Table S1. PCR conditions

Both forward and reverse primers were tagged with Illumina adapter, pad and linker sequences. PCR enrichment was performed in a 50 μL reaction containing 30ng template, fusion PCR primer and PCR master mix. PCR cycling conditions were as follows:

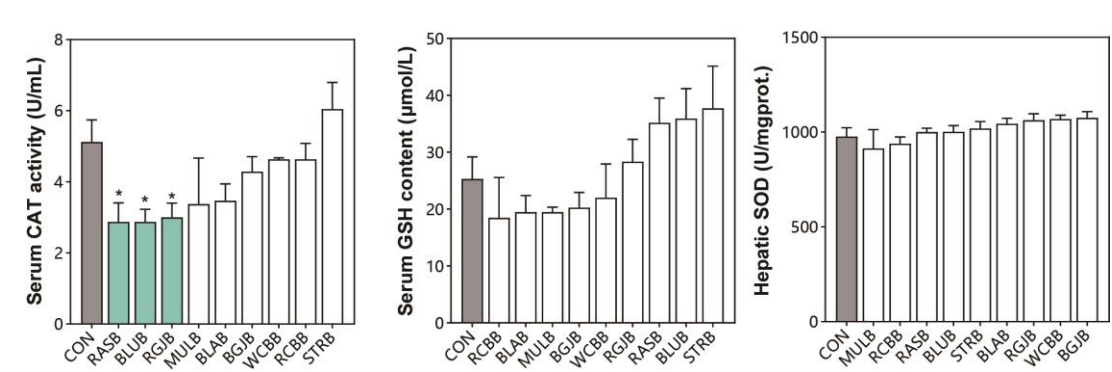| Temperature	Time	Number of cycles
95°C	3 minutes	/
95°C	45 seconds	
56°C	45 seconds	30 cycles
72°C	45 seconds	
72°C	10 minutes	/

Figure S1. Influence of berry extracts on the antioxidant capacities of healthy objects. Error bars were expressed as mean ± SEM (n = 7/group). Statistical significance was determined by Mann-Whitney *U* test for two groups comparisons. *, compared with control group. *, *P* < 0.05; **, *P* < 0.01.
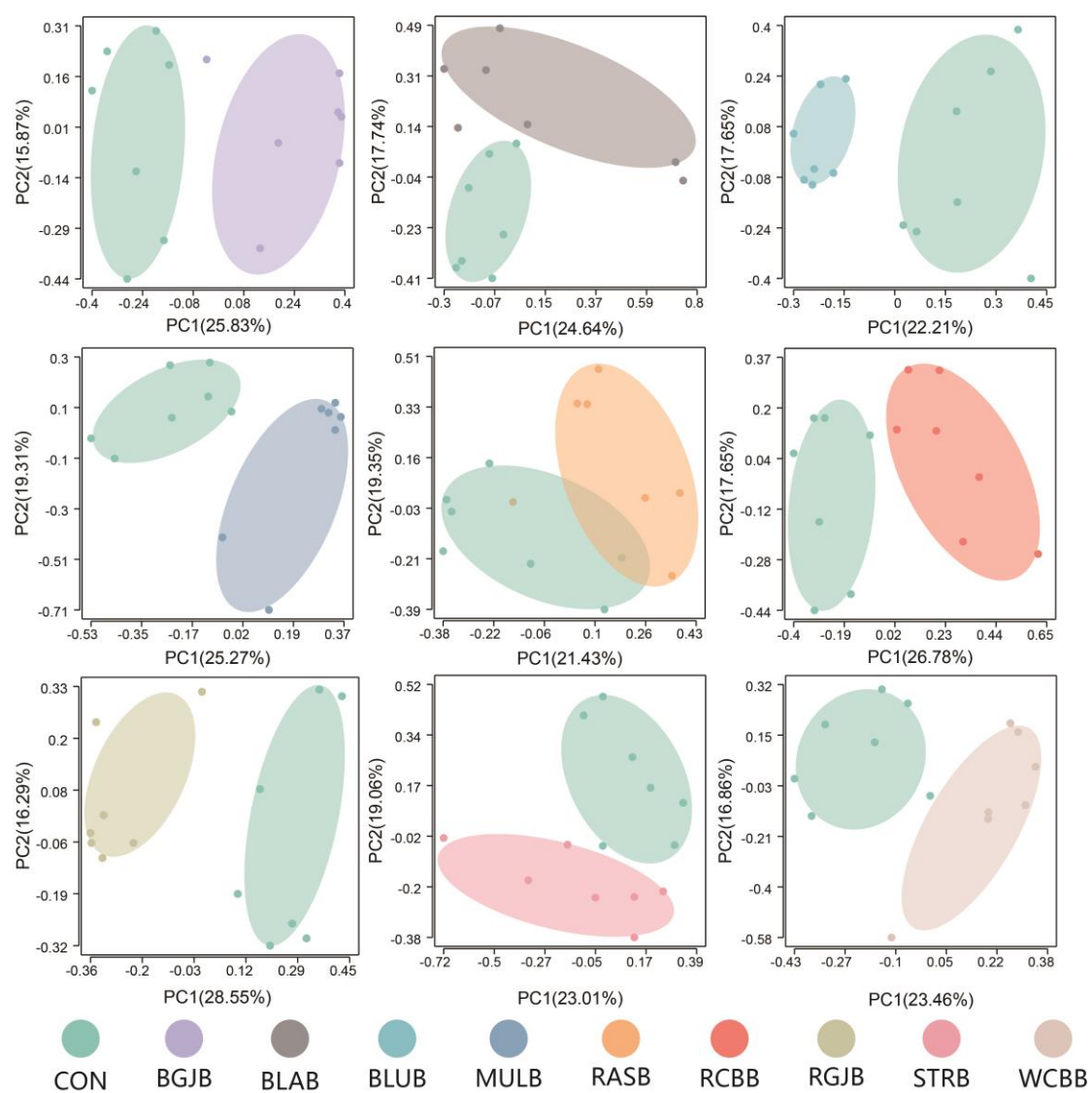
Figure S2. Principal component analysis (PCA) plot of the gut microbiota composition at the operational taxonomic unit (OTU) level from different groups (n = 7/group).
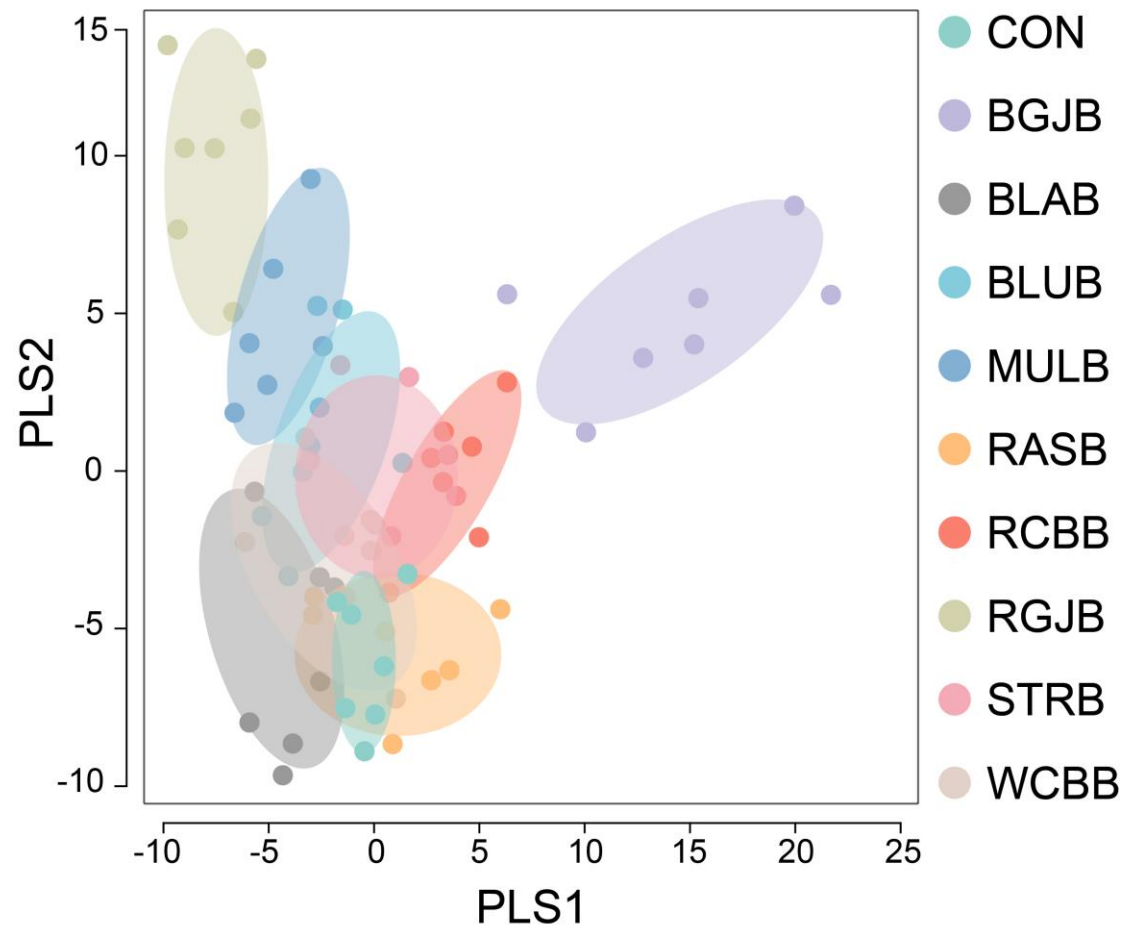
Figure S3: Partial least squares discriminant analysis (PLS-DA) of the gut microbiota composition at the operational taxonomic unit (OTU) level from different groups (n = 7/group).
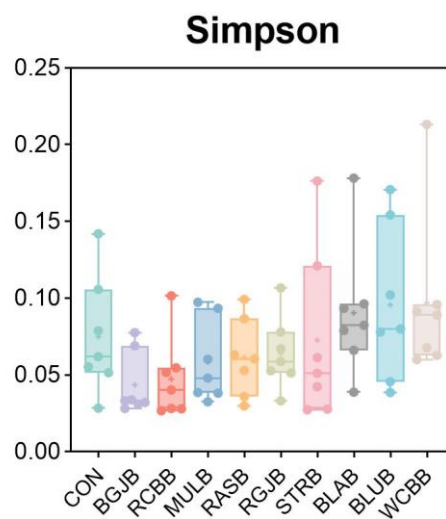

Figure S4: Alpha diversity analysis of gut bacterial diversity (Simpson index) from different mouse groups (n = 7/group).
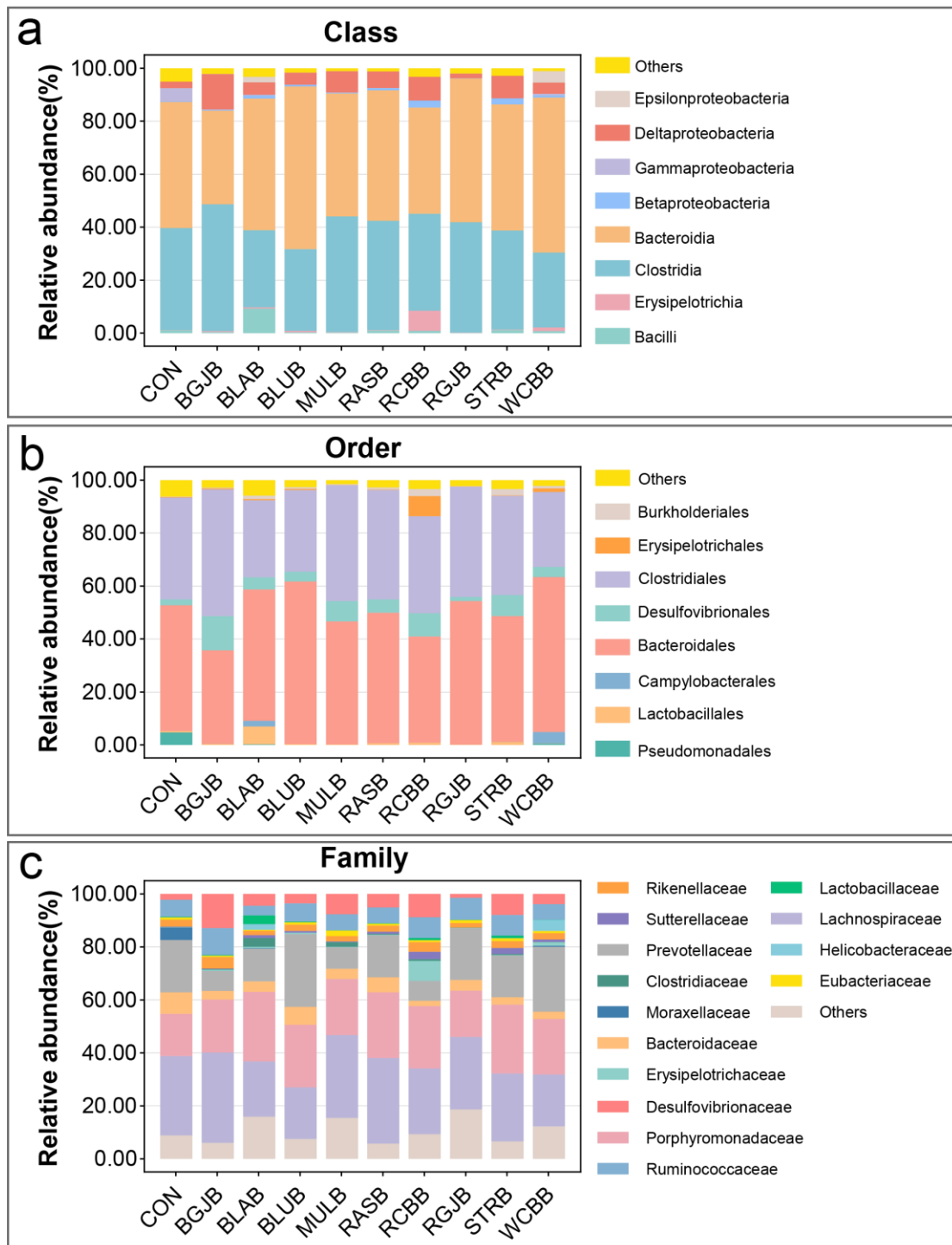
Figure S5. Bacterial taxonomic profiling at the (a) class level, (b) order level and (c) family level of gut bacteria from different mouse groups (n = 7/group).
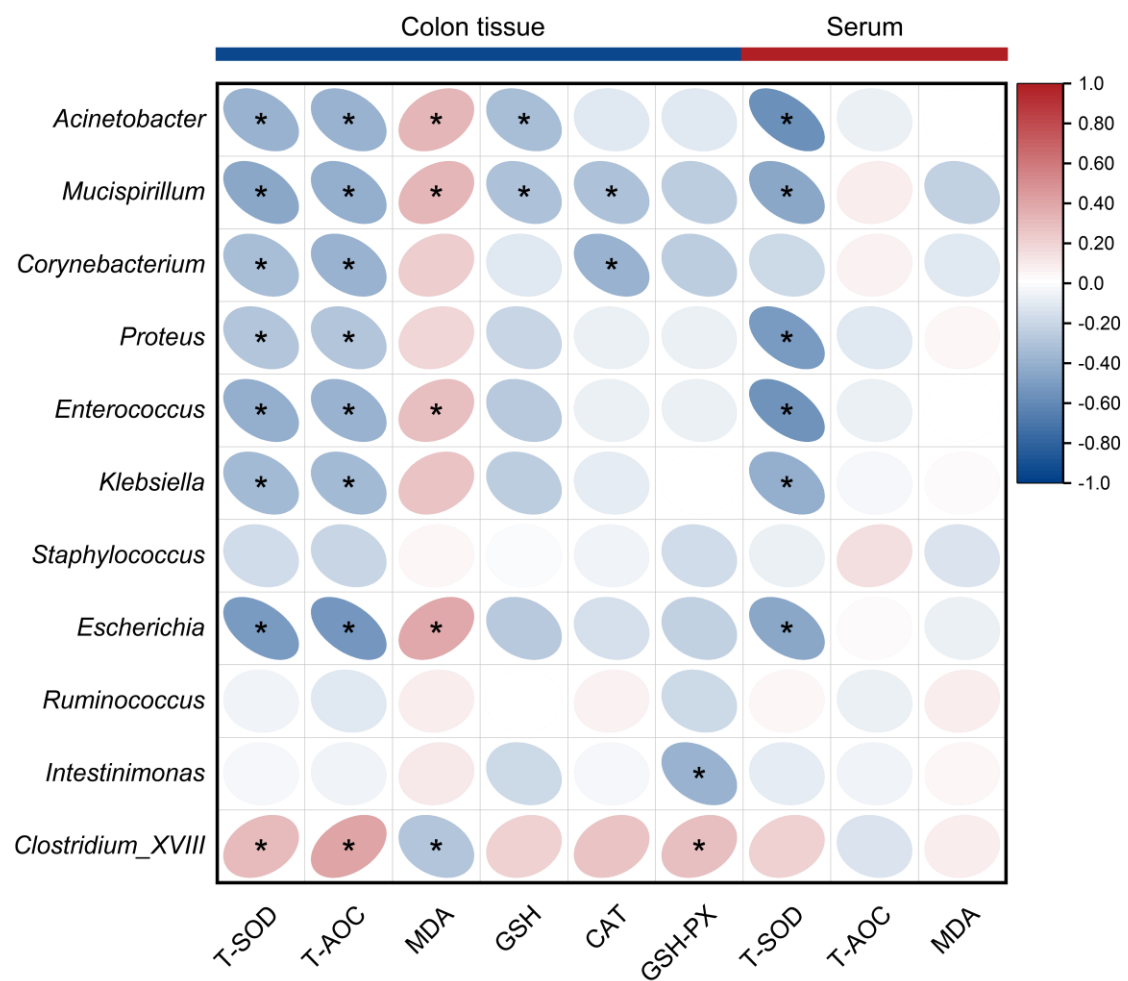
Figure S6: Spearman correlation analysis between gut microbiota and *in vivo* antioxidant indices. The red color denotes a positive correlation, while blue color denotes a negative correlation. The intensity of the color is proportional to the strength of Spearman correlation. *, $P < 0.05$.