

Description of Additional Supplementary files

File name: Supplementary Data 1

Description: Metadata of spatial transcriptomics datasets and the list of differentially expressed genes identified in this study.

File name: Supplementary Data 2

Description: Differentially expressed genes identified in germ cell lineage populations, together with Gene Ontology (GO) enrichment results for cluster-specific upregulated genes.

File name: Supplementary Data 3

Description: Differential expression analysis of epigenetic modification-related genes in germ cell populations.

File name: Supplementary Data 4

Description: Differentially expressed genes identified in supporting cell lineage populations, together with Gene Ontology (GO) enrichment results for cluster-specific upregulated genes.

File name: Supplementary Data 5

Description: Differentially expressed genes associated with interstitial and mesenchymal cell lineage populations and Gene Ontology (GO) enrichment analysis of upregulated genes in each cluster.

File name: Supplementary Data 6

Description: Comprehensive summary of cell–cell communication interactions between germ cells and surrounding neighboring cells (within one spatial grid) across different developmental stages.