



# Comparative multi-omics analyses reveal the breed effect on the colonic host-microbe interactions in pig.

Liang Huang<sup>1,2</sup>, Shiqi Luo<sup>1,2</sup>, Shuqi Liu<sup>1,2</sup>, Mingliang Jin<sup>1,2</sup>, Yizhen Wang<sup>1,2</sup>, Xin Zong<sup>1,2</sup>

<sup>1</sup>Key Laboratory of Molecular Animal Nutrition, Ministry of Education, College of Animal Sciences, Zhejiang University, Hangzhou, China

<sup>2</sup>Key Laboratory of Animal Nutrition and Feed Science in Eastern China, Ministry of Agriculture, College of Animal Sciences, Zhejiang University, Hangzhou, China



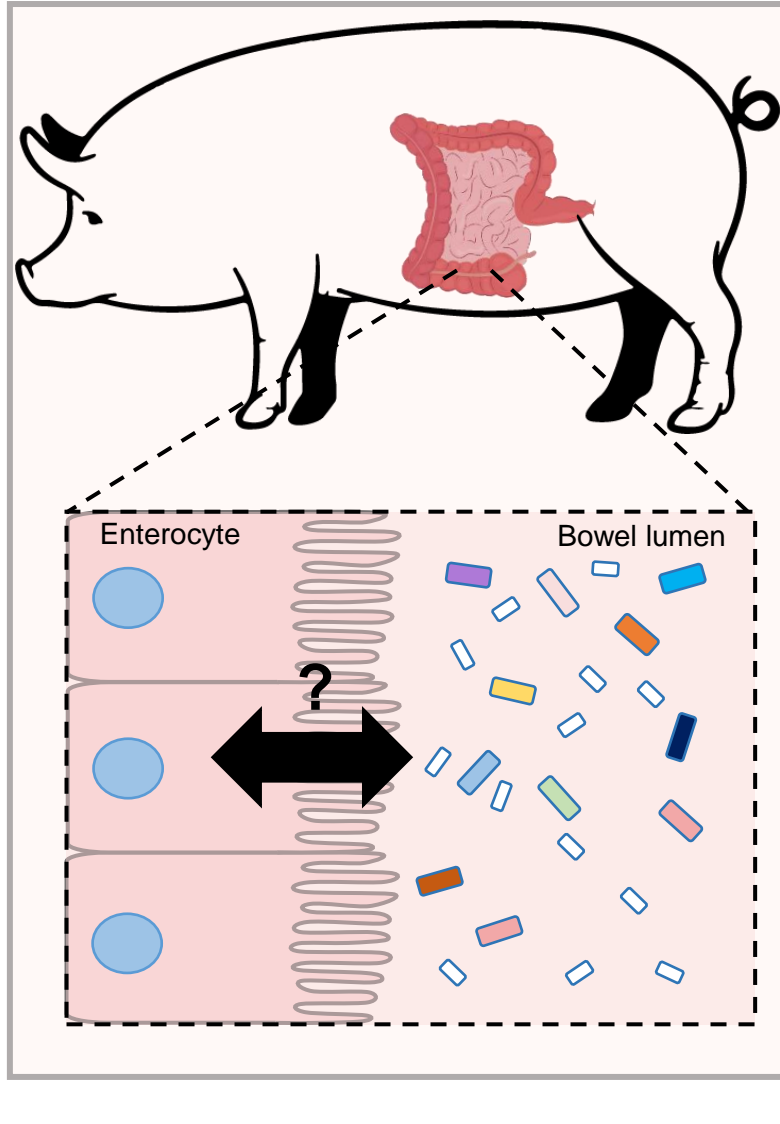
Liang Huang, Shiqi Luo, Shuqi Liu, Mingliang Jin, Yizhen Wang, Xin Zong. 2024. Comparative multi-omics analyses reveal the breed effect on the colonic host-microbe interactions in pig. *iMetaomics* 1: e8.

<https://doi.org/10.1002/imo2.8>

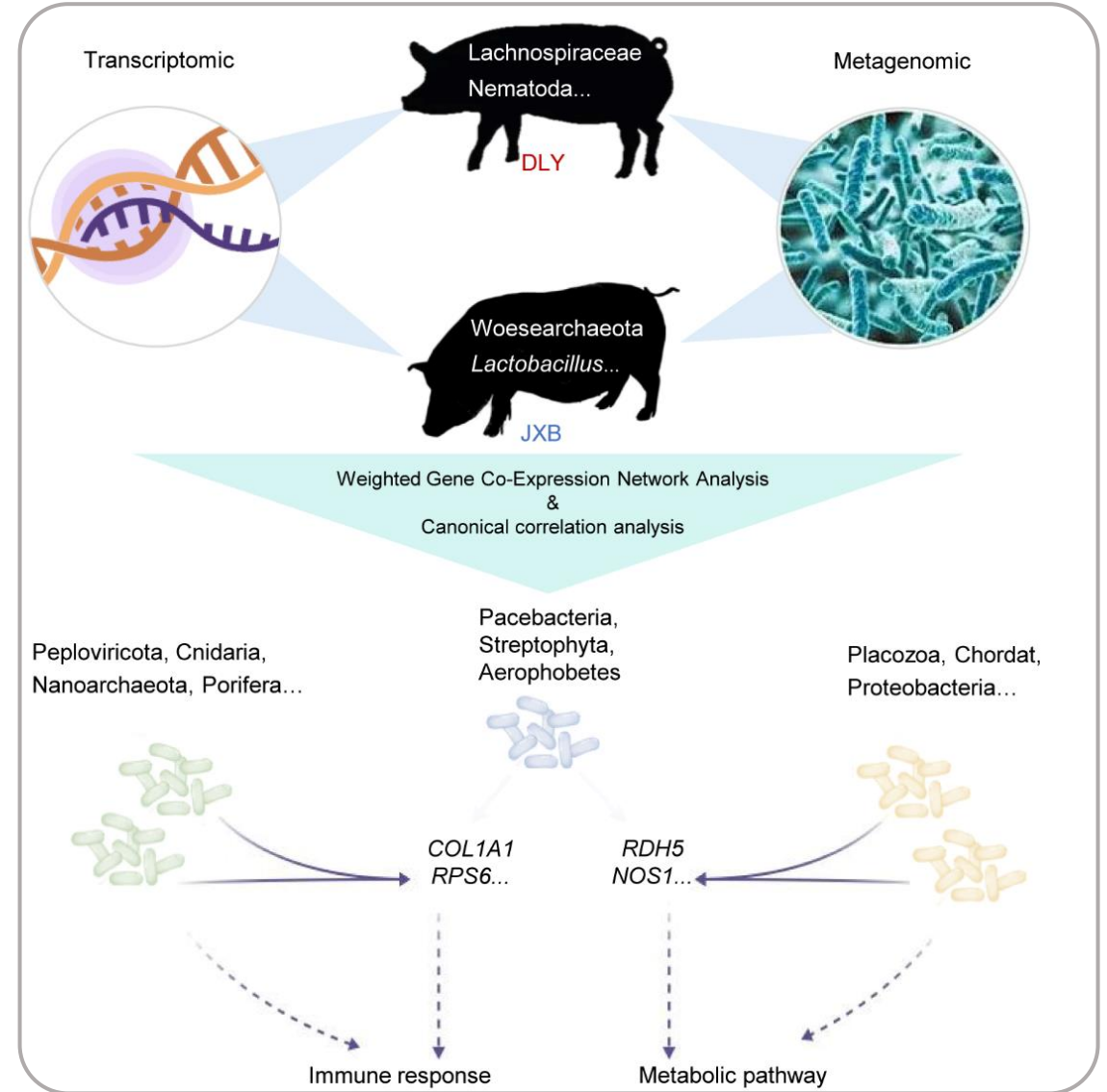


# Introduction

## Host-gut microbe interactions in pig

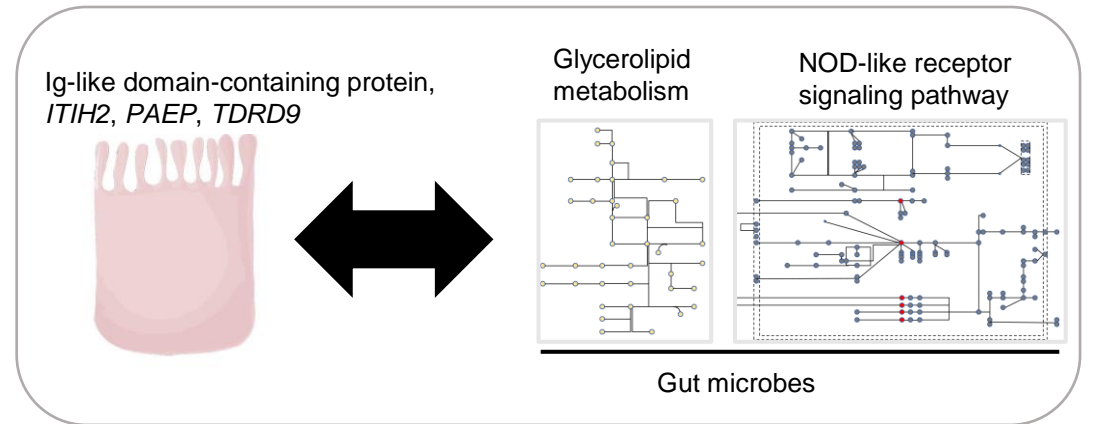
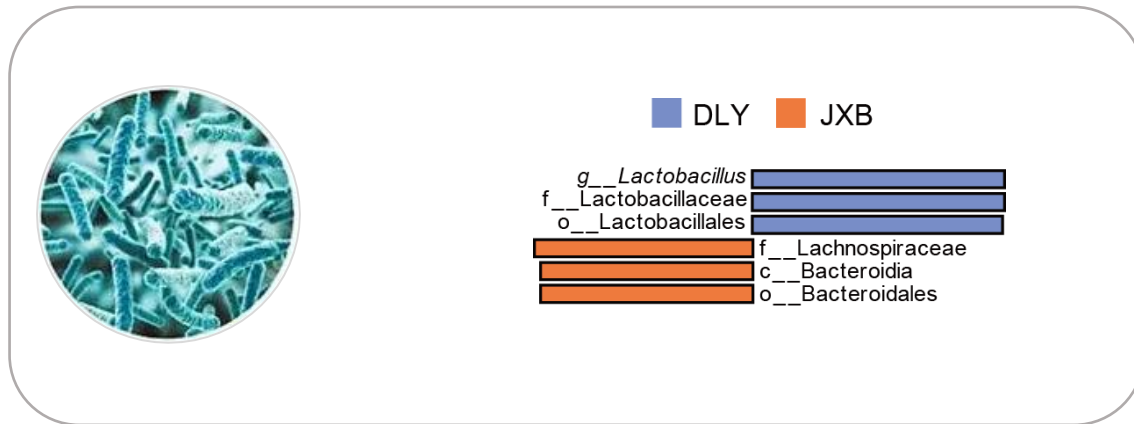
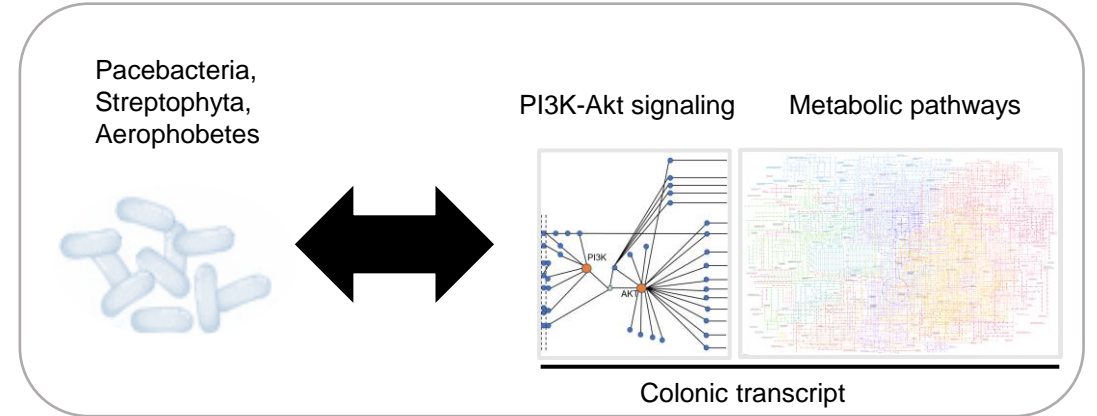
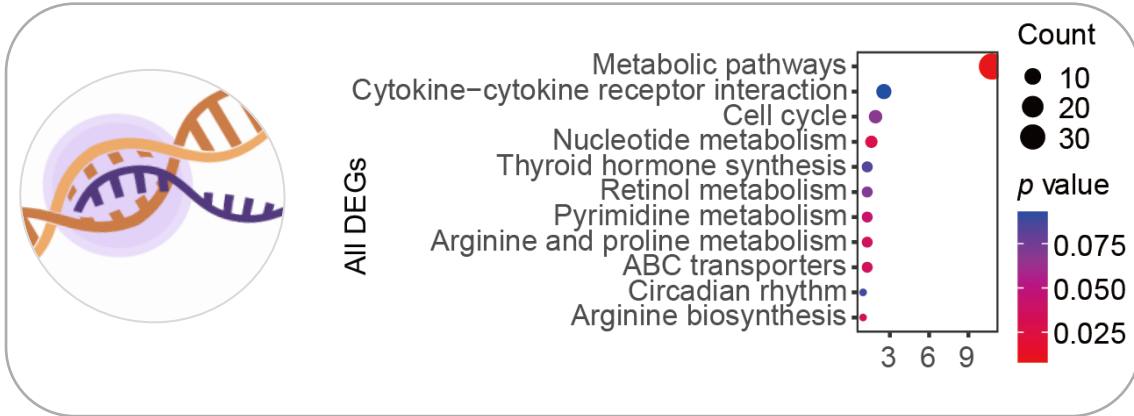


## Workflows





# Highlights





# Microbial composition

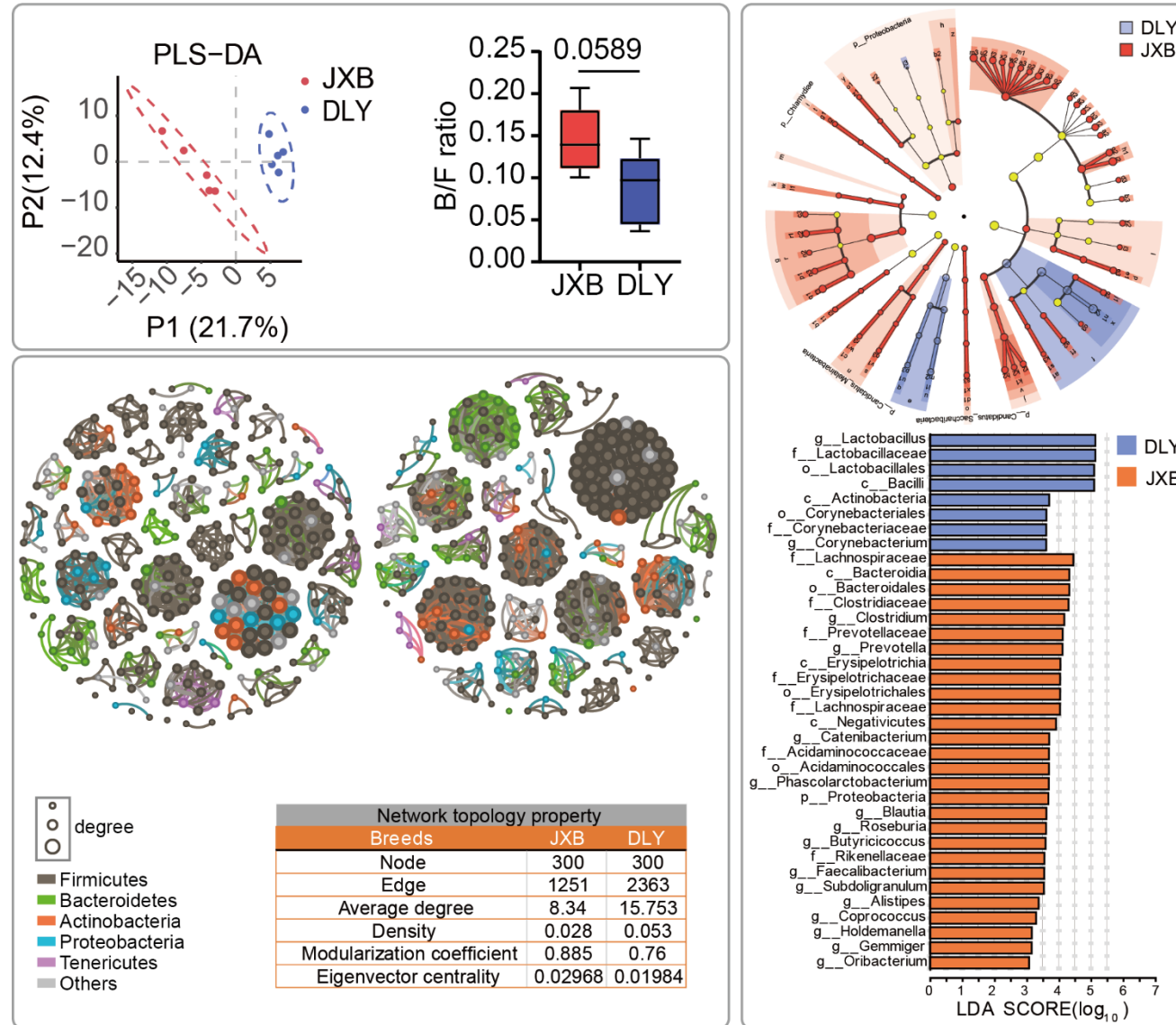


Figure 1. Composition of gut bacteria in the Jiaxing Black (JXB) and Duroc × Landrace × Yorkshire (DLY) pigs



# Comparison of colon gene expression signatures

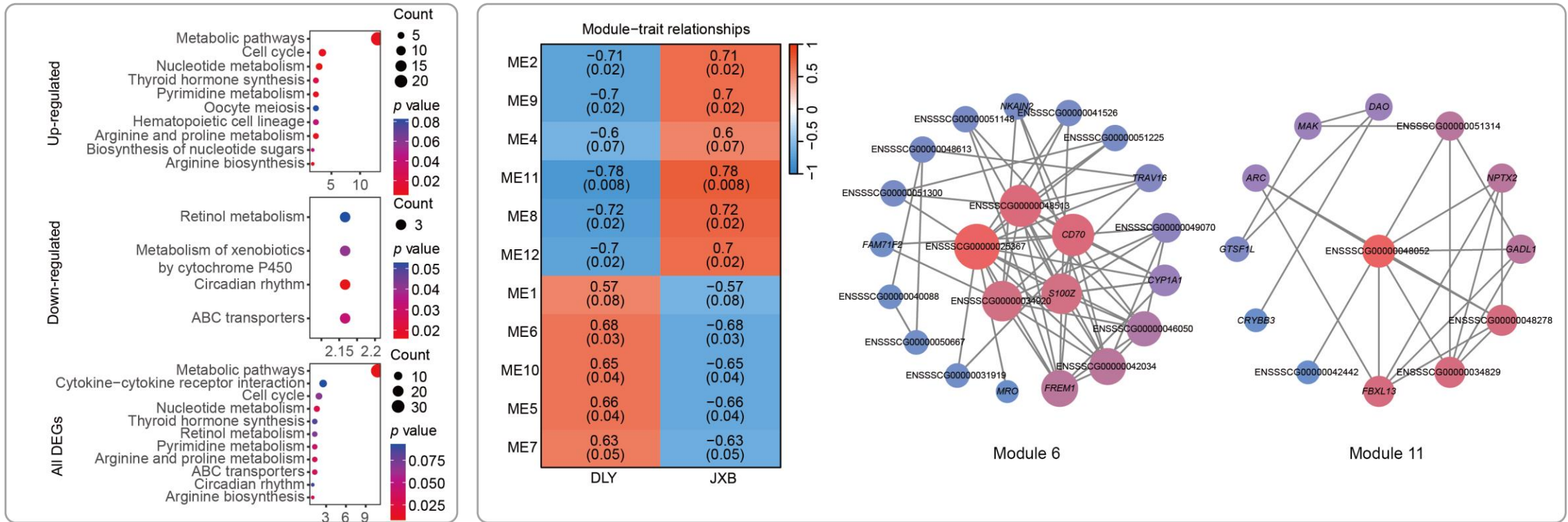


Figure 2. Transcriptional changes of gene sets in the Jiaxing Black (JXB) and Duroc × Landrace × Yorkshire(DLY) pigs

# Interactions between host pathways and the gut microbiota

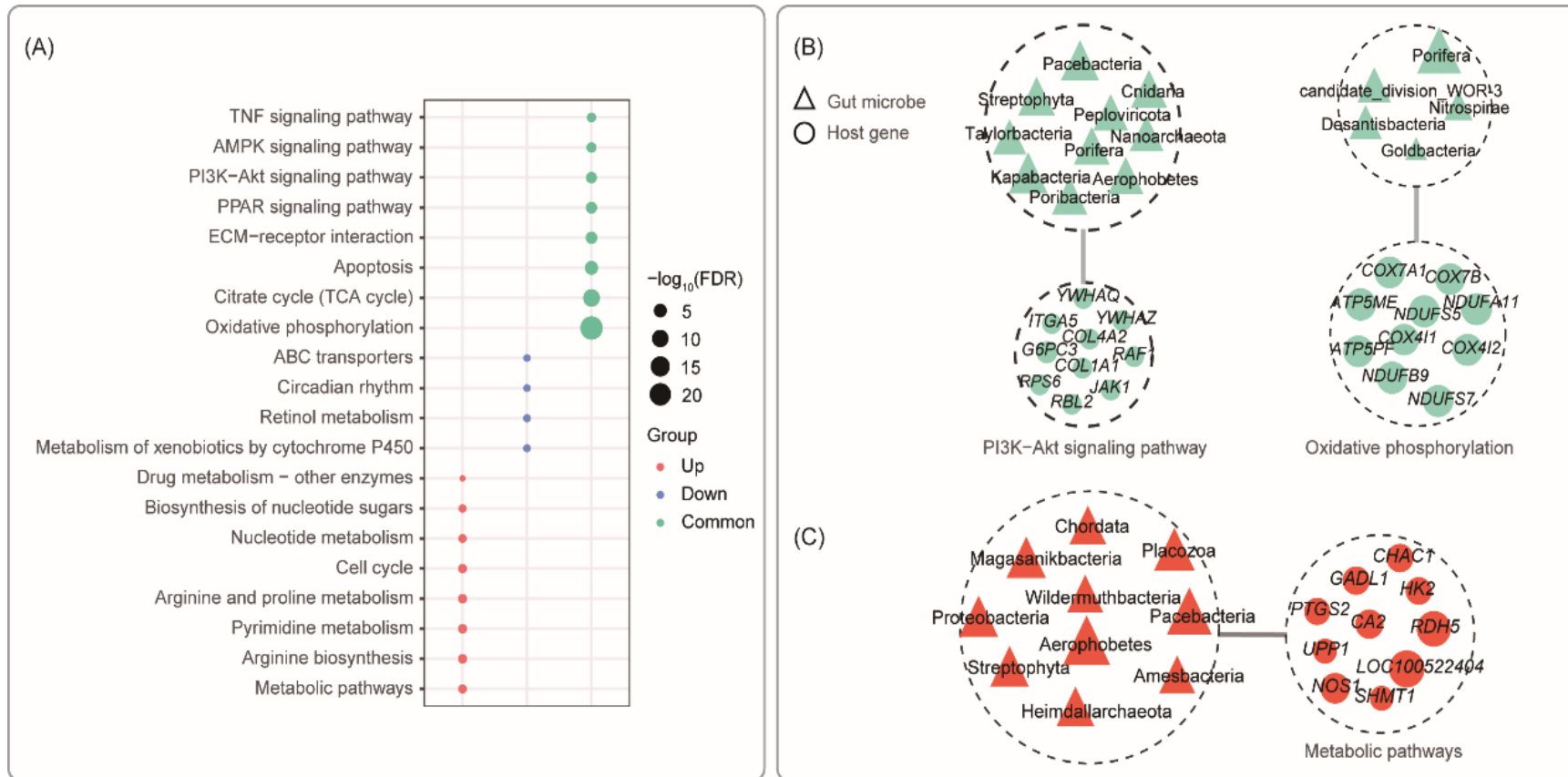


Figure 3. Host pathway-gut microbiota interactions in the Jiaxing Black (JXB) and Duroc  $\times$  Landrace  $\times$  Yorkshire (DLY) pigs



# Regulation of gut microbiome by host genes

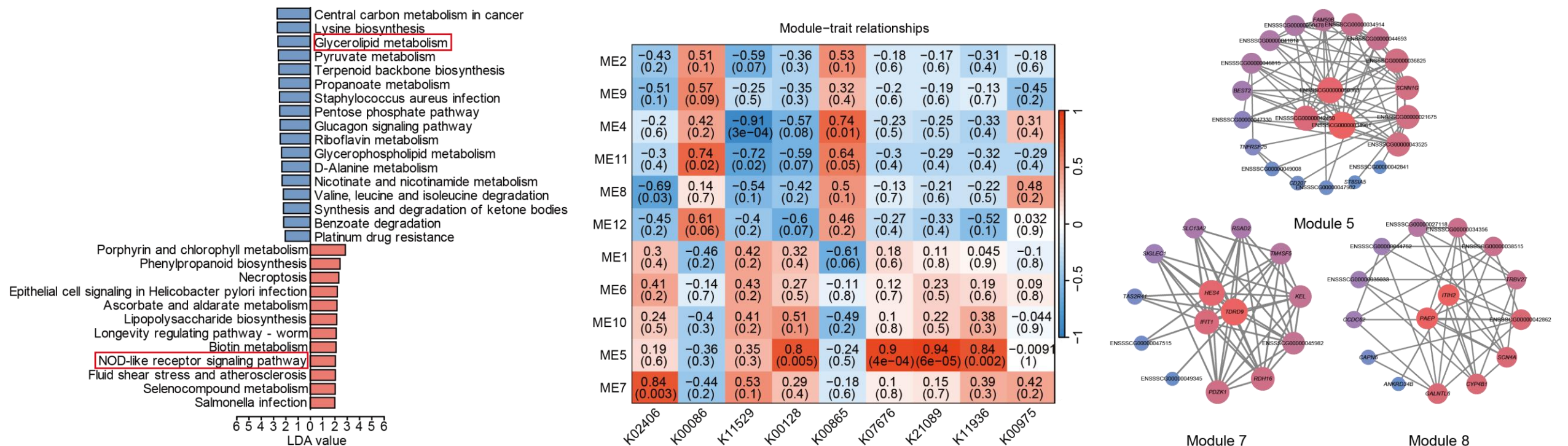


Figure 4. Functional differences of gut microbiota between the Jixing Black (JXB) and Duroc × Landrace × Yorkshire (DLY) pigs



# Summary

- ❑ In this study, we present the differences in colonic transcript levels and gut microbiota composition between Jiaxing black pig (JXB) and Duroc × Landrace × Yorkshire (DLY);
- ❑ The regulatory effects of gut microbes on the host colonic and, in turn, the host on the gut bacterial immune response and metabolism were determined, and key genes and microbiota were identified;
- ❑ These findings provide insights into the mechanisms of gut microbiota and their potential applications in animal production.

Liang Huang, Shiqi Luo, Shuqi Liu, Mingliang Jin, Yizhen Wang, Xin Zong. 2024. Comparative multi-omics analyses reveal the breed effect on the colonic host-microbe interactions in pig. *iMetaomics* 1: e8.

<https://doi.org/10.1002/imo2.8>



“[iMeta](#)” (IF **23.7**) is a Wiley partner journal launched by iMeta Science Society of scientists in bioinformatics and metagenomics in 2022. It aims to publish high-quality papers targeting a broad and diverse audiences. Its scope is similar to that of Nature Biotechnology, Nature Microbiology, Cell Host & Microbe. It unique features include video submission, bilingual publishing, and social media dissemination with 500,000 followers. It has been published 190+ papers and been cited for 3400+ times since 2022, and indexed by [ESCI](#), [PubMed](#), [Google](#), and [Scopus](#).

“[iMetaomics](#)” is sister journal of “iMeta” launched in 2024, with target IF>10, and its scope is similar to Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics, and Bioinformatics. All submissions are welcomed!

Society: <http://www.imeta.science>  
Publisher: <https://wileyonlinelibrary.com/journal/imeta>

Submission: <https://wiley.atyponrex.com/journal/IMT2>  
<https://wiley.atyponrex.com/journal/IMO2>

 [office@imeta.science](mailto:office@imeta.science)

 [Promotion Video](#)

 [iMetaScience](#)

 [iMetaScience](#)