

## **Does gut microbiota regulate brooding in geese?**

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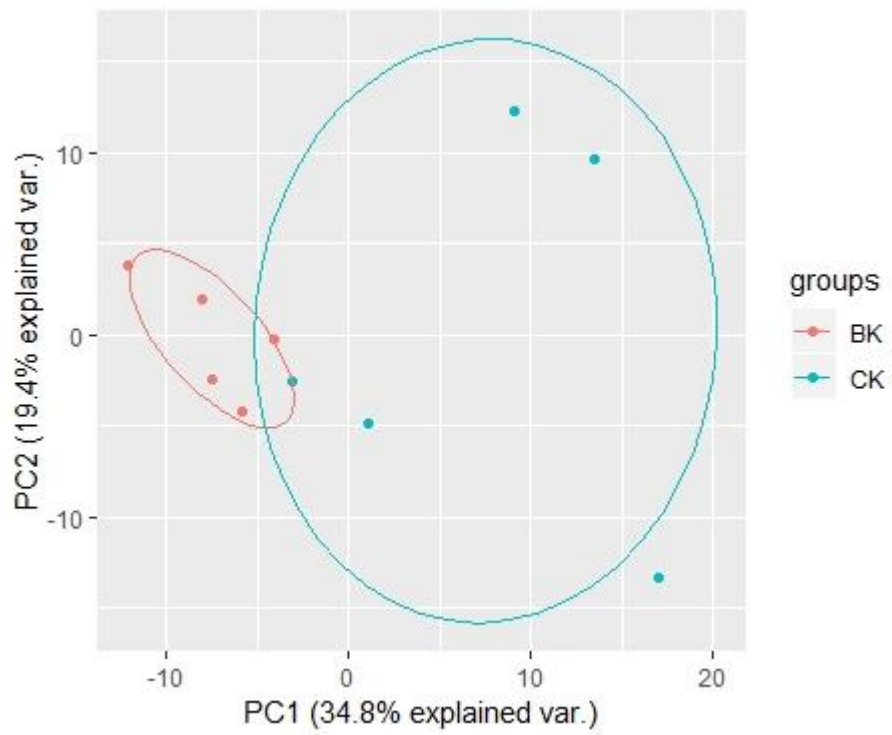
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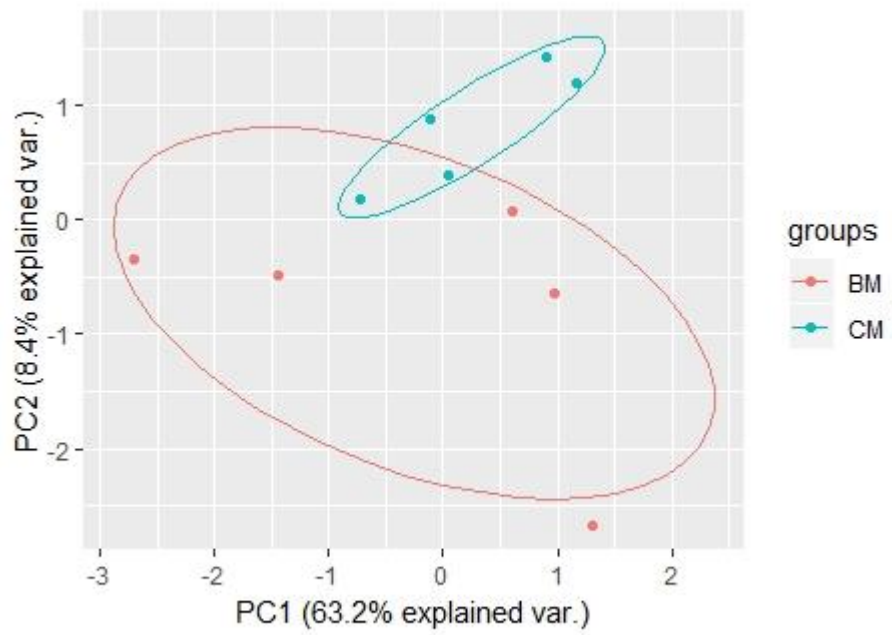
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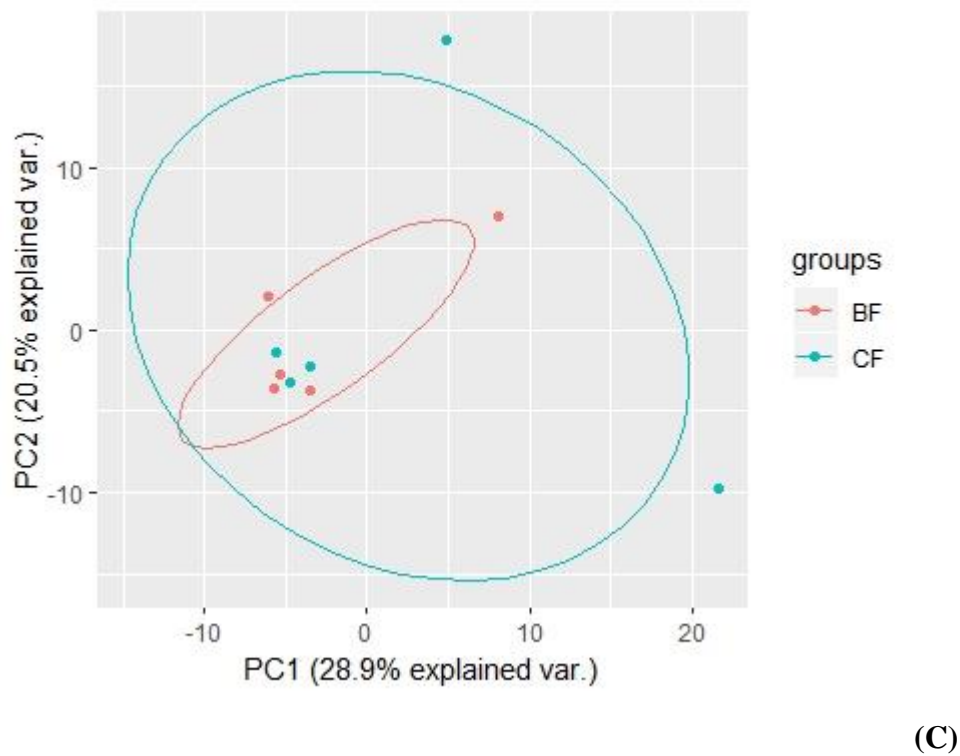
## Supplementary material



(A)

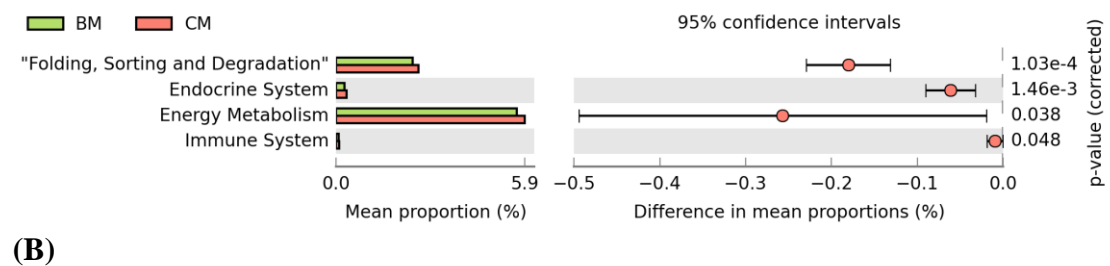
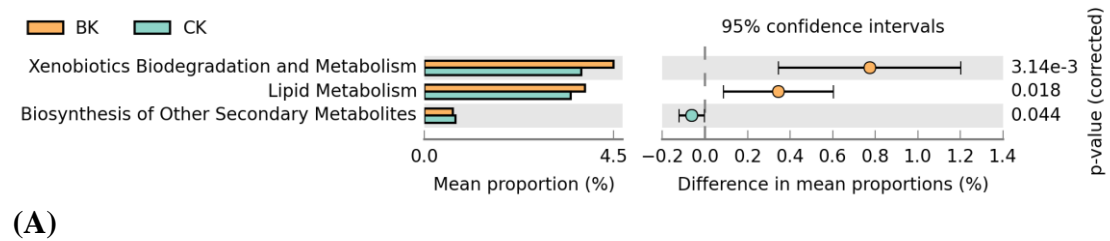


(B)



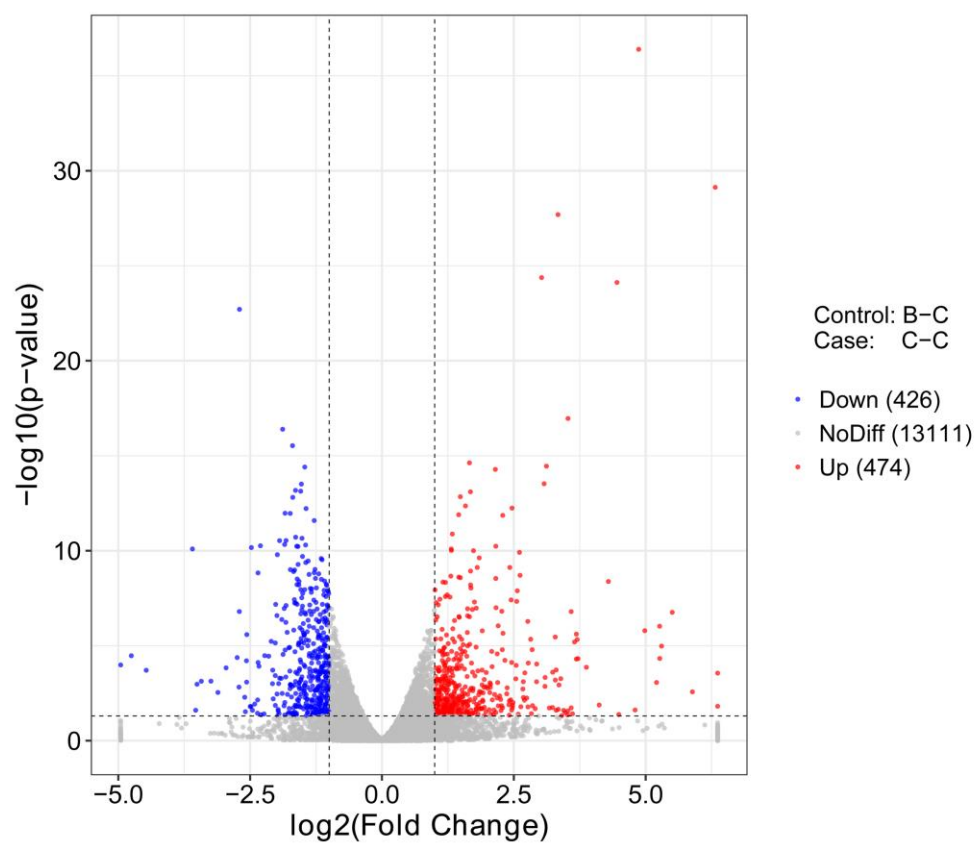
**Figure S1.** Genus-level microorganism principal components analysis (PCA).

Jejunum (A), cecum (B), and manure (C).

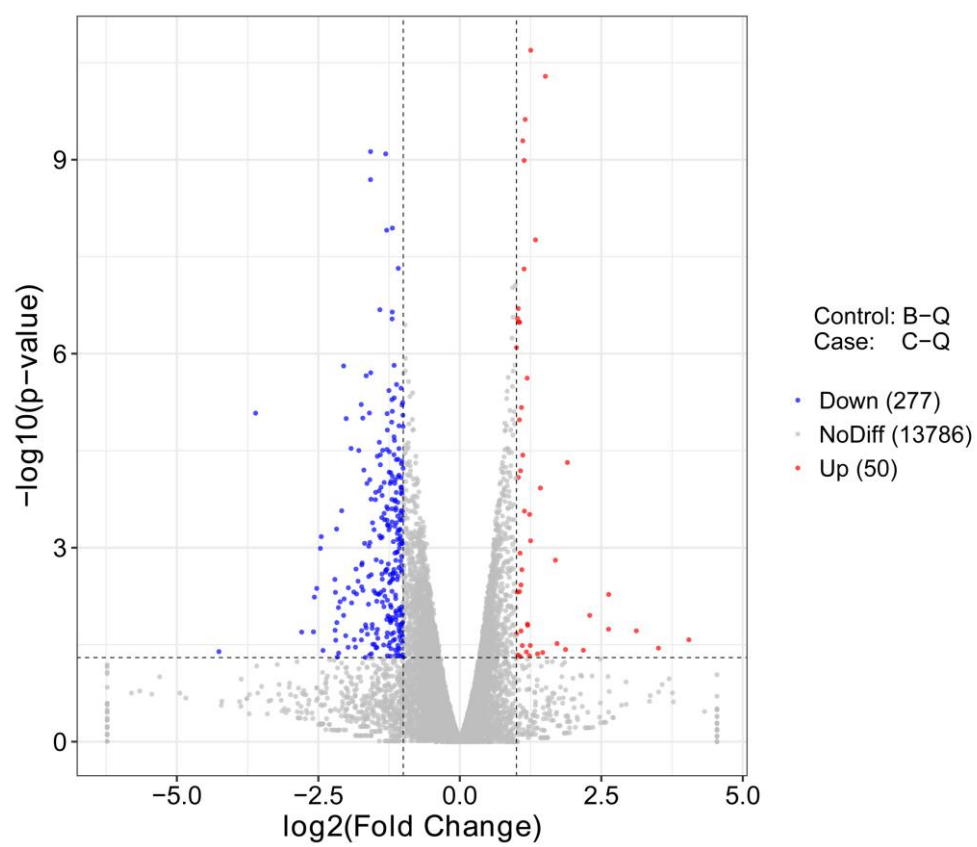


**Figure S2.** Second functional groups with different metabolism of gut microbiota.

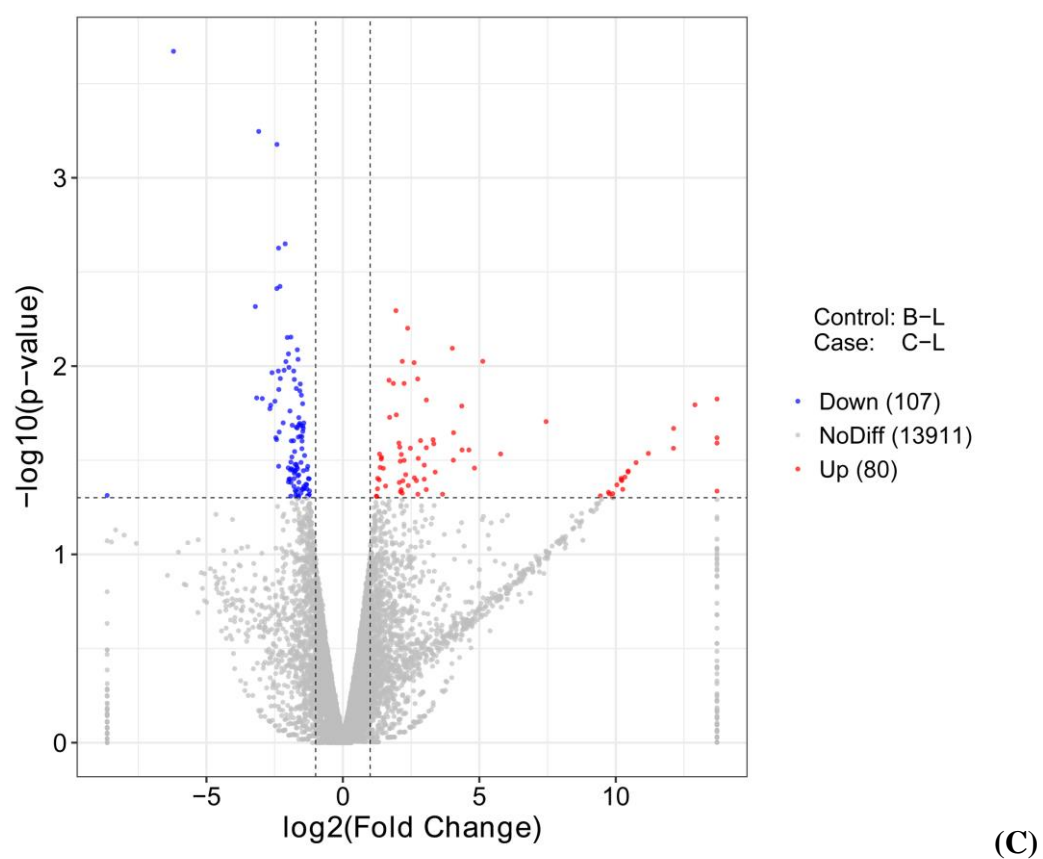
Jejunum (A) and cecum (B).



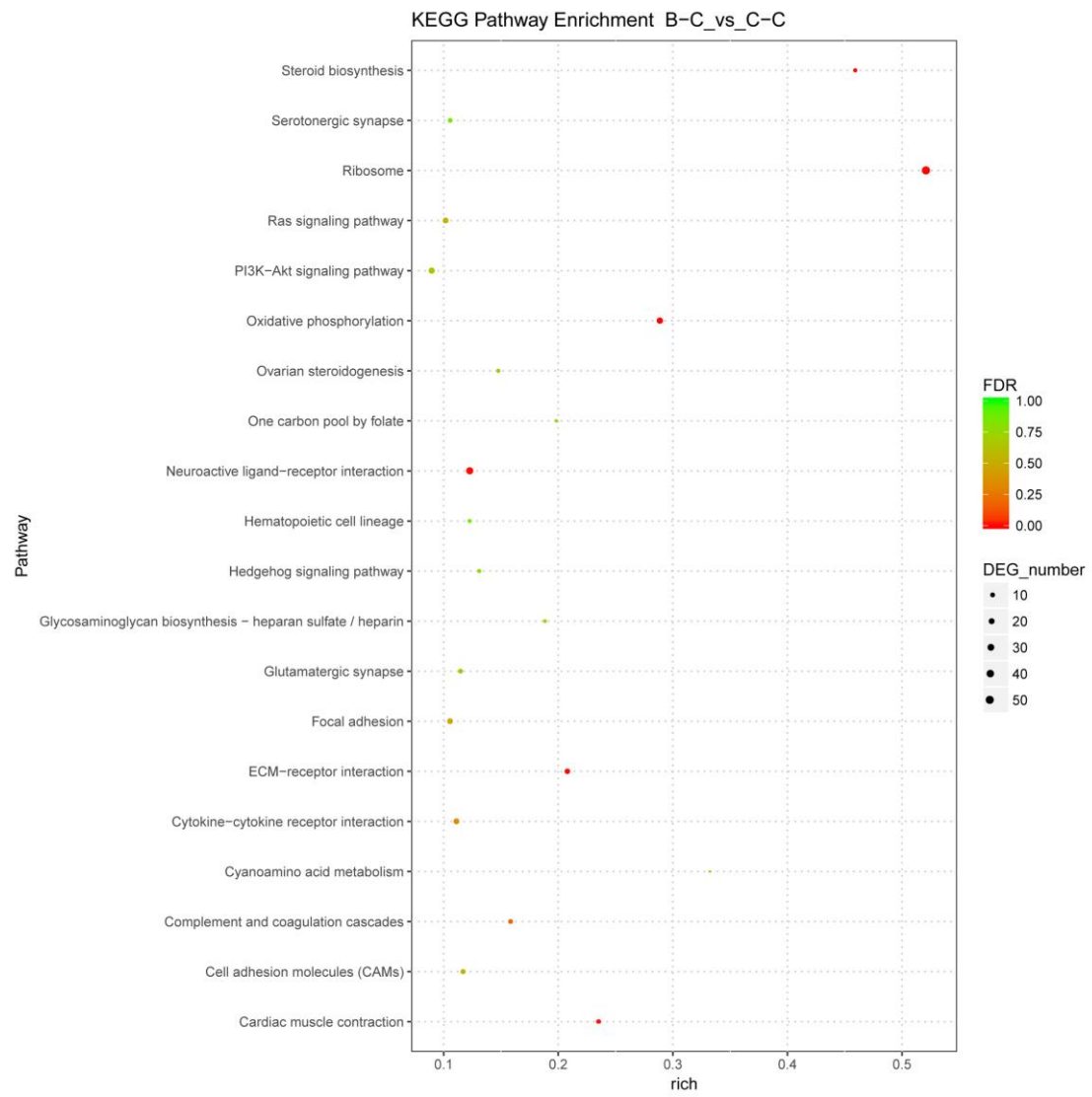
(A)



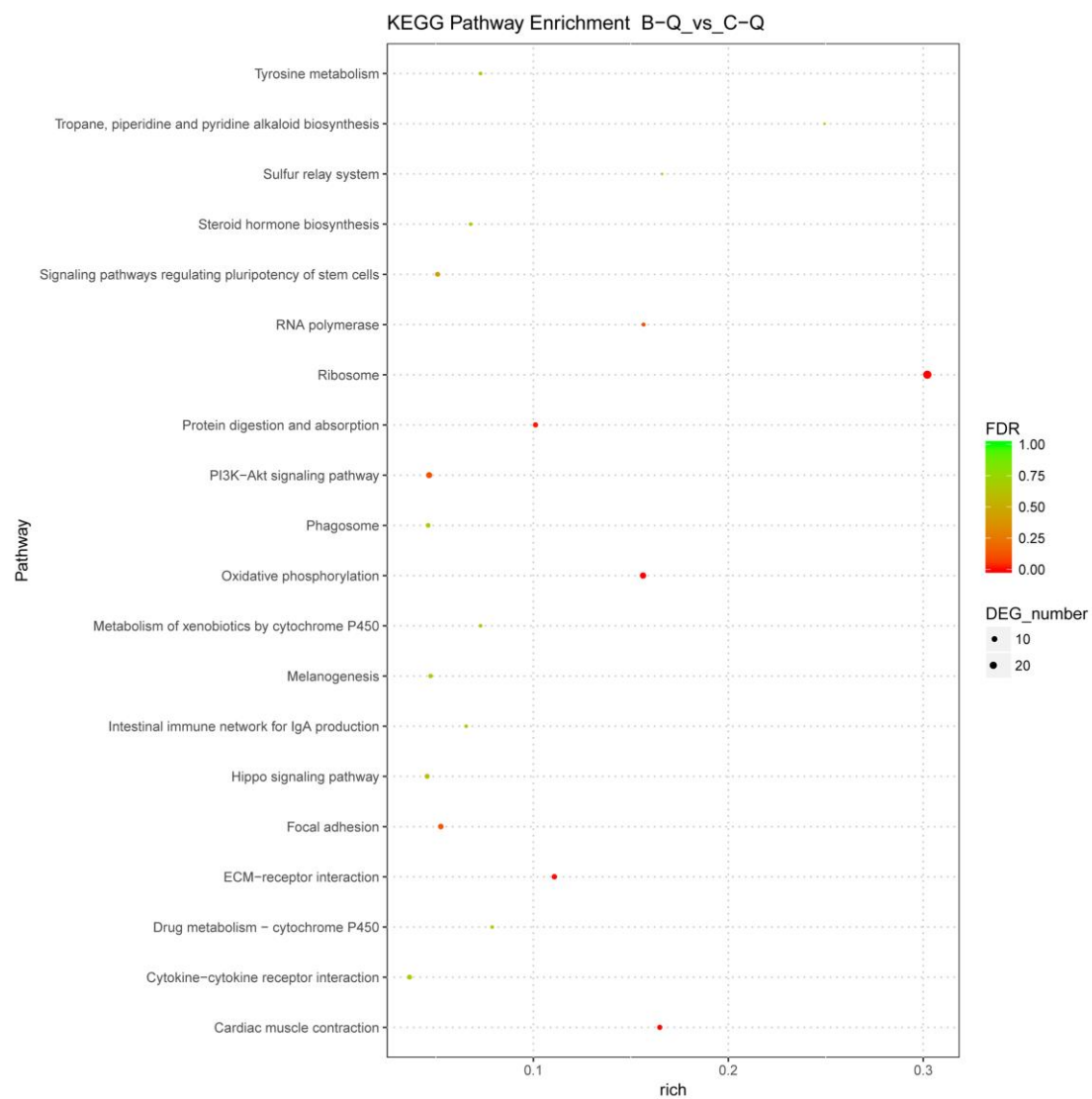
(B)



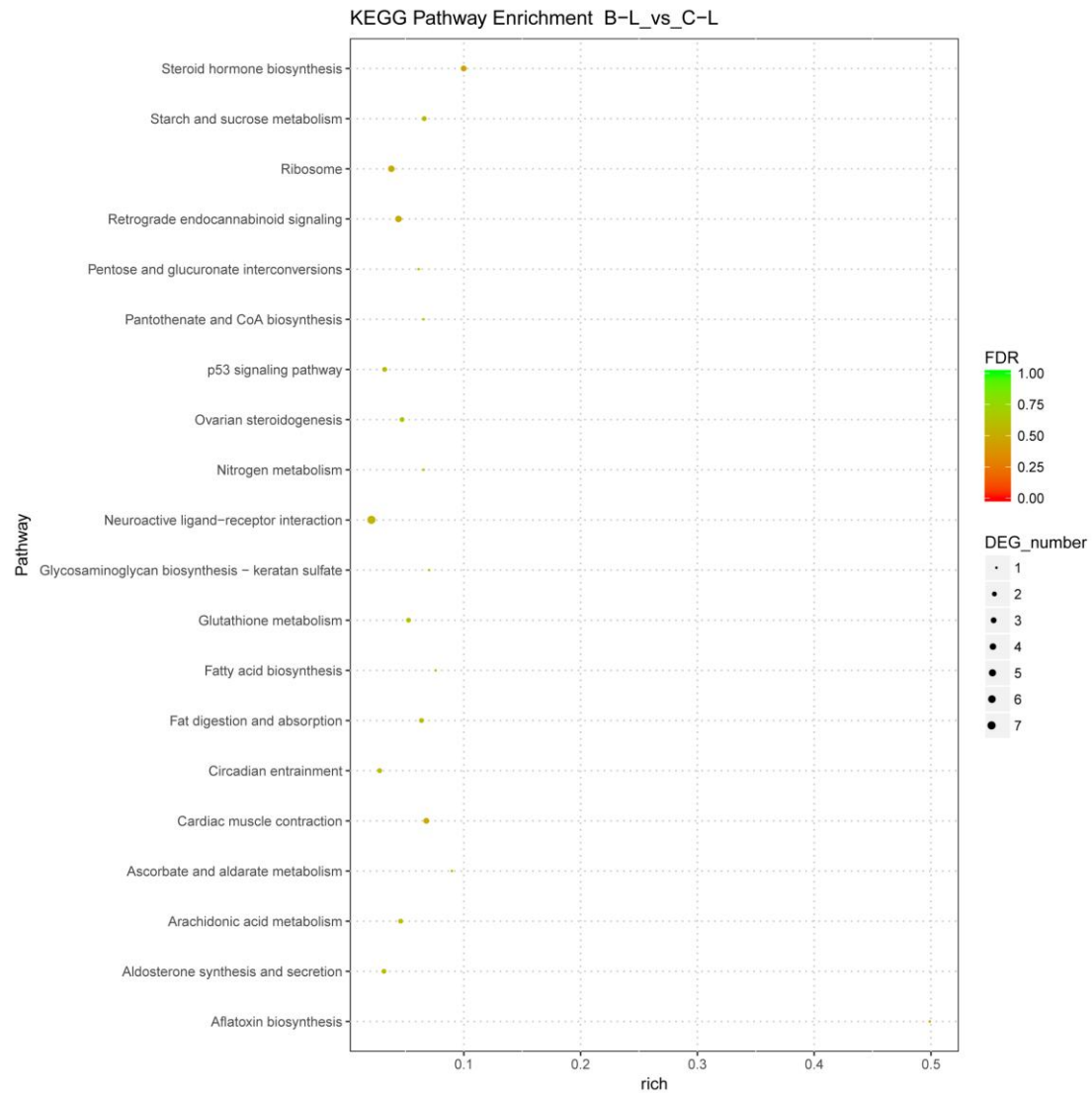
**Figure S3.** Volcano map of differentially expressed genes in pituitary, thalamus, and ovary. (A) Pituitary; (B) thalamus; (C) ovary. The two vertical dashed lines in the figure are twice the difference threshold; the horizontal dashed line is the threshold for the  $P$  value,  $P = 0.05$ .



(A)



(B)



(C)

**Figure S4.** KEGG (Kyoto Encyclopedia of Genes and Genomes) diacylglycerol (DAG) enrichment analysis. Figure S4A shows the pituitary significantly different KEGG pathways: (1) ribosome, majority in downregulated genes; (2) oxidative phosphorylation, majority in downregulated genes; (3) extracellular matrix (ECM)–receptor interaction, majority in upregulated genes; (4) steroid biosynthesis, majority in upregulated genes; (5) neuroactive ligand–receptor interaction, majority in upregulated genes; (6) cardiac muscle contraction, majority in downregulated genes. Figure S4B shows the significantly different KEGG pathways in the thalamus: (1)



ribosome, majority in downregulated genes; (2) oxidative phosphorylation, majority in downregulated genes; (3) cardiac muscle contraction, majority in downregulated genes; (4) ECM–receptor interaction, majority in downregulated genes; (5) protein digestion and absorption, majority of downregulated genes. Figure S4C shows that the ovary does not have any significantly different KEGG pathways.