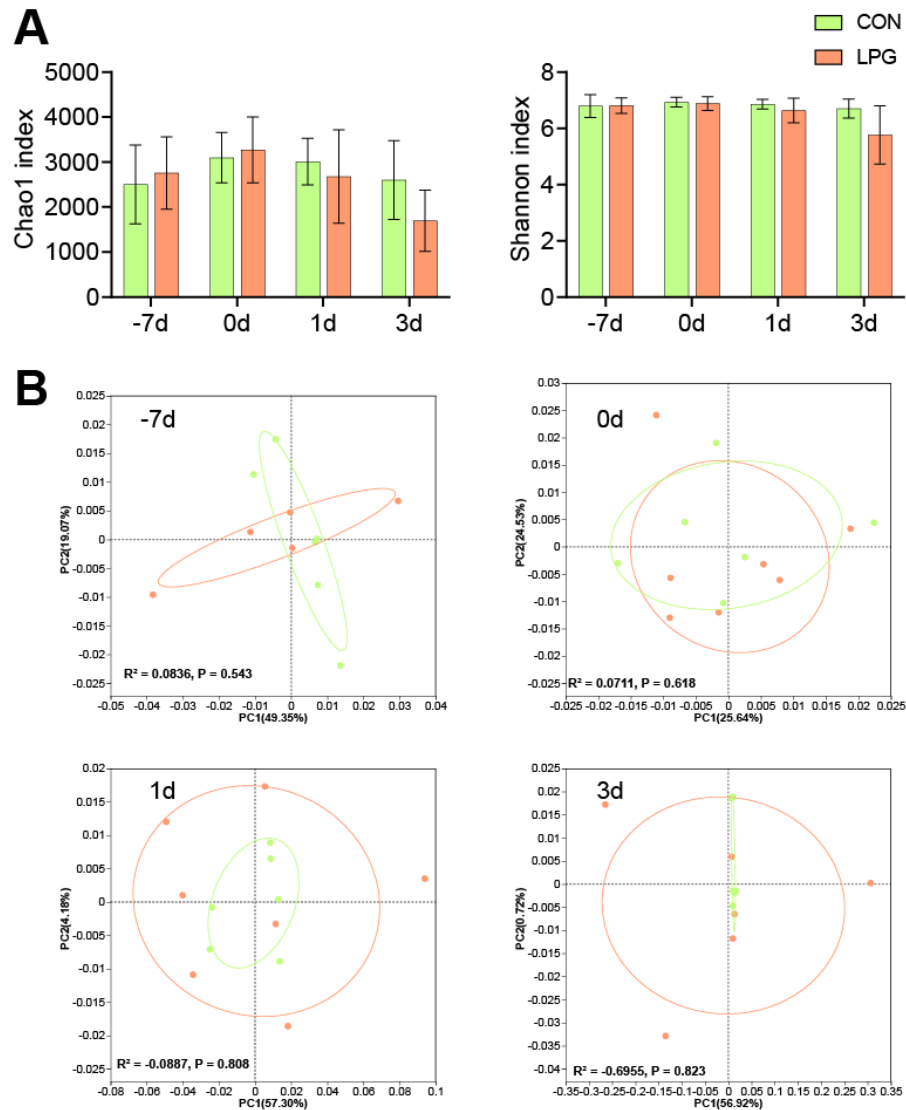


1 Supplementary table 1:

2 The formulation and chemical composition of TMR in close-up and fresh cow (DM basis)

Items	Prepartum		Postpartum
	LPG	CON	
Ingredient, %			
Corn silage	55.99	55.65	52.17
Oat hay	11.20	11.13	4.7
Leymus chinensis	8.61	8.56	-
Alfalfa hay	-	-	6.69
Steam-flaked corn	6.24	6.21	10.99
Molasses	-	-	2.88
Soybean meal	9.04	8.99	9.85
Corn gluten meal	-	-	1.98
Soybean hull	1.89	2.90	5.59
DDGS	5.17	5.14	2.98
Fat powder	-	-	0.56
Synthetic zeolite	1.29	-	-
Premix	0.39	0.39	0.27
Magnesium oxide	0.17	-	-
Ammonium chloride	-	0.13	-
Magnesium sulfate	-	0.90	-
Calcium carbonate	-	-	0.77
Rumen buffer	-	-	0.28
Salt	-	-	0.2
Yeast culture	-	-	0.07
Nutrient composition			
NE _L , Mcal/kg	1.57	1.59	1.70
CP, %	13.8±0.5	14.4±0.2	16.4±0.3
NDF, %	34.7±1.8	33.3±1.7	25.9±1.2
ADF, %	19.4±1.3	19.2±1.0	15.3±0.6
Starch, %	14.7±1.2	14.0±0.7	19.2±1.6
Ether extract, %	4.32±0.72	4.34±0.68	4.91±0.83
Ash, %	8.75±0.25	7.91±0.10	7.44±0.17
Ca, %	0.37±0.04	0.37±0.04	1.10±0.08
P, %	0.32±0.01	0.32±0.005	0.35±0.01
Mg, %	0.41±0.05	0.45±0.03	0.28±0.004



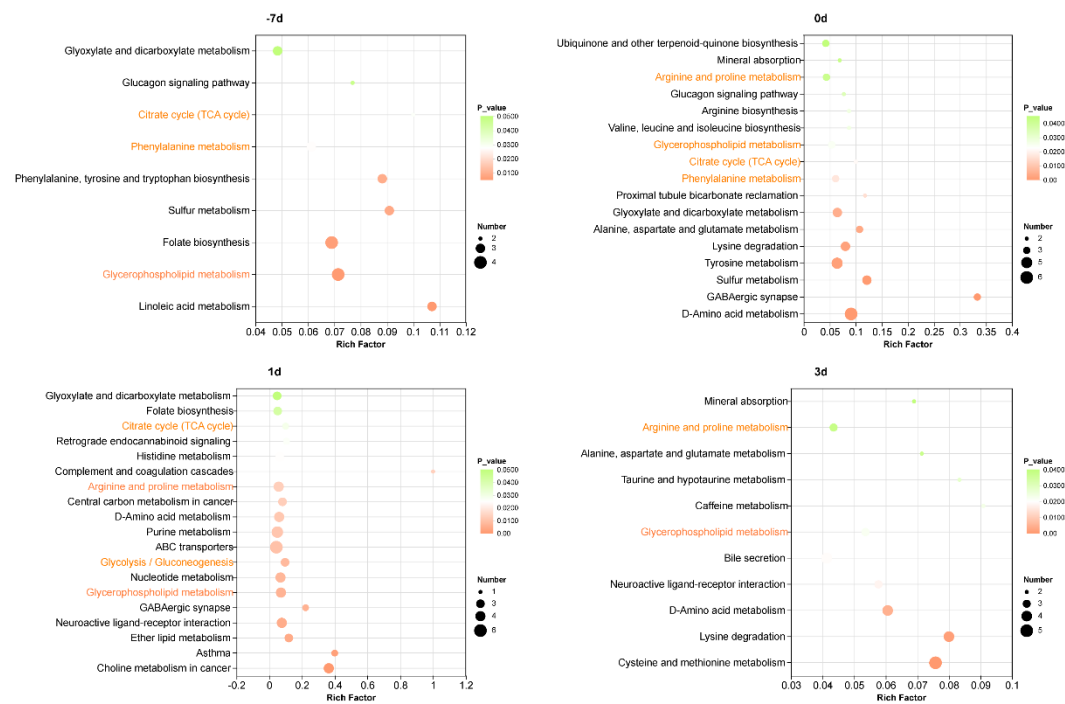
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5 Supplementary figure 1: Peripartum low-phosphorus status on α -diversity and β -
6 diversity of rumen microbiota during the transition period. (A) Chao1 richness index
7 and Shannon diversity index of rumen microbiota at -7 d, 0 d (calving), 1 d, and 3 d
8 relative to parturition in cows under low-phosphorus status (LPG) and control cows
9 (CON). (B) Principal coordinate analysis (PCoA) based on Bray Curtis dissimilarity
10 showing time-resolved separation of rumen microbial community structure between
11 LPG and CON cows at -7 d, 0 d (calving), 1 d, and 3 d. Ellipses indicate 95% confidence
12 intervals.

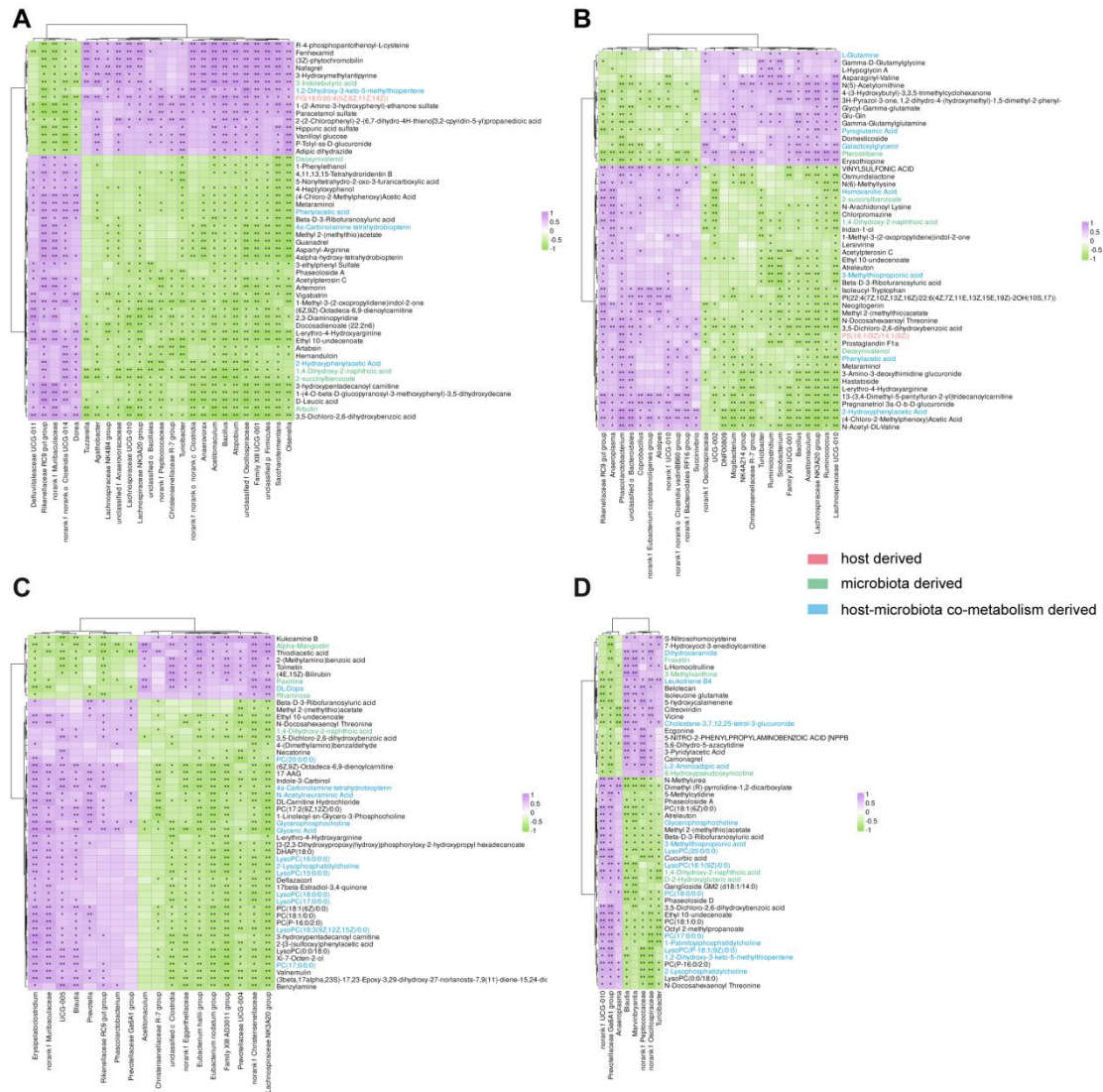


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14 Supplementary figure 2: Differential metabolites in the glycerophospholipid metabolic
 15 pathway of bovine plasma. (A) prepartum 7 days, (B) parturition, (C) postpartum 1 day,
 16 and (D) postpartum 3 days. Data for CON are shown in green, and data for LPG are
 17 shown in orange.



19 Supplementary figure 3: Enrichment of differential metabolic pathways.



Supplementary figure 4: Correlation heatmap of hindgut microbiota and plasma differential metabolites. (A) prepartum 7 days, (B) parturition, (C) postpartum 1 day, and (D) postpartum 3 days. Metabolites are color-coded: red (host-derived), green (microbiota-derived) and blue (host-microbiota co-metabolism-associated).