

Supplementary Figure S2. Microarray-based comparison between number of differentially expressed genes in extra-pulmonary organs as a result of *S. aureus* pneumonia alone (SA, n = 5 liver, n = 5 kidney) versus combination of pneumonia and mechanical ventilation (MV+SA, n = 5 liver, n = 5 kidney). Note the large increase in the number of differentially expressed genes in liver and kidney when mice with pneumonia are expose to MV. For each condition (SA, MV+SA), organ-specific differential gene expression was determined relative to control mice (n = 5 for kidney, n = 3 for liver) using a Bayesian implementation of the parametric *t*-test coupled with false discovery rate (FDR) analysis based on Benjamini-Hochberg adjustment of *P*-values. An adjusted *P*-value < 0.01 was used to identify significant differential gene expression.

