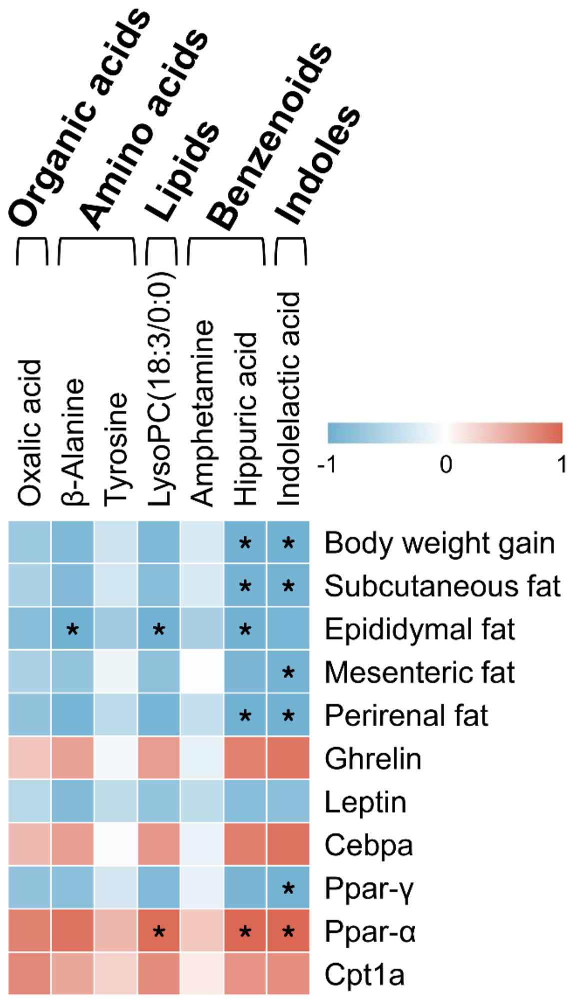
Supplementary figure 1. Obesity-related hormone level in the plasma of probiotic-administered mice. (A) Graphs showing the results of quantitative analysis of hormones with decreasing tendency, namely, adiponectin, insulin, PAI-1, and resistin. (B) Graphs showing the results of quantitative analysis of hormones with no change in level, namely, GIP and glucagon. Values represent the mean ± SD (n = 6 per group). Significance is indicated by *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, and ****$p < 0.0001$ as compared with the ND group. ***HFD***, High fat diet; ***HFDPC***, HFD group treated with BEPC22; ***HFDLP***, HFD group treated with BELP53*;* ***HFDF,*** HFD group treated with the combination of two strains.



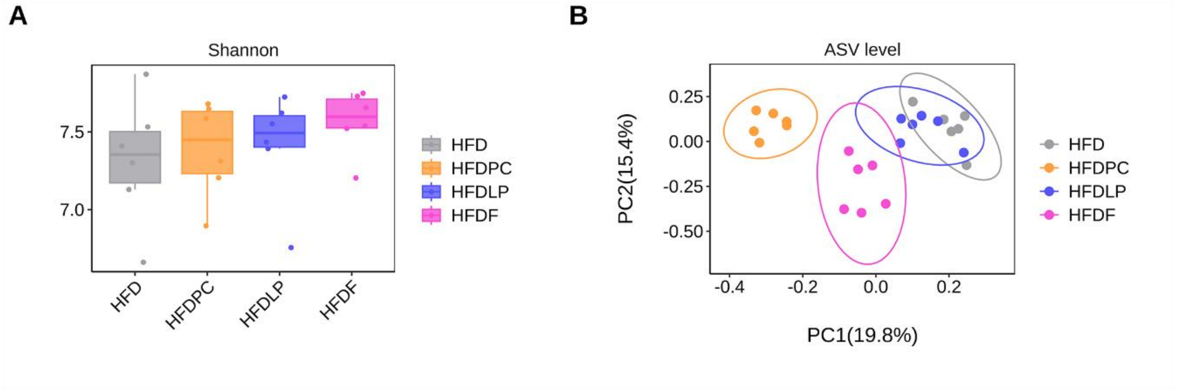
Supplementary figure 2. mRNA expression of obesity-related genes in the liver and white adipose tissue. (A–B) Graphs showing results of the qPCR analysis of *Ppar-α* and *Ucp2* in the liver and (C–E) *Ppar-γ*, *Fasn*, and *Cpt1a* in the epididymal adipose tissue. Values represent the mean ± SD (n = 6 per group). Significance is indicated by **p* < 0.05, ***p* < 0.01, ****p* < 0.001, and *****p* < 0.0001 as compared with the ND group. *BEPC22*, *Lacticaseibacillus paracasei*; *BELP53*, *Lactiplantibacillus plantarum*; *Ppar-α* or *γ*, Peroxisome proliferator-activated receptor alpha or gamma; *Ucp2*, Uncoupling protein2; *Fasn*, Fatty acid synthase; *Cpt1a*, Carnitine palmitoyltransferase1a.



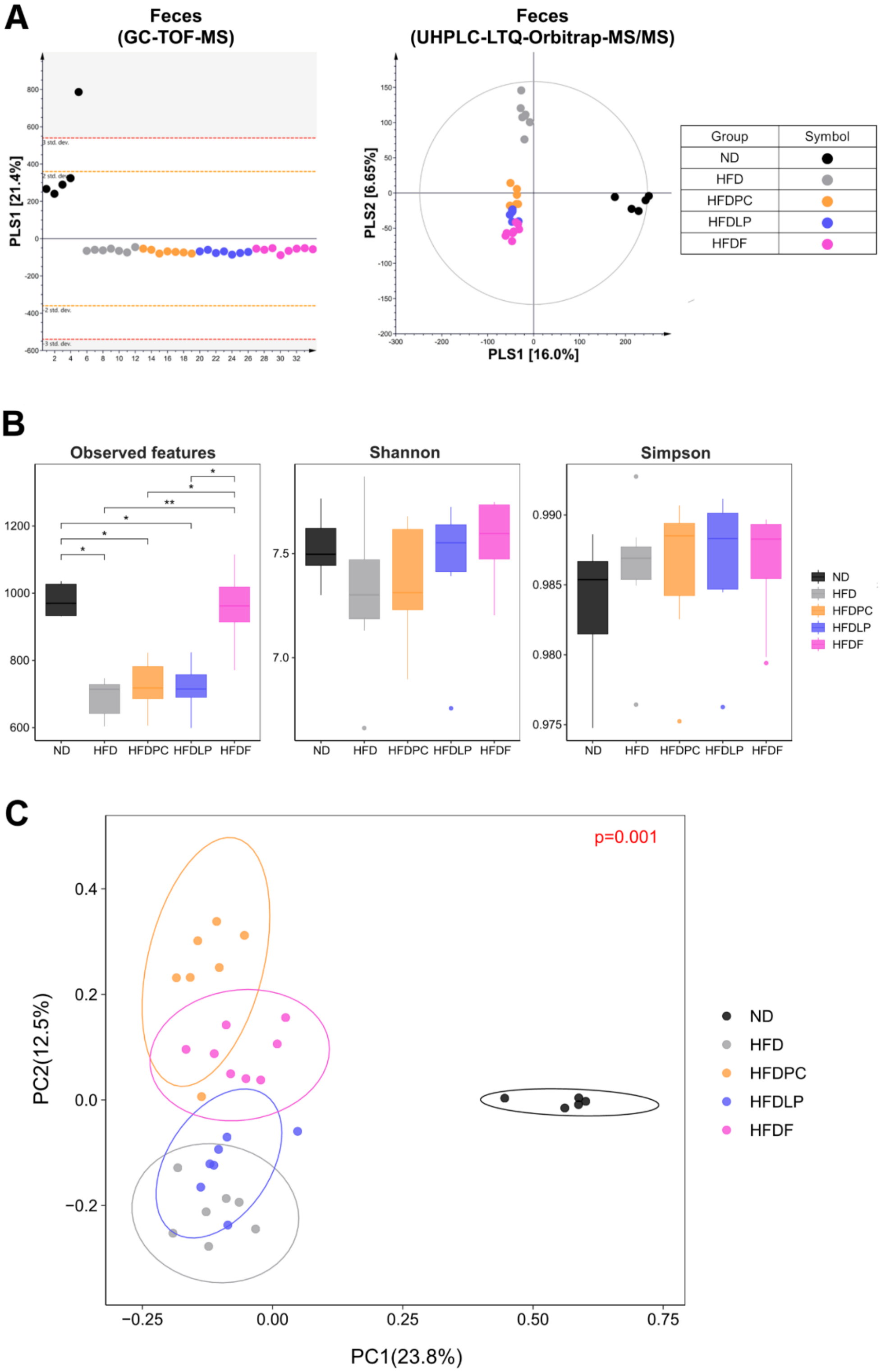
Supplementary figure 3. Correlation map between the metabolite levels of faeces and observed mouse phenotypes. Each square implies Pearson's correlation coefficient between metabolites and assayed activities. Red indicates a positive (0 < r < 1) correlation, and blue indicates a negative (−1 < r < 0) correlation. Asterisks indicate *p*-values < 0.05.



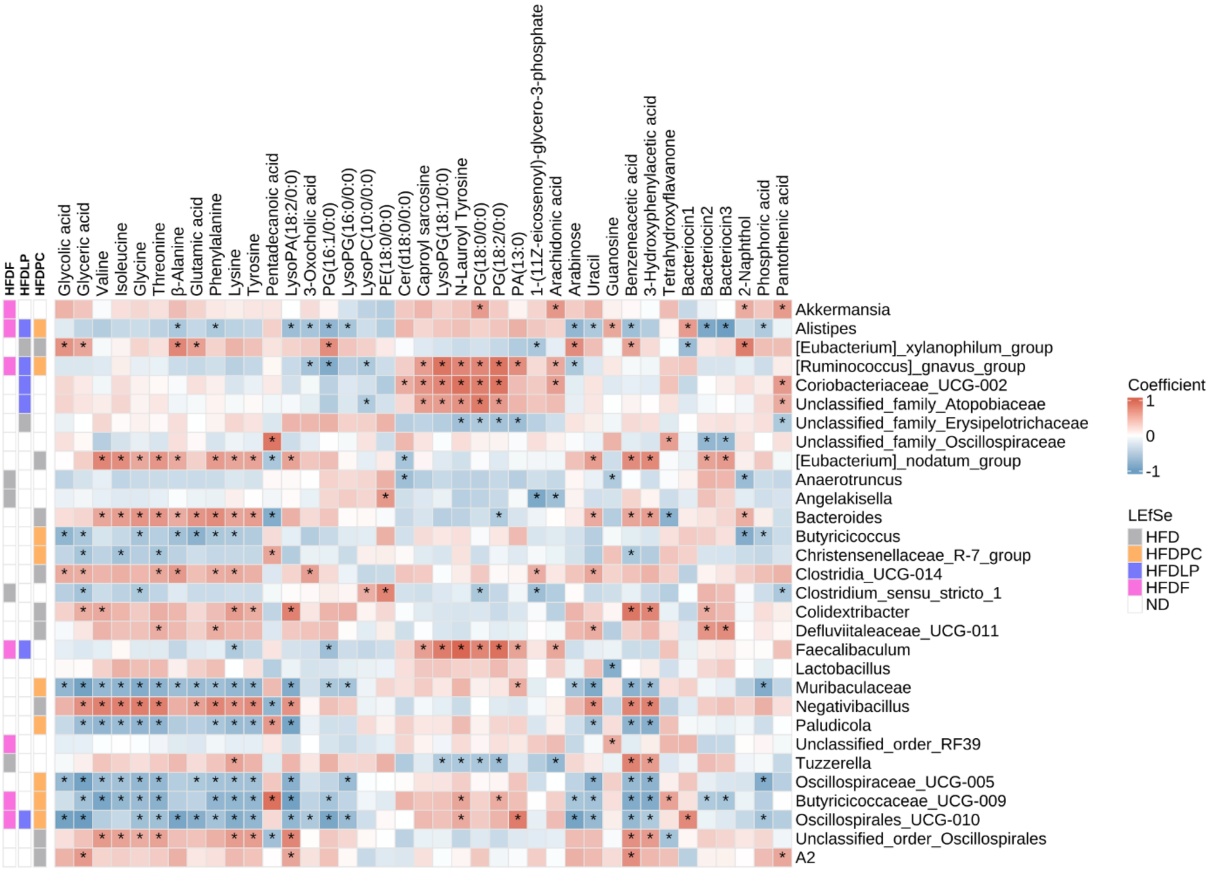
Supplementary figure 4. Correlation map between the metabolite levels of plasma and observed mouse phenotypes. Each square implies Pearson’s correlation coefficient between metabolites and assayed activities. Red indicates a positive ($0 < r < 1$) correlation, and blue indicates a negative ($-1 < r < 0$) correlation. Asterisks indicate *p*-values < 0.05.



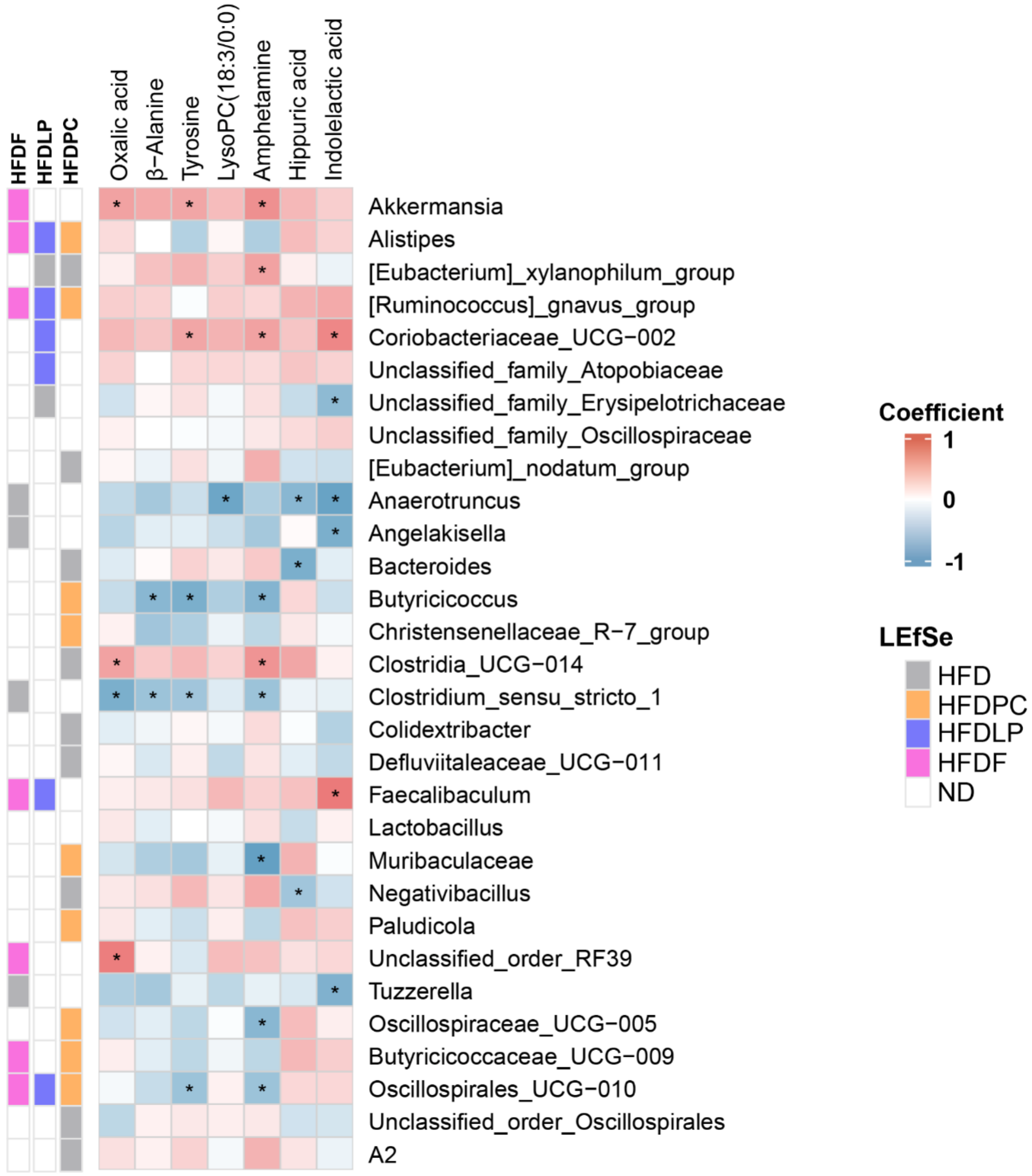
Supplementary figure 5. Comparison of the gut microbiota diversity between the groups. Alpha diversity comparisons using (A) the Shannon index. Beta diversity at (B) the ASV level as revealed by principal component analysis.



Supplementary figure 6. Comparison of the gut microbiota diversity between the groups including ND group. Sparse partial least-squares discriminant analysis (PLS-DA) score plots for the metabolome of faeces five groups based on GC-TOF-MS and UHPLC-LTQ-Orbitrap-MS/MS data sets (A). Alpha diversity comparisons using (B) the Observed features, Shannon index and Simpson index. Beta diversity at (C) the ASV level as revealed by principal component analysis.



Supplementary figure 7. Correlation map between the metabolite levels of faeces and observed gut microbiota. Each square implies Pearson's correlation coefficient between metabolites and assayed activities. Red indicates a positive (0 < r < 1) correlation, and blue indicates a negative (−1 < r < 0) correlation. Asterisks indicate *p*-values < 0.05.



Supplementary figure 8. Correlation map between the metabolite levels of plasma and observed gut microbiota. Each square implies Pearson's correlation coefficient between metabolites and assayed activities. Red indicates a positive (0 < r < 1) correlation, and blue indicates a negative (−1 < r < 0) correlation. Asterisks indicate *p*-values < 0.05.