Fig. S1 Schematic diagram of experimental design. CPs, Bus, Bus + CPs treated mice, respectively. Collected sample and intestinal content to conduct 16s rRNA sequencing followed by bioinformatic analysis.

Fig. S2 The bioinformatic analysis of gut microbiota. (A) The species richness in Ctrl, CPs, Bus, and Bus +CPs groups. (B)The microbiota relative abundance at the genus level.

Fig. S3 The bioinformatic analysis of gut microbiota. (A)The heatmap of dominant bacteria at the phylum level. (B) The figure of random forest classification. (C) The abundance of dominant bacteria at the phylum level.

Fig. S4 (A) Extended error bar plot showing the functional pathway that had differences between the Ctrl and Bus groups. (B) Extended error bar plot showing the functional pathway that had differences between the Bus and Bus + CPs groups.

Table S1 Information on the antibodies used in this paper.

Antibodies	**Vendor**	**Dilution**
HSD17β1 (IF)	Bioss (bs-6603R)	1:150
CYP17A1 (IF)	Bioss (bs-6695R)	1:150
Claudin1 (IF)	Bioss (bs-1428R)	1:500
Zo-1 (IF)	Bioss (bs-1329R)	1:500
Occludin (IF)	Bioss (bs-10011R)	1:150
VASA (IF)	Abcam(ab13840)	1:150
Desmoglein2 (IF)	Abcam (ab150372)	1:150

Table S2 Primers used for quantitative RT-PCR.

Genes	**GenBank**	**Forward primer sequences**	**Reverse primer sequences**
Cldn1	NC_000082.7	CTTGACCCCCATCAATGC	CACCTCCCAGAAGGCAGA
Cldn3	NC_000071.7	GCAAGCAGACTGTGTGTCGT	TACCGTCACCACTACCAGCA
Cldn5	NC_000082.7	ACGGGAGGAGCGCTTTAC	GTTGGCGAACCAGCAGAG
Pmp22	NC_000077.7	AGCTGTCCCTTTGAACTGAAAC	CCCCAACAAGAGTAGGAGCA
Gapdh	NC_000072.7	ACCACAGTCCATGCCATCAC	TCCACCACCCTGTTGCTGTA