Deciphering functional groups of rumen microbiome and their underlying potentially causal relationships in shaping host traits

Ming-Yuan Xue[1,2], Yun-Yi Xie[1], Xin-Wei Zang[1], Yi-Fan Zhong[1], Xiao-Jiao Ma[1], Hui-Zeng Sun[1,3*], Jian-Xin Liu[1,3*]

[1]Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou 310058, China

[2]Xianghu Laboratory, Hangzhou 311231, China

[3]Ministry of Education Key laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou 310058, China

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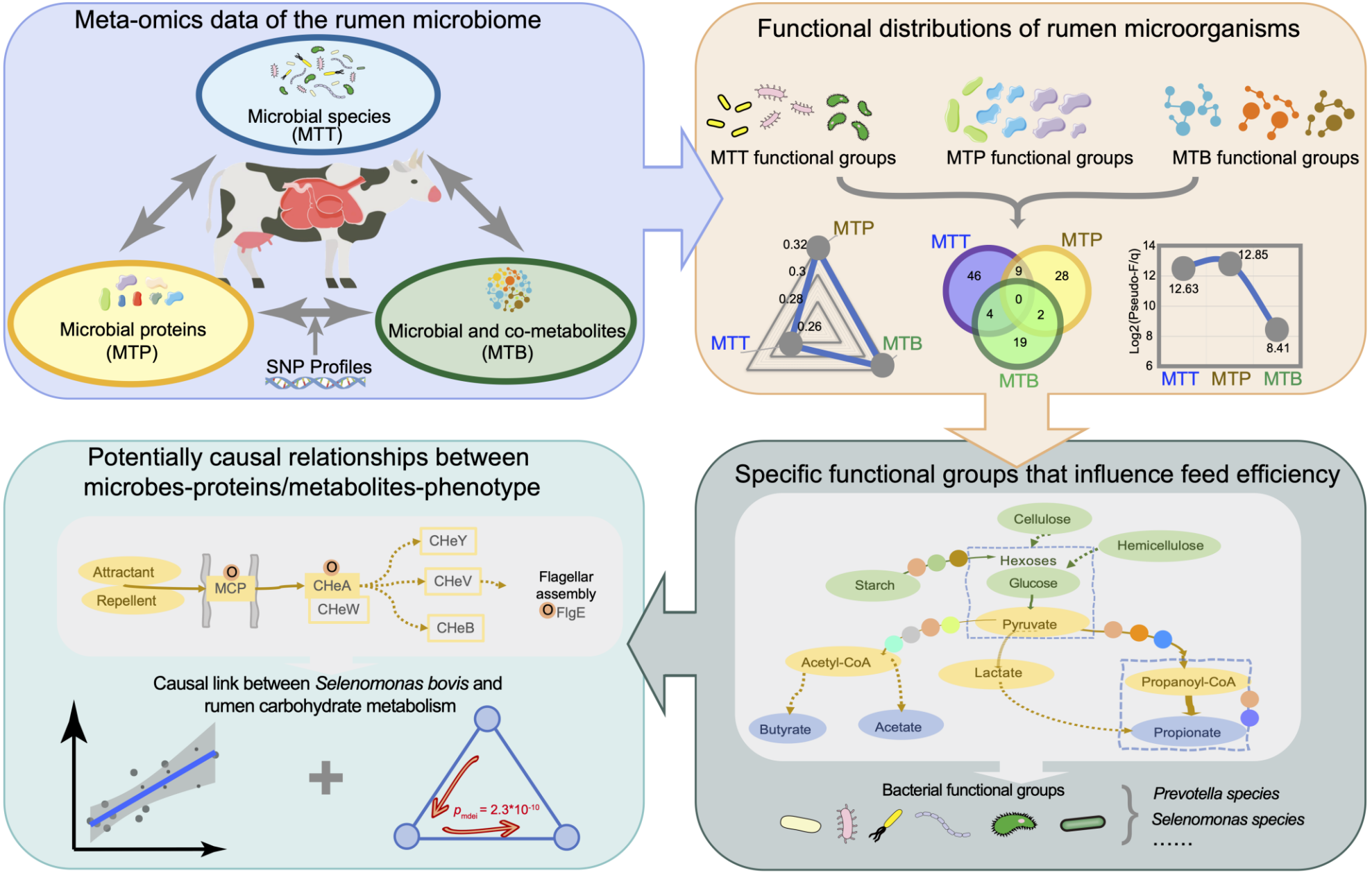
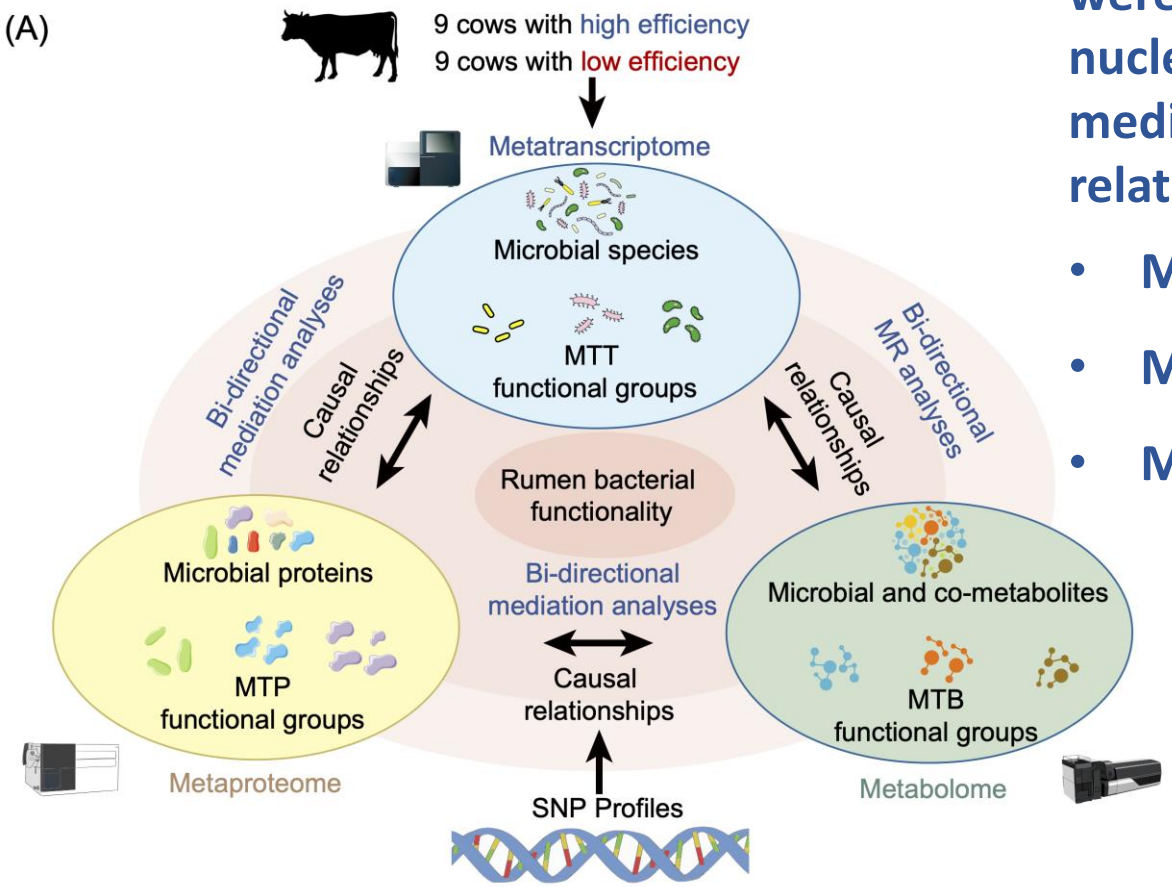
Highlights

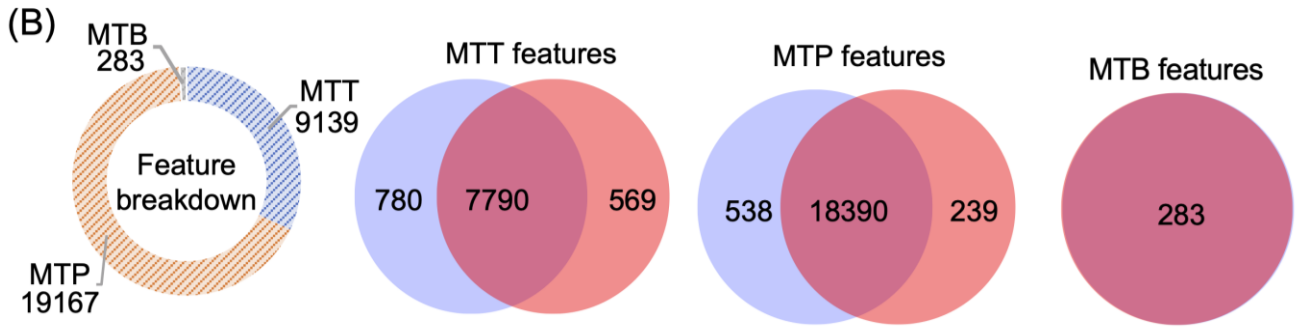

Meta-omics data of the rumen microbiome
Microbial species (MTT)
Microbial proteins (MTP)
Microbial and co-metabolites (MTB)
SNP Profiles
Functional distributions of rumen microorganisms
MTT functional groups
MTP functional groups
MTB functional groups
MTP
MTT
MTB
0.32
0.3
0.28
0.26
46
9
28
0
4
2
19
Log2(Pseudo-F/q)
14
12
10
8
6
12.63
12.85
8.41
Specific functional groups that influence feed efficiency
Cellulose
Hemicellulose
Hexoses
Starch
Glucose
Pyruvate
Acetyl-CoA
Lactate
Propanoyl-CoA
Butyrate
Acetate
Propionate
Bacterial functional groups
Prevotella species
Selenomonas species
.....
Potentially causal relationships between microbes-proteins/metabolites-phenotype
Attractant
Repellent
MCP
CHeA
CHeW
CHeY
CHeV
CHeB
Flagellar assembly
FlgE
Causal link between Selenomonas bovis and rumen carbohydrate metabolism
p_{mdei} = 2.3*10^{-10}

Materials and methods

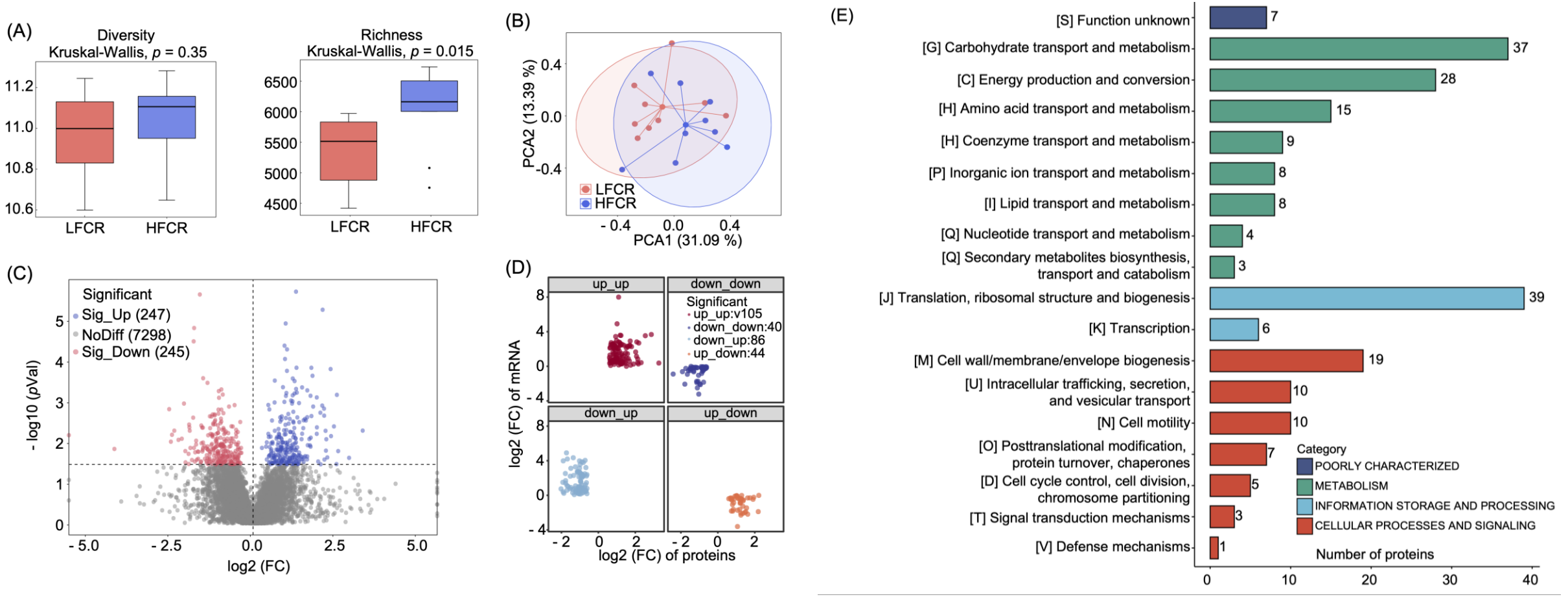


A total of 28,589 features from three different omics platforms were initially identified, and we included a total of 20,571 single nucleotide polymorphisms (SNP) loci from 298 dairy cattle as a mediating factor for investigating the potentially causal relationship behind the omics-based relationships.

- MTT——9,139 microbial taxa
- MTB——283 metabolite features
- MTP——19,167 proteins



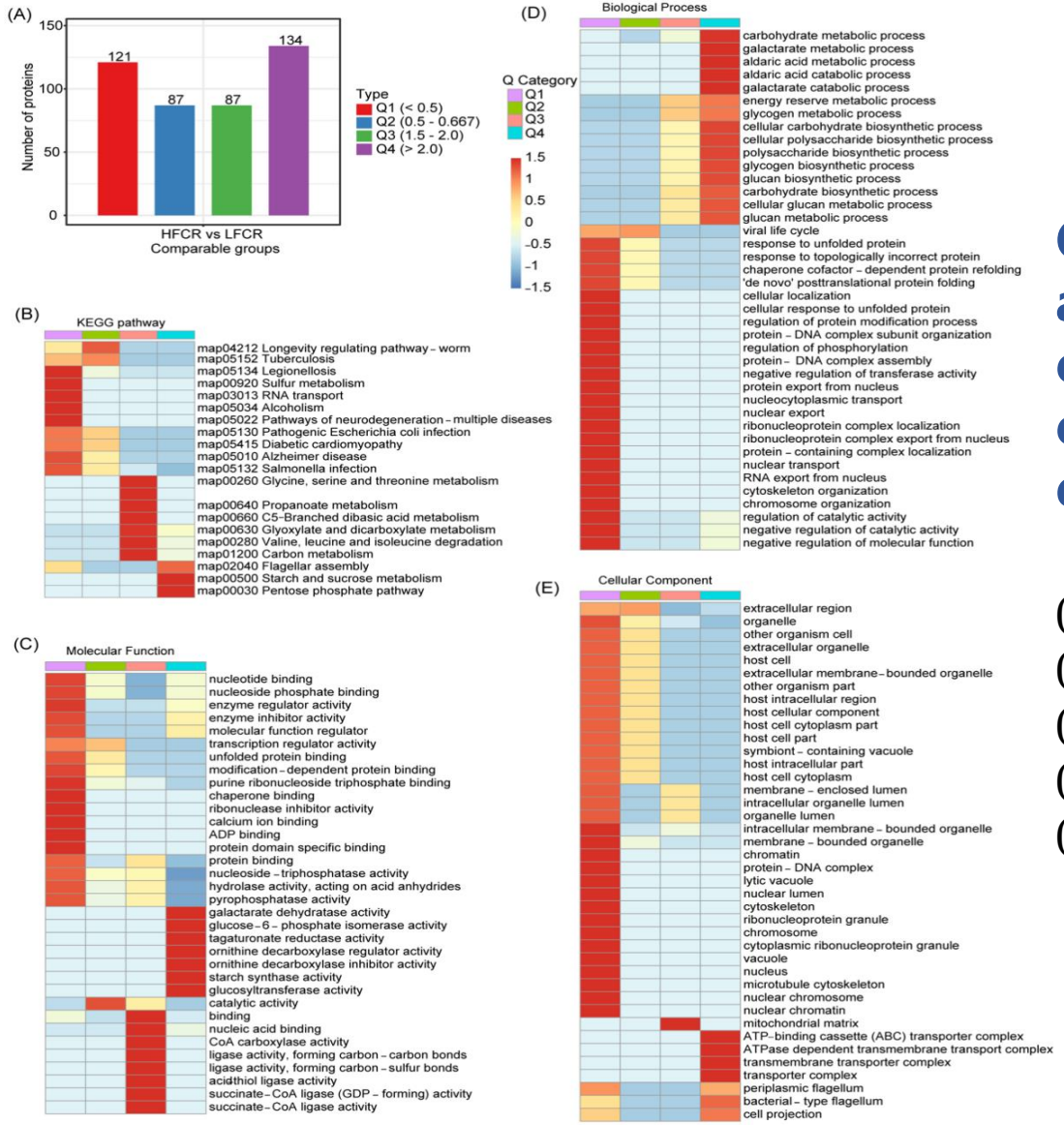
The functionality of rumen microbiota based on metaproteomics



Main metaproteome features of the rumen microbiota

(A) Box plot representing alpha diversity and richness indices of the metaproteome from the rumen of cows with differential feed efficiencies. (B) principal component analysis (PCA) plot representing beta diversity of metaproteomic data from rumen microbes of cows with differential feed efficiencies. (C) Volcano plot comparing proteins from rumen microbes of cows with differential feed efficiencies. (D) Correlation analysis between significantly differential transcriptomic features and significantly differential proteomic features. (E) Functional classification of significantly upregulated cluster of orthologous groups of protein (COGs). LFCR, low feed conversion ratio; HFCR, high feed conversion ratio; FC, fold change.

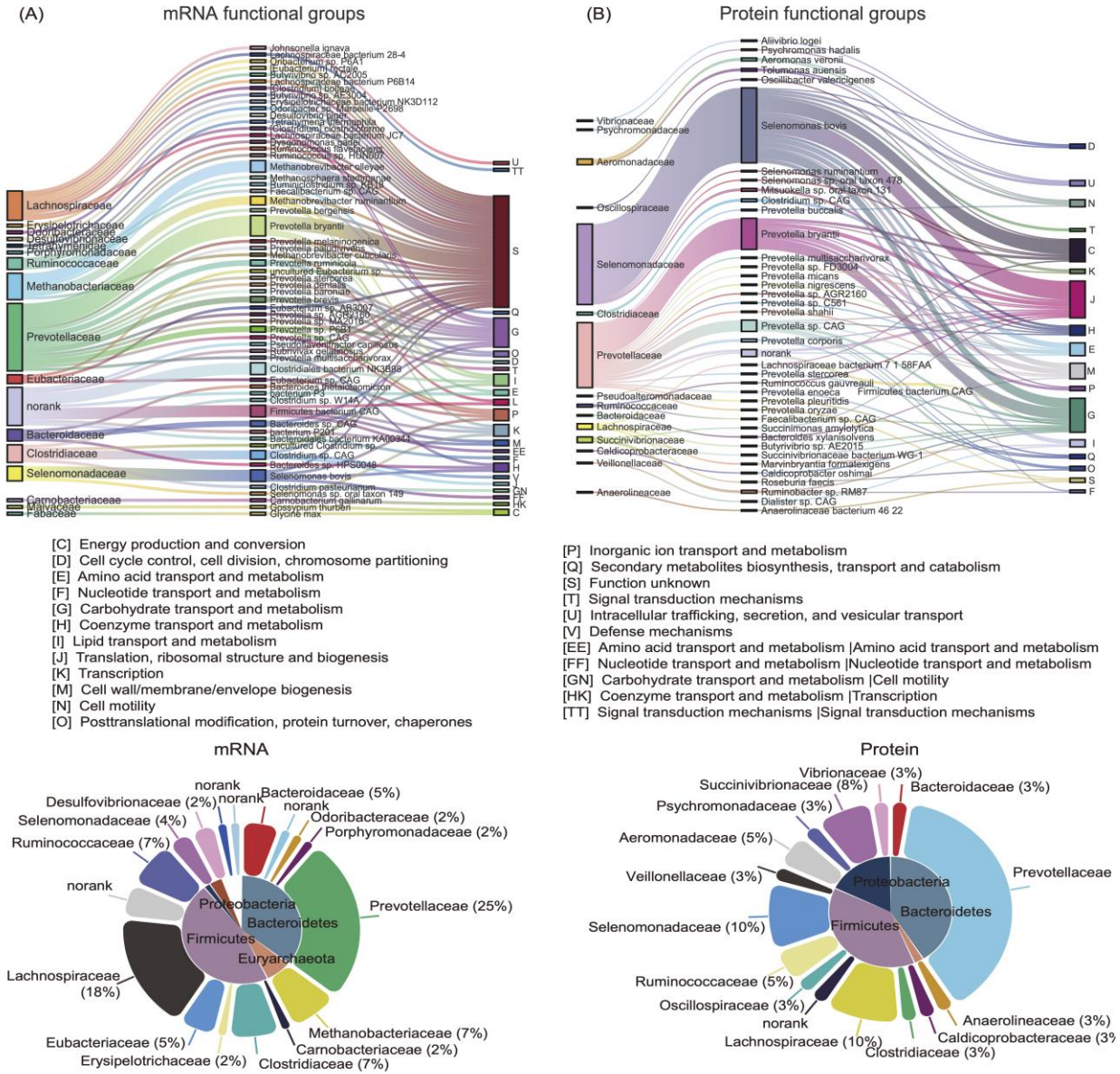
The difference between potential and actual functional groups of rumen microbiota



Cluster results to identify functional correlations among differentially expressed proteins in comparison groups after performing GO classification and enrichment of differentially expressed proteins in various comparison groups.

(A) Comparison of clusters in the two groups.
(B) Heatmap showing classification of pathways.
(C) Heatmap showing classification of molecular functions.
(D) Heatmap showing classification of biological process functions.
(E) Heatmap showing classification of cellular component functions.

The difference between potential and actual functional groups of rumen microbiota

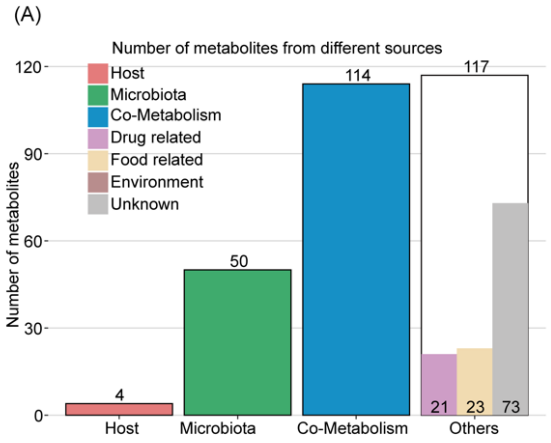


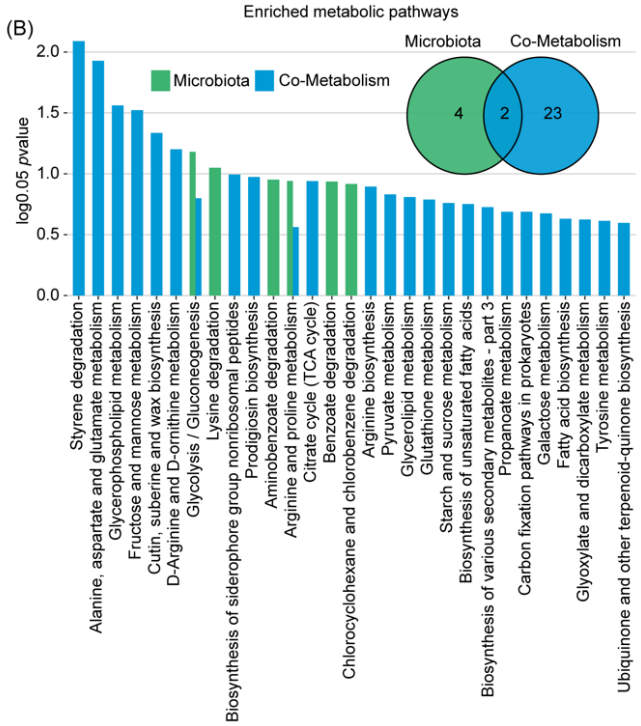
Comparison of rumen microbial functional groups related to high feed efficiency in dairy cows based on metatranscriptomics and metaproteomics.

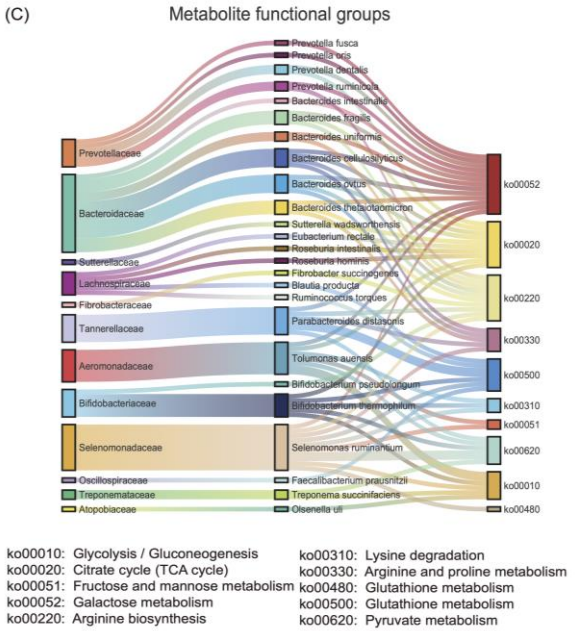
(A) The Sankey diagrams of the taxonomic and functional mapping relationships of rumen microbial functional groups related to high feed efficiency, analyzed based on metatranscriptomics data.

(B) The Sankey diagrams display the taxonomic and functional mapping relationships analyzed based on metaproteomics data.

The difference between potential and actual functional groups of rumen microbiota





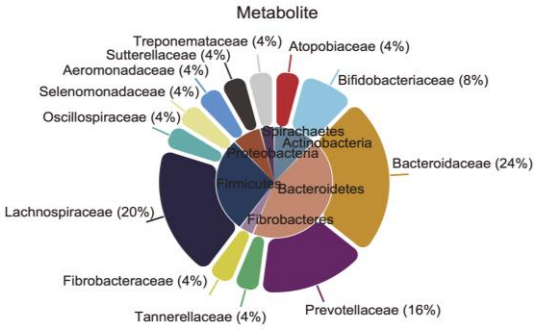


Metabolomics-based rumen microbial functional groups related to high feed efficiency in dairy cows.

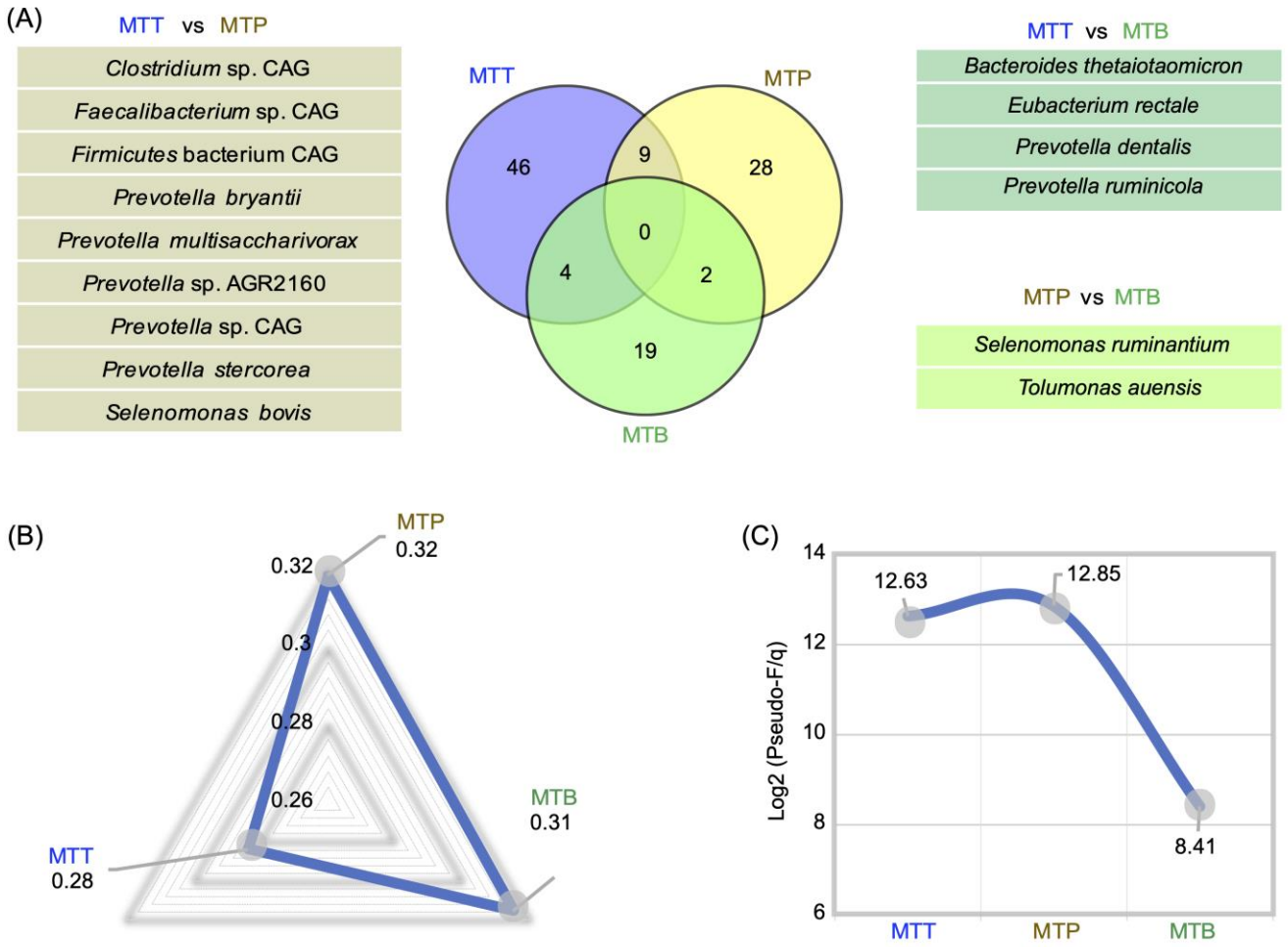
(A) Discriminating the origins of rumen microbial metabolites from the bulk metabolome using the MetOrigin workflow.

(B) Metabolic pathway enrichment analysis according to different origins, including both microbial and cometabolism metabolites.

(C) Taxonomic and functional mapping relationships analyzed based on metabolomics.



The difference between potential and actual functional groups of rumen microbiota

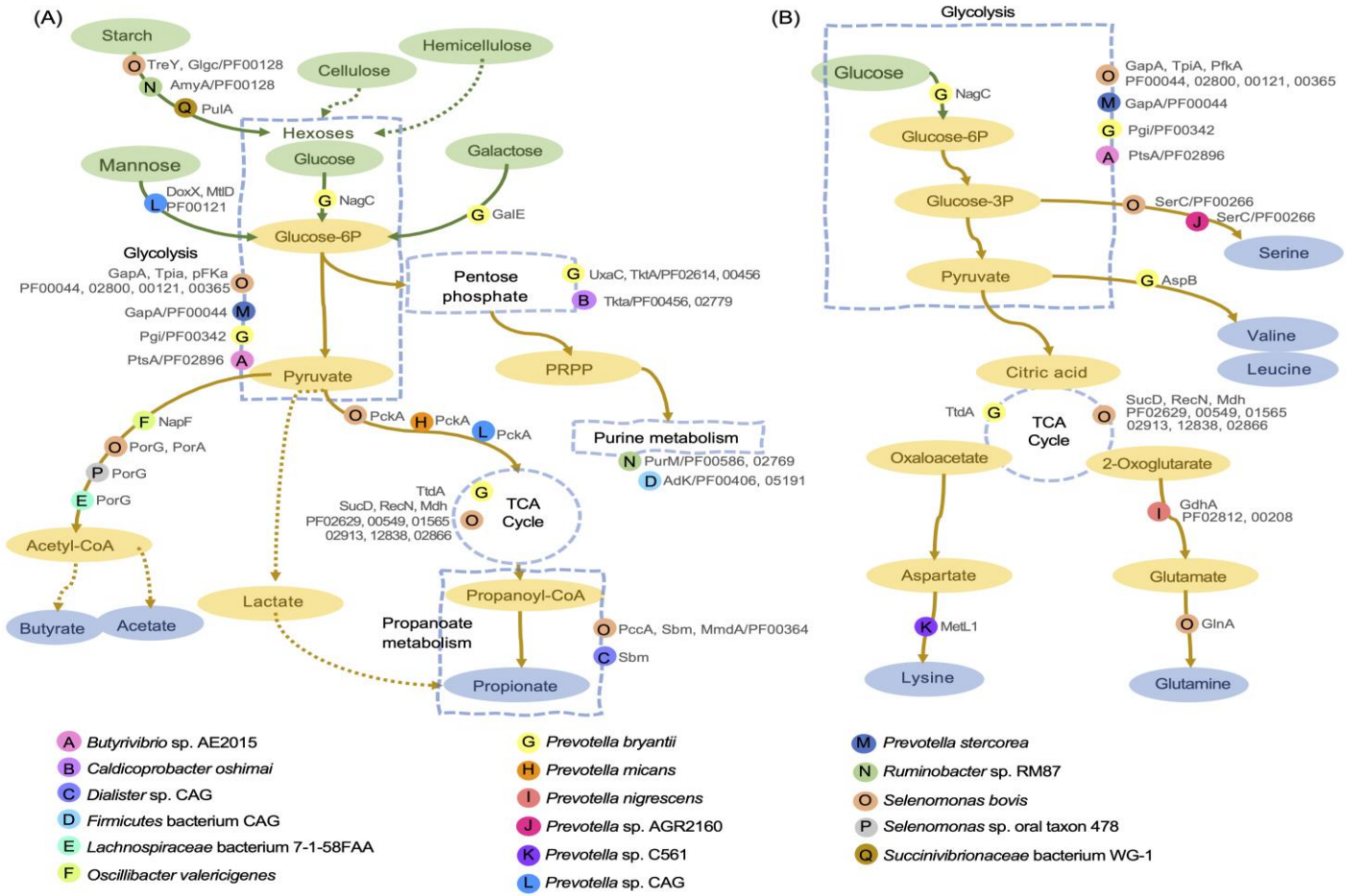


Comparison of rumen functional groups analyzed by different omics data.

(A) Venn diagram showing overlaps of rumen microbial functional groups related to high feed efficiency based on MTT, MTP, and MTB.

(B) Comparison of discriminatory power for feed efficiency of each functional group, as calculated by permutational multivariate analysis of variance (PERMANOVA) R2 values (C) and $\log_2$ (Pseudo-F/q) values. Input values of omics data were determined by PERMANOVA of Bray–Curtis-based beta diversity. CAG, co-abundance gene group.

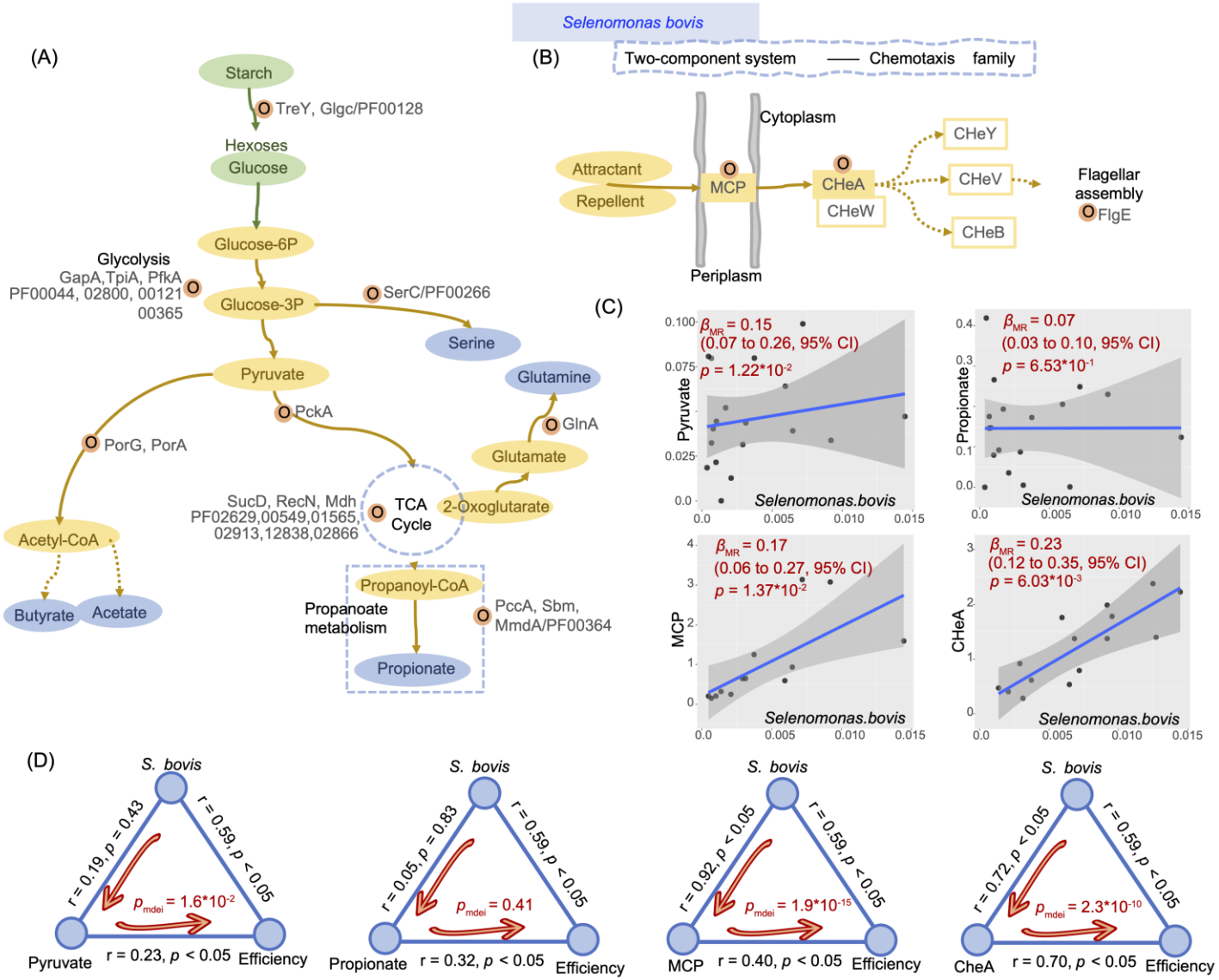
Rumen functional groups in high-feed-efficiency cows exerted important functions through key proteins



Pattern diagrams representing the role of key proteins involved in critical metabolic pathways in the rumen microbial functional groups based on the metaproteome.

(A) Carbohydrates metabolism. (B) Nitrogen metabolism.

Potentially Causal relationships between S. bovis and functional proteins/metabolites contributed to high feed efficiency



The proteins involved in the metabolic pathways in which Selenomonas bovis participates in the rumen function of high feed-efficient dairy cows and their causal relationships with key functions.

- Proteins involved in key nutrient metabolism (A) and bacterial chemotaxis (B) functions played by *S. bovis* and their participating metabolic pathways.
- (C) Causal relationships between *S. bovis* and functional proteins/metabolites as assessed by Mendelian randomization (MR) analysis, with the MR effect size (β) and 95% confidence interval (CI) represented.
- (D) The direct mediation effects of *S. bovis* on feed efficiency through key functional proteins/metabolites, along with corresponding p values derived from mediation analysis (p_{mdei}). MCP, methyl-accepting chemotaxis proteins; CI, confidence interval.

Summary

- In our study, we reported the protein-level information in the rumen and integrated holo-omics to explore functional groups and redundancy across RNA, protein, and metabolite levels.

- Additionally, we found a causal link between Selenomonas bovis and rumen carbohydrate metabolism, potentially mediated by bacterial chemotaxis and a two-component regulatory system, impacting feed utilization efficiency of dairy cows.

- Our findings suggest a potentially nuanced understanding of the mapping of the rumen microbiota to its functional endpoints and its association with phenotypes. The platform offers features such as online vector graphic editing, one-click execution, email reminders, tool popularity analysis, video tutorials, aiming to facilitate user access and utilization.

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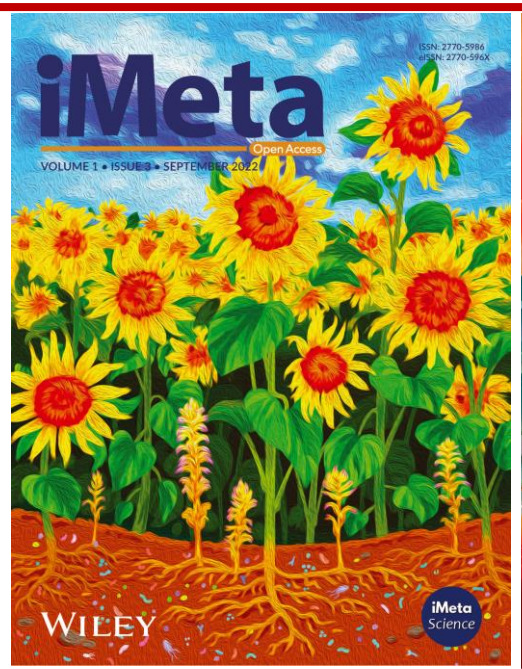

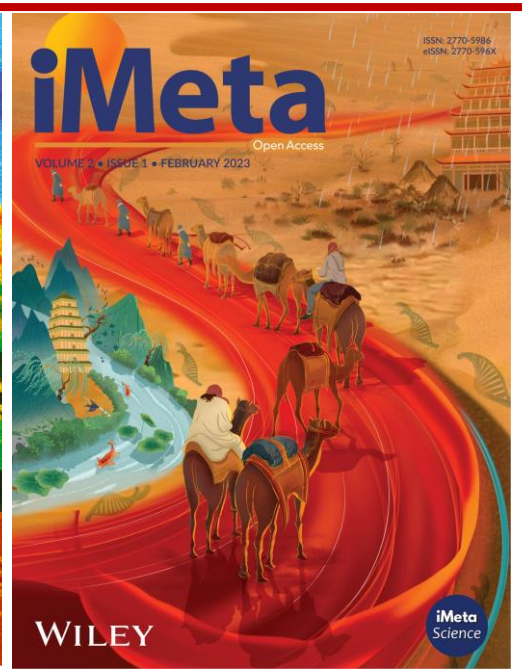

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