

## Supplementary Materials

**Figure S1.** Violin plots of the selected marker genes in the different clusters.

**Figure S2.** The expression of 32 cell-specific genes in porcine testicular cells.

**Figure S3.** A heatmap of 32 cell-specific genes in porcine testicular cells.

**Figure S4.** Feature plots (t-distributed stochastic neighbor embedding [t-SNE]) of 32 cell-specific marker genes in each cluster.

**Figure S5.** Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis for myoid cells (MCs), endothelial cells (ECs), and natural killer (NK) cells/macrophages.

**Figure S6.** Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis for spermatogonia (SPG), spermatocytes (SPCs), spermatids (SPTs), and sperm (SP) cells.

**Table S1.** Information for all the single cells.

**Table S2.** Metrics summary.

**Table S3.** Functional enrichment analysis of Sertoli cells (SCs).

**Table S4.** Functional enrichment analysis of Leydig cells (LCs).

**Table S5.** Functional enrichment analysis of myoid cells (MCs). **Table S6:** Functional enrichment analysis of endothelial cells (ECs).

**Table S7.** Functional enrichment analysis of natural killer (NK) cells/macrophages.

**Table S8.** Functional enrichment analysis of spermatogonia (SPG).

**Table S9.** Functional enrichment analysis of spermatocytes (SPCs). **Table S10:** Functional enrichment analysis of spermatids (SPTs). **Table S11:** Functional enrichment analysis of sperm (SP) cells.