

Figure legends

Figure S1. Relatively stable of lung microbiota in sham group. **A-B:** Analysis of alpha diversity of lung microbiota by Chao1 analysis and Simpson analysis, respectively. **C:** Analysis of differences between groups based on permutational multivariate analysis of variance. **D-E:** Relative abundance of lung microbiota at phylum and genus, respectively. Q: control group. S3h, S1d, S3d, S7d and S14d: 3 h, 1 d, 3 d, 7 d and 14 d after sham surgery.

Figure S2. Relatively stable of gut microbiota in sham group. **A-B:** Analysis of alpha diversity of gut microbiota by Chao1 analysis and Simpson analysis, respectively. **C:** Analysis of differences between groups based on permutational multivariate analysis of variance. **D-E:** Relative abundance of gut microbiota at phylum and genus, respectively. Q: control group. S3h, S1d, S3d, S7d and S14d: 3 h, 1 d, 3 d, 7 d and 14 d after sham surgery.

Figure S3. Relatively stable of histopathology and biomarkers of bacterial translocation in plasma. **A:** Lung HE staining. **B:** Quantification of histological injury score. Data are depicted as mean \pm SD with $*P < 0.05$ compared to Q, $^{\#}P < 0.05$ compared to S3h by one-way ANOVA. **C:** MPO activity of lung tissue. Q: control group. Data are depicted as mean \pm SD with $*P < 0.05$ compared to Q, $^{\#}P < 0.05$ compared to S3h by one-way ANOVA. **D-F:** Levels of plasma LBP, sCD14 and zonulin, respectively. **G:** Intestinal lysozyme immunohistochemistry. Black arrow indicated lysozyme. Blue arrow indicated the villi of the small intestine. Scale bar = 200 μ m. **H:** The DAB staining intensity. Q: control group. S3h, S1d, S3d, S7d and S14d: 3 h, 1 d, 3 d, 7 d and 14 d after sham surgery. Scale bar = 100 μ m.