

Figure S1. Raw data of the dataset GSE112013 from single-cell RNA sequencing of the adult testis were filtered and normalized. (A) The low-quality data of the dataset were filtered as follows: Genes expressed in <3 cells and samples with <50 cells were detected. (B) No correlation was present between the percentage of mitochondrial genes and the sequencing depth. A positive correlation was detected between the gene number and sequencing depth ($R=0.86$; $P<0.05$). (C) The data were log-normalized and genes with larger coefficients of variation were selected. 1,500 differential genes with the largest standard deviation of expression in all cells were selected for subsequent analysis and the top 10 differential genes were displayed. Mt, mitochondrial genes.

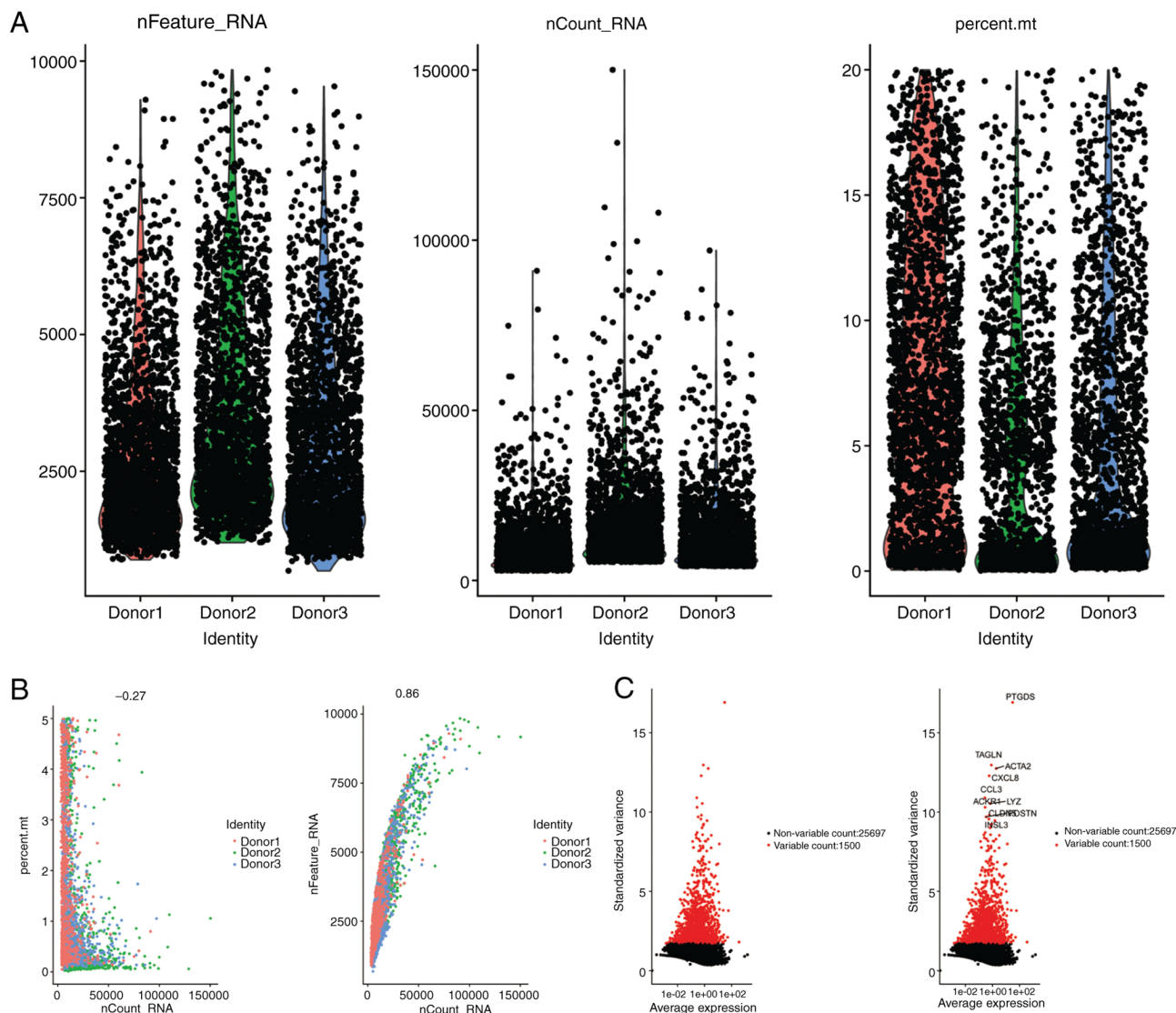


Figure S2. Raw data of the dataset GSE120506 from single-cell RNA sequencing of infant testis were filtered and normalized. (A) The filtered data of the dataset. (B) No correlation was present between the percentage of mitochondrial genes and the sequencing depth. A positive correlation was detected between the gene number and sequencing depth ($R=0.97$, $P<0.05$). (C) The data were log-normalized and genes with a larger coefficient of variation were selected. A total of 5,000 differential genes with the largest standard deviation of expression in all cells were selected for subsequent analysis and the top 10 differential genes were displayed. Mt, mitochondrial genes.

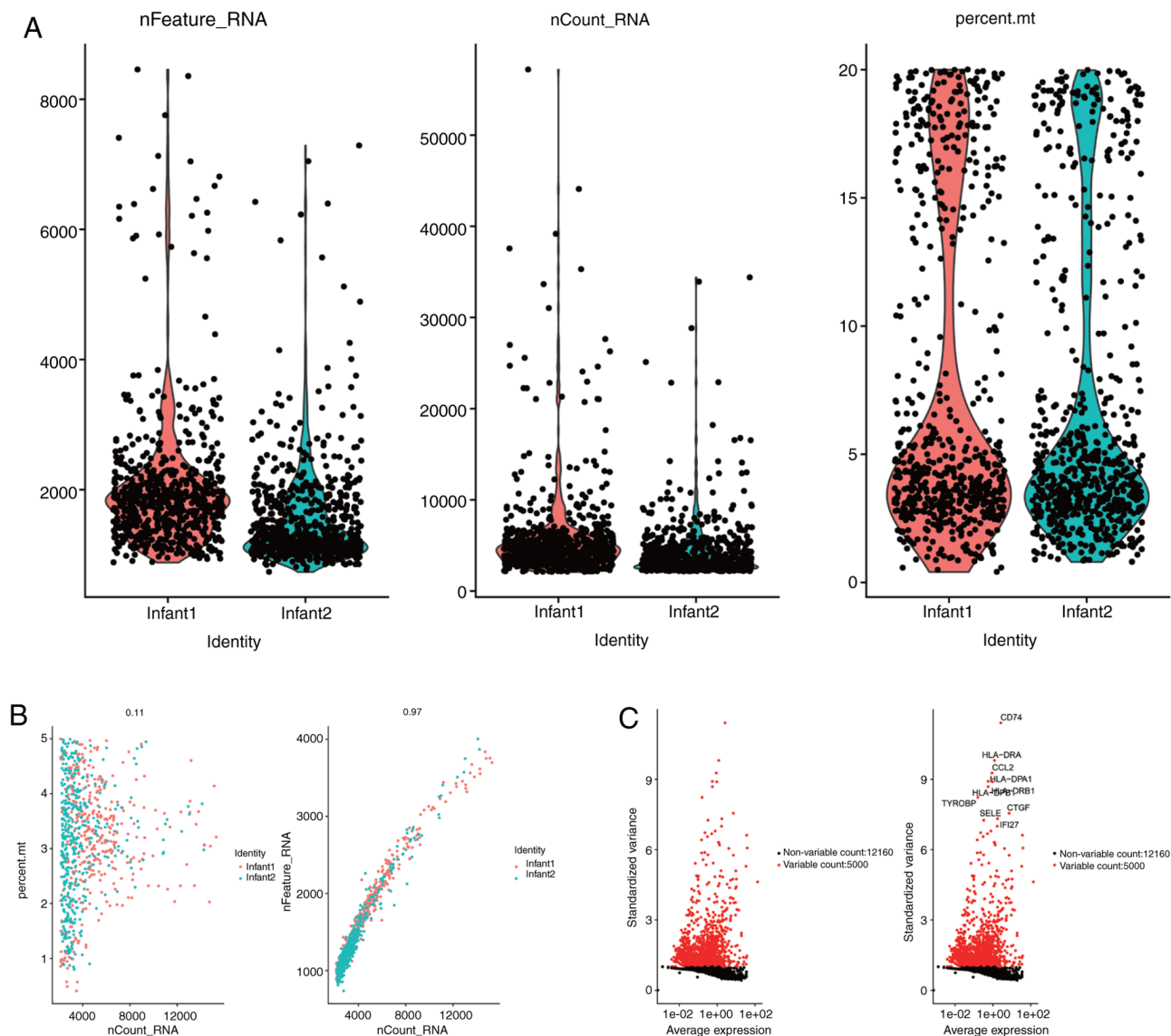


Figure S3. PCA of the dataset GSE112013 from single-cell RNA sequencing of adult testis. (A) A PCA algorithm was used to analyze the dataset. (B) The top 20 genes in the top 4 PCs and the correlation between genes and each component. (C) Heat map displaying the marker genes in the top 4 PCs. (D) P-value and mean distribution of the 20 PCs. PCA, principal component analysis.

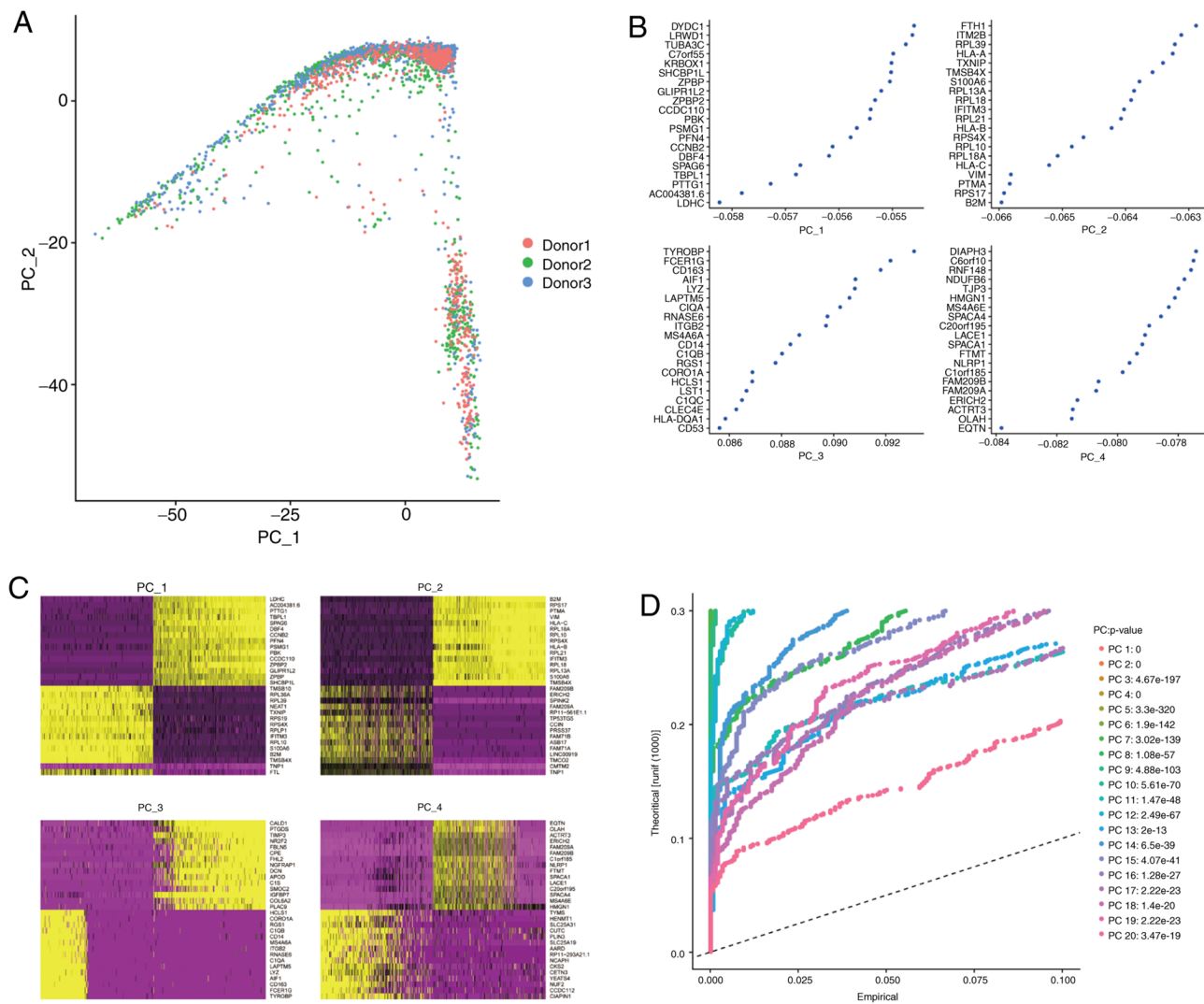


Figure S4. PCA of the dataset GSE120506 from single-cell RNA sequencing of infant testis. (A) A PCA algorithm was used to analyze the dataset. (B) The top 20 genes in the top 4 PC and the correlation between genes and each component. (C) Heat map displaying the marker genes in the top 4 PC. (D) P-value and mean distribution of the 20 PCs. PCA, principal component analysis.

