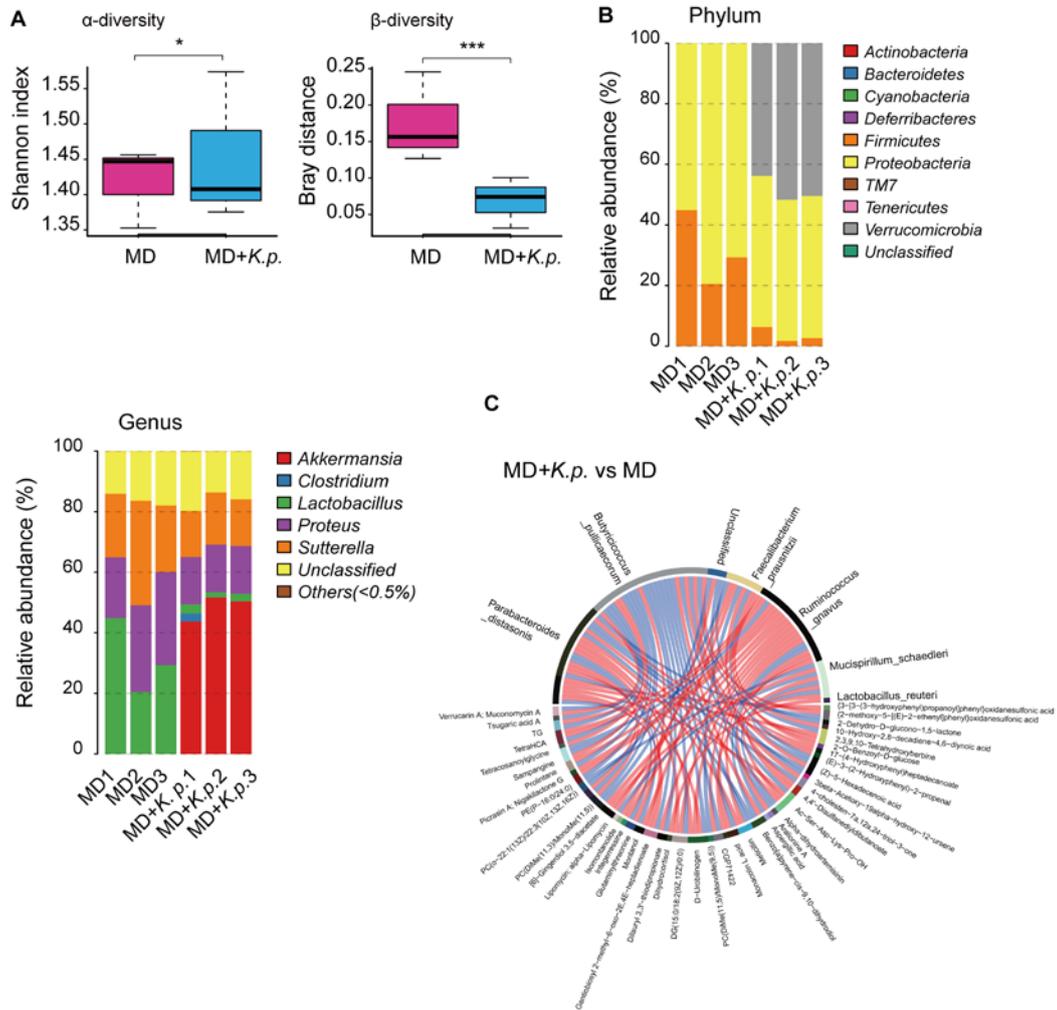


SUPPLEMENTARY FIGURE 1. Differential metabolites and KEGG pathway enrichment.

(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.



SUPPLEMENTARY FIGURE 2. Association of cecum metabolites and gut microbiomes.

(A) α -diversity (Shannon index) and β -diversity (Bray-Curtis similarity index) of 16S rRNA genes from *K. pneumoniae*-infected, gut microbiota-depleted mice and gut microbiota-depleted controls. (B) Discriminative OTUs abundance of taxonomic distributions at phylum and genus levels between *K. pneumoniae*-infected, gut microbiota depleted mice and gut microbiota-depleted controls. (C) Chord Chart of gut microbiota with corresponding metabolites at species level in *K. pneumoniae*-infected, gut microbiota-depleted mice and gut microbiota-depleted

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.