



SUPPLEMENTARY FIGURE 1. Differential metabolites and KEGG pathway enrichment.

(A) Hierarchical clustering heatmap of metabolites identified in cecum contents from *K. pneumoniae*-infected, microbiota-depleted mice versus microbiota-depleted controls. Red denotes increased expression; green denotes decreased expression. (B) Selected examples of KEGG pathway enrichment. Disturbances on propionate and butyrate metabolisms are highlighted in red color. The *P* values are determined using Hypergeometric test and Benjamini-Hochberg FDR correction (A). MD, gut microbiota-depleted mice.

controls. Conditions: $r > 0.8$ & $p < 0.05$. The P values are determined using two-tailed Wilcoxon rank-sum test (**B**). $*P < 0.05$, $***P < 0.001$. MD, gut microbiota-depleted mice.