



A gut microbiome-lipid axis in early pregnancy is associated with metabolic dysregulation and diabetes risk

Zhonghan Sun¹, Chang He¹, Xiaonan Ma¹, Ping Wu², Tianlei Wang³,
Jiaying Yuan⁴, Yanni Pu¹, Xiaofeng Zhou¹, Zhendong Mei⁵, Huiling Song¹,
Yetong Wang¹, Haiyan Yue¹, Yuanqing Fu⁶, Jusheng Zheng⁶,
An Pan², Da Chen⁷, Shangyu Hong¹, Xiong-Fei Pan³, Yan Zheng¹

¹ Fudan University

² Huazhong University of Science and Technology

³ West China Second University Hospital, Sichuan University

⁴ Shuangliu Maternal and Child Health Hospital

⁵ Harvard University

⁶ Westlake University

⁷ Jinan University

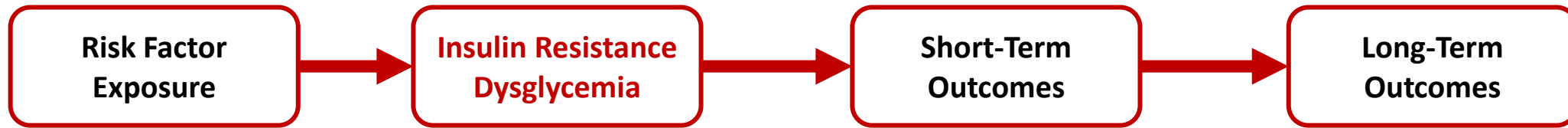


Zhonghan Sun, Chang He, Xiaonan Ma, Ping Wu, Tianlei Wang, Jiaying Yuan, Yanni Pu, et al. 2026. A Gut Microbiome-lipid Axis In Early Pregnancy Is Associated With Metabolic Dysregulation And Diabetes Risk. *iMeta* 5: e70166.
<https://doi.org/10.1002/imt2.70166>



Background

GDM Affects Both Mothers and Offspring



	Pregnancy	Birth	Postpartum
Mother	Preeclampsia	Difficult Delivery	Diabetes  ~10-fold
Child	Fetal Growth Restriction	Adverse Birth Outcomes	Growth Impairment, CVD, T2DM



Early-pregnancy changes may precede GDM diagnosis



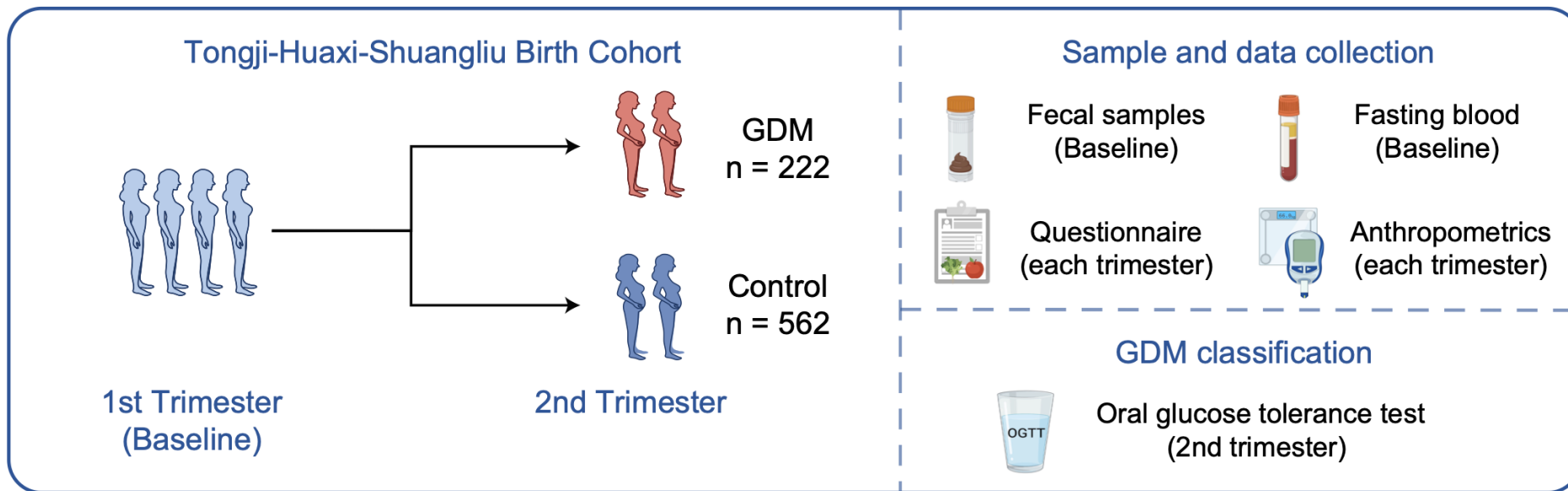
Highlights

- First-trimester microbiome and lipidome profiles revealed early molecular signatures preceding GDM diagnosis.
- Integrated analyses linked *Ruminococcus bicirculans* to GDM-related metabolic dysregulation through glycosphingolipid metabolism.
- Animal and cell experiments showed that *Ruminococcus bicirculans* and LacCer 24:1 improved insulin tolerance and modulated hepatic AKT signaling.
- Combined microbial and lipid risk scores identified women at high GDM risk in early pregnancy.



Study Design

Study Design



Measurements

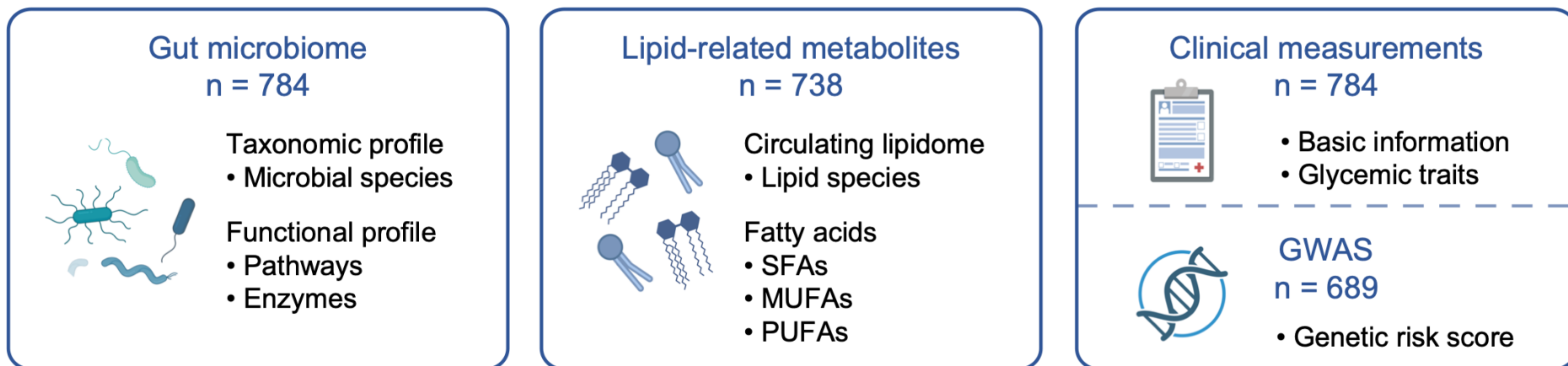
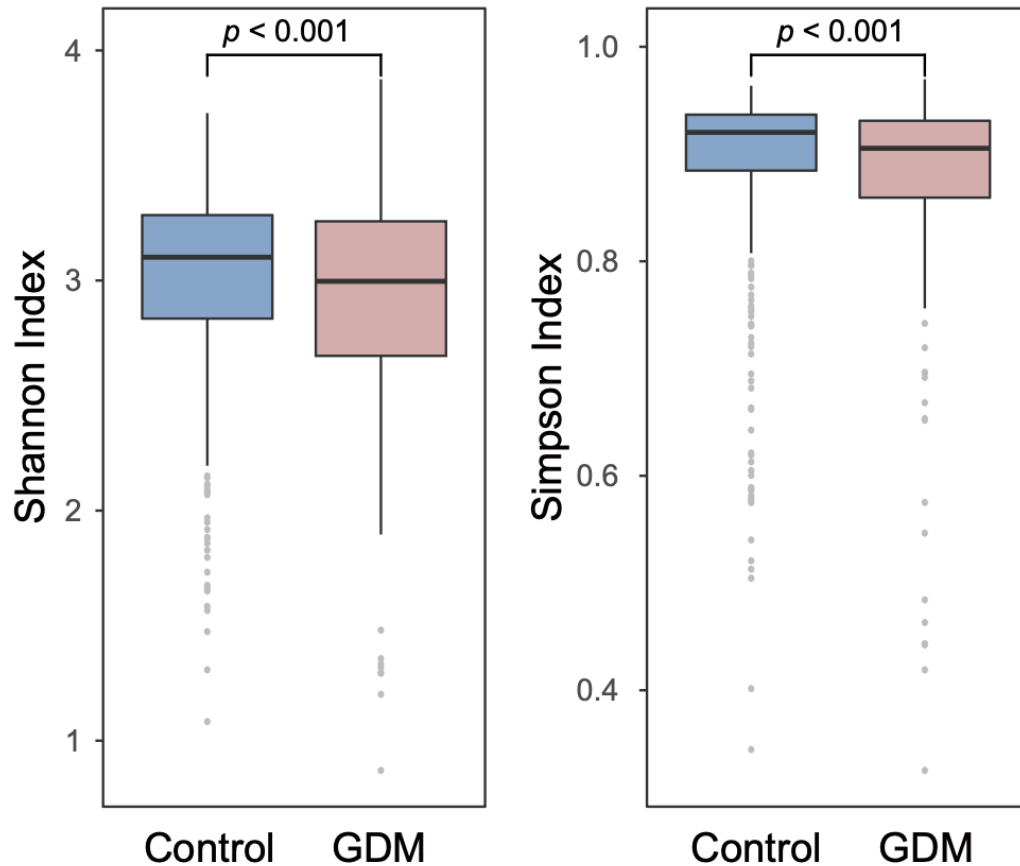


Figure 1. Study design, multi-omics measurements, and analytical framework.



Gut Microbiome Alterations Precede GDM Diagnosis

Gut Microbial Diversity



Gut Microbial Community Structure

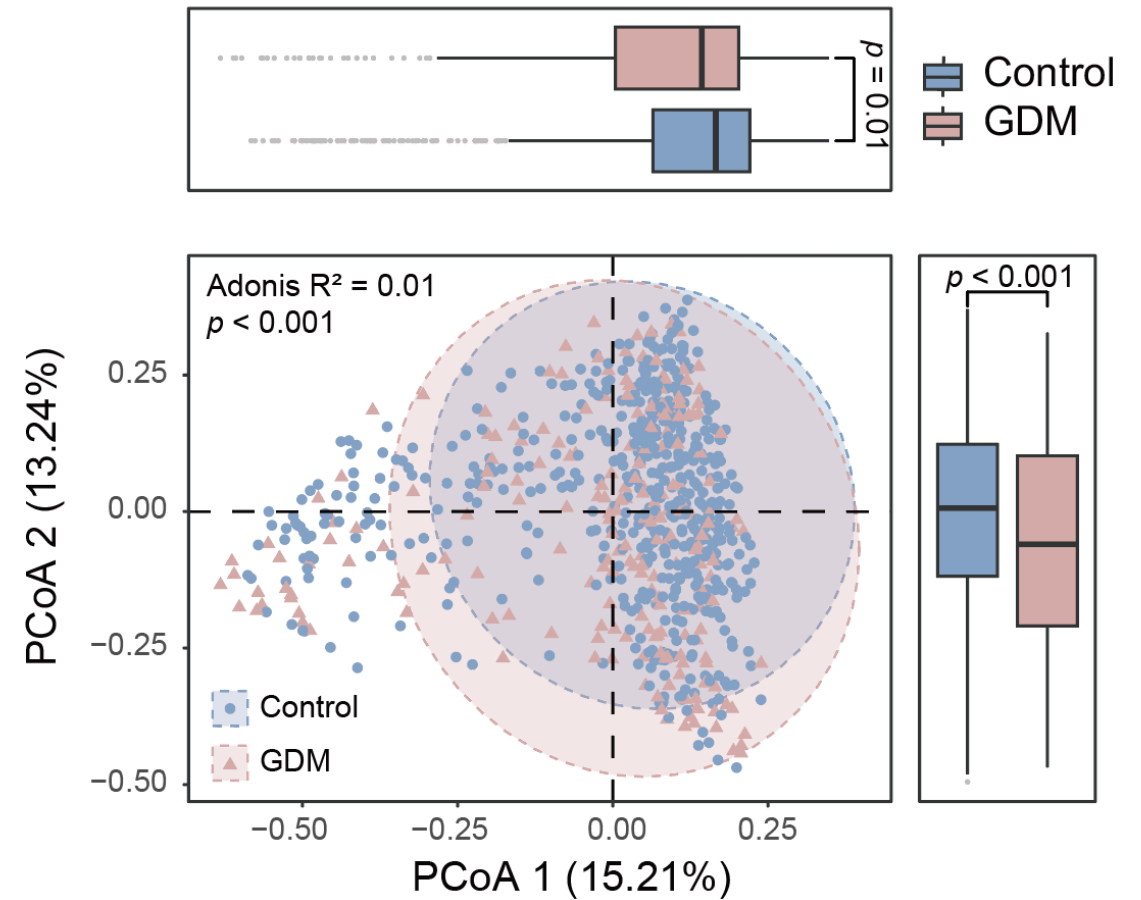


Figure 2A-B. Early-pregnancy gut microbial diversity and composition in relation to later GDM.

Twenty-six Microbial Species Are Associated with GDM Risk

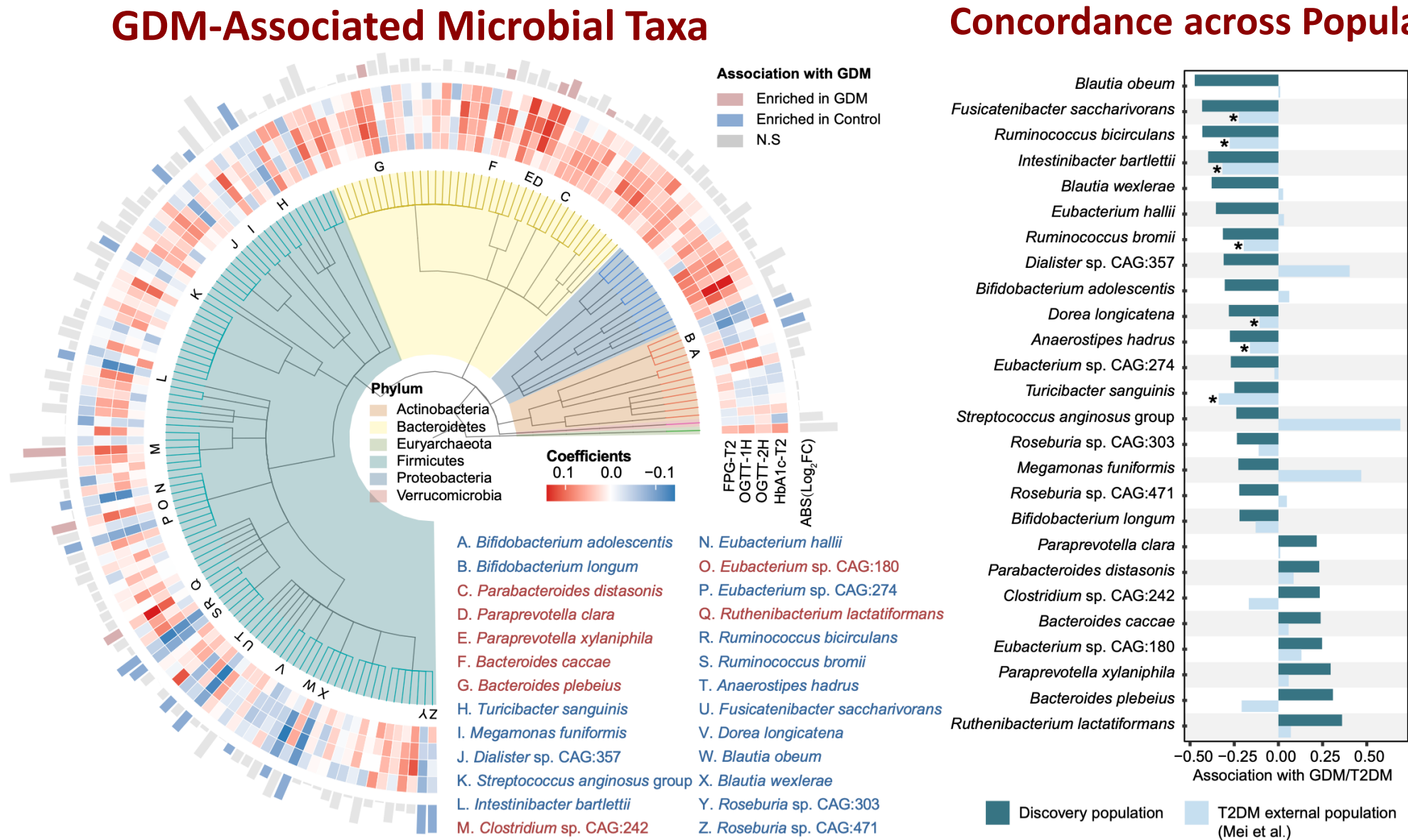
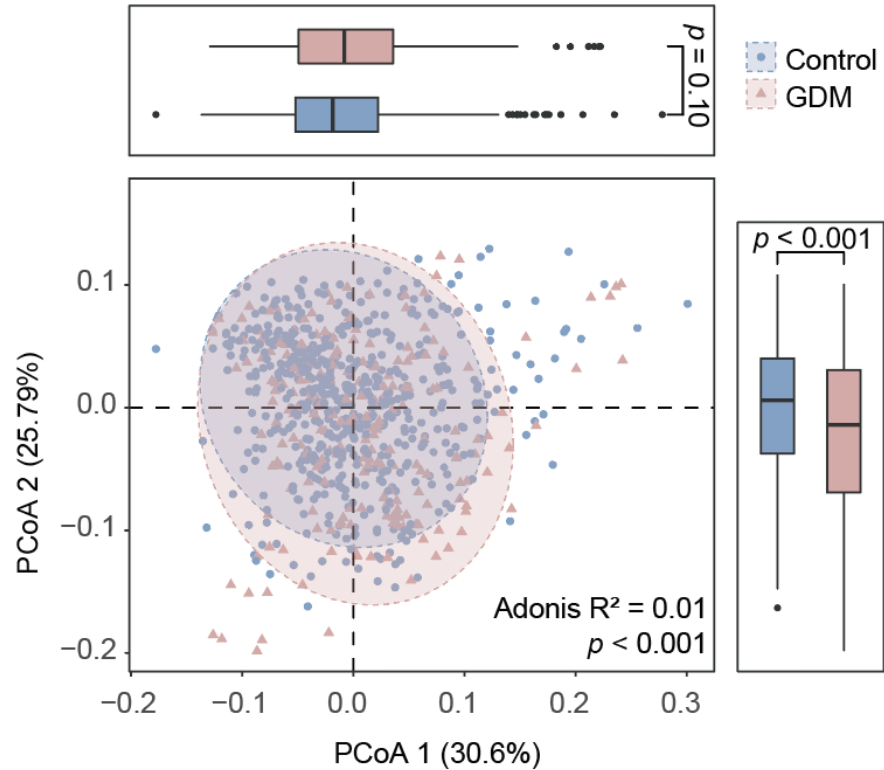


Figure 2D-E. Microbial species associated with later GDM and concordance across populations.

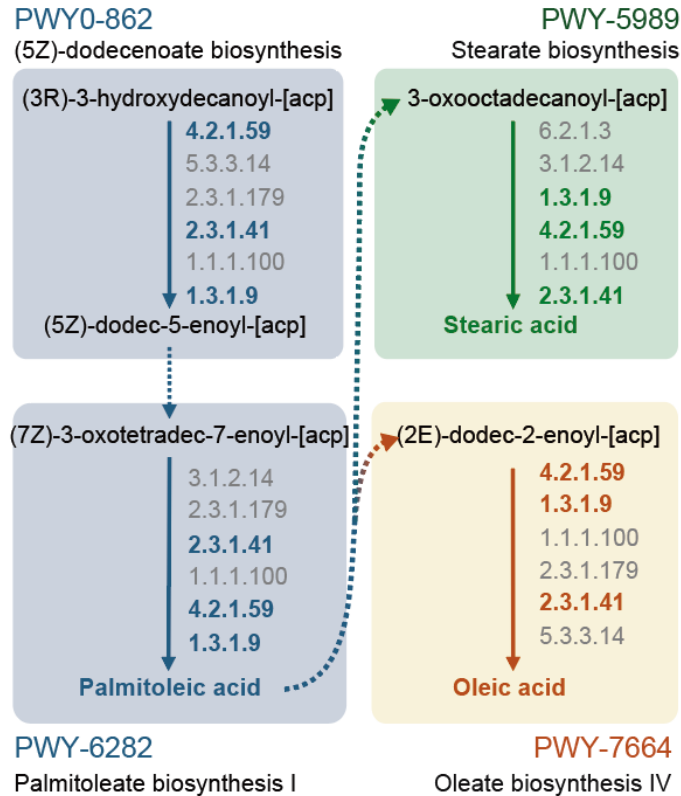


Microbial Functions Shift toward Lipid Biosynthesis

Microbial Functional Profile



Fatty Acid Biosynthesis Pathways



Key Enzymes and Circulating Fatty Acids

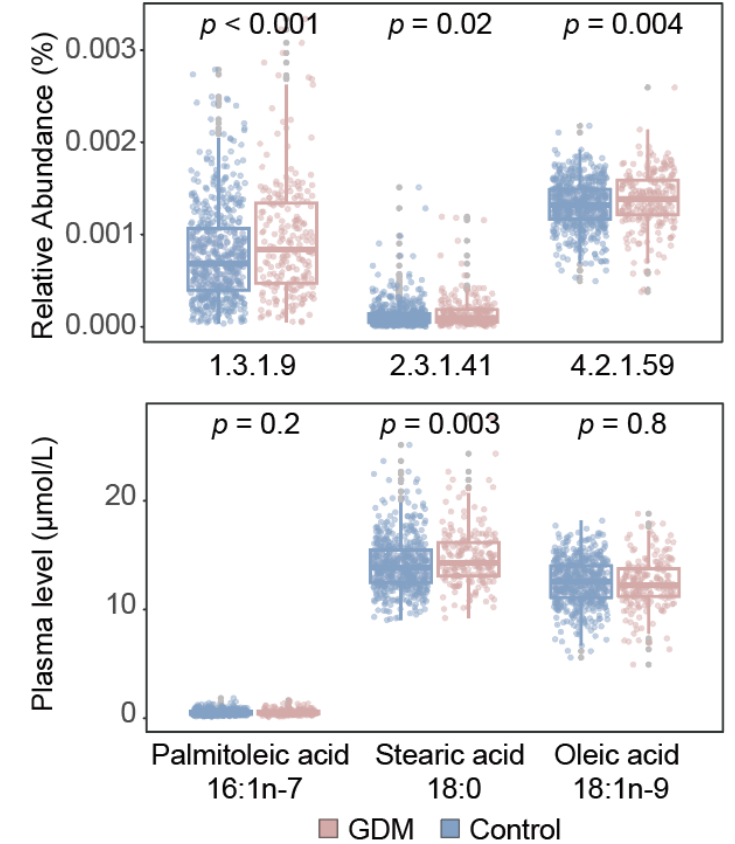
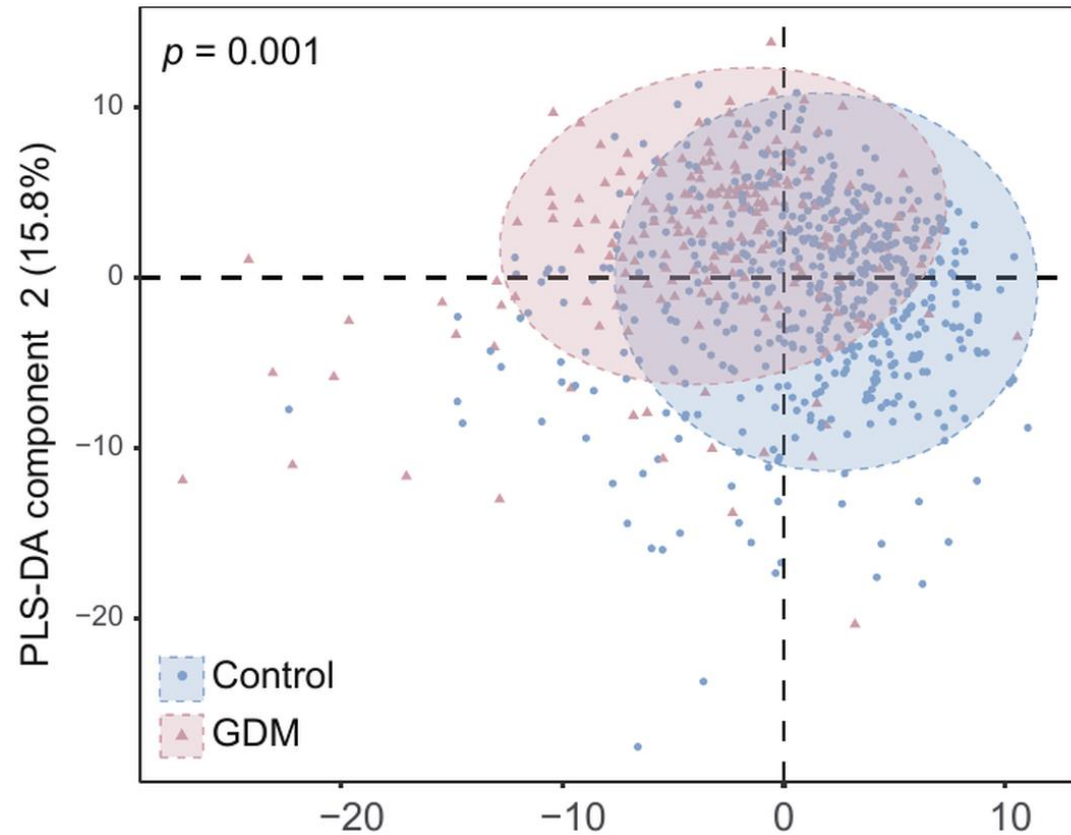


Figure 3A-E. Microbial functional features linked to the risk of later GDM.

Plasma Lipidome Is Remodeled Before GDM Diagnosis

Overall Lipidomic Profile



Lipid Classes and GDM Risk

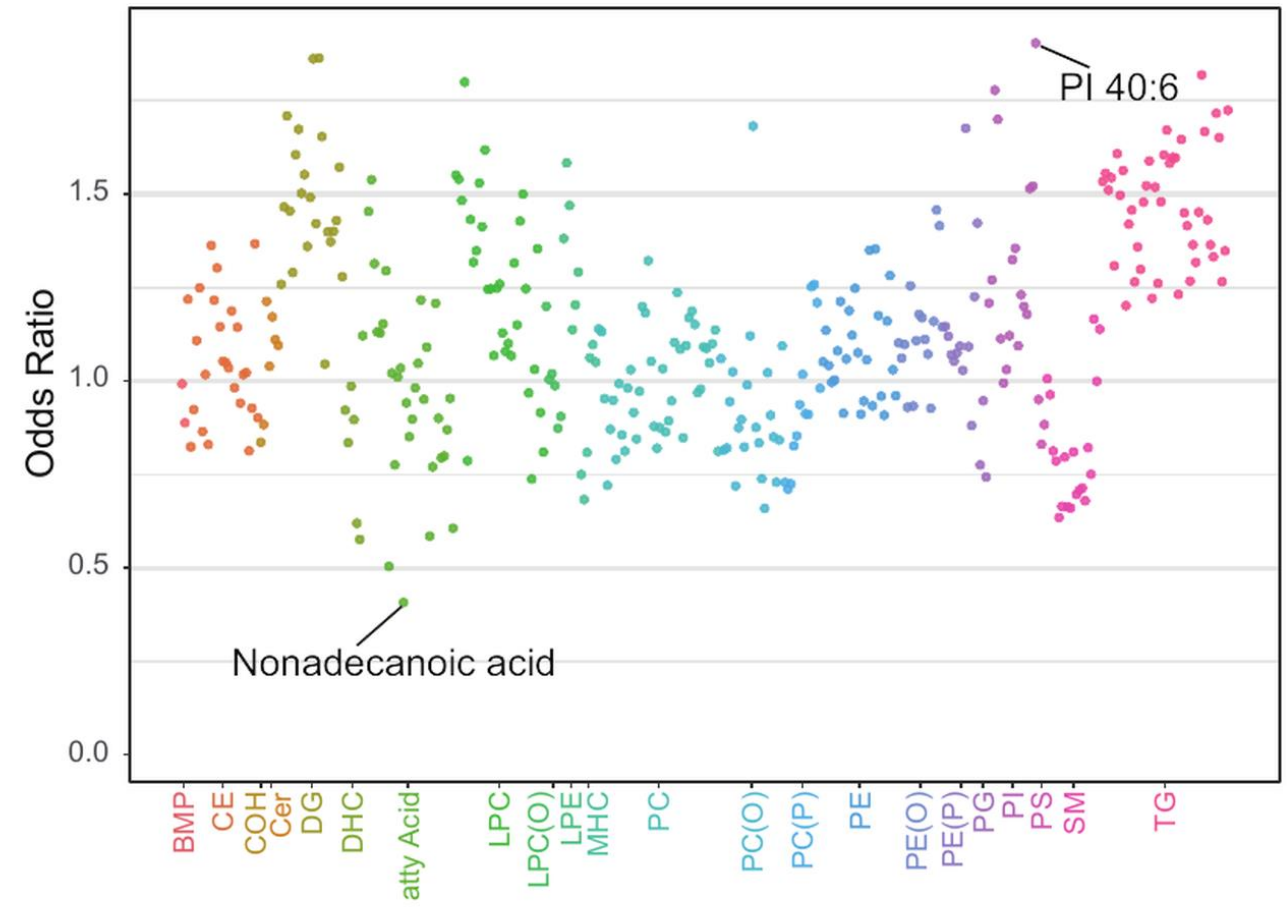
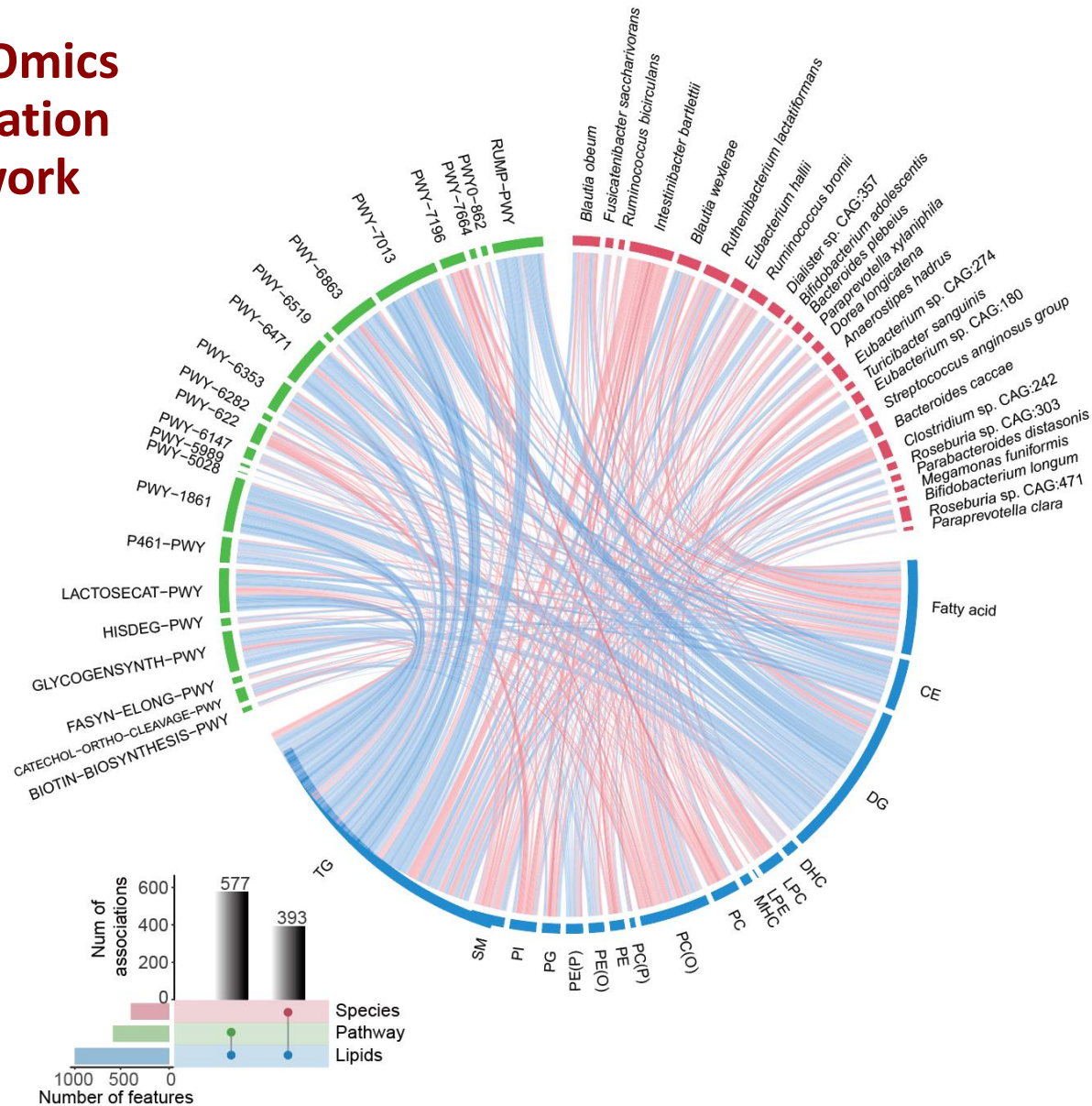


Figure 4A-B. Early-pregnancy plasma lipidomic alterations associated with later GDM.

Microbial Changes Are Associated with Host Lipid Alterations

Cross-Omics Association Network



Lipidomic Mediation

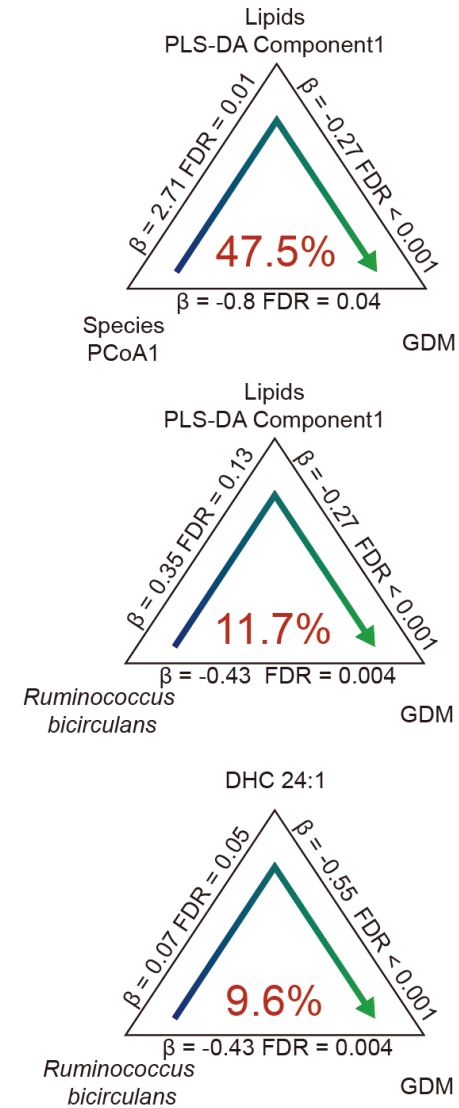


Figure 4C, G-I. Cross-omics microbiome-lipid associations and lipidomic mediation effects.



R. bicirculans Produces LacCer 24:1 Anaerobically

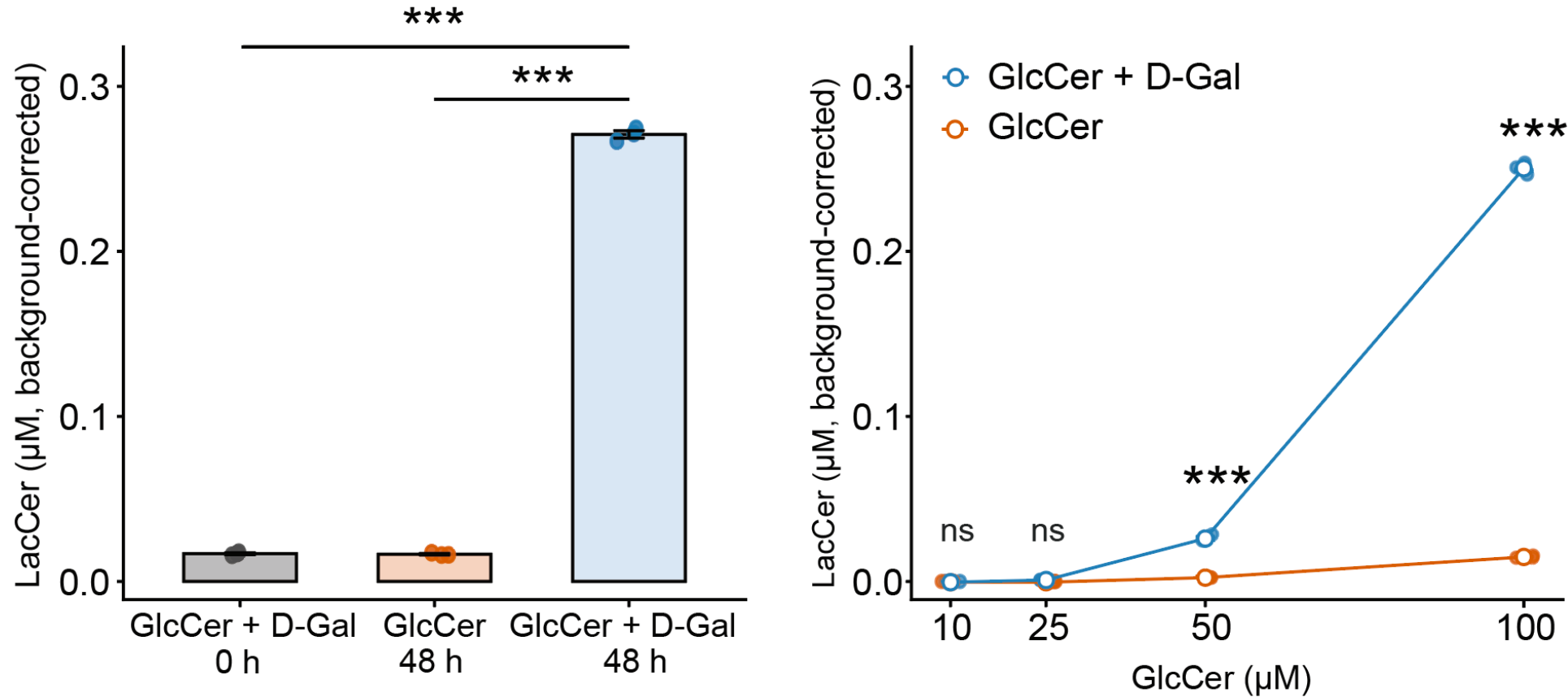
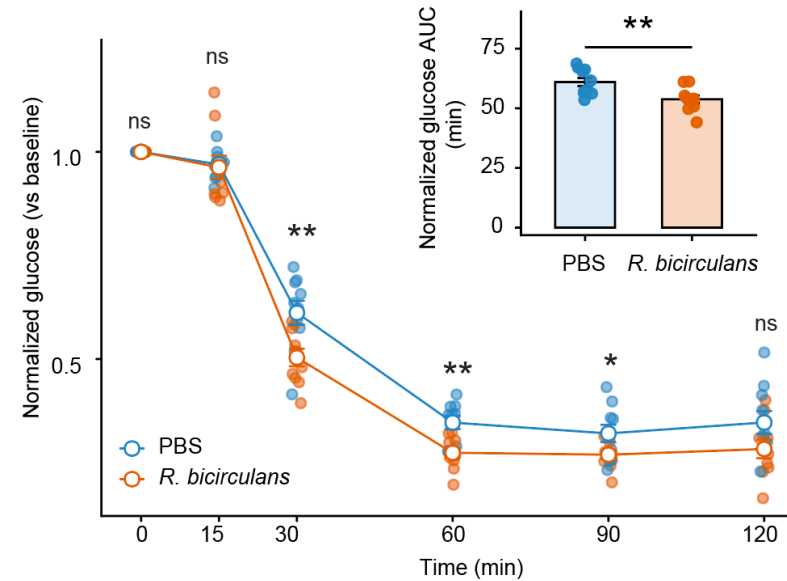
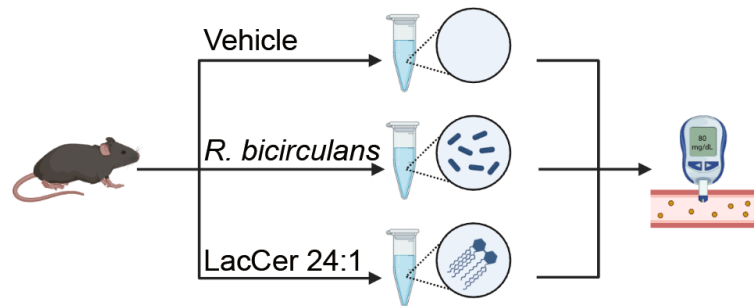
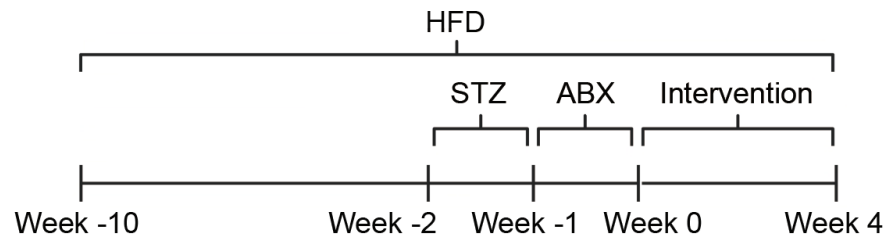


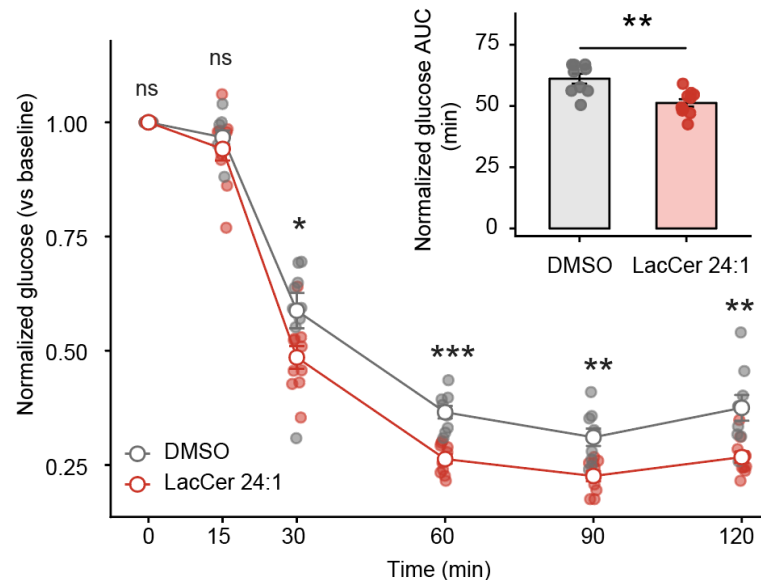
Figure 5A-B. Anaerobic production of LacCer 24:1 by *R. bicirculans*.

R. bicirculans and LacCer 24:1 Improve Insulin Tolerance

Animal Study Design



**Bacterial
Colonization**

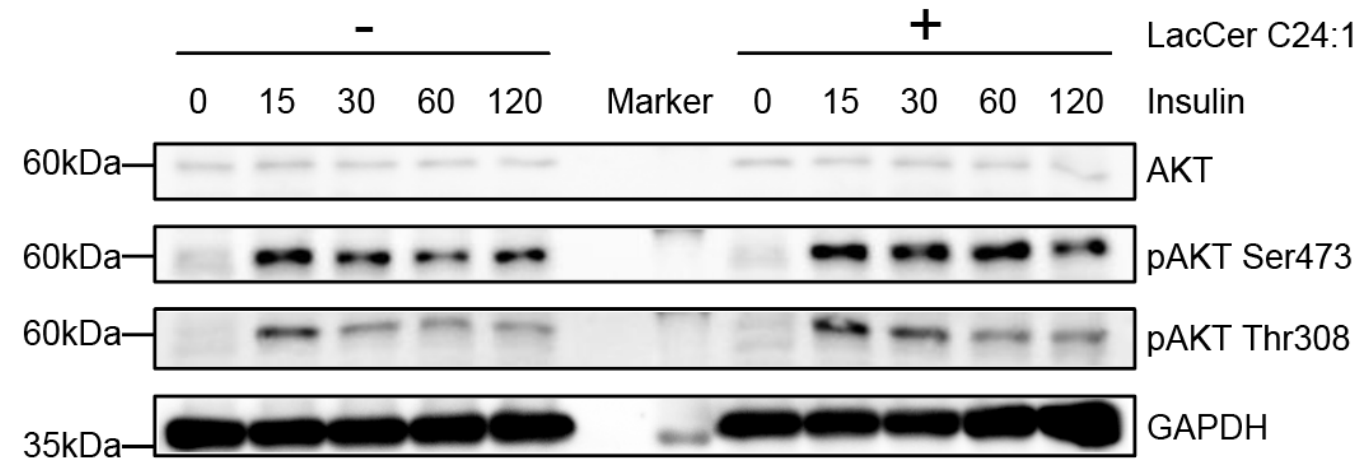


**LacCer 24:1
Administration**

Figure 5C-E. *R. bicirculans* colonization or LacCer 24:1 administration improves insulin tolerance in mice.

LacCer 24:1 Modulates Hepatic AKT Signaling

AKT Phosphorylation



Microbe-Lipid Link to Insulin Signaling

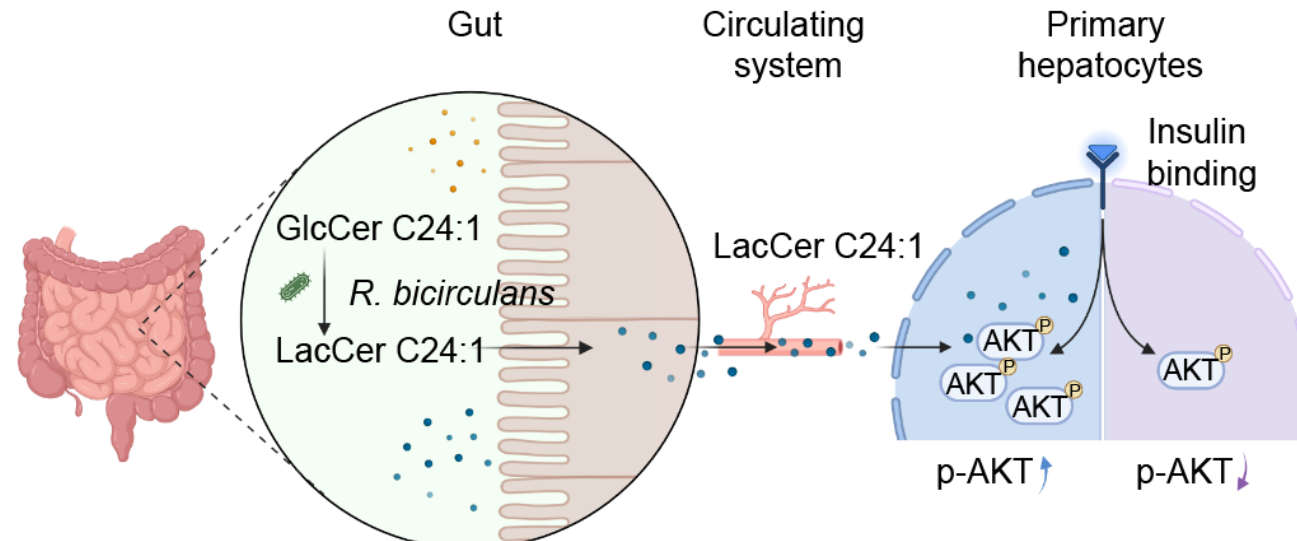


Figure 5F-G. LacCer 24:1 modulates AKT phosphorylation in primary hepatocytes and the proposed model.



Multi-Omics Integration Improves GDM Discrimination

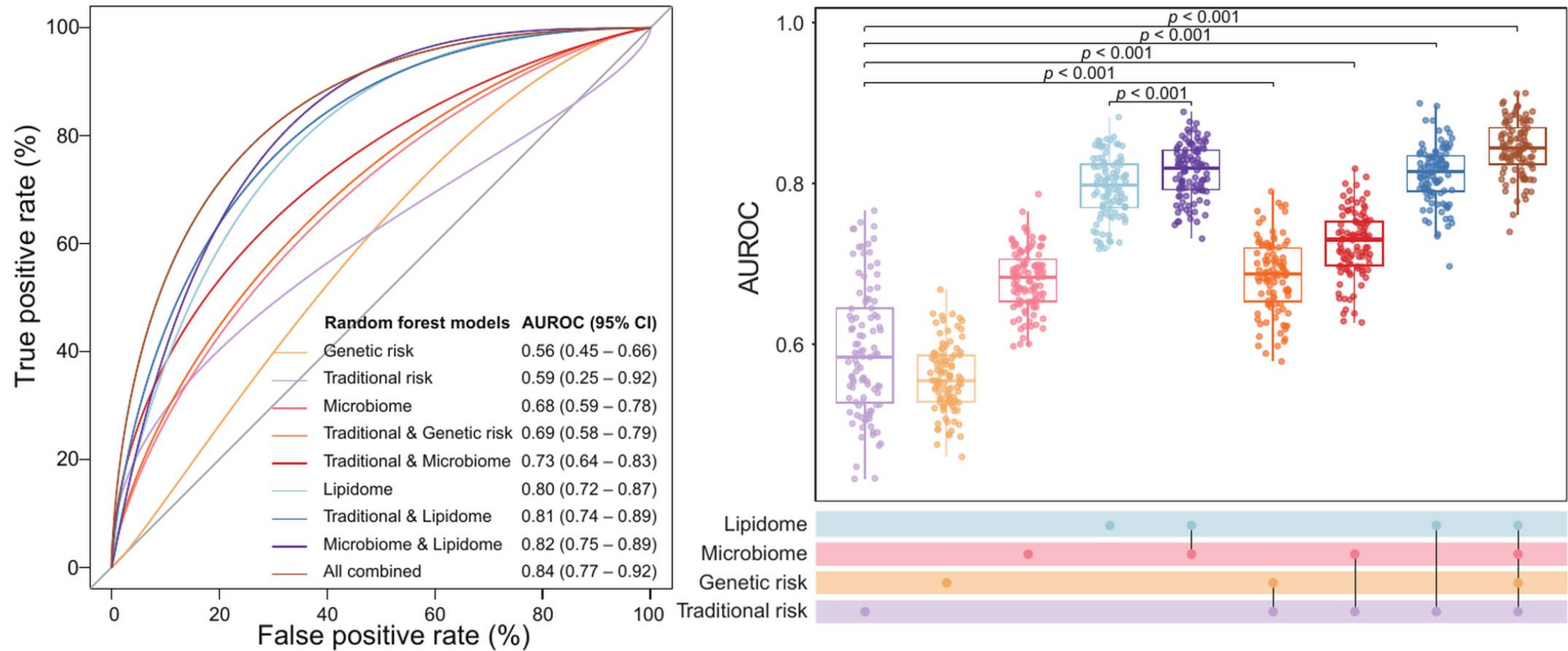
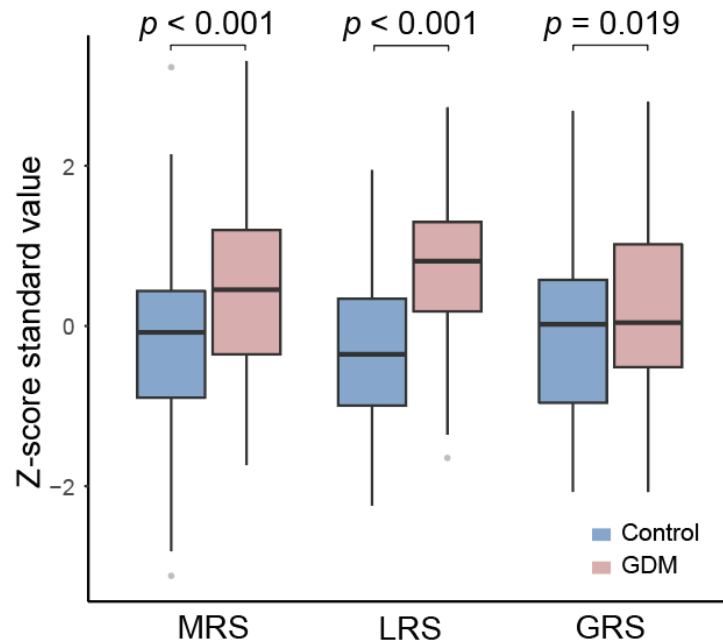


Figure 6A-C. Integrating microbiome and lipidomic features improves early-pregnancy discrimination of later GDM.



Microbial and Lipid Scores Identify High-Risk Women

Microbial, Lipid, and Genetic Scores



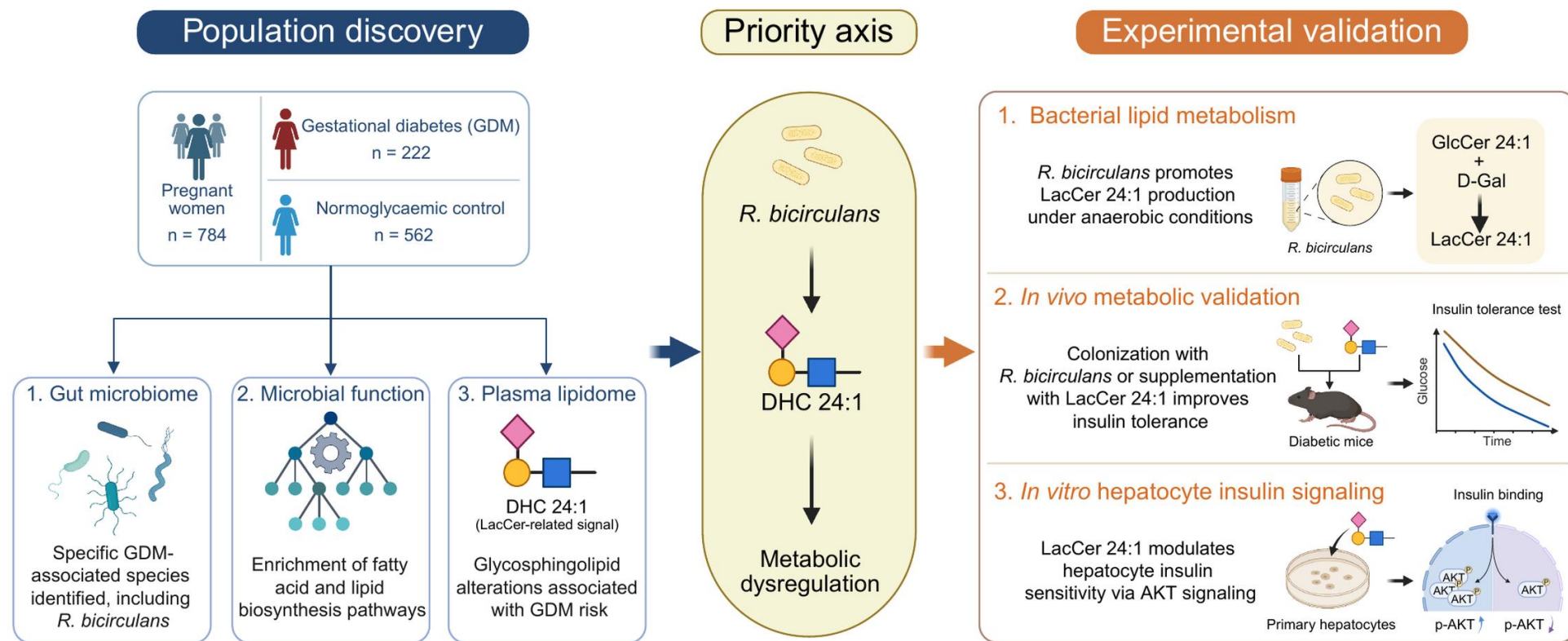
Combined Scores and GDM Risk

		MRS			Relative excess risk due to interaction
		Low	High	Total	
LRS	Low	Ref.	1.29 (0.61, 2.74)	Ref.	11.83 (3.93, 19.73)
	High	5.64 (3.02, 11.03)	19.19 (10.63, 36.81)	8.24 (5.51, 12.61)	
GRS	Low	Ref.	2.76 (1.66, 4.66)	Ref.	1.36 (-0.30, 3.02)
	High	1.09 (0.59, 1.98)	4.44 (2.68, 7.53)	1.39 (0.99, 1.96)	
Total		Ref.	2.74 (1.96, 3.86)	-	-

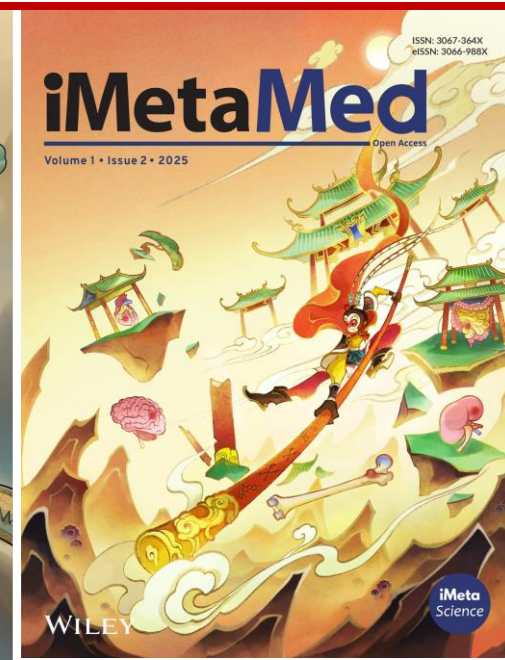
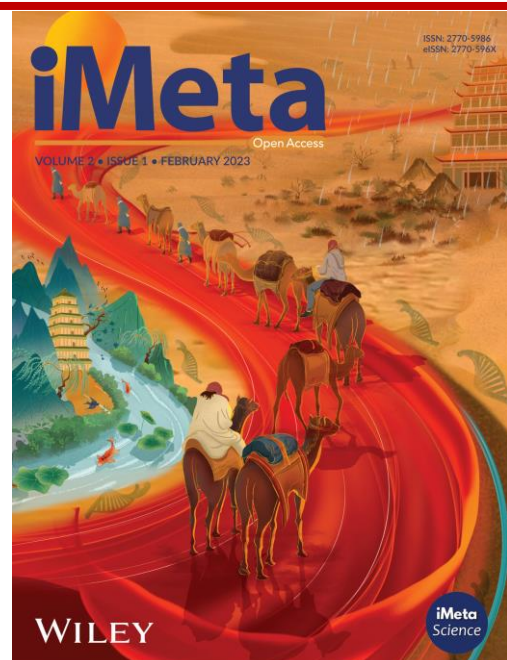
Figure 6D-E. Microbial, lipid, and genetic risk scores and their joint associations with later GDM.



Summary



- ❑ GDM-related gut microbial and lipidomic changes were already evident in early pregnancy, before clinical diagnosis.
- ❑ Population and experimental findings support a link between microbial glycosphingolipid metabolism and host insulin responses.
- ❑ Microbiome and lipidome data may improve early GDM risk stratification, pending external validation.



“**iMeta**” launched in 2022 by iMeta Science Society, **impact factor (IF) 44.4**, **ranking top 47/22643 in the world**. It aims to publish innovative and high-quality papers with broad and diverse audiences. Its scope is similar to *Cell*, *Nature* and *Science*. Its unique features include video abstract, bilingual publication, and social media with 800,000 followers. Indexed by [SCIE/ESI](#), [PubMed](#), [Google Scholar](#) etc.

“**iMetaOmics**” launched in 2024, indexed by [ESCI](#), [PubMed](#), [Google Scholar](#), with a **target IF>15**, and its scope is similar to *Nature Communications*, *Science Advances*, *Advanced Science*, *Nucleic Acids Research*, etc.

“**iMetaMed**” launched in 2025, with a target IF>15, similar to *Med*, *Cell Reports Medicine*, *eBioMedicine*, *eClinicalMedicine* etc.



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

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

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



[iMetaScience](#)



[iMetaScience](#)



office@imeta.science

imetaomics@imeta.science



[Promotion Video](#)

Update
2026/6/17