

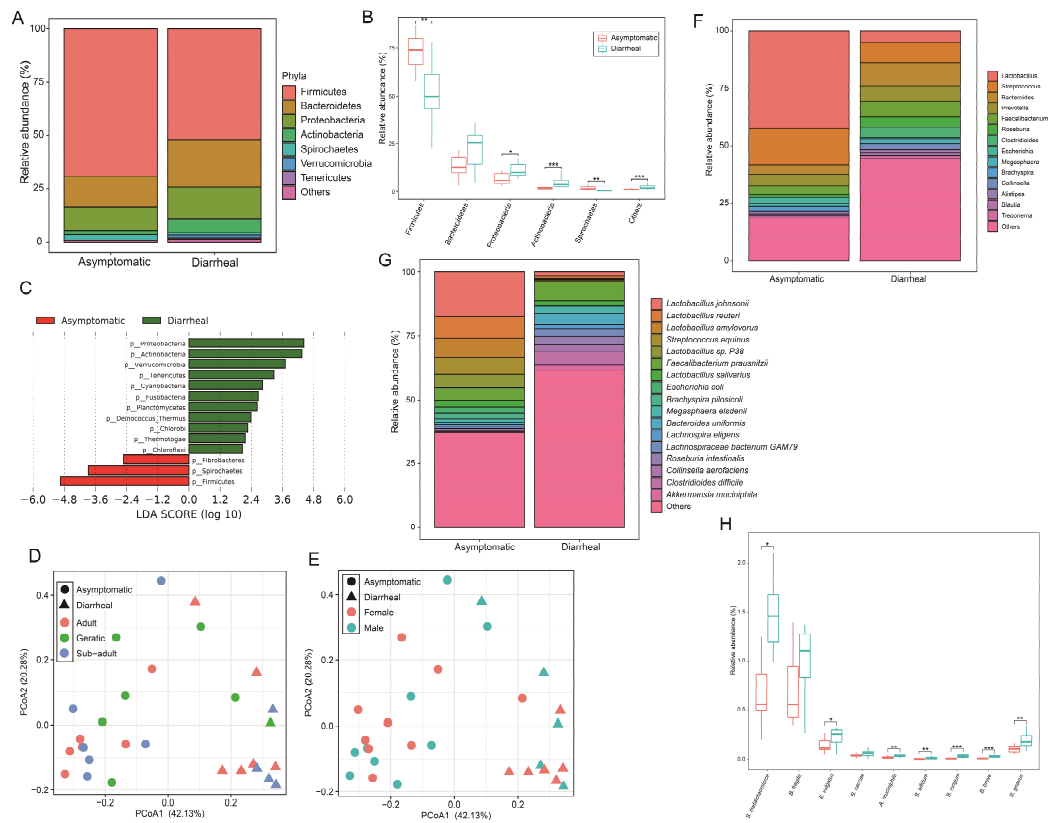


Fig. S1 The gut microbiome of chronic diarrhea RMs and asymptomatic RMs. (A) The distribution of main bacterial phyla with abundance more than 1% in all samples. (B) The comparison of main bacterial phyla. *, p-value <0.05; **, p-value <0.01; ***, p-value <0.001. (C) The difference of phylum-level relative abundance between gut bacteria of asymptomatic RMs and chronic diarrhea RMs by LEfSe ($p < 0.05$ and $LDA > 3$). (D) PCoA plot based on Bray-Curtis distance of genus-level relative abundance profile of RMs gut microbiomes with different ages (adonis, $R^2 = 0.04153$, $P = 0.842$). (E) PCoA plot based on Bray-Curtis distance of genus-level relative abundance profile of RMs gut microbiomes with different gender (adonis, $R^2 = 0.01849$, $P = 0.842$). (F) The distribution of main bacterial genera. (G) The distribution of main bacterial species. (H) The comparison of mucin-degradation species. *, p-value <0.05; **, p-value <0.01; ***, p-value <0.001.

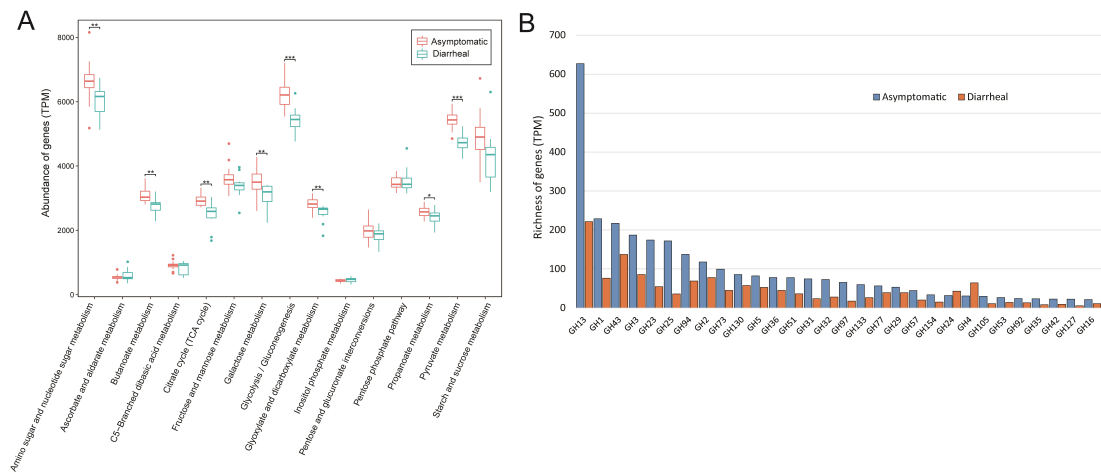


Fig. S2 The functional comparison of gut microbiome. (A) The abundance comparison of gene associated with carbohydrate metabolism. *, p-value <0.05; **, p-value <0.01; ***, p-value <0.001 (B) The abundance of main GHs family in gut.

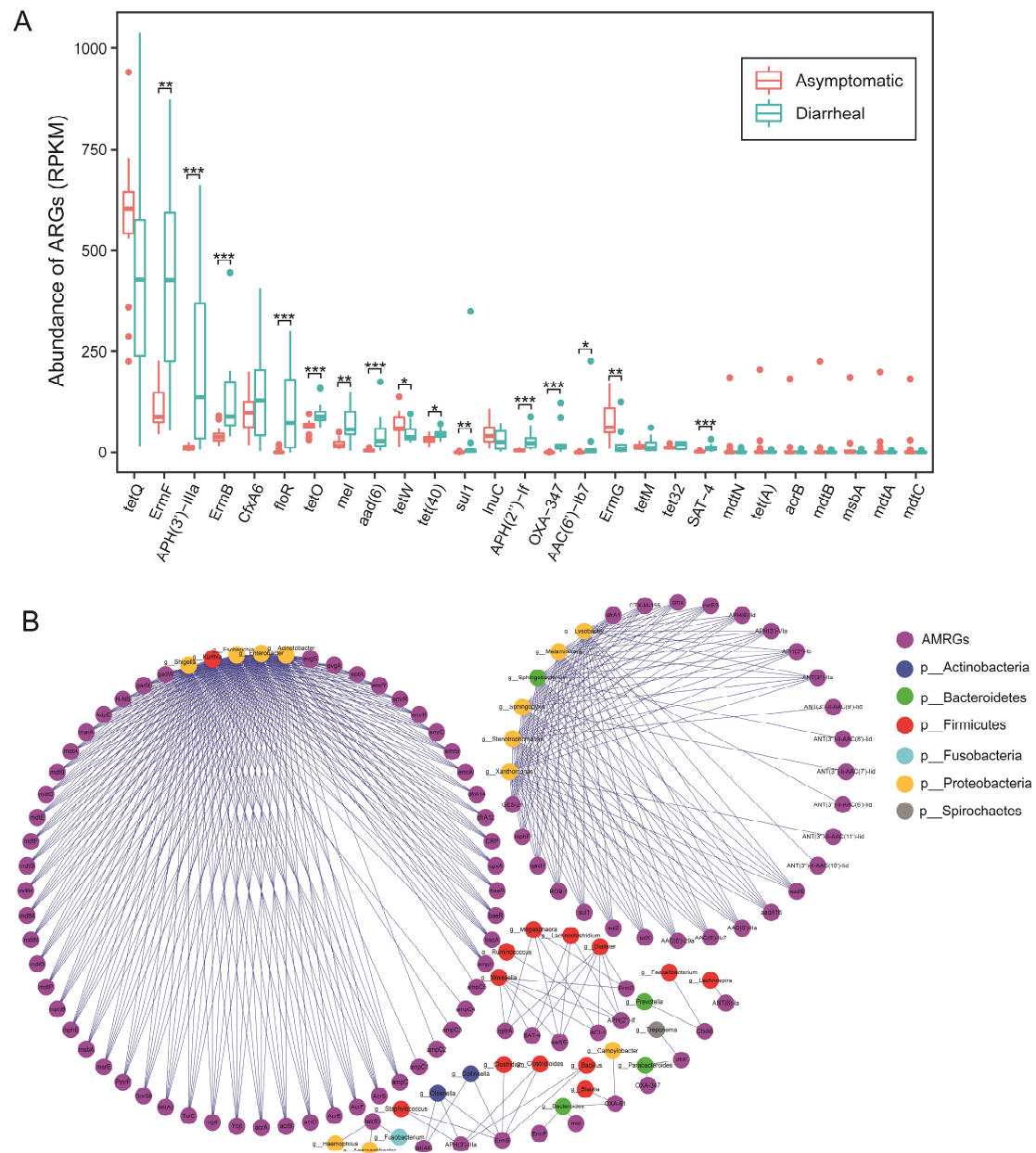


Fig. S4 The antibiotic resistance in gut microbiome of asymptomatic and chronic diarrhea RMs. (A) The abundance comparison of prevalent ARGs in gut microbiome of asymptomatic and chronic diarrhea RMs. The symbol * means $p < 0.05$; the symbol ** means $p < 0.01$; the symbol *** means $p < 0.001$. (B) The correlation between the abundance of gut microbiome and ARGs ($R^2 > 0.7$)