Figure S1. Quality control and integration of snRNA-seq data from human ovarian tissues. (A) Distributions of gene counts (nFeature_RNA), RNA counts (nCount_RNA) and mitochondrial content (percent.mt). (B) Associations between percent.mt and nCount_RNA (left), and between nFeature_RNA and nCount_RNA (right). (C) Identification of highly variable genes for downstream analysis. (D) Principal component analysis illustrating cell-cycle phase distribution (G1, S and G2M). (E) UMAP of all samples colored by age group (young vs. aged). (F) UMAP of individual samples following integration. (G) Heatmap of top differentially expressed genes across clusters. (H) Cell type annotation and counts for the eight major ovarian cell types. SMC, smooth muscle cells; TC, theca cells; M, macrophages; F, fibroblasts; SC, stromal cells; EC, endothelial cells; GC, granulosa cells; EpiC, epithelial cells.

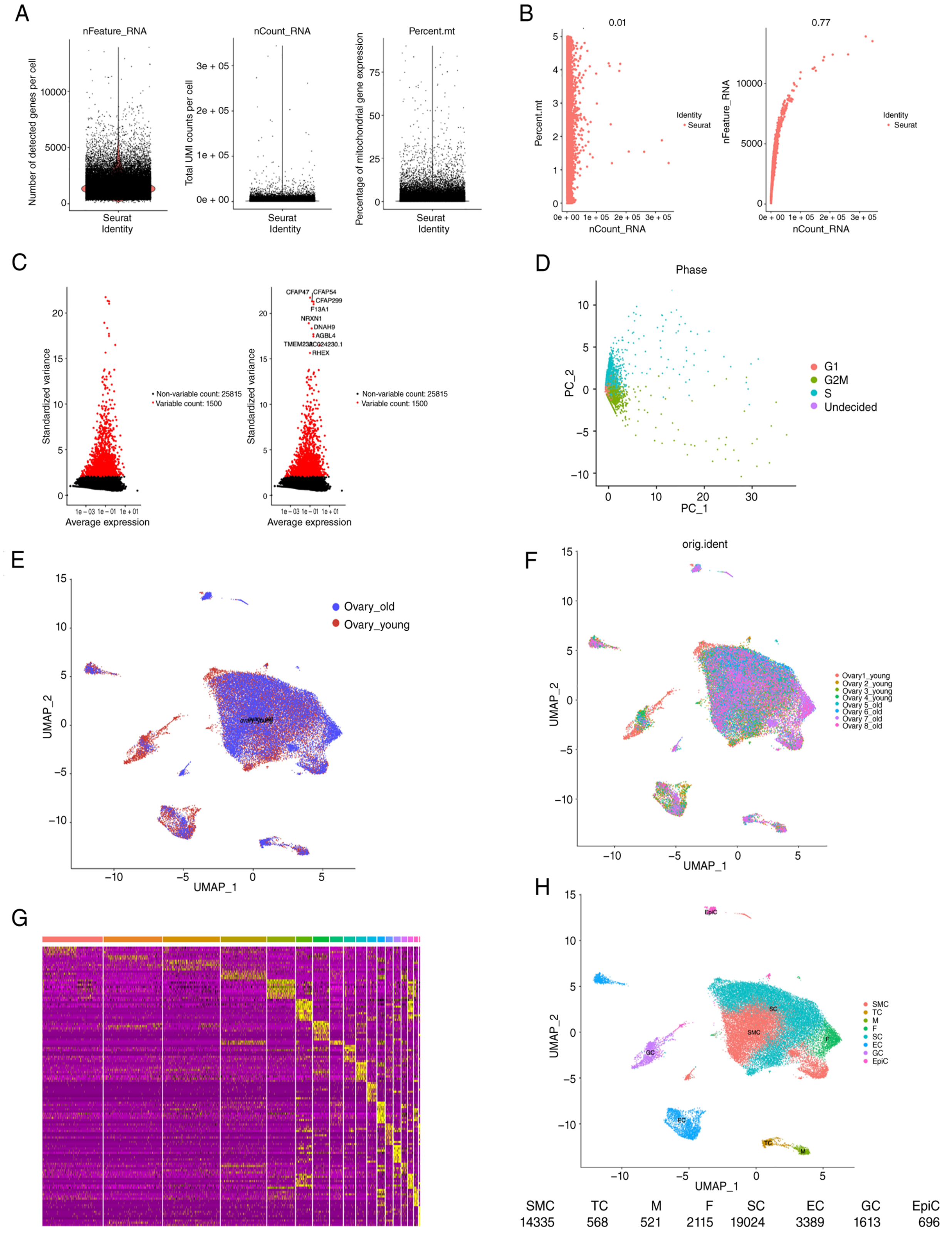

Figure S2. Clustering and cell type annotation across individual ovarian samples. (A) UMAP plots of 20 clusters in each individual sample (four young and four aged). (B) UMAP plots illustrating annotated cell types across all individual samples.

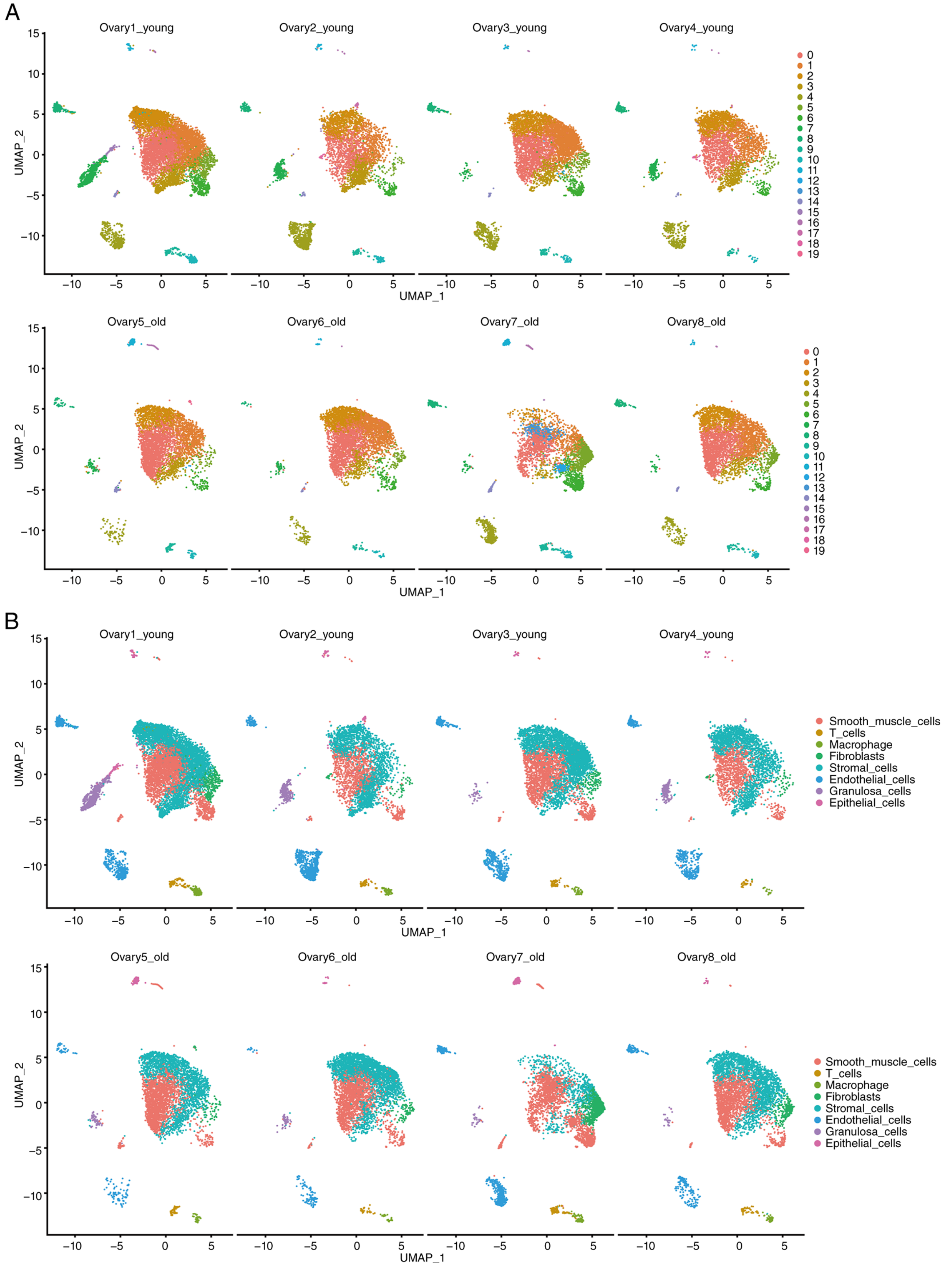

Figure S3. Age-associated changes in inflammatory and antioxidant gene expression in human ovaries. (A) UMAP plots illustrating the spatial expression of NLRP3 in young and aged ovarian samples. (B) Dot plot illustrating inflammatory gene expression (G*SDMD*, *NLRP3*, *GZMA* and *GZMB*) across ovarian cell types. (C) Violin plots illustrating increased NLRP3 expression in macrophages in aged ovaries. (D) UMAP plots showing *SOD1* expression patterns in young and aged ovaries. (E) Dot plot illustrating antioxidant gene expression (*NQO1*, *PRDX1*, *GSTP1*, *SOD3* and *SOD1*) by age group. (F) Violin plots illustrating reduced SOD1 expression across cell types in aged ovaries.

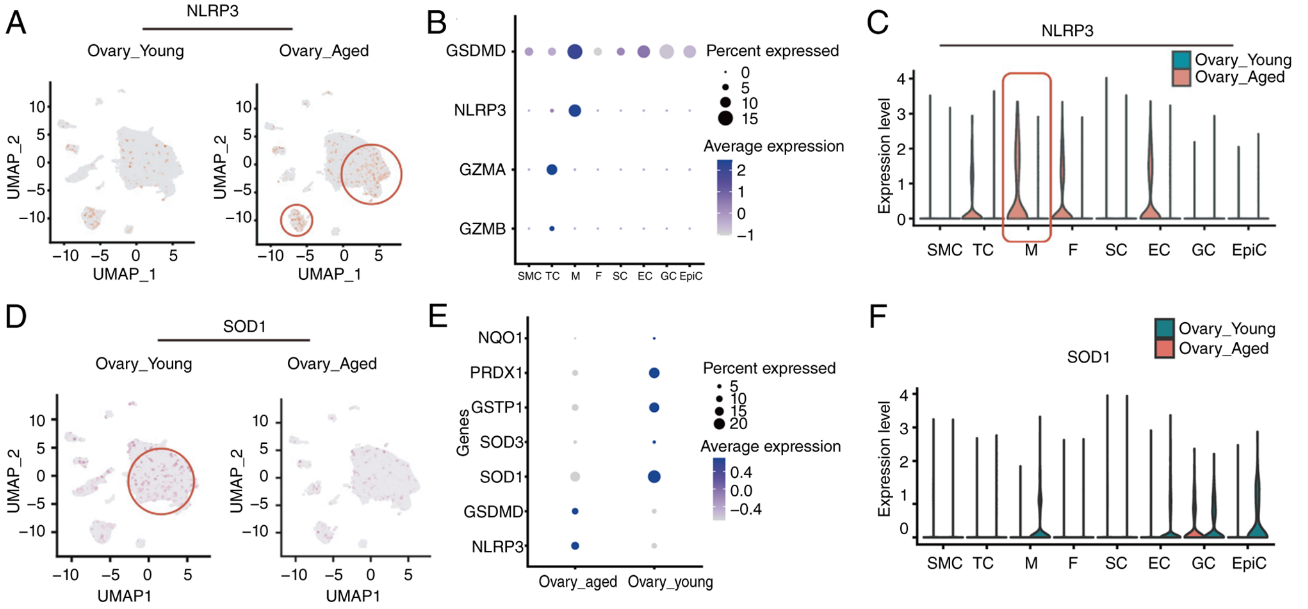

Figure S4. Global signaling changes in aged ovaries and activation of growth- and inflammation-related pathways. (A) FGF, PDGF, and IGF signaling networks in young and aged ovaries based on sender-receiver interactions. (B) Heatmaps comparing FGF signaling strength across cell types in young and aged ovaries. (C) Dot plot of ligand-receptor interactions enriched in aged ovaries, including *VEGFA-VEGFR1, FGF7-FGFR1, CXCL12-CXCR4* and *IL-1β-IL-1R1*.