

Supplementary Materials

Figure S1. PCP regulates the microecological diversity and composition of lung tissue. Note: Z: control group (n=5); M: model group (n=5); P/PCP: PCP group (n=5). (A) PLS-DA analysis (lung microecology) (B-C) LEfSe analysis (lung microecology), LDA>3.

Figure S2. PCP regulates the diversity and composition of the gut microbiota. Note: Z: control group (n=5); M: model group (n=5); P/PCP: PCP group (n=5). (A) Species distribution map of microbial community at gate level (lung microecology) (B-D) LEfSe analysis (gut microecology), LDA>4.

Figure S3. PCP regulates the diversity and composition of the gut microbiota. Note: Z: control group (n=5); M: model group (n=5); P/PCP: PCP group (n=5). (A) PLS-DA analysis (gut microecology) (B) Species distribution map of microbial community at phylum level (gut microecology) (C-D) Wilcoxon test ($p<0.05$) for relative abundance analysis of gut flora.

Figure S4. Differentially expressed metabolites (DEM). Note: Control group (n=5); Model group (n=5); PCP: PCP group (n=5). The LC-MS Identified 178 significantly altered DEM, $p<0.05$.

Figure S5. 20 species of the most relevant DEM. (A) Model VS control: 20 different metabolites (Correlation analysis uses the Pearson correlation coefficient to measure the degree of linear correlation between two metabolites. Red indicates a positive correlation and blue indicates a negative correlation. A larger dot indicates a higher correlation coefficient between the two variables.) (B) PCP VS Model: 20 different metabolites.