



Supplementary Figure S2. Information on human samples and quality control of single-cell RNA-seq; related to Fig. 1. (A) Summary information for the testicular samples for single-cell RNA-seq. (B) Violin plots showing the percentages of mitochondrial genes detected in each cell type. (C) UMAP plots showing the cell distributions for the young (red) and old (blue) groups. (D) UMAP plots showing the cell distributions for each sample. Cells are coloured and annotated to the right. (E) Relative proportions of different cell types in the samples analysed. (F) UMAP plots showing the expression profiles of cell type-specific marker genes for the indicated cell types in human testis. The colour key, ranging from grey to brown, indicates low to high gene expression levels. SSCs, spermatogonial stem cells; Diff-SPGs, differentiating spermatogonia; SPCs, spermatocytes; RSs, round spermatids; ESs, elongating spermatids; SCs, Sertoli cells; LCs, Leydig cells; PTMs, peritubular myoid cells; Ms, macrophages; ECs, endothelial cells; SMCs, smooth muscle cells; UMAP, uniform manifold approximation and projection.