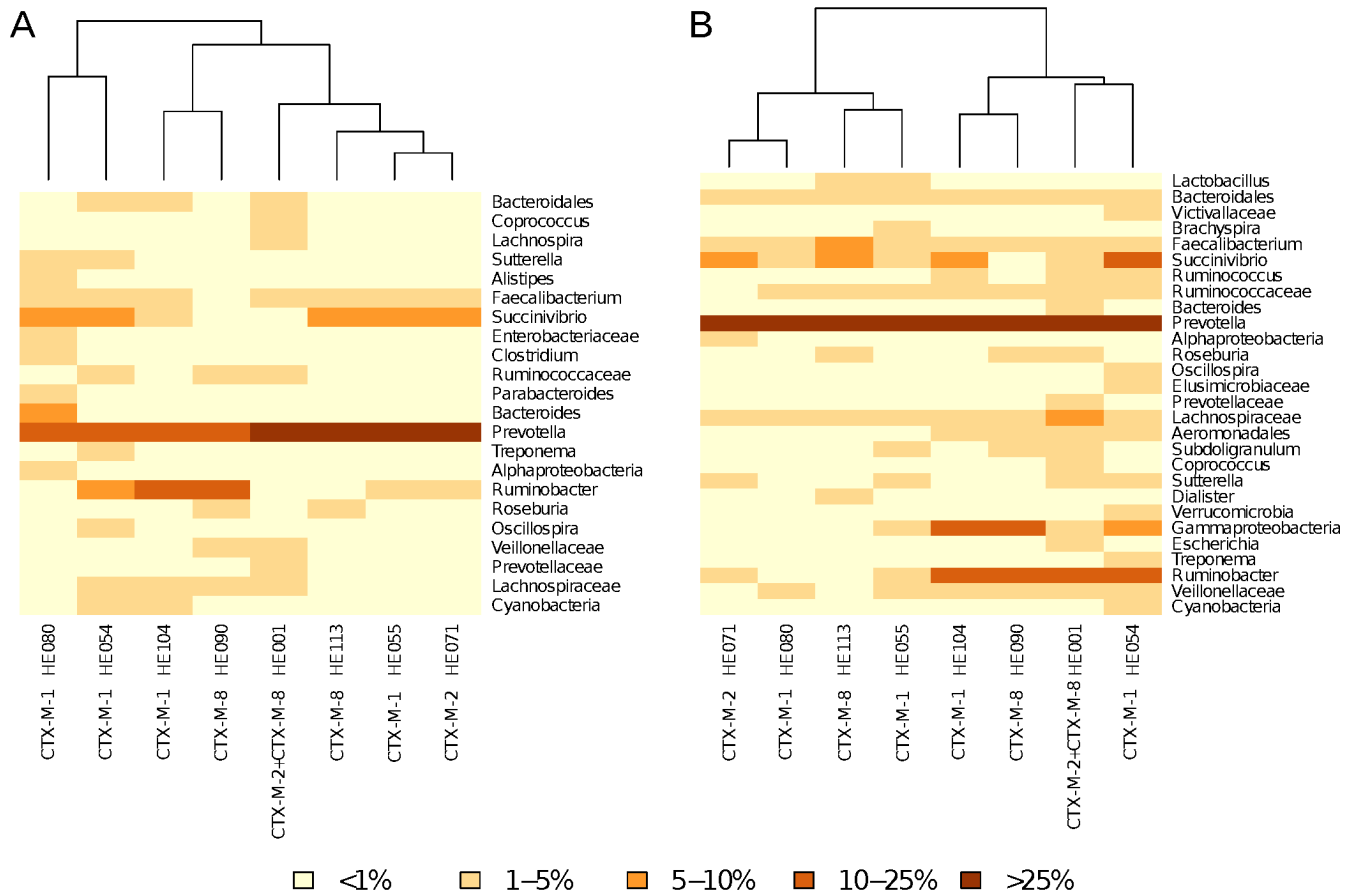


Supplementary Figure 1. Analysis of beta diversity. PCoA of weighted UniFrac distances among (A) total microbial communities and (B) active bacterial communities.



Supplementary Figure 2. Relationship between bacterial composition and CTX-M gene for the carrier individuals. Heat maps of (A) total microbiota and (B) active microbiota. The CTX-M gene carried by each individual is shown with the name of the sample. Colours in the figure depict the percentage range of sequences assigned to main taxa (abundance >1% in at least one sample).