Alterations in the gut microbiome and metabolisms in pregnancies with fetal growth restriction

Running title: Gut dysbiosis and metabolic disorders in FGR

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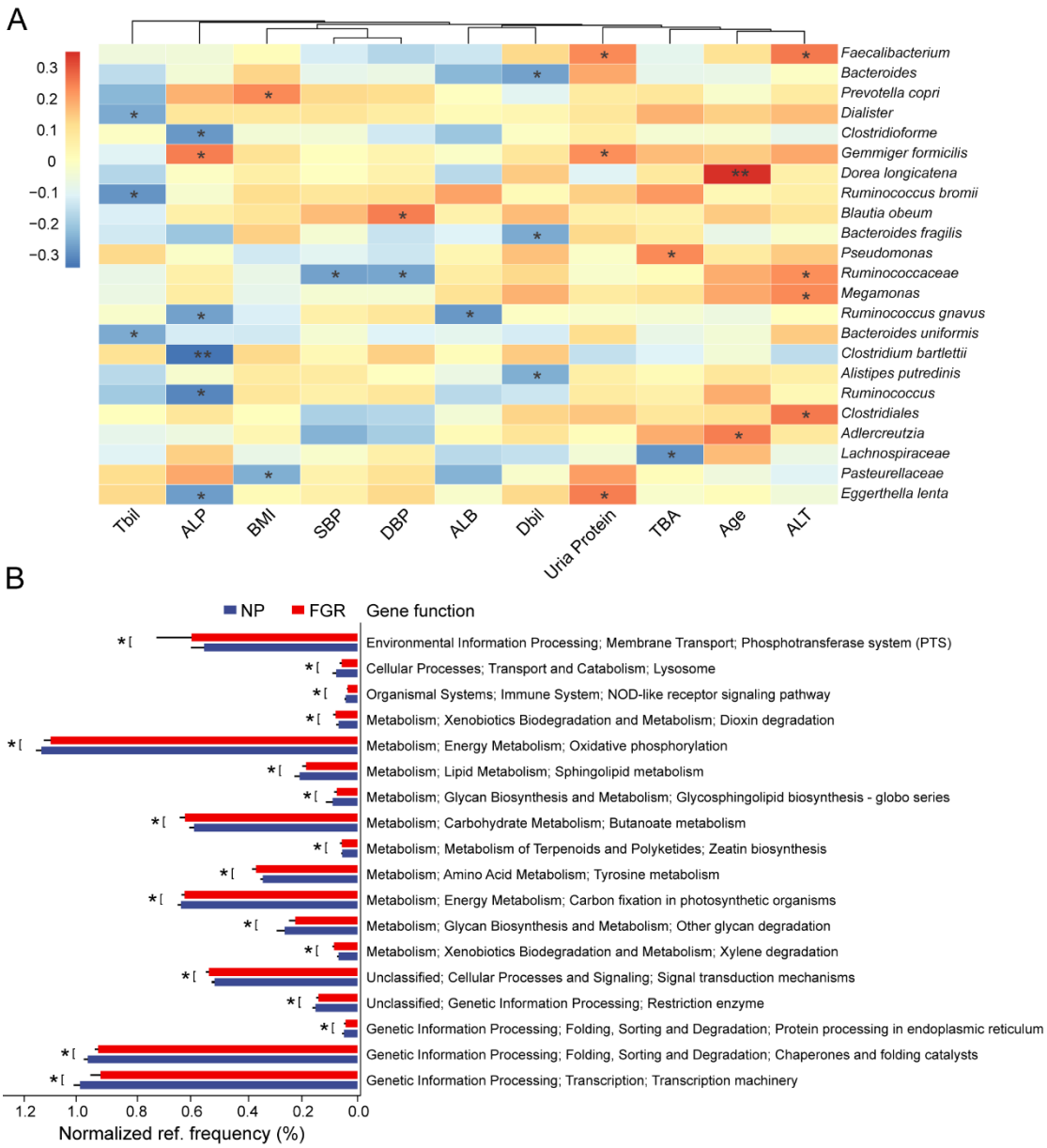
Supplementary materials

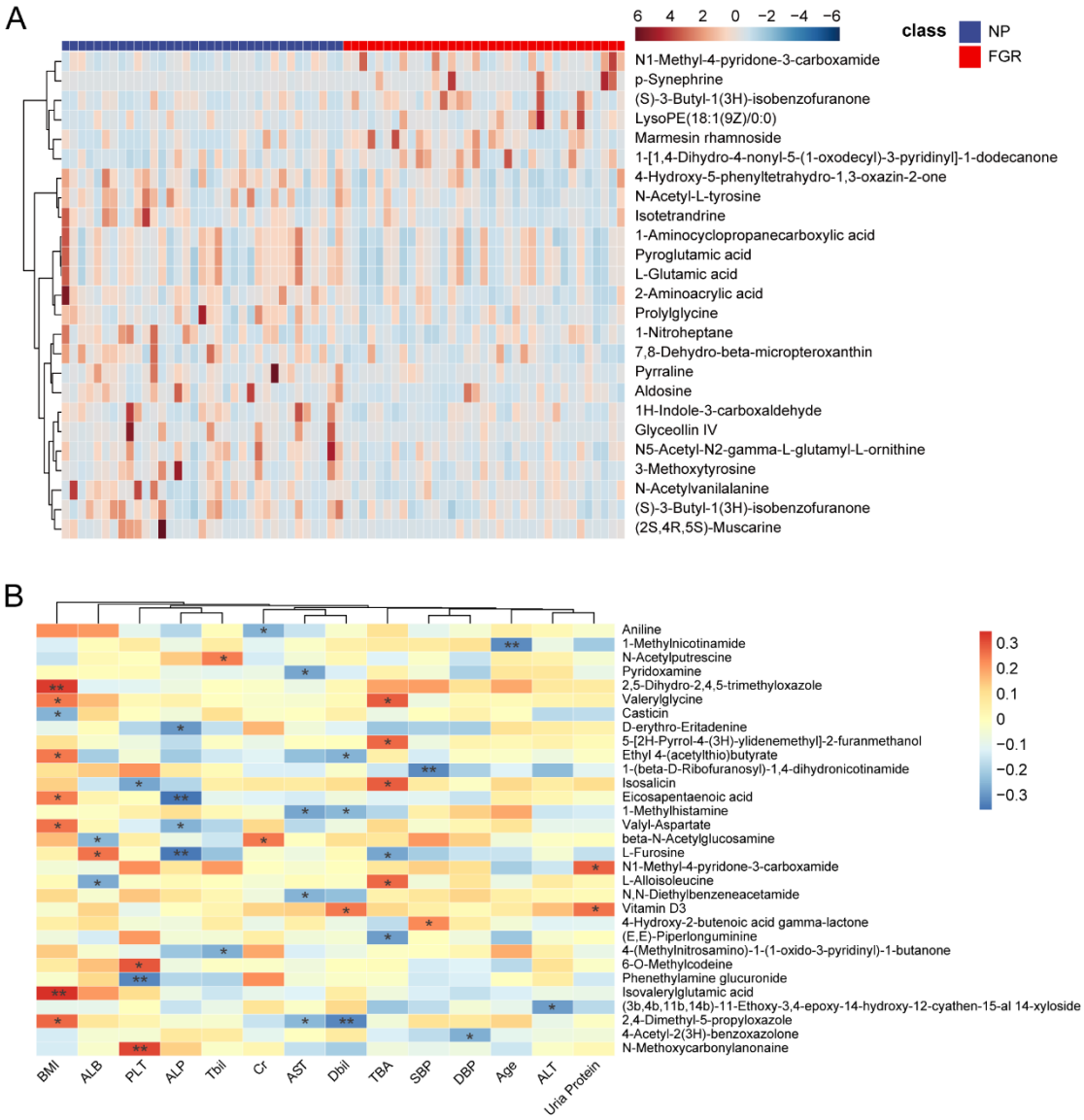
Supplementary Table 1

	NP Group (n=31)	FGR Group (n=19)	*P*
Maternal features			
Age (y)	30.10±4.99	28.60±3.53	0.3322
Gestational Age (w)	39.80±1.18	37.20±1.77	<0.001
BMI (kg/m^2)	26.80±3.00	26.30±3.97	0.6154
SBP (mmHg)	117 (112-124)	124 (120-138)	0.0024
DBP (mmHg)	68.90±7.97	77.42±8.25	0.0009
PLT (×10^9/L)	229.6±59.76	250.8±54.14	0.2025
ALT (U/L)	10.27±2.97	11.87±4.98	0.2157
AST (U/L)	14.9 (12.8-17.8)	17.5 (13.2-21.8)	0.1647
ALP (U/L)	158 (131-181)	139 (117-179)	0.4662
ALB (g/L)	36.36±2.02	35.23±3.83	0.2462
TBA (μmol/L)	3.3 (2.4-5.8)	3.1 (2.6-4.6)	0.6807
TBil (μmol/L)	8.0 (7.0-9.7)	6.6 (5.5-8.2)	0.0031
DBil (μmol/L)	1.4 (1.1-1.9)	1.1 (0.8-1.5)	0.0227
Cr (μmol/L)	45.0 (42.0-49.0)	51.0 (40.0-56.0)	0.3182
Fetal features			
NW (g)	3310±301.6	2151±239.2	<0.0001
BPD (mm)	92.0 (86.0-95.0)	83.0 (75.0-87.0)	<0.0001
HC (mm)	328 (317-334)	296 (274-311)	<0.0001
AC (mm)	334 (325-345)	286 (269-303)	<0.0001
FL (mm)	72 (69-73)	63 (58-67)	<0.0001
AFV (mm)	48.8±11.6	36.7±9.0	0.0001

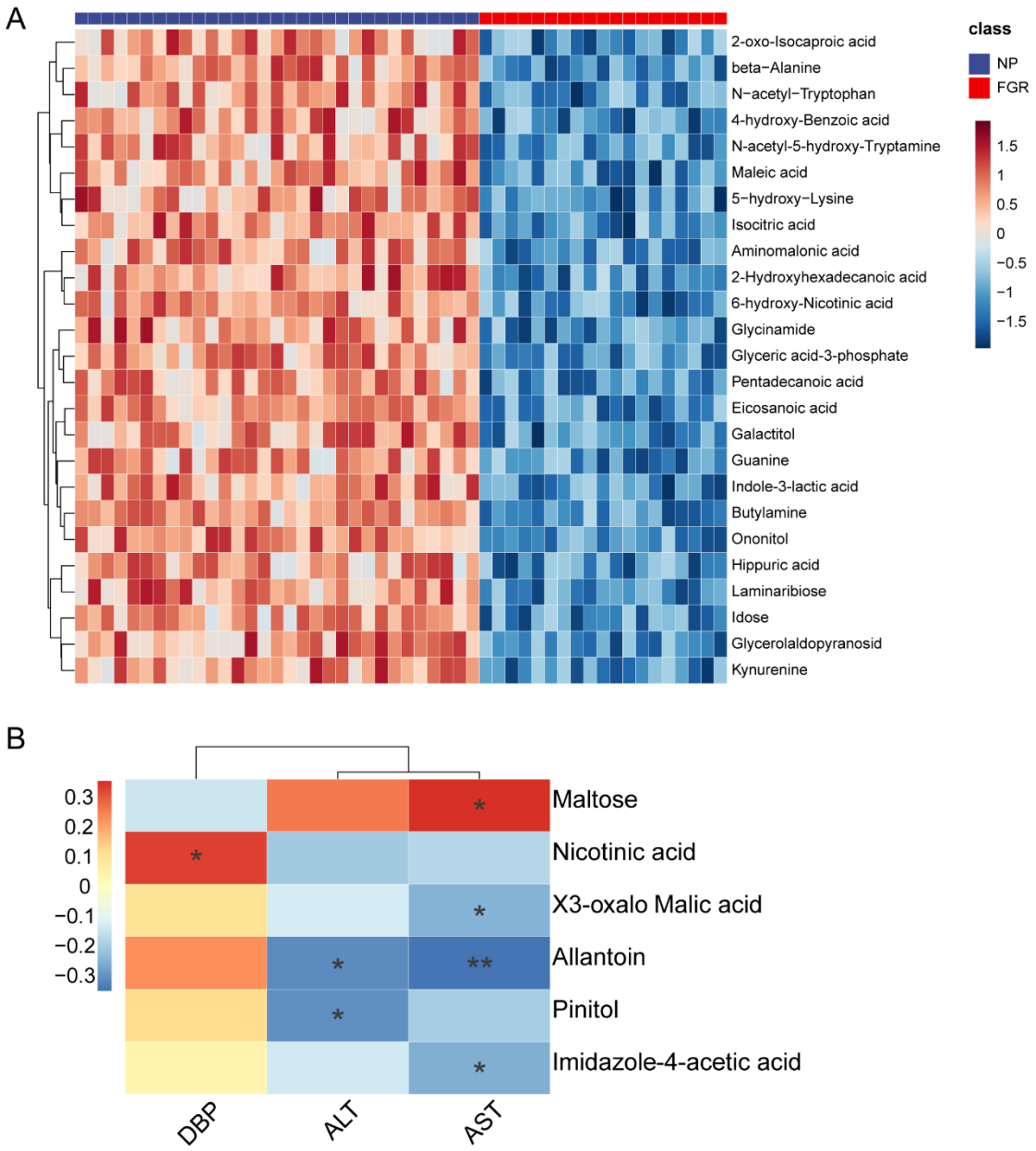
Data was assessed for normality using the Shapiro-Wilk normality test, and was presented as mean ± SD or median (interquartile range). For normally distributed data, Student's *t*-test with Welch's correction was performed between two groups. For non-normal distributed data, Mann–Whitney U test was performed between two groups. BMI, body mass index; G, gravidity; P, parity; SBP, systolic blood pressure; DBP, diastolic blood pressure; PLT, platelet; ALT, alanine aminotransferase; AST, aspartate aminotransferase; ALP, alkaline phosphatase; ALB, albumin; TBil, total bilirubin; DBil, direct bilirubin; Cr, creatinine; NW, neonatal weight; BPD, biparietal diameter; HC, head circumference; AC, abdominal circumference; FL, femur length; AFV, amniotic fluid volume.



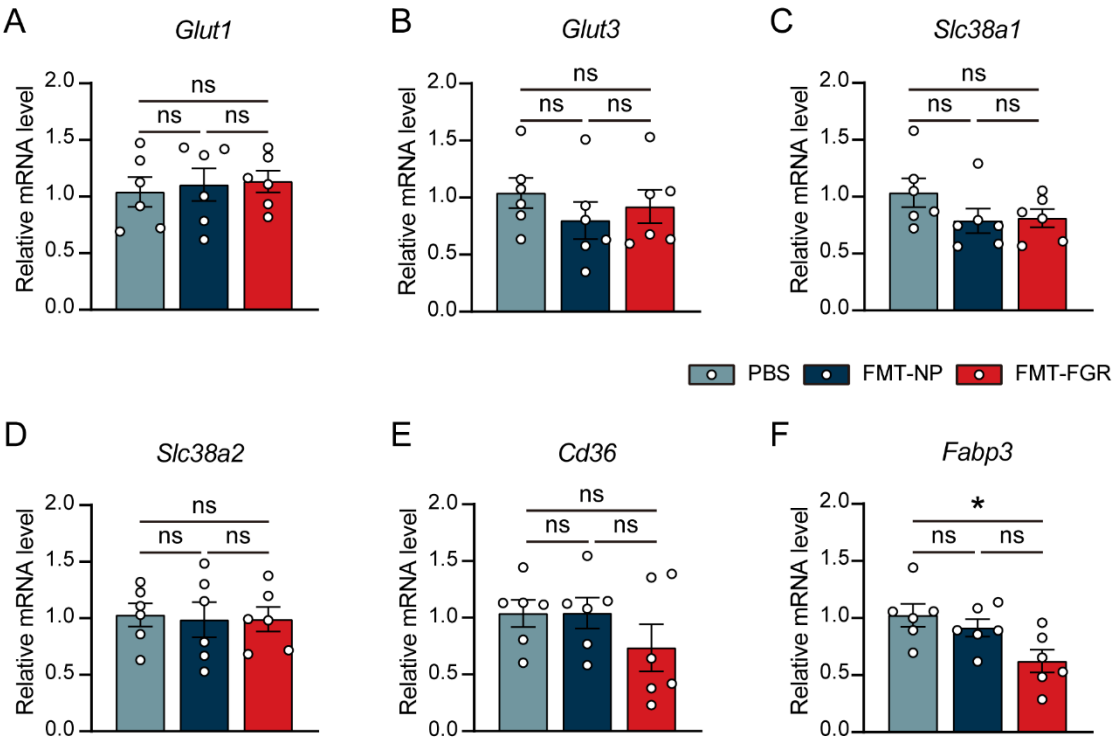
Supplementary Figure 1 (A) Correlation heatmap of maternal gut microbiota and maternal clinical manifestations. Data was processed by Spearman's correlation test. **(B)** KEGG pathways predicted by PICRUSt analysis. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. NP, n = 35; FGR, n = 35)



Supplementary Figure 2 (A) The top 25 abundant metabolites. **(B)** Correlation heatmap of maternal gut metabolites and maternal clinical manifestations. Data was processed by Spearman's correlation test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. NP, n = 35; FGR, n = 35.



Supplementary Figure 3 (A) The top 25 abundant metabolites. **(B)** Correlation heatmap of maternal serum metabolites and maternal clinical manifestations. Data was processed by Spearman's correlation test. **P* < 0.05, ***P* < 0.01. NP, n = 31; FGR, n = 19.



Supplementary Figure 4 The expression of glucose transporters (*Glut1* and *Glut3*), amino acid transporters (*Slc38a1* and *Slc38a2*) and fatty acid transporters (*Cd36* and *Fabp3*) at the mRNA level in the placenta, normalized to *18S*. Data was presented as mean ± SEM. One-way ANOVA test was conducted followed by Bonferroni test. **P* < 0.05, ns, not significant. n = 6 /group.