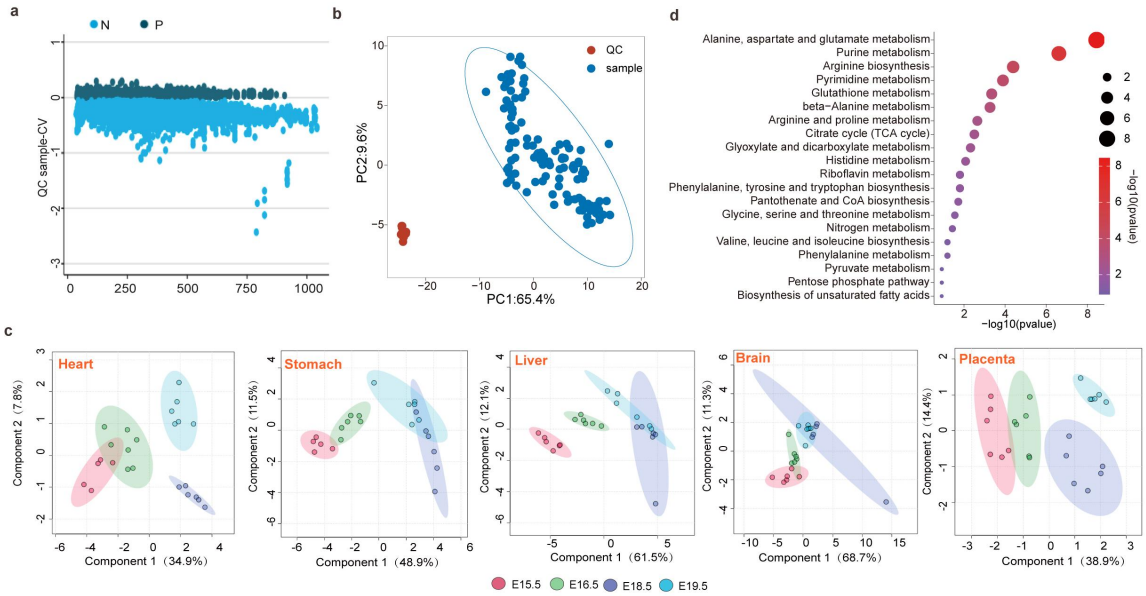
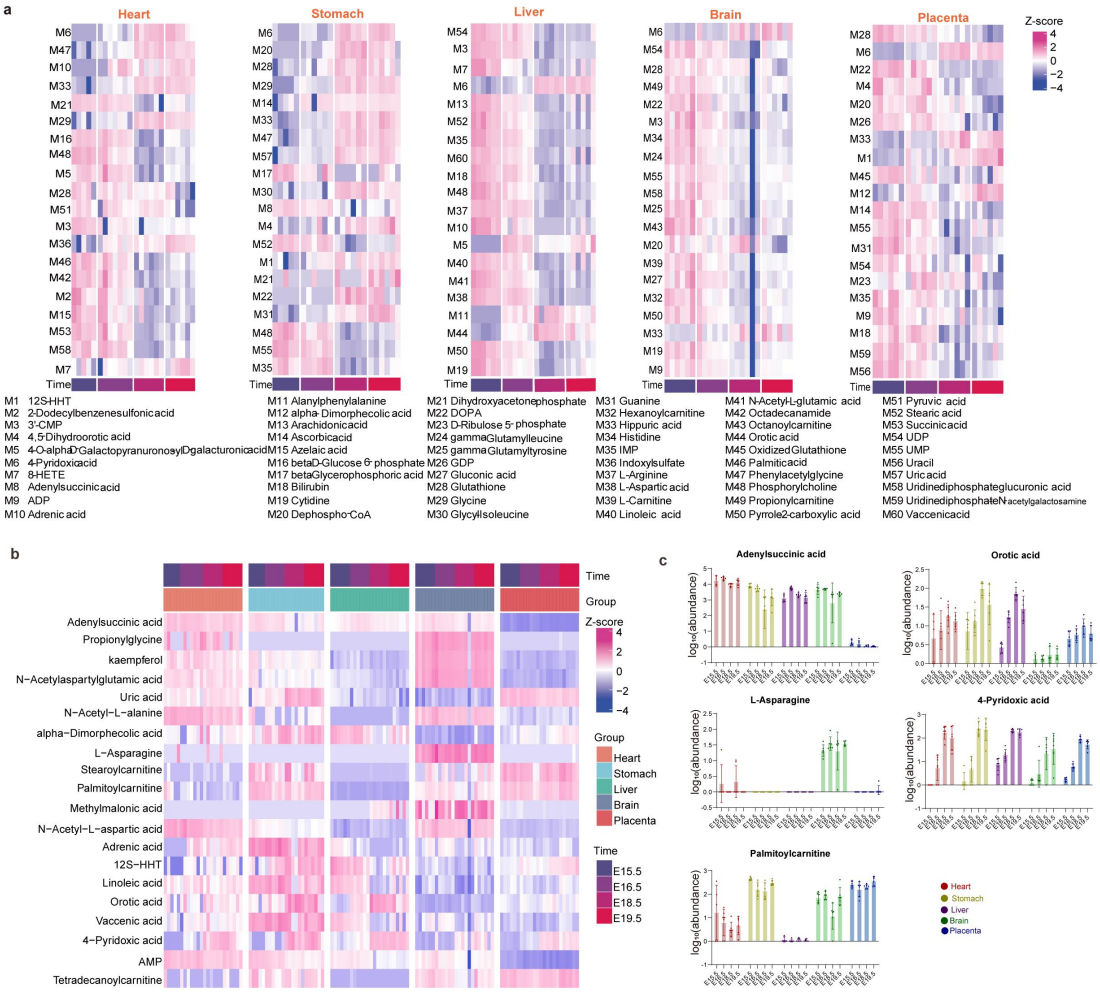


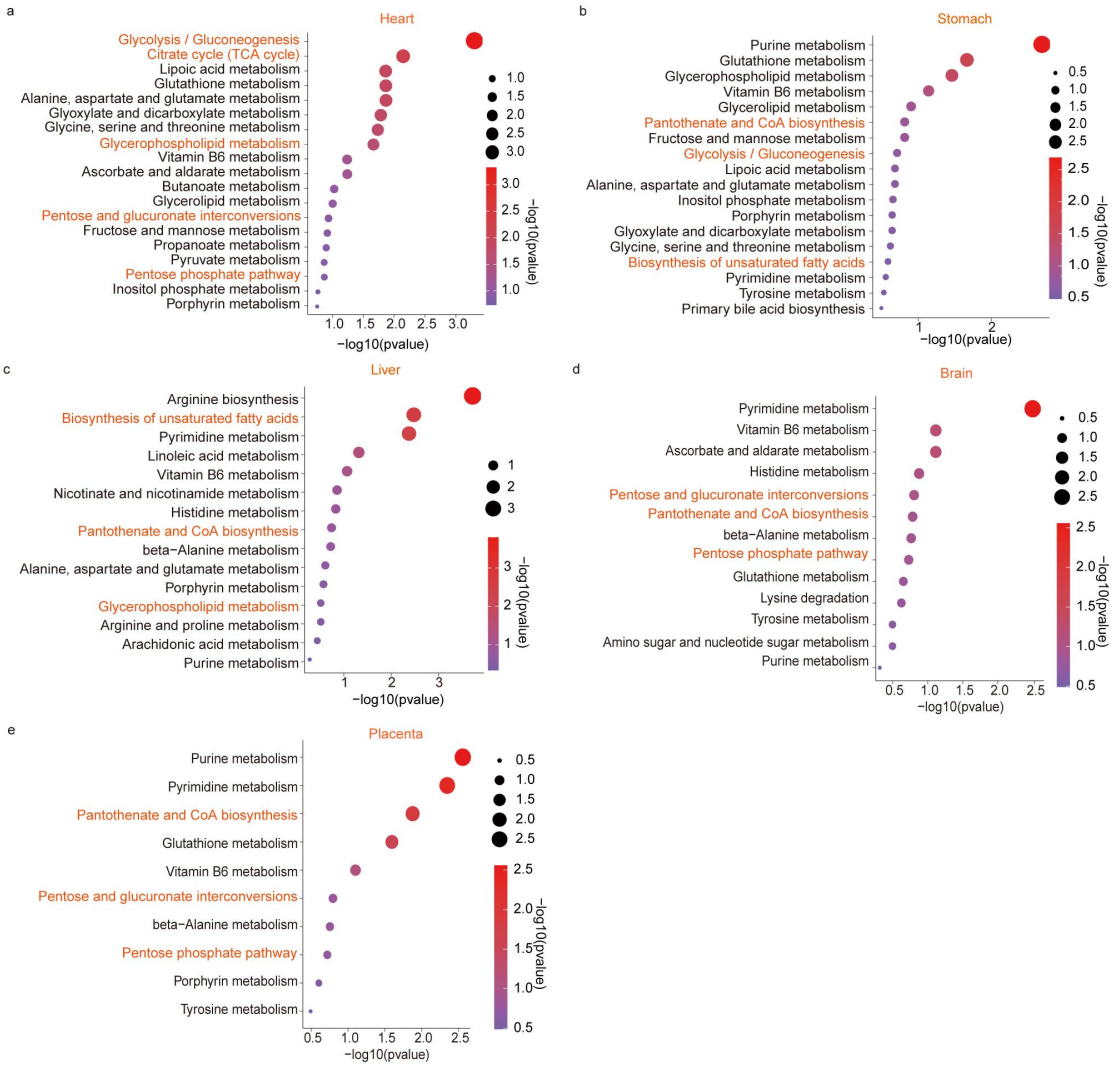
Supplementary Fig. 1 Metabolic characteristics of different organs during late gestation.

a, The coefficient of variation of QC samples, where light blue N represents the negative ion mode and dark blue P represents the positive ion mode. **b,** PCA analysis of QC samples and organ samples, with QC samples represented by red points in the figure. **c,** PLS-DA analysis of heart, stomach, liver, brain, placenta. Different organ samples were separated at different times. **d,** The KEGG enrichment of all identified metabolites. The color of the bubble represents the value of -log10 (p value).



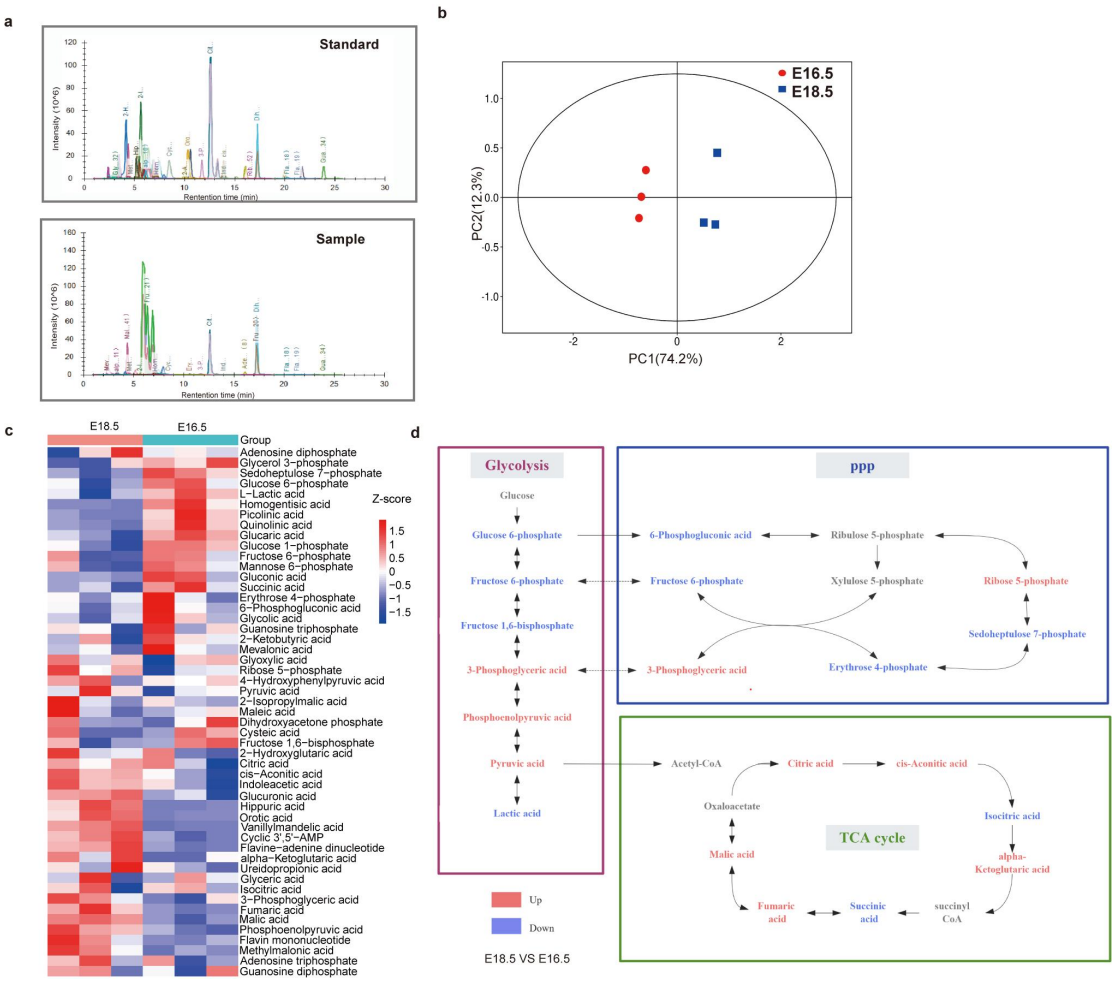
Supplementary Fig. 2 Differential metabolites of different organs during late gestation.

a, Heatmaps of top 20 differential metabolites in each of the 5 organs at E15.5-E19.5. All differential metabolite codes are M1-M60, names for each number at the bottom, colors represent different developmental times. **b,** Heatmap of different metabolites of different organs at E15.5-E19.5. The top of 20 differential metabolites were screened through PLS-DA analysis, with color indicating the abundance of the metabolites, red indicating higher level, and blue indicating lower level. **c,** The $\log_{10}$(abundance) of characteristic metabolites in 5 organs at E15.5 to E19.5. The sample sizes were: n=5 (heart and stomach at E15.5), n=7 (heart at E16.5), and n=6 (all other groups)**.** Error bars represent mean ± SD.



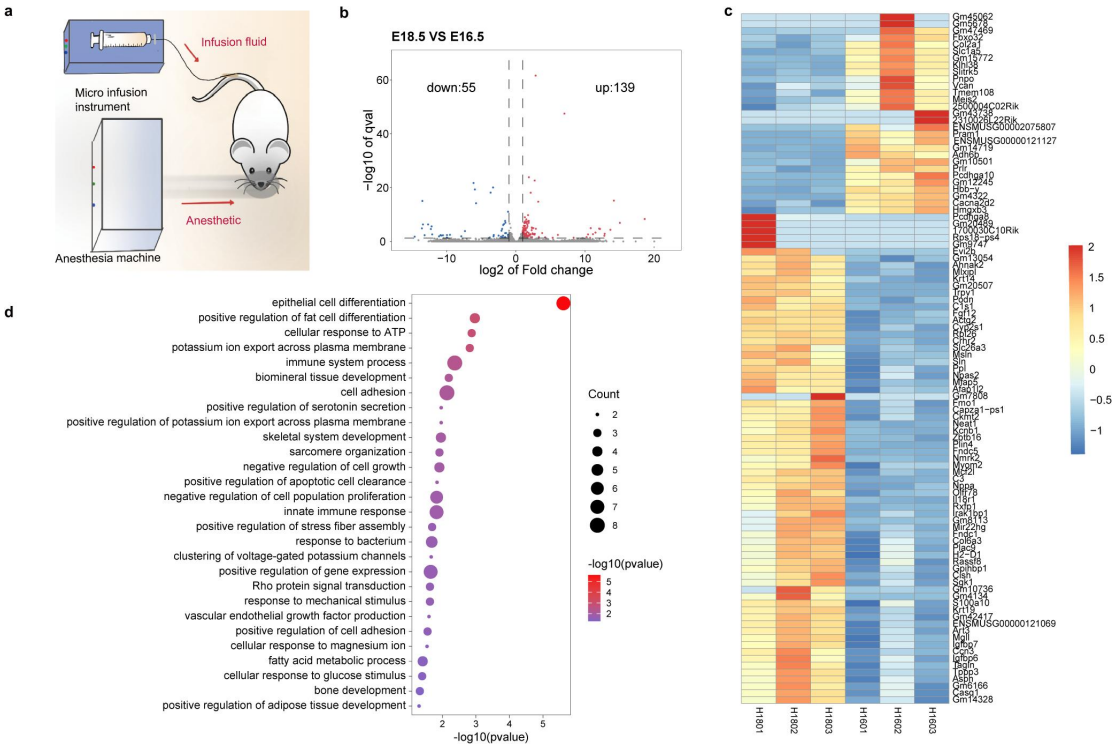
Supplementary Fig. 3 KEGG enrichment of metabolites of major organs.

a-e, The KEGG enrichment of top 20 differential metabolites in the heart (a), stomach (b), liver (c), brain (d) and placenta (e) at E15.5-E19.5. The color of the bubble represents the value of -log10 (p value)**.**



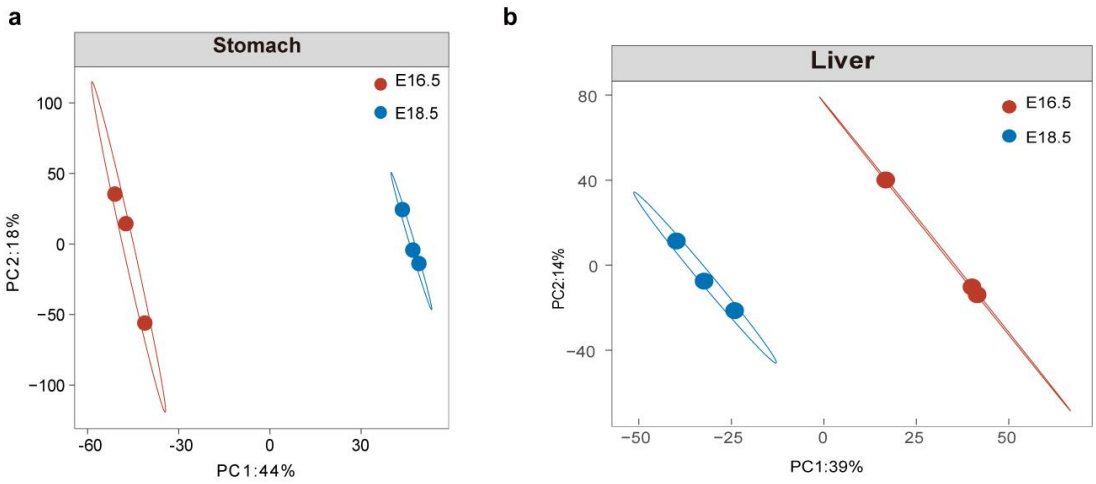
Supplementary Fig. 4 Targeted metabolomics of heart in late gestation.

a, Chromatogram of central carbon cycle targeted metabolites in heart. The upper figure shows quantitative detection of mixed standard samples, and the lower figure shows quantitative detection of samples. **b,** OPLS-DA analysis of targeted metabolites of E16.5 and E18.5 samples (n=3 per group). **c,** Heatmap showed the abundance of targeted metabolites in heart at E16.5 and E18.5 (n=3 per group), red indicating higher level and blue indicating lower level. **d,** Targeted metabolite related metabolic pathways. Highlighted in red represented upregulated metabolites at E18.5, blue represented downregulated metabolites, and gray represented undetected metabolites (created with Biorender).

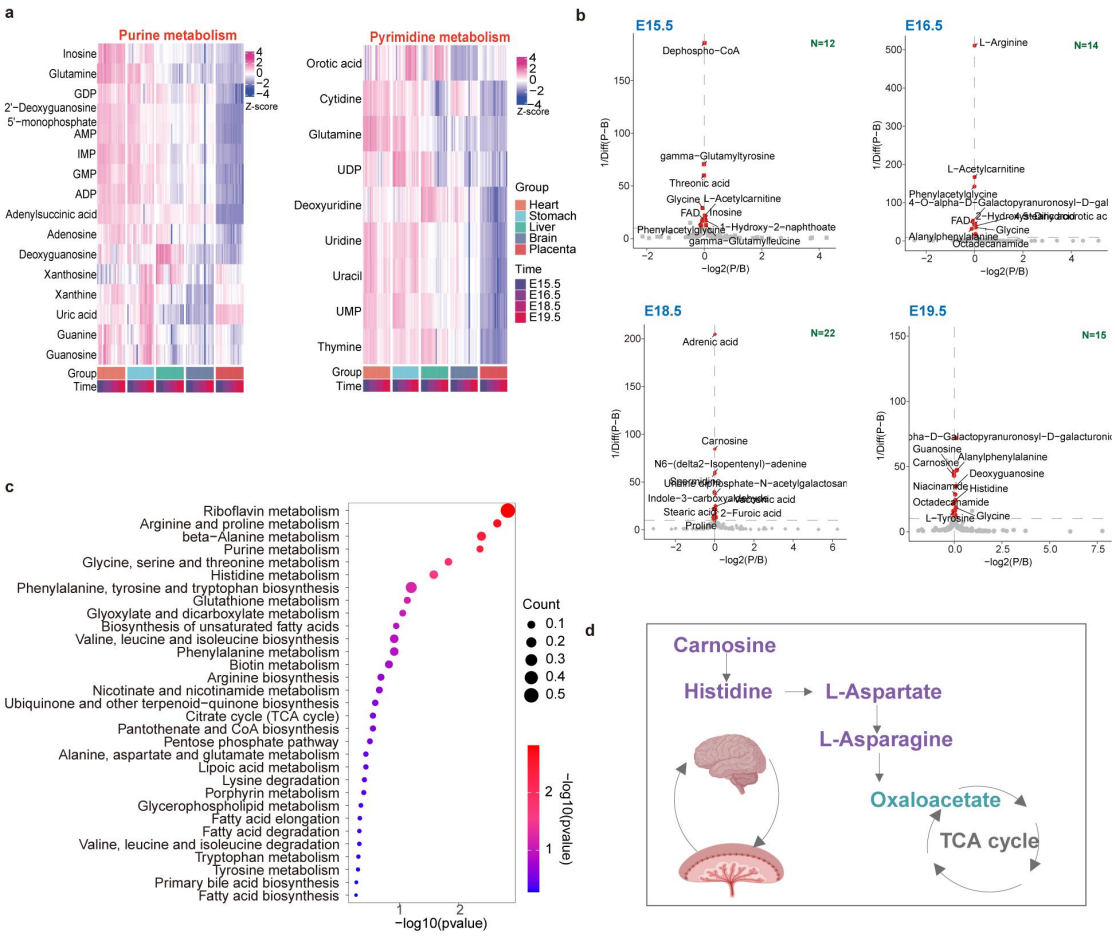


Supplementary Fig. 5 Metabolic flux and transcriptome of heart in late gestation.

a, Infusion pattern diagram of ^{13}C glucose isotopes in pregnant mice. **b,** Volcano diagram of differentially expressed genes in heart between E16.5 and E18.5 (n=3 per group). **c**, Heatmap of top 100 differential expression genes between E16.5 and E18.5. **d,** GO enrichment of upregulated differential expression genes between E16.5 and E18.5.



Supplementary Fig. 6 PLS-DA analysis of protein in stomach (a) and liver (b) at E16.5 and E18.5.



Supplementary Fig. 7 Metabolic characteristics of brain and placenta in late gestation.

a, Heatmap of metabolites in purine and pyrimidine metabolism pathway of different organs from E15.5 to E19.5. Colors indicating the abundance of the metabolites, red represented higher level, and blue represented lower level. **b.** Metabolites with similar abundance in the placenta and brain. The similar metabolites were determined based on the ratio of metabolites in the brain and placenta being greater than 0.95. Different time points from left to right. **c,** KEGG enrichment analysis of metabolites with all similar abundance between brain and placenta. **d,** Schematic diagram of metabolic pathways of carnosine and histidine in brain and placenta (created with Biorender).