



比较多组学分析揭示 品种对猪结肠宿主-微生物 相互作用的影响

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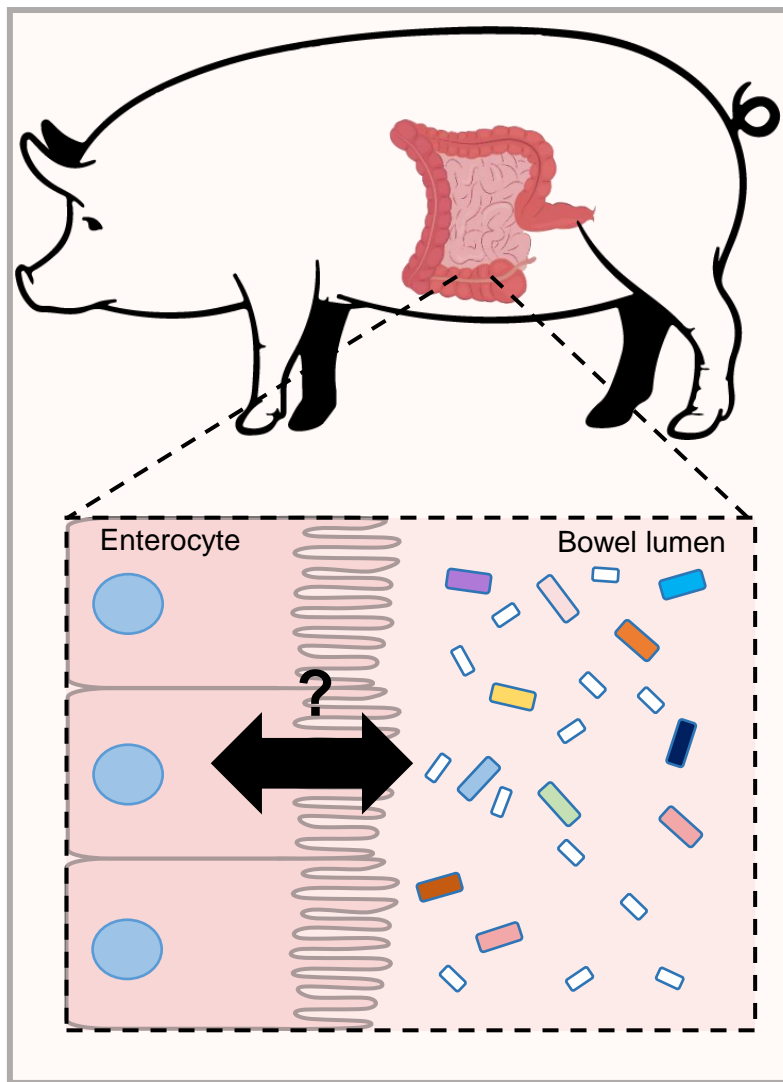
Liang Huang, Shiqi Luo, Shuqi Liu, Mingliang Jin, Yizhen Wang, Xin Zong. 2024. Comparative multi-omics analyses reveal the breed effect on the colonic host-microbe interactions in pig. *iMetaomics* 1: e8.

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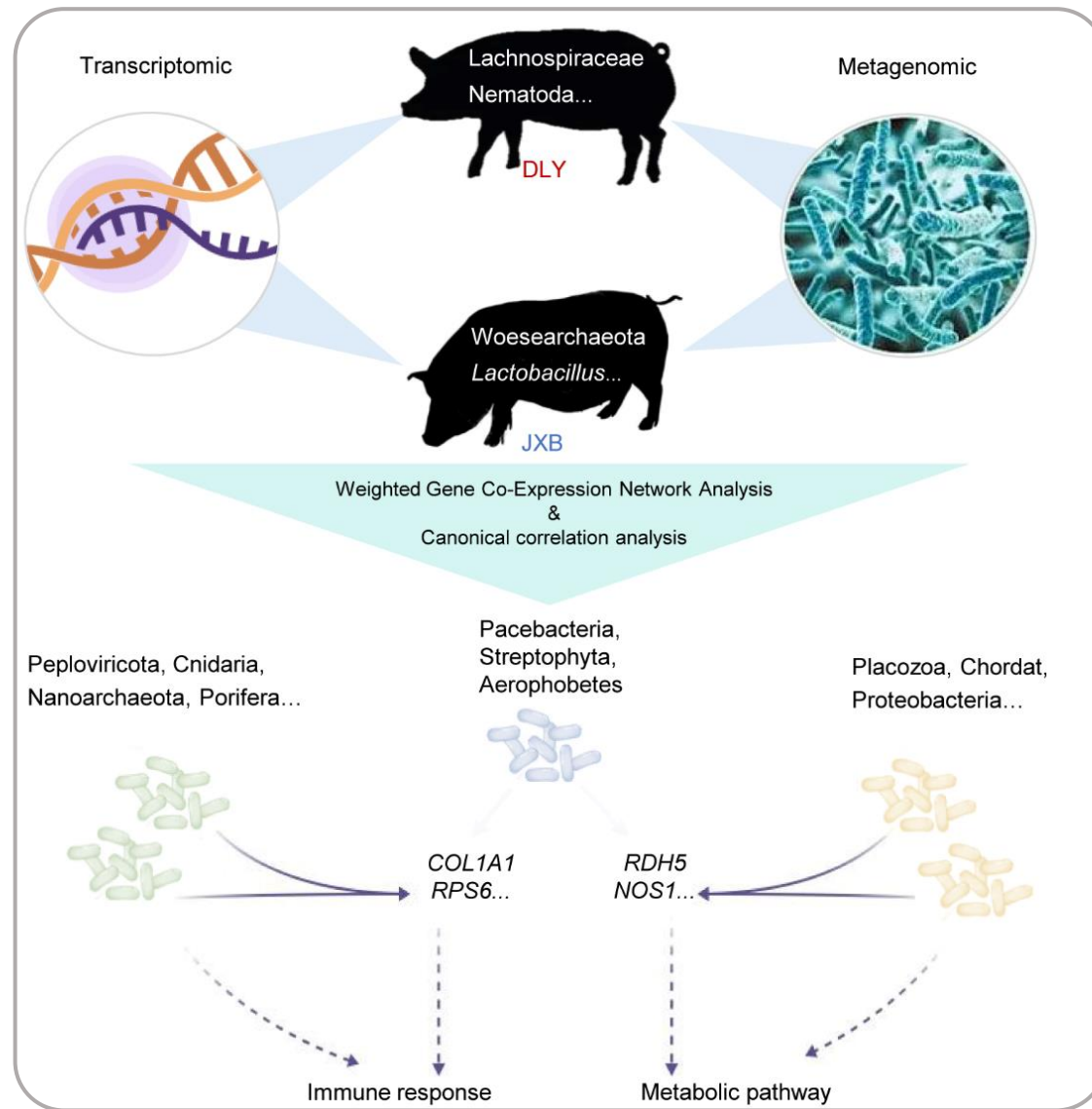


简介

猪肠道菌群与宿主的相互作用

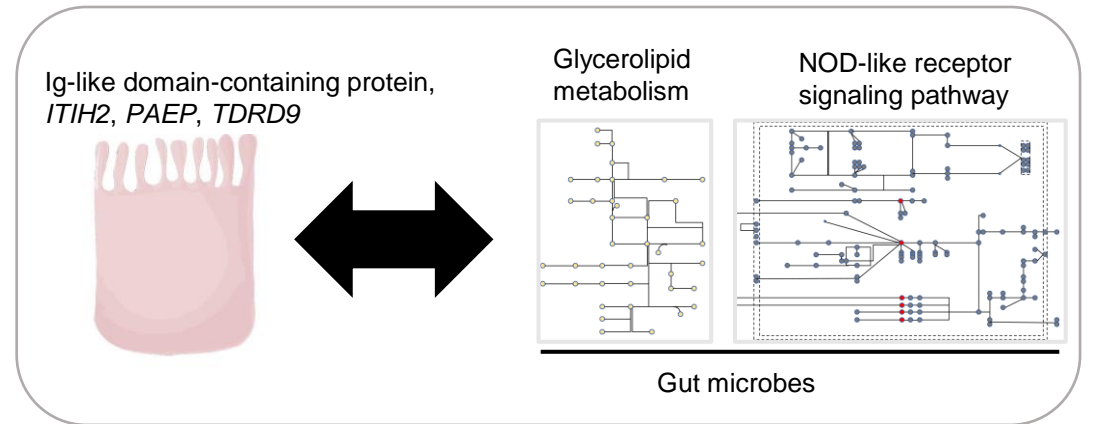
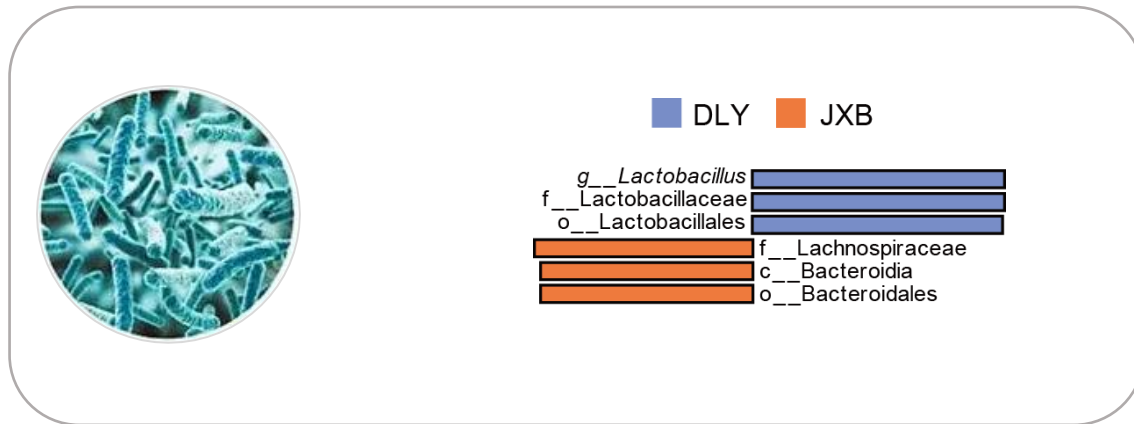
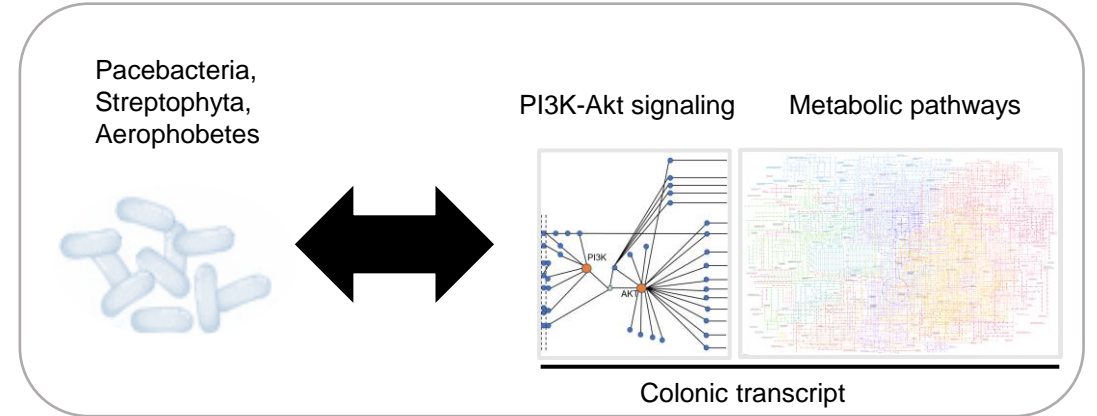
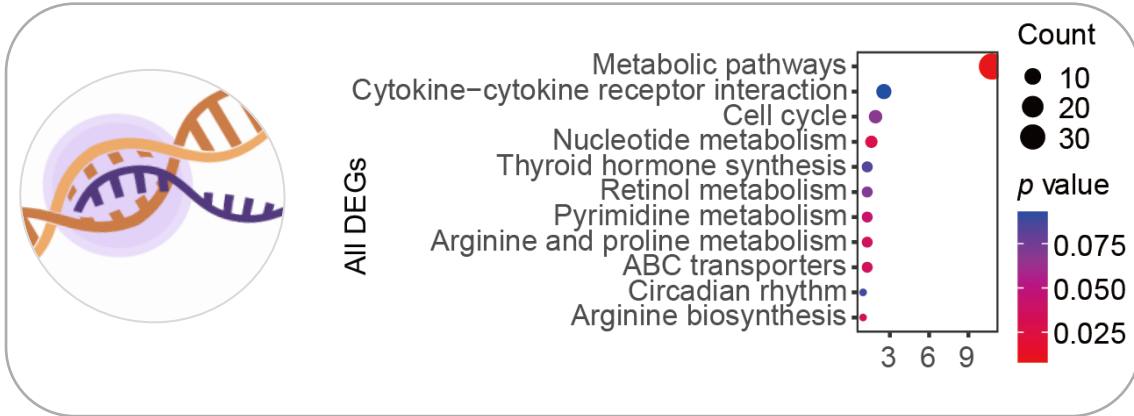


技术路线





亮点





微生物组成

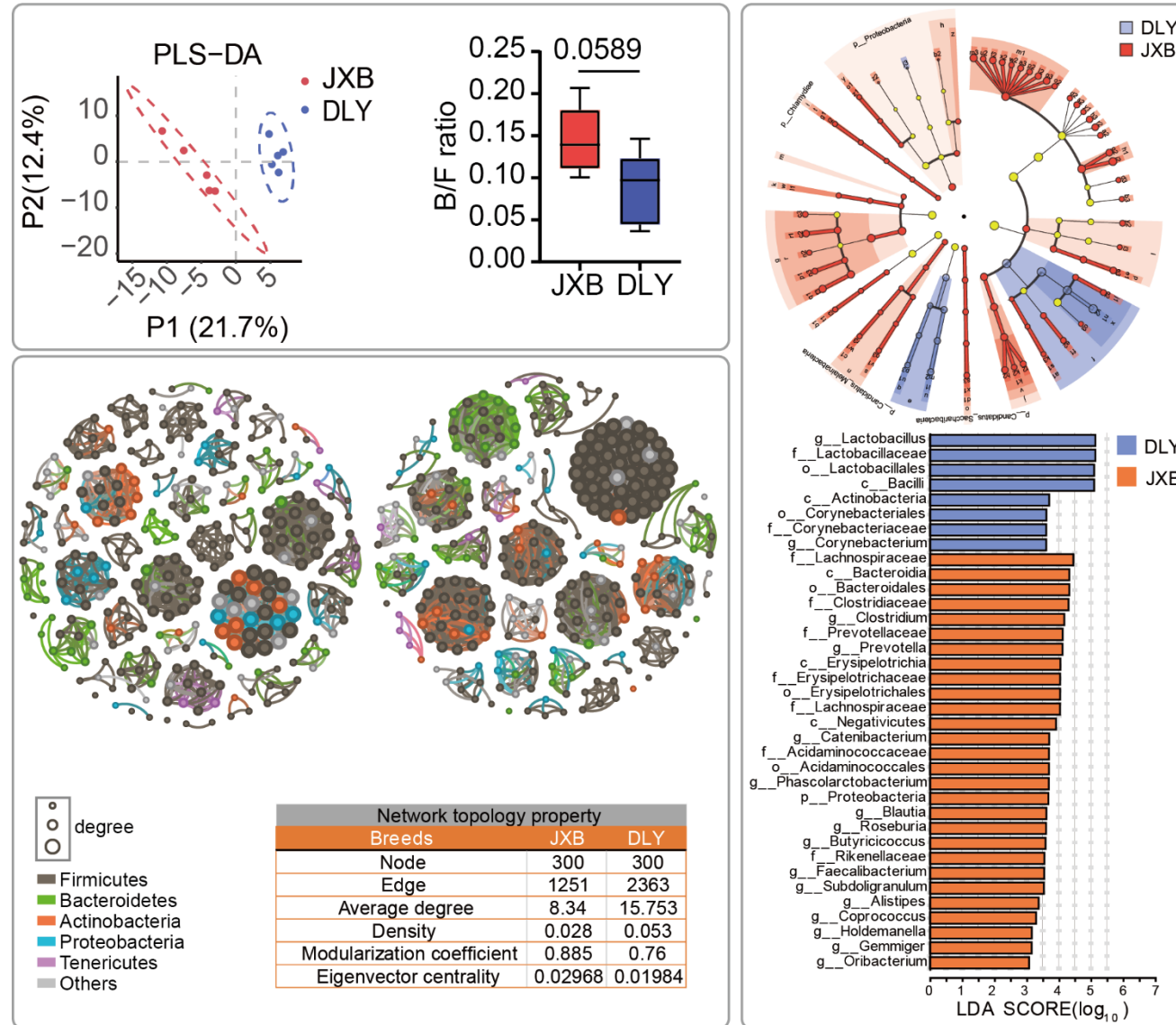


Figure 1. Composition of gut bacteria in the Jiaxing Black (JXB) and Duroc × Landrace × Yorkshire (DLY) pigs



结肠基因表达谱的比较

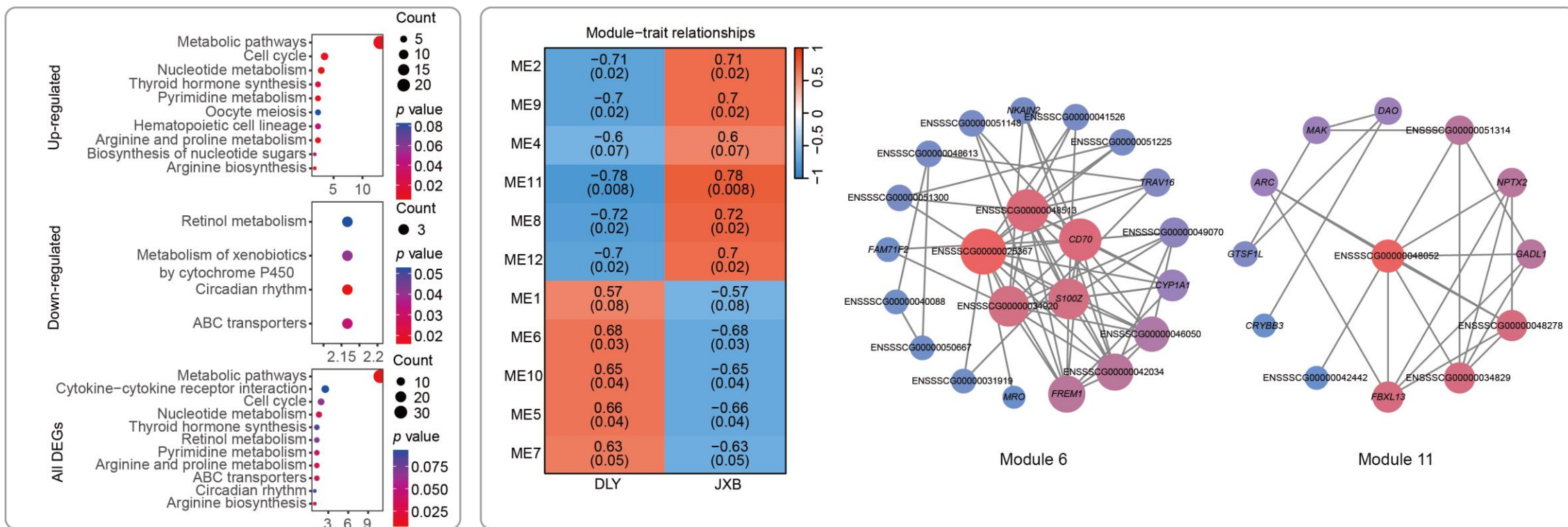


Figure 2. Transcriptional changes of gene sets in the Jiaxing Black (JXB) and Duroc × Landrace × Yorkshire(DLY) pigs



宿主途径和肠道微生物群之间的相互作用

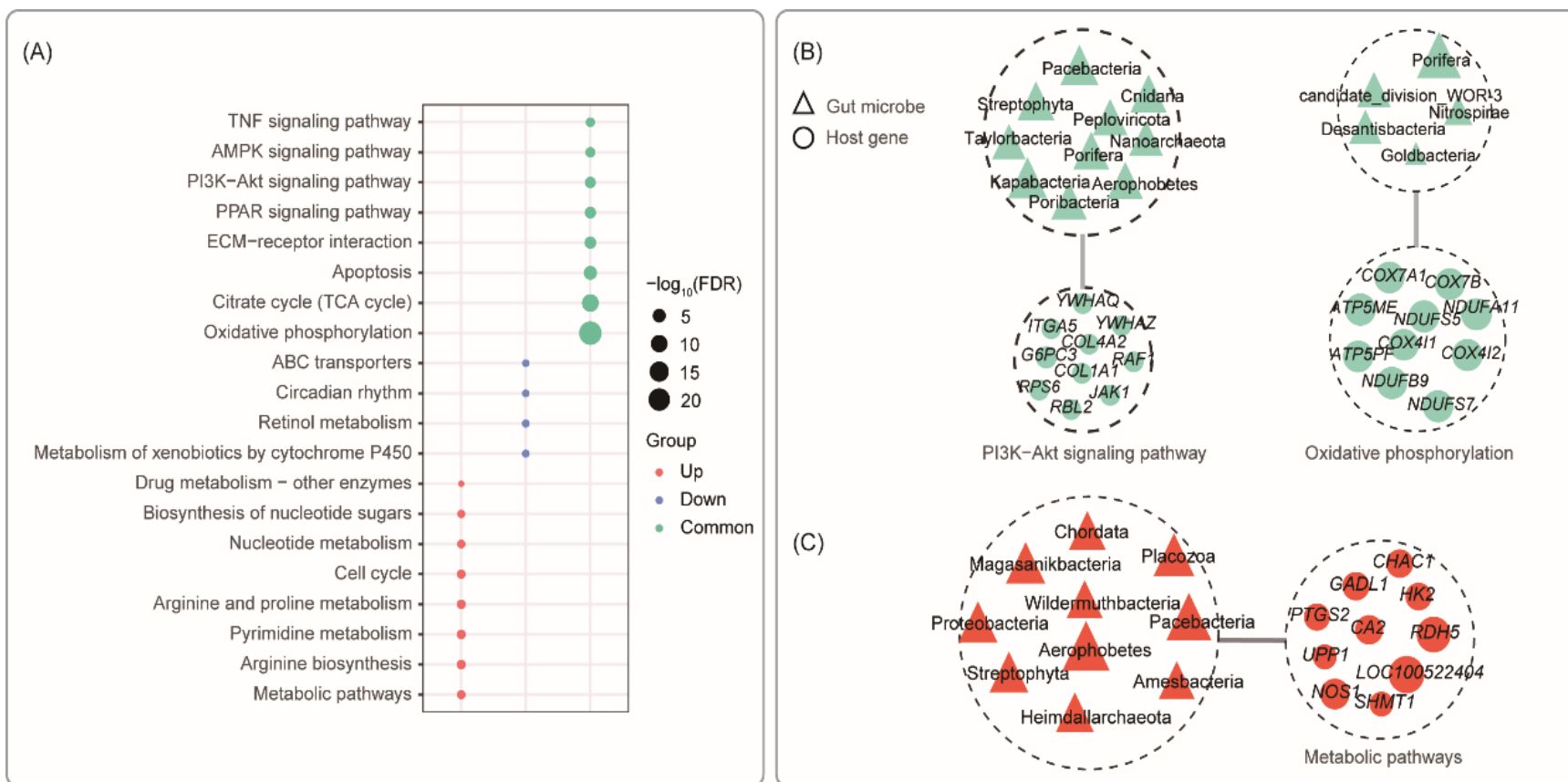


Figure 3. Host pathway-gut microbiota interactions in the Jiaxing Black (JXB) and Duroc \times Landrace \times Yorkshire (DLY) pigs



宿主基因对肠道菌群的调节

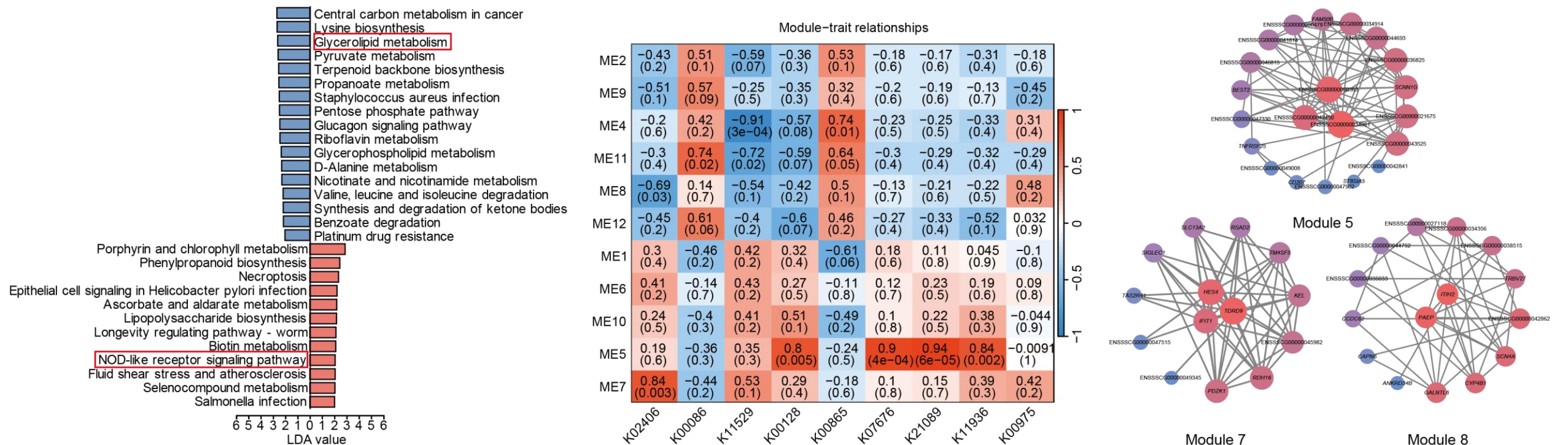


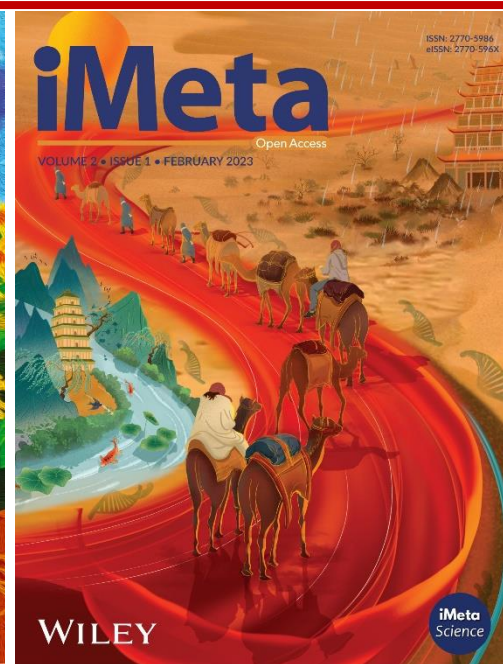
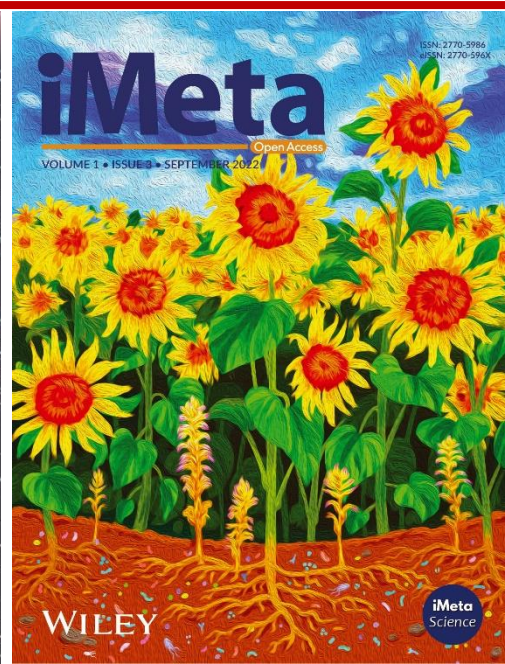
Figure 4. Functional differences of gut microbiota between the Jiaying Black (JXB) and Duroc × Landrace × Yorkshire (DLY) pigs



总结

- ❑ 在这项研究中，我们介绍了嘉兴黑猪（JXB）和杜长大猪（DLY）结肠转录水平和肠道菌群组成的差异；
- ❑ 确定了肠道微生物对宿主结肠，以及宿主反过来对肠道微生物免疫应答和代谢的调控作用，确定了关键基因和菌群。
- ❑ 这些发现为了解肠道菌群的作用机制及其在畜牧业生产中的潜在应用提供参考。

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