

Supplementary figure legends

Figure S1. Spatiotemporal analysis and distribution of 15 clusters in the young and aged ovaries.

(A) PCA clustering graph of two samples; (B) Spots distribution plots of 15 clusters in the young and aged ovaries; (C) The top 10 specifically expressed genes in 15 clusters.

Figure S2. GO and KEGG analysis of 15 clusters.

(A) GO and KEGG analysis for cluster 1; (B) GO and KEGG analysis for cluster 2; (C) GO and KEGG analysis for cluster 3; (D) GO and KEGG analysis for cluster 4; (E) GO and KEGG analysis for cluster 5; (F) GO and KEGG analysis for cluster 6; (G) GO and KEGG analysis for cluster 7; (H) GO and KEGG analysis for cluster 8; (I) GO and KEGG analysis for cluster 9; (J) GO and KEGG analysis for cluster 10; (K) GO and KEGG analysis for cluster 11; (L) GO and KEGG analysis for cluster 12; (M) GO and KEGG analysis for cluster 13; (N) GO and KEGG analysis for cluster 14; (O) GO and KEGG analysis for cluster 15.

Figure S3. DEGs between the young and aged ovary transcriptomes.

(A) Violin plots of *Akr1b10* in different clusters; (B) PPI network of top 200 DEGs between the aged and young ovaries; (C) Hub genes between old and young ovaries using Cytohubba topological method BottleNeck; (D) Split violin plot of the top 10 hub genes between the aged and young ovaries.

Figure S4. Gene expression patterns in ovarian follicles.

(A) Venn plot showing overlapping up-regulated genes in aged ovarian follicles; (B) Venn plot showing overlapping down-regulated genes in aged ovarian follicles; (C) Spatial distribution and box plots showing expression patterns of *Egr1*, *Ptgs2*, and *Gsta4* in aged and young cluster 4, 8, and 10; (D) The top 5 GO terms (BP, CC, and MF) in three follicle clusters; (E) The top 20 KEGG terms in three follicle clusters.

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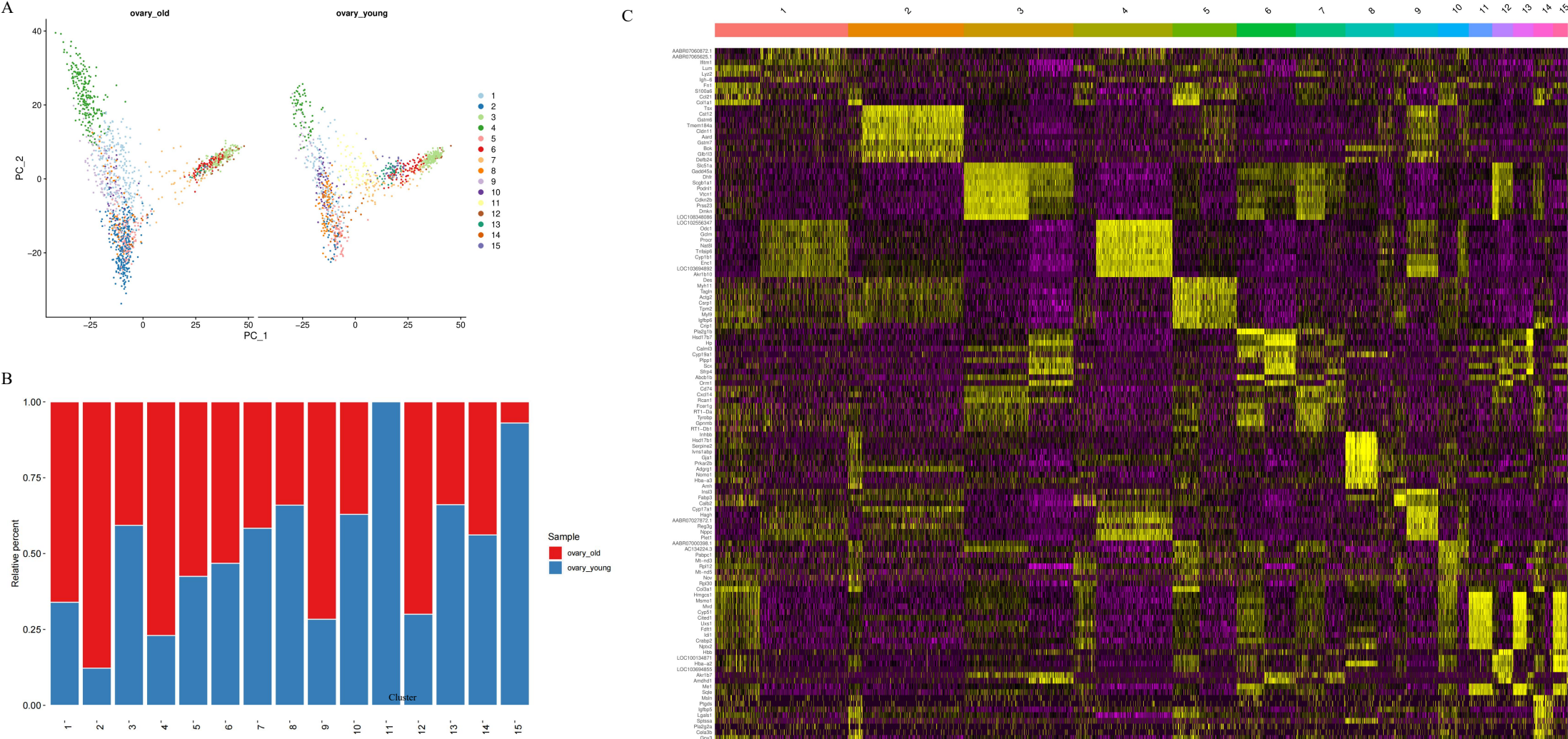


Figure S3. DEGs between the young and aged ovary transcriptomes.

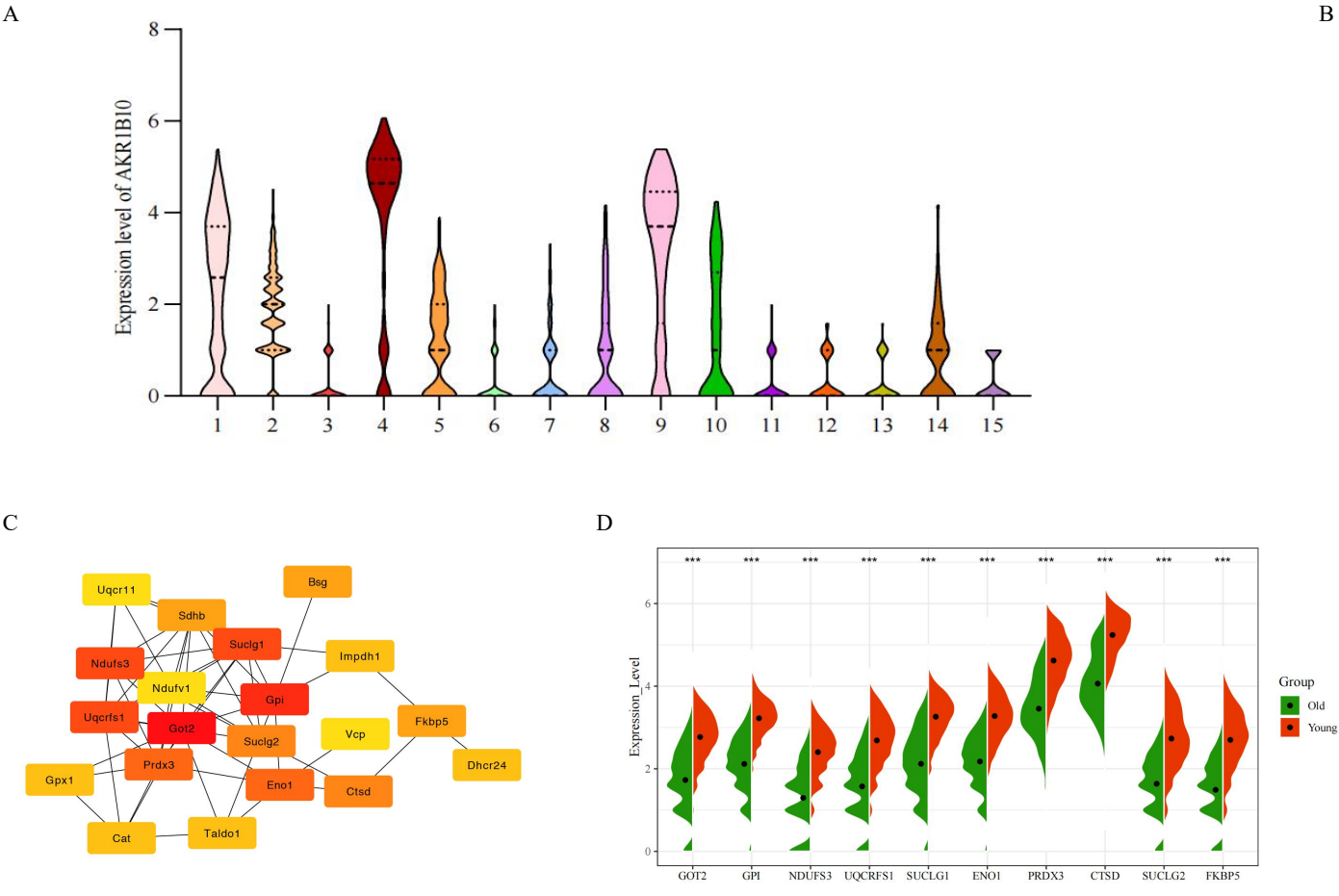


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