Whole-genome sequencing and intestinal metagenome sequencing revealed the carriage and transmission of *Salmonella enterica* in Xinjiang, China

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Keywords: Whole-genome sequencing; Metagenome sequencing; Gut; *Salmonella*; healthy people; Xinjiang, China.

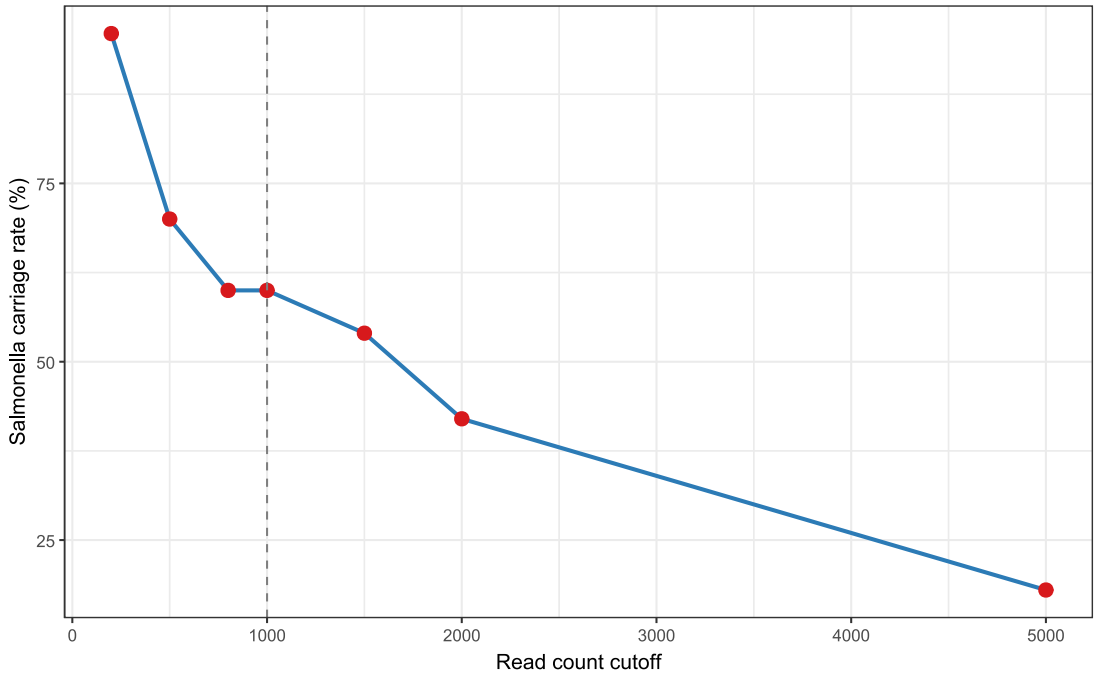


Figure S1. Changes in *Salmonella* carriage rate across different read count cutoffs. Sensitivity analysis shows the variation of estimated *Salmonella enterica* carriage rate under a gradient of read count thresholds. The vertical dashed line marks the 1000-read cutoff used in this study, which falls within the stable plateau of carriage rate.

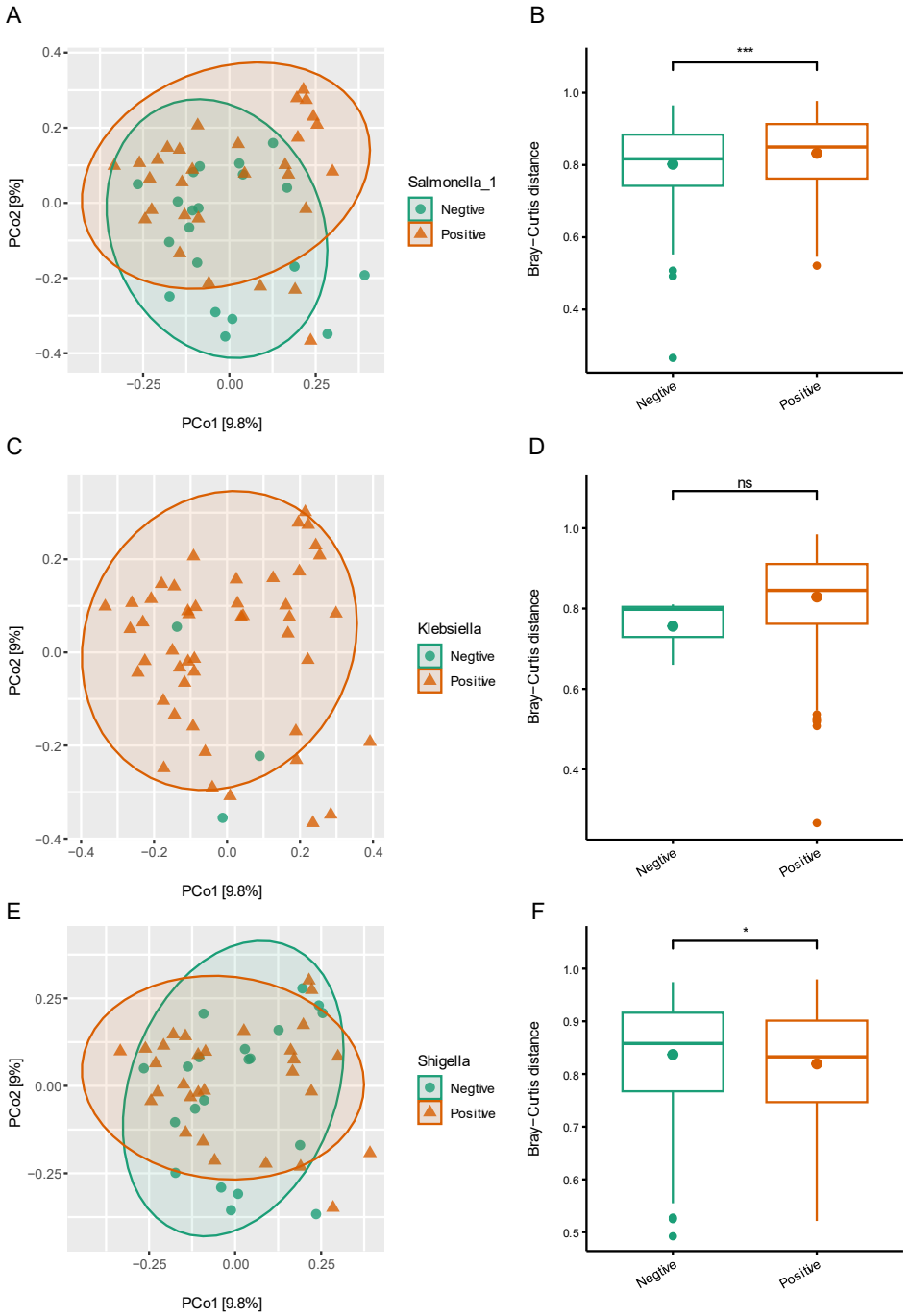


Figure S2. Intestinal archaeal β-diversity of 50 healthy individuals stratified by *Salmonella*, *Klebsiella*, and *Shigella* carriage status. (A, C, E) Boxplots of Bray-Curtis distances for *Salmonella*, *Klebsiella*, and *Shigella* groupings, respectively. (B, D, F) PCoA plots (Bray-Curtis) for *Salmonella*, *Klebsiella*, and *Shigella* groupings (PCo1=9.8%, PCo2=9%). PCoA showed no distinct clustering between groups, whereas ASV-level Bray-Curtis distances revealed significant compositional differences ($p < 0.0001$ for *Salmonella*, $p < 0.05$ for *Shigella*; adonis test).

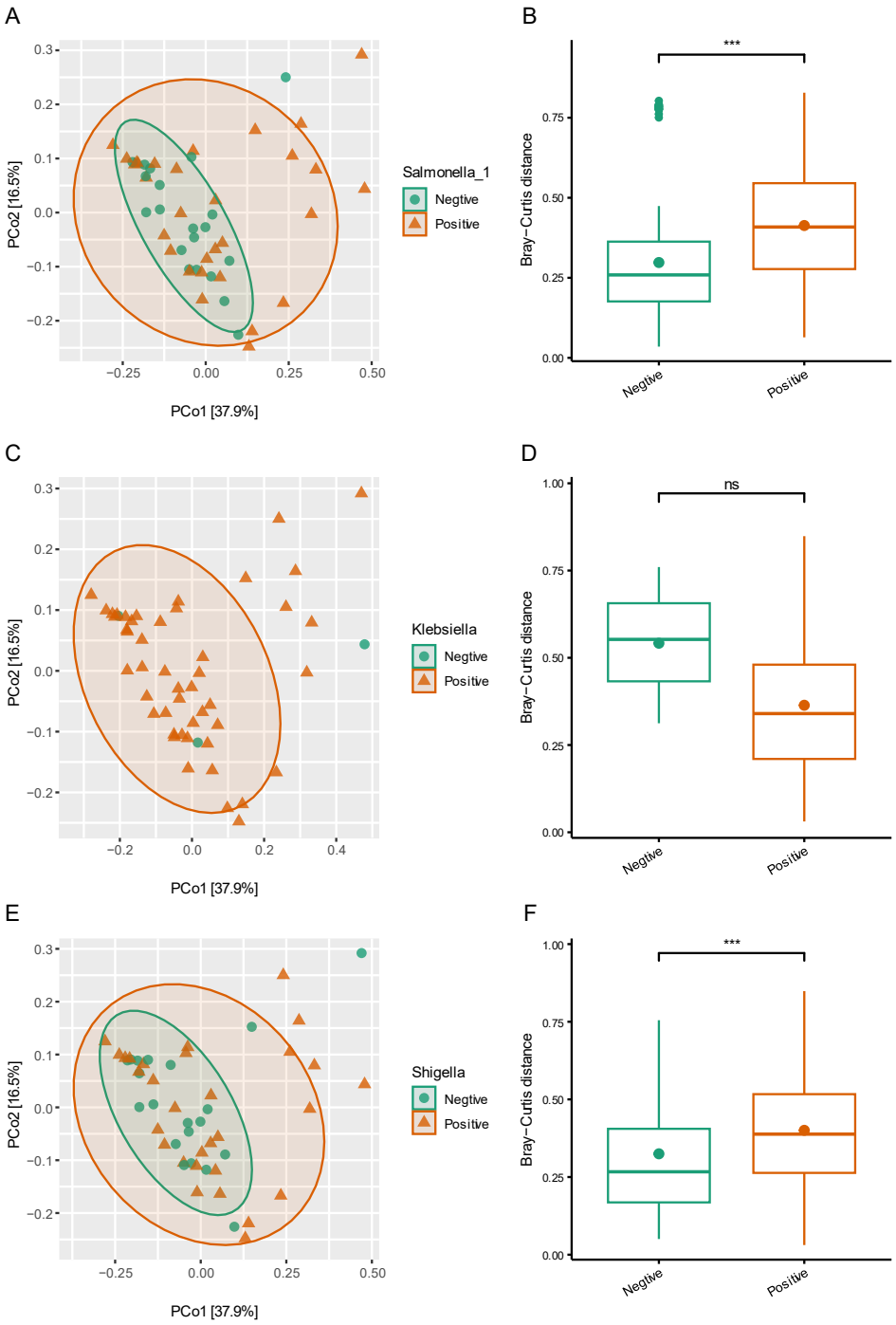


Figure S3. Intestinal viral β-diversity of 50 healthy individuals stratified by *Salmonella*, *Klebsiella*, and *Shigella* carriage status. (A, C, E) Boxplots of Bray-Curtis distances for *Salmonella*, *Klebsiella*, and *Shigella* groupings, respectively. (B, D, F) PCoA plots (Bray-Curtis) for *Salmonella*, *Klebsiella*, and *Shigella* groupings (PCo1=37.9%, PCo2=16.5%). PCoA showed no distinct clustering between groups, whereas ASV-level Bray-Curtis distances revealed significant compositional differences ($p < 0.0001$ for *Salmonella*, $p < 0.0001$ for *Shigella*; adonis test)