



Integrating genome-wide and transcriptome-wide association studies to uncover the host-microbiome interactions in bovine rumen methanogenesis

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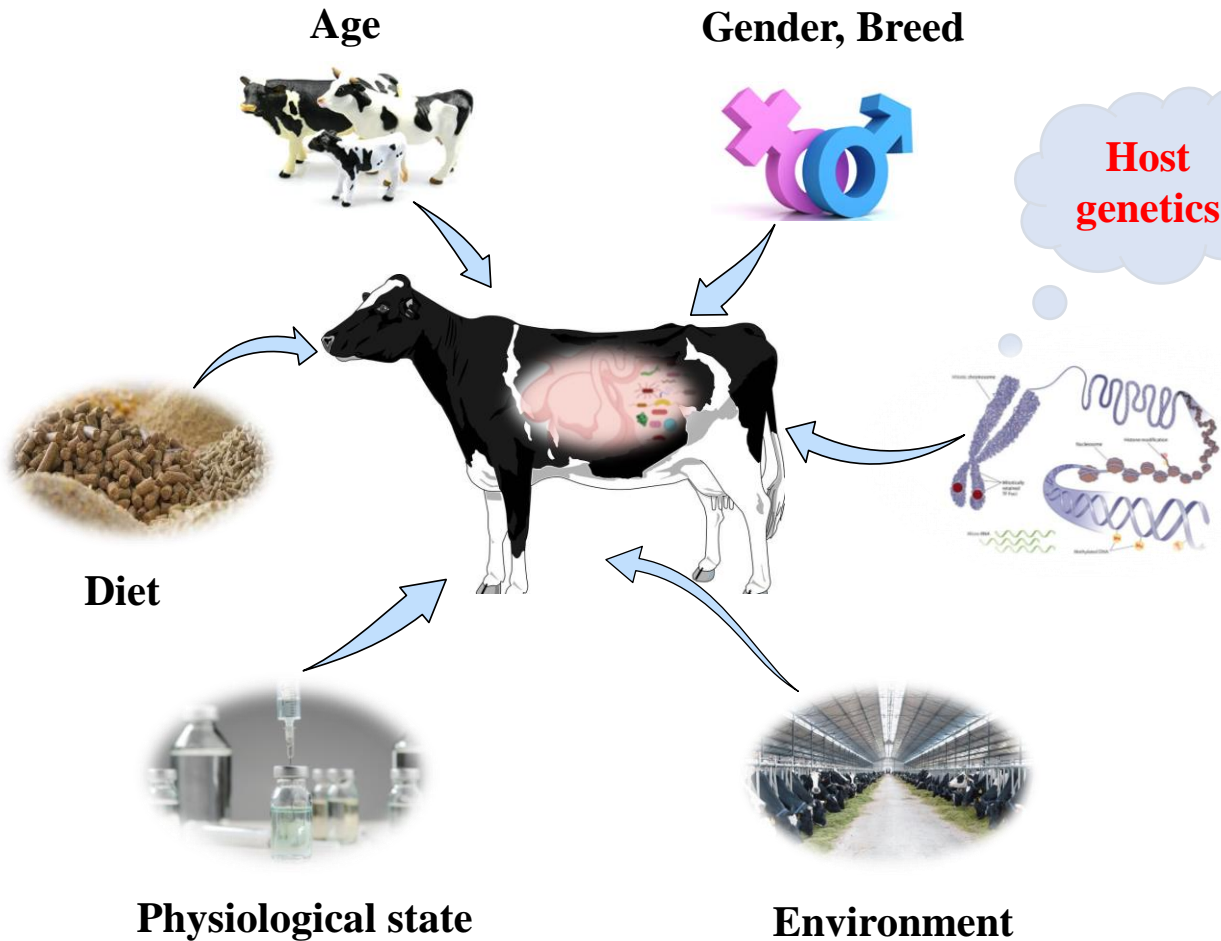


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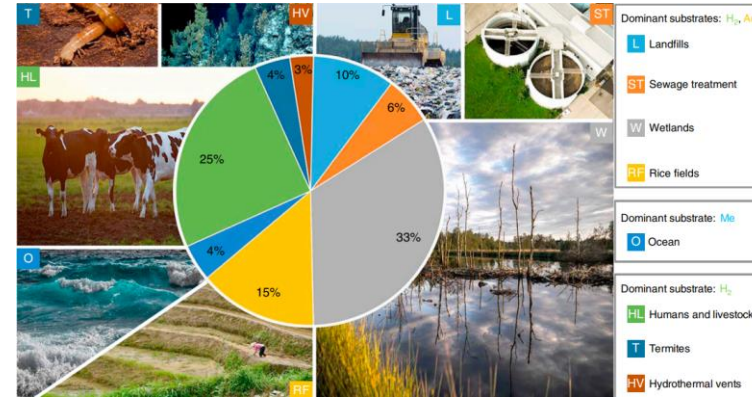


Background

Host genetics is one of the factors affecting rumen microbiota of dairy cows

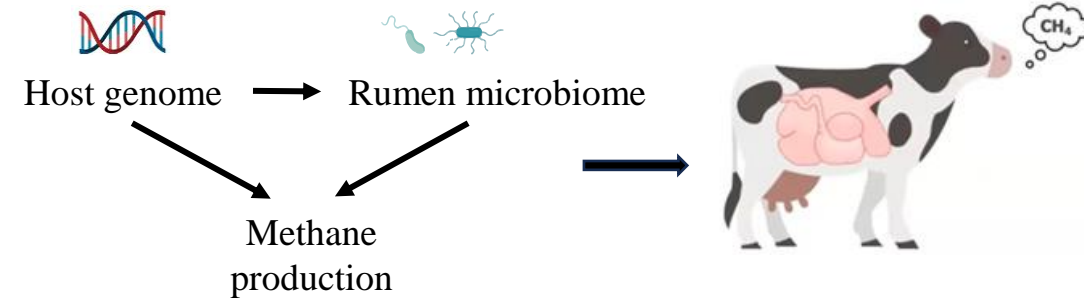


Methane emissions have become an important selection trait in dairy cow breeding



Cattle contribute the majority of livestock production emissions of methane.

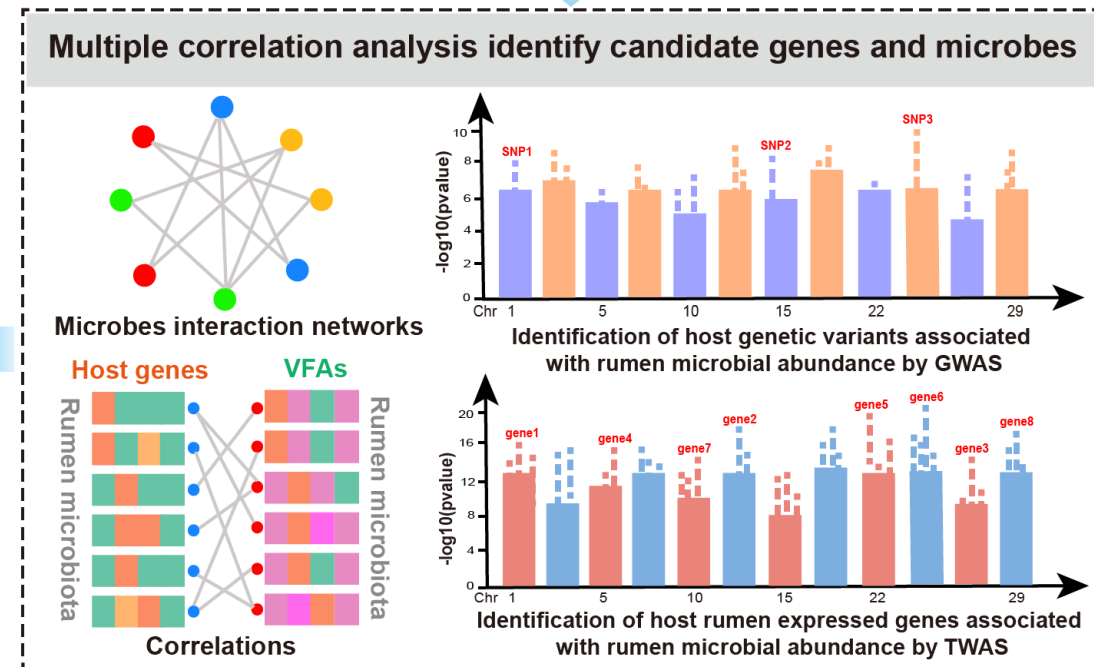
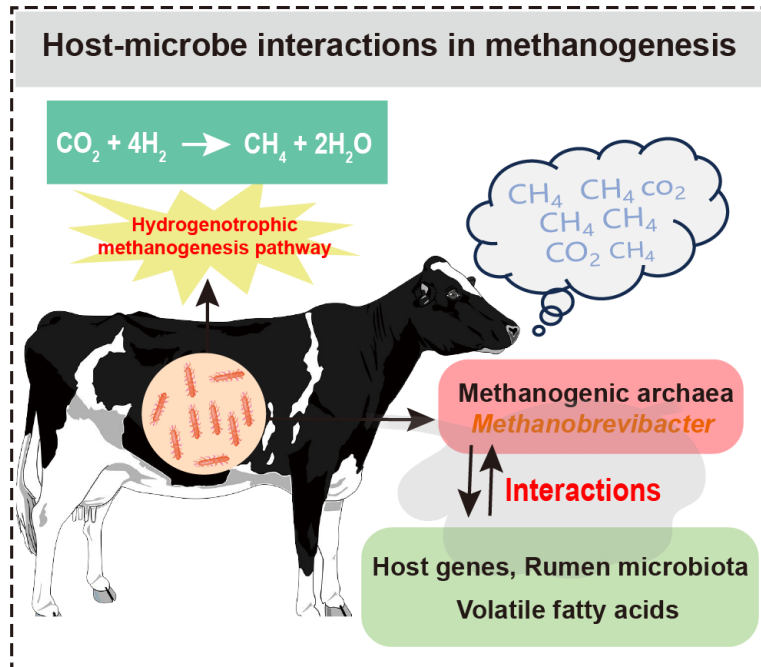
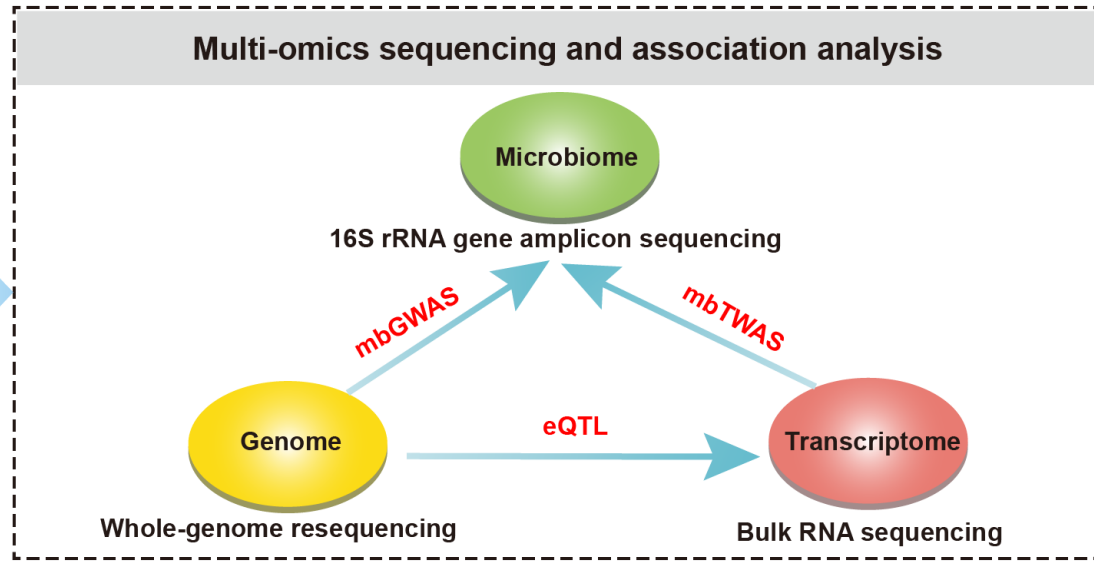
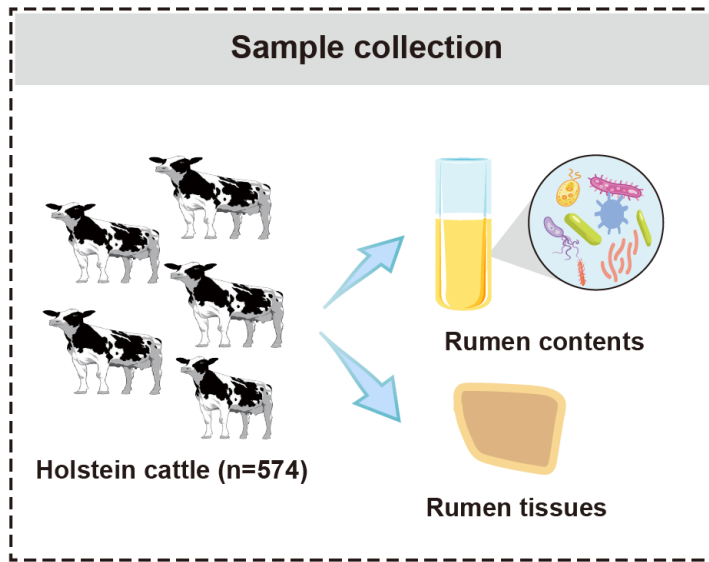
Zhe Lyu, et al. Current Biology



To elucidate how host genome and rumen microbiome affect rumen microbiota composition and abundance, thereby regulating methane emissions from dairy cows.



Highlights



Landscape of rumen microbiota using a single large cohort of Holstein cattle

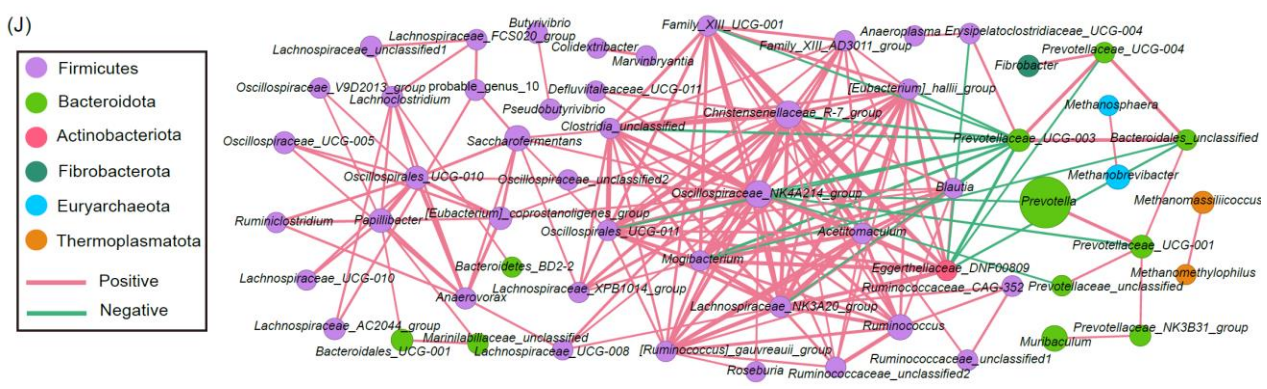
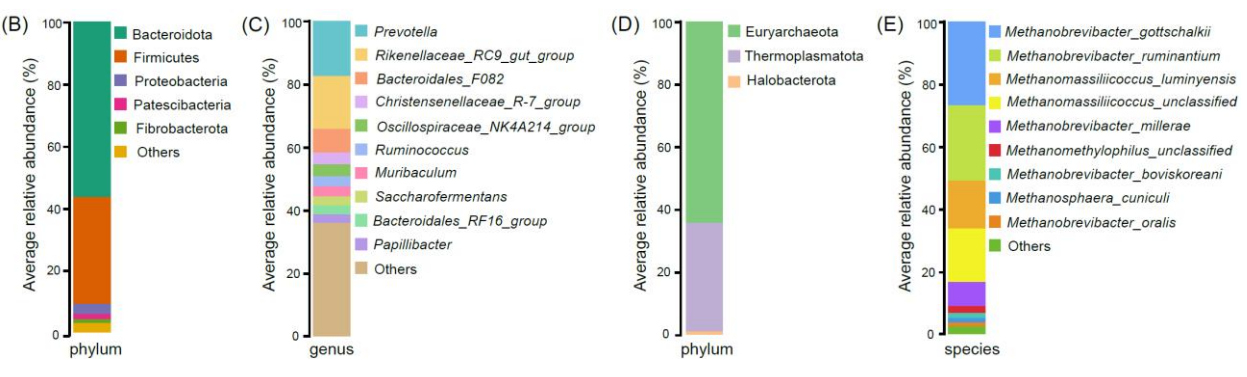
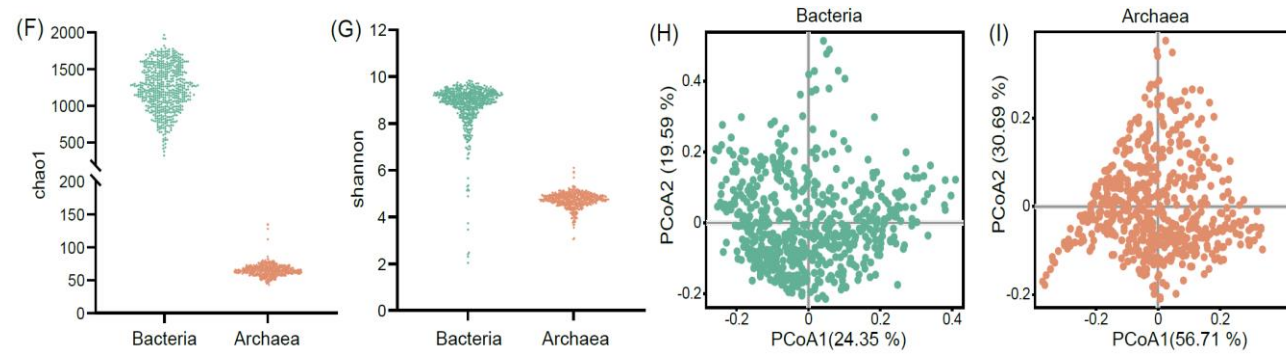
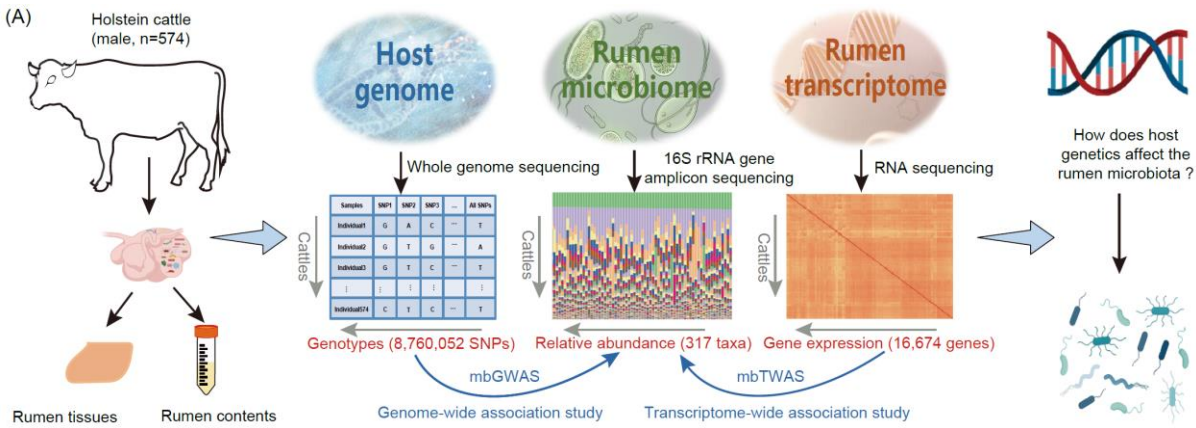
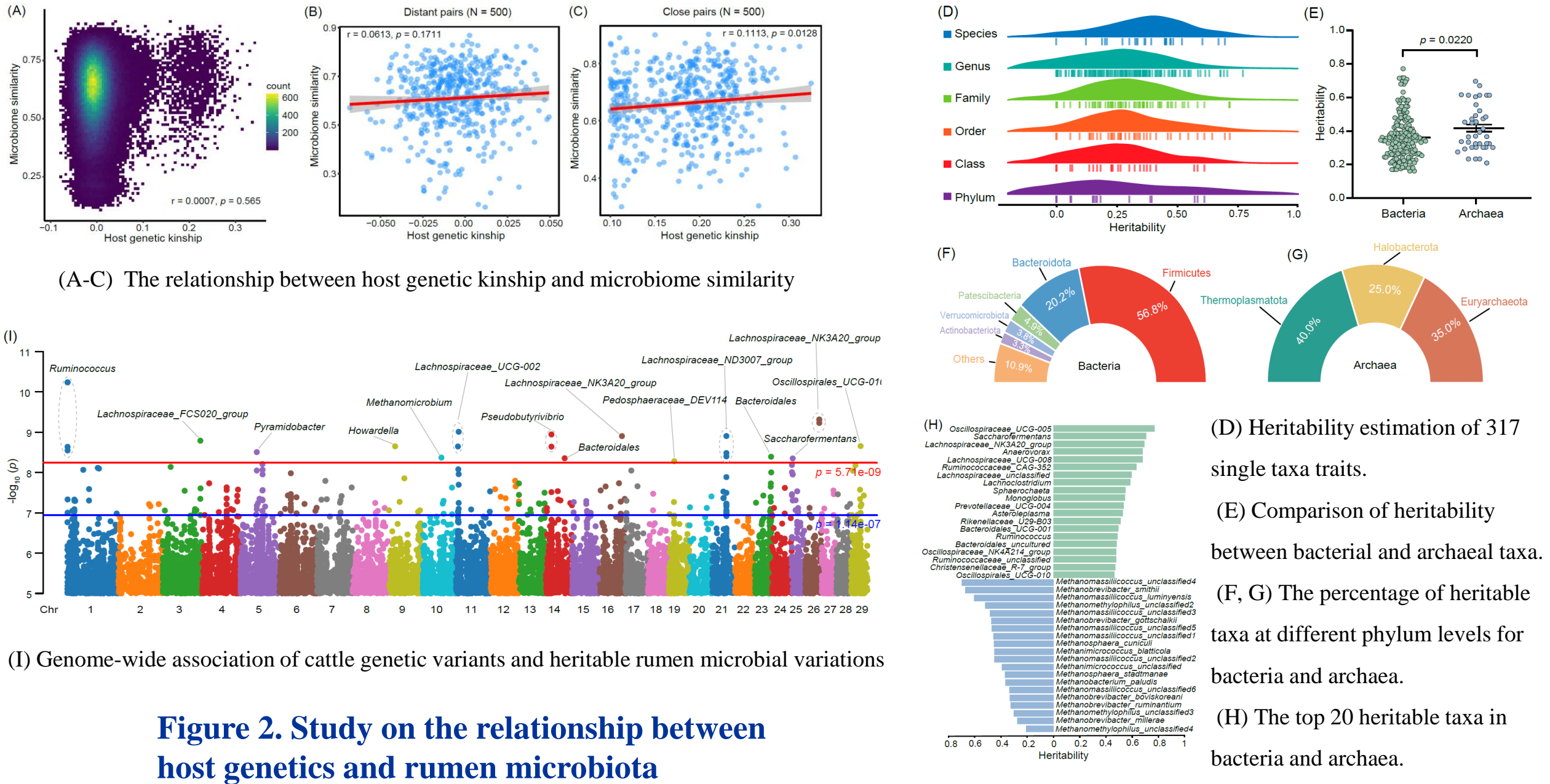


Figure 1. Study design and the composition and community structure of rumen microbiota



Host genetic factors affect the rumen microbiota



(A-C) The relationship between host genetic kinship and microbiome similarity

(D) Heritability estimation of 317 single taxa traits.

(E) Comparison of heritability between bacterial and archaeal taxa.

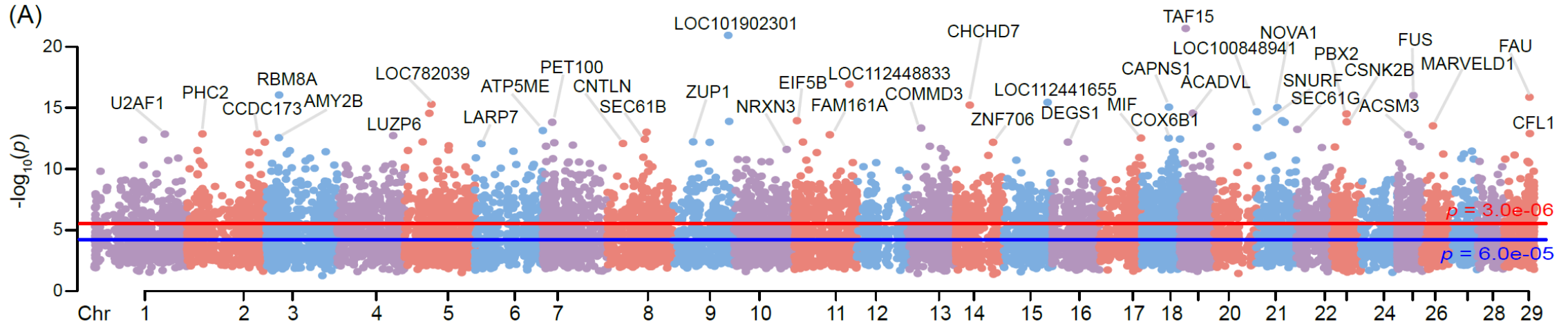
(F, G) The percentage of heritable taxa at different phylum levels for bacteria and archaea.

(H) The top 20 heritable taxa in bacteria and archaea.

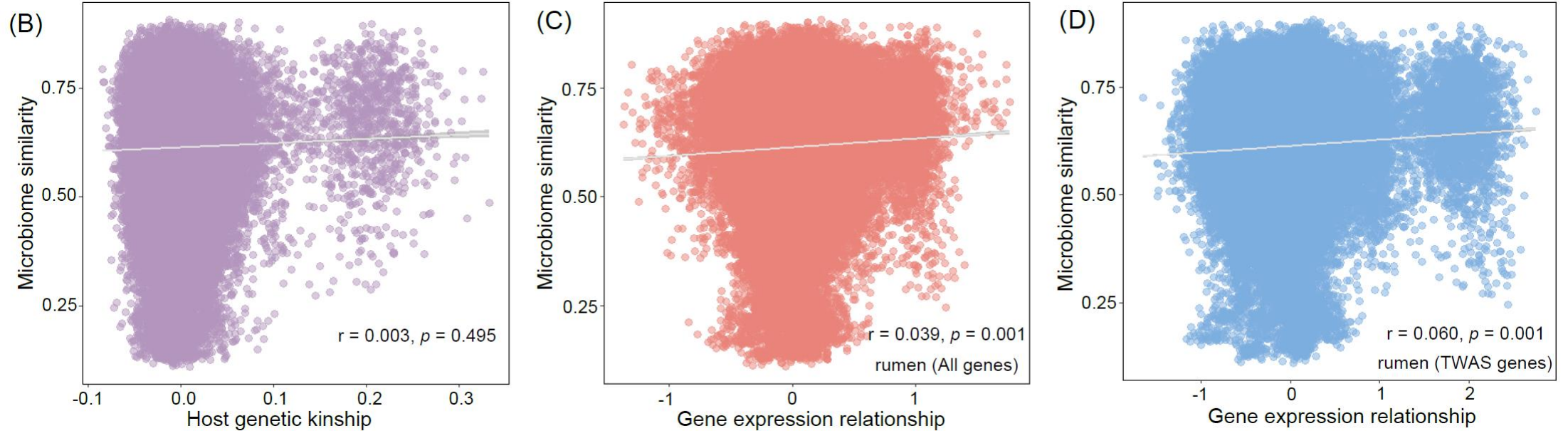
Figure 2. Study on the relationship between host genetics and rumen microbiota



TWAS atlas of rumen microbiota



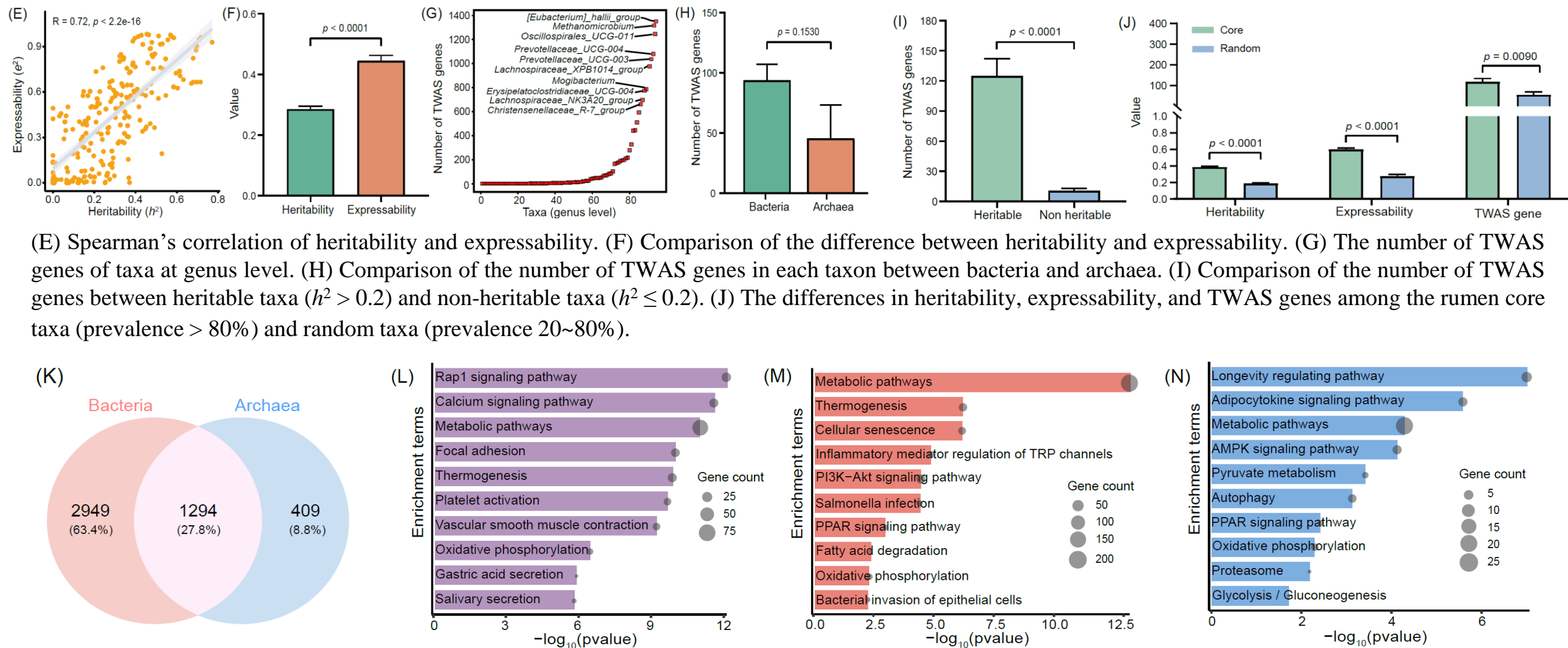
(A) Transcriptome-wide association of rumen gene expression and rumen microbial abundance



(B-D) The correlations between host genetic kinship, gene expression relatedness and microbiome similarity



TWAS atlas of rumen microbiota

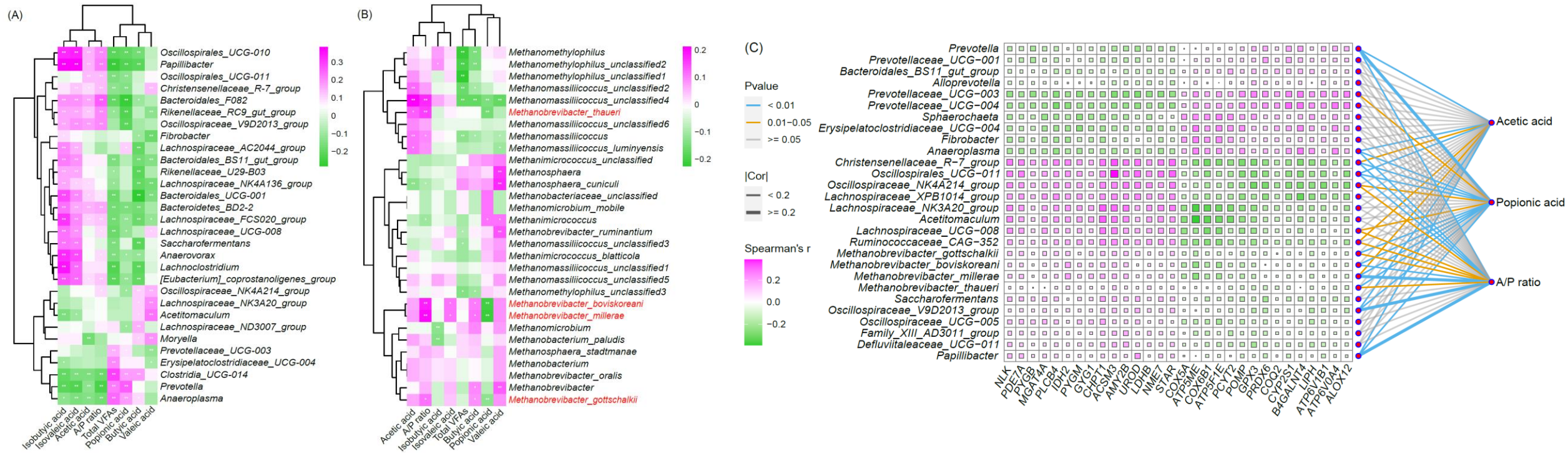


(K) The overlapping TWAS genes between rumen bacteria and archaea.

(L-M) Functional enrichment analyses for bacteria and archaea shared TWAS genes, bacteria-specific genes, and archaea-specific genes, respectively.

Figure 3. Characteristics of the TWAS atlas of rumen microbiota

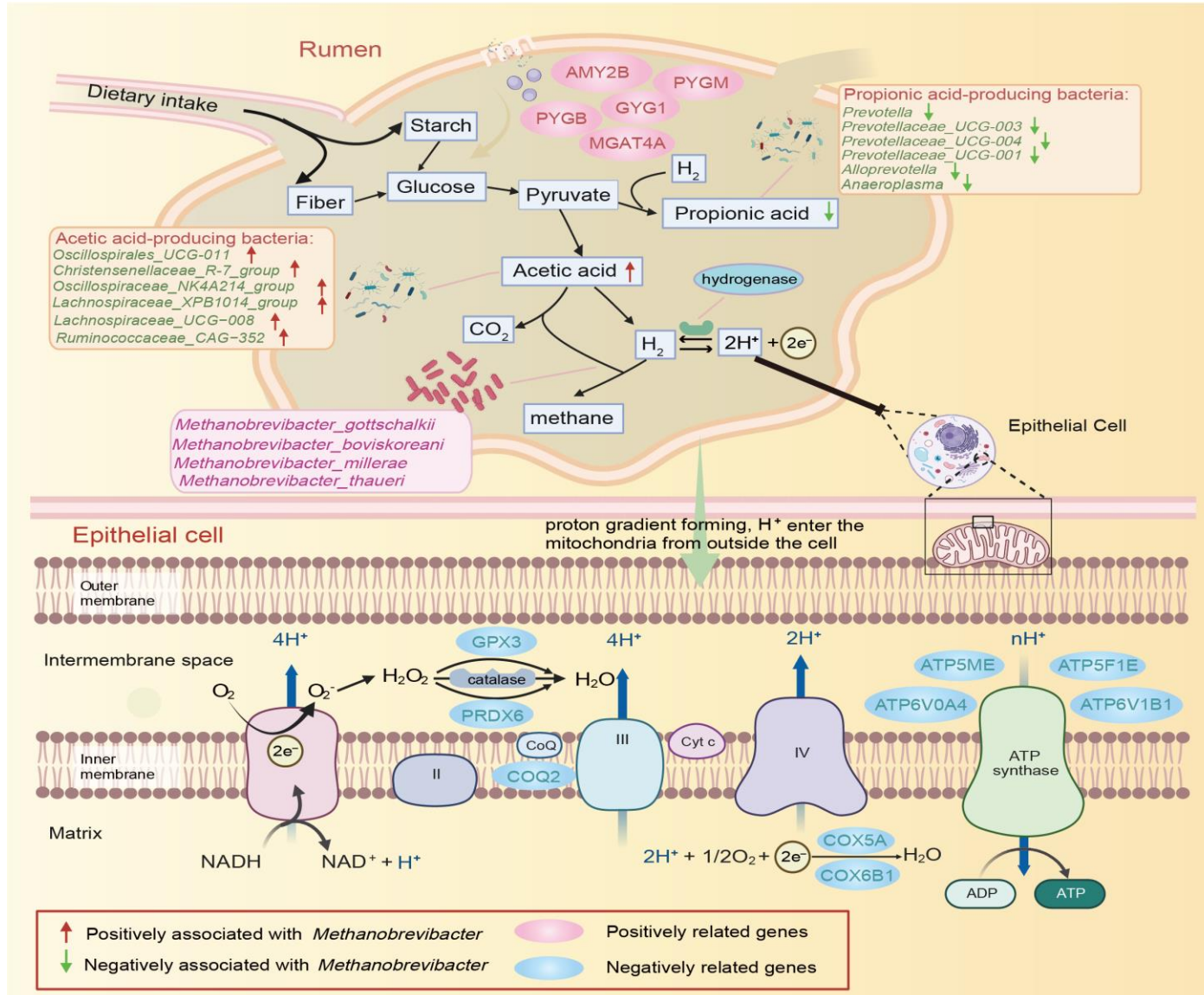
Multiple correlation analysis discovers promising genes and microbes in methanogenesis



- (A) The correlations between rumen bacterial taxa and volatile fatty acids (VFAs).
- (B) The correlations between rumen archaeal taxa and VFAs.
- (C) Multiple correlation analyses among host rumen genes, rumen microbiota and volatile fatty acids. Only correlation coefficients < -0.2 or > 0.2 and adjusted p values < 0.05 are displayed. * represents $p < 0.05$, ** represents $p < 0.01$.

Figure 5. Multiple correlation networks of genes-taxa-VFAs

Multiple correlation analysis discovers promising genes and microbes in methanogenesis



➤ The upper part illustrates the potential process by which high expression of the rumen epithelial amylase and glycogen genes leads to more extensive breakdown of starch into glucose in the rumen, which reduces the niche advantage of starch-utilizing bacteria and increases opportunities for acetate-producing microorganisms to acquire nutrients. This promotes a shift in rumen fermentation towards acetate-type fermentation. Acetate-type fermentation results in increased hydrogen production, which in turn enhances the abundance of *Methanobrevibacter*, a genus of methanogenic archaea.

➤ The lower part exhibits the potential process of electron transfer and hydrogen ion transport in the mitochondrial oxidative respiratory chain of host rumen epithelial cells. When genes for rumen epithelial hydrogen ion transport and oxidative phosphorylation are highly expressed, the pathways for hydrogen utilization in the rumen increase, thereby reducing the abundance of *Methanobrevibacter* in the rumen.

Figure 6. Overview of putative ruminal carbohydrate and hydrogen metabolism pathways in methanogenesis



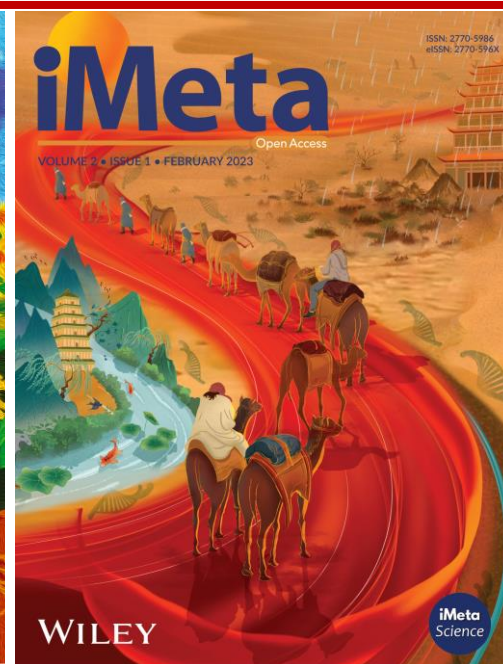
Summary

- ❑ In this study, we systematically evaluated the effect of host genetic variants and rumen gene expressions on bovine rumen microbial abundance variation.
- ❑ Our results highlight the TWAS is a promising method for determining the host and microbiota associations at gene expression level.
- ❑ By combining multiple relationship networks (genes-taxa-VFAs), we observed that host-microbe interactions in the rumen methanogenesis are primarily involved in substrate hydrogen metabolism and transport.
- ❑ Overall, these findings provide novel insights into the host-microbiome interactions in methanogenesis and offer valuable guidelines for genetic regulation and microbial management strategies to mitigate methane emissions in ruminants.

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