Supplementary Figure S1

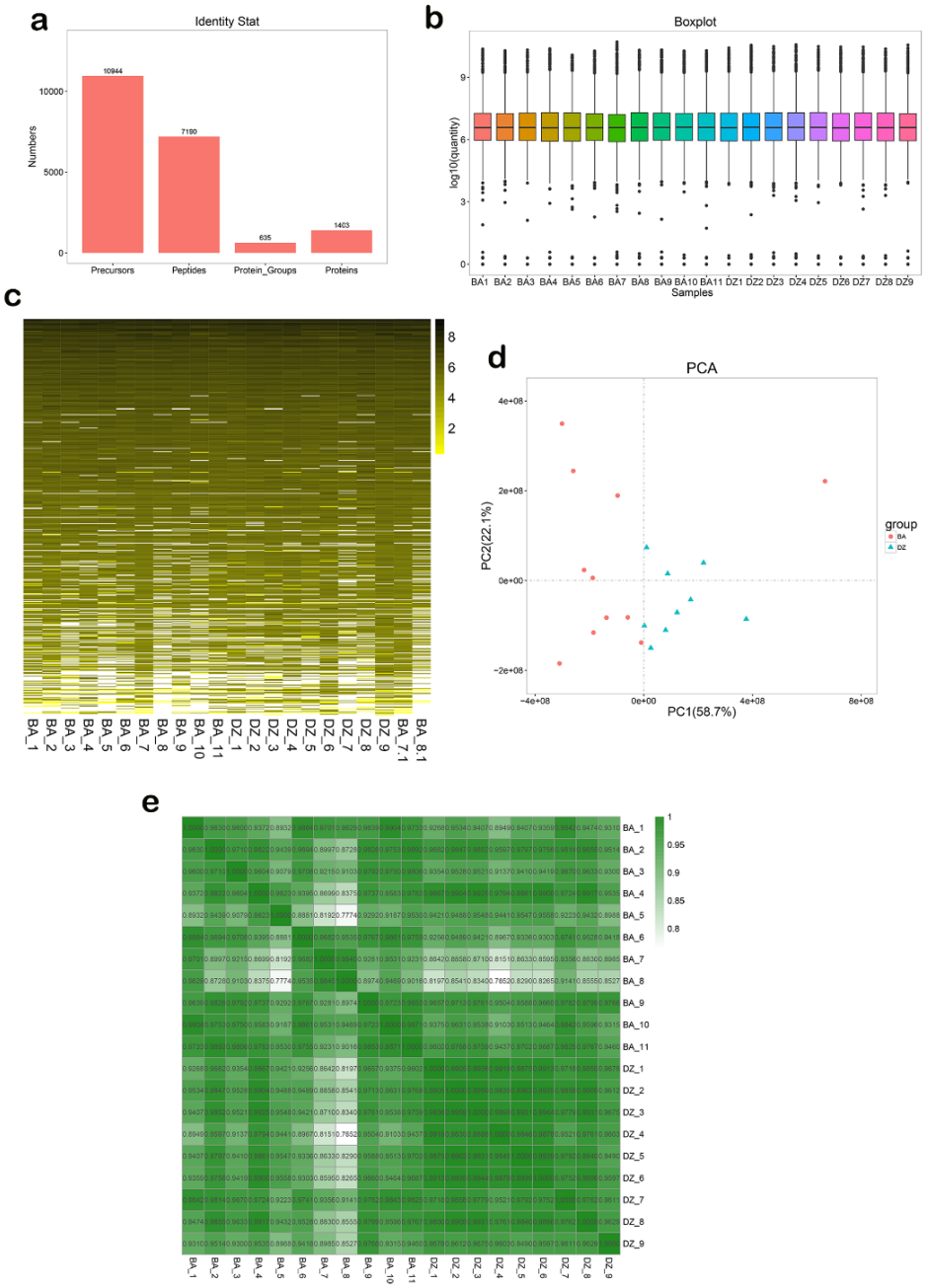

Figure S1. (a) Identification of serum protein via proteomics analysis. (b) Box diagram showing the peak-intensity distributions of mass spectrum signals for all samples. (c) A quantification heatmap for all serum proteins found by proteomics analysis. (d) PCA analysis of all serum proteins in 20 samples detected via proteomics analysis. (e) Correlation heatmap for the serum samples subjected to proteomics analysis.

Supplementary Figure S2

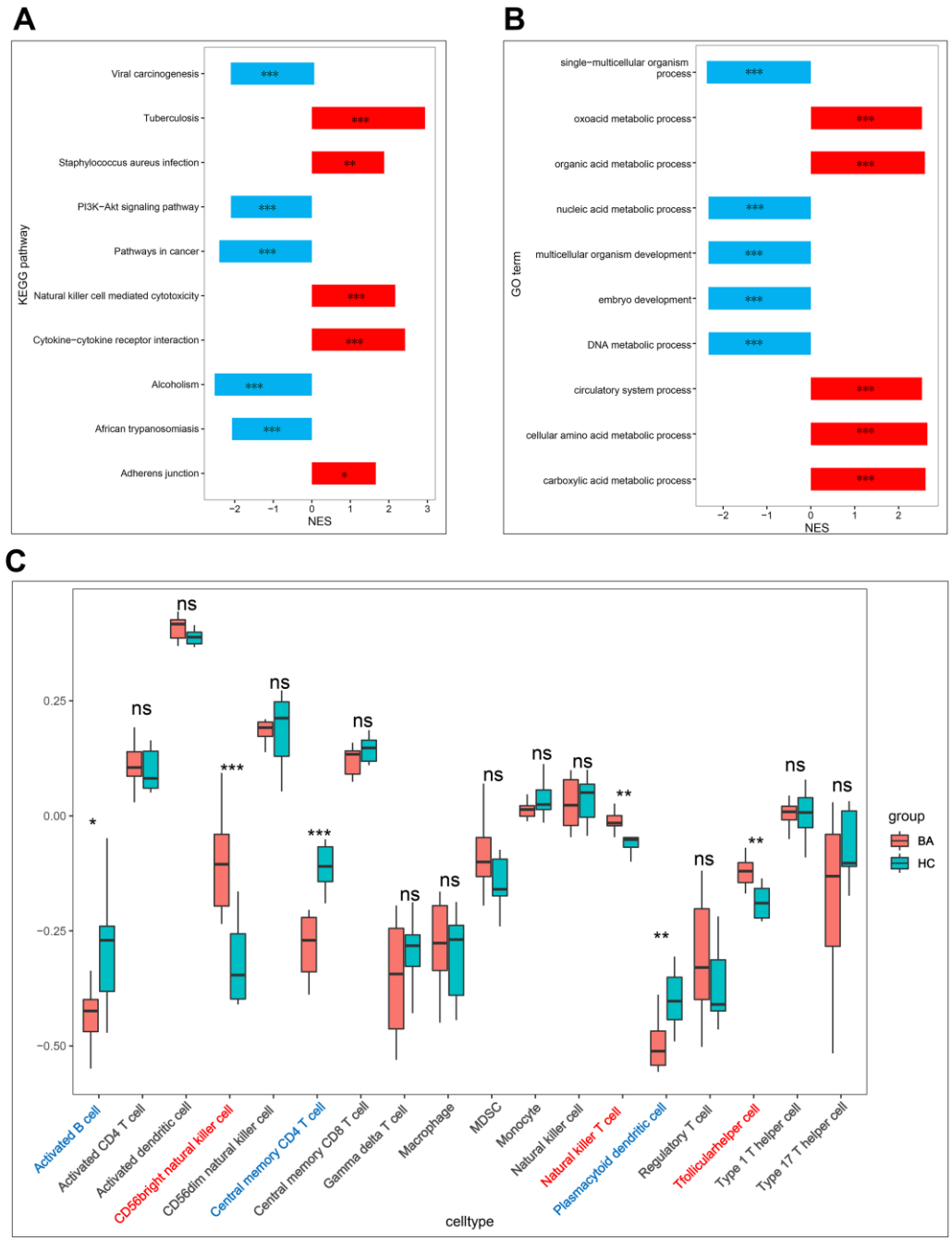

Figure S2. (A) The top 5 KEGG pathways upregulated in BA (red) and the top five KEGG pathways downregulated in BA (blue). *P < 0.05; **P < 0.01; ***P < 0.001; two-tailed T test. (B) The top 5 GO terms upregulated in BA (red) and the top five GO terms downregulated in BA (blue). ***P < 0·001, two-tailed T test. (C) Immune cell-infiltration analysis. ns, P > 0.05; *P < 0.05; **P < 0.01; ***P < 0.001; two-tailed T test. Immune cell types that showed significantly increased infiltration in BA are marked in red, immune cells that showed significantly decreased infiltration in BA are marked in blue.

Supplementary Figure S3

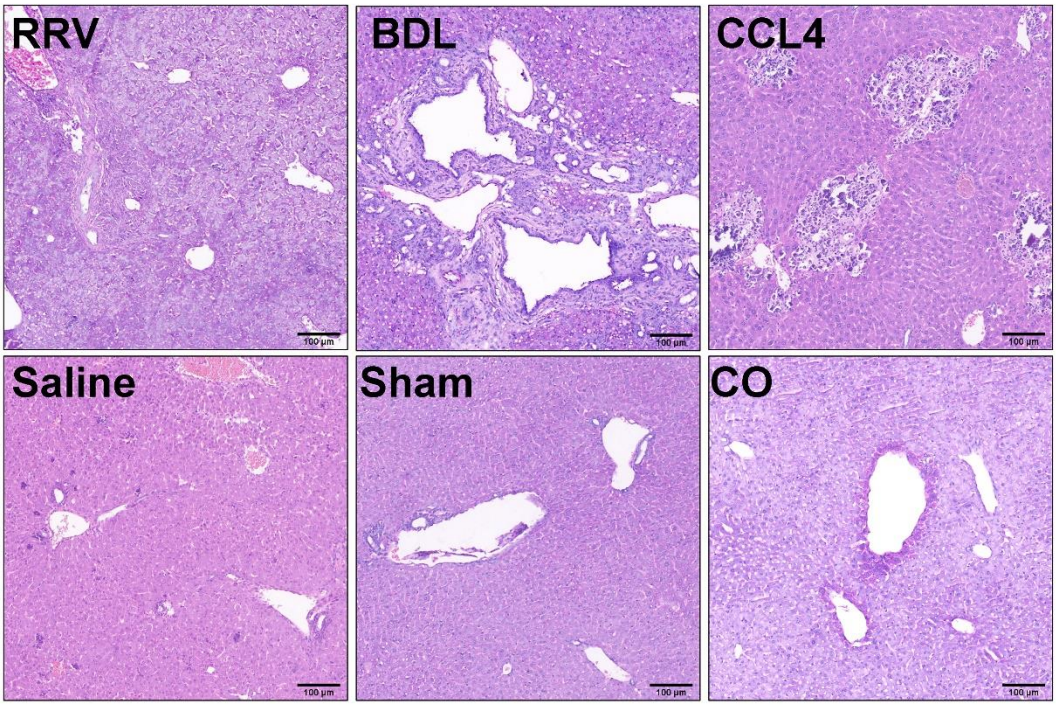

Figure S3. HE staining of liver sections from the experimental mouse models (Original magnification, ×100; Scale bars, 100μm).

Supplementary Figure S4

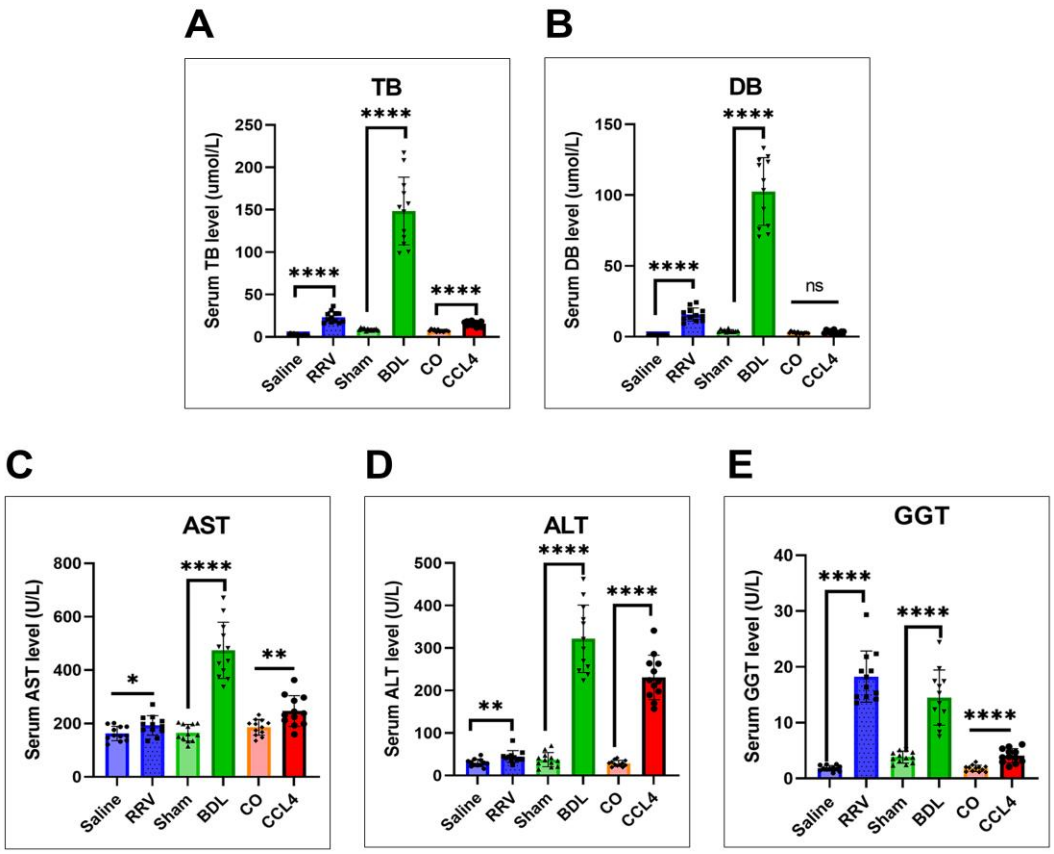

Figure S4. (A) Serum levels of total bilirubin in the experimental mouse models. (B) Serum levels of direct bilirubin in the experimental mouse models. (C) Serum levels of AST in the experimental mouse models. (D) Serum levels of ALT in the experimental mouse models. (E) Serum levels of GGT in the experimental mouse models. n = 12 for each group; ns, $P > 0{\cdot}05$; *$P < 0{\cdot}05$; **$P < 0{\cdot}01$; ***$P < 0{\cdot}001$; ****$P < 0{\cdot}0001$; two-tailed T test.