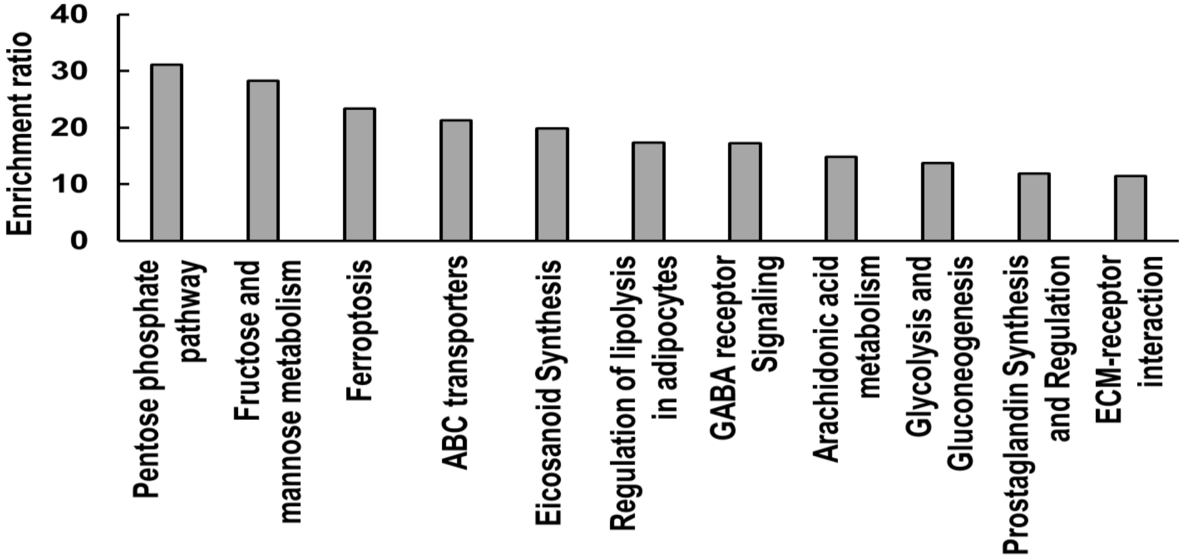
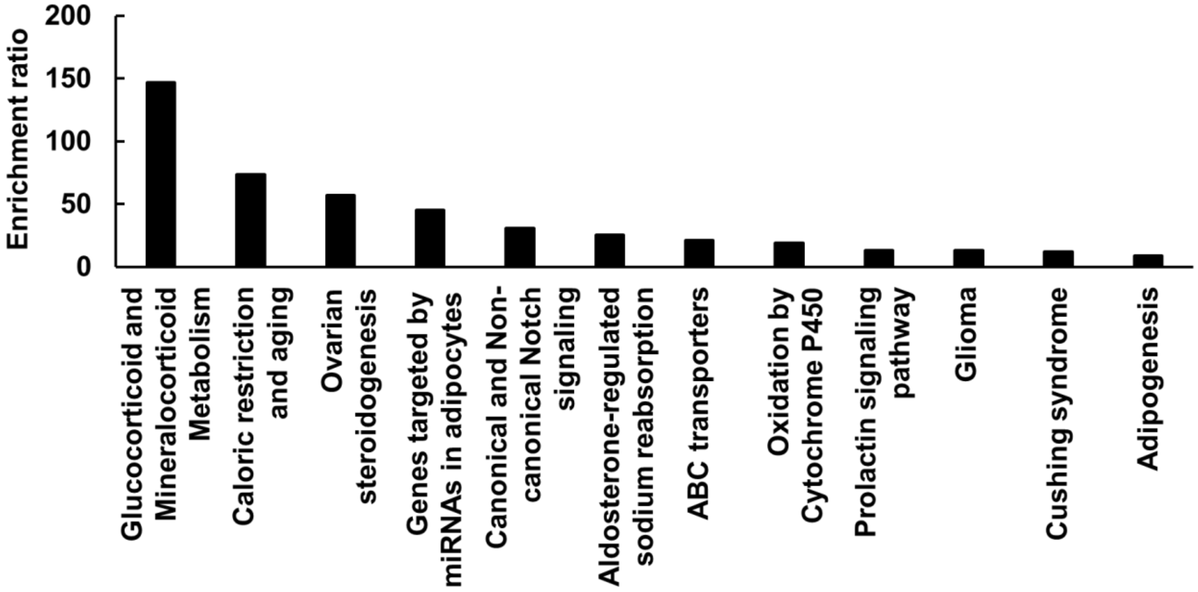
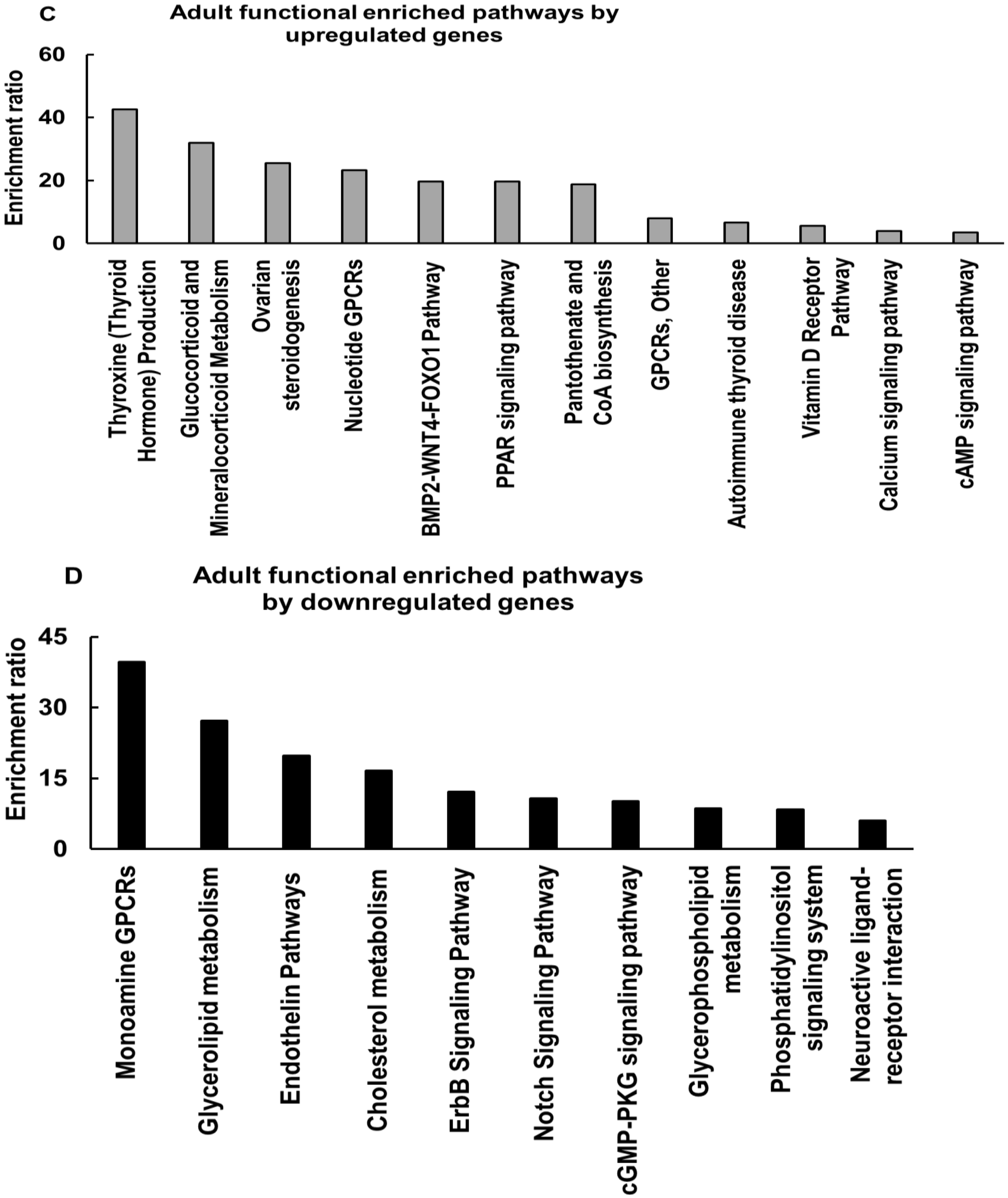
Supplemental Fig.1



A Fetal functional enriched pathways by upregulated genes



B Fetal functional enriched pathways by downregulated genes



Supplemental Fig 1. Bioinformatic analysis of the RNA-seq data. Genes differentially expressed were evaluated *in silico* using Function Enrichment software showing upregulated and downregulated canonical pathways in fetal D90 (A, B) and adult Y2 (C, D) ovaries, respectively.