

## 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.