

Description of Additional Supplementary Files

Supplementary Data 1 -(related to Figure 2): Quality metrics for all samples. First tab: Abbreviations. Second tab: Quality filters including cell numbers before and after filtering, and mitochondrial content for each sample analyzed. Third tab: Drop-seq quality metrics. Forth tab: 10x Genomics quality metrics.

Supplementary Data 2 -(related to Figure 2): Cellular composition of pre- (isthmus, ampulla, and fimbria) and pre-/post-menopausal (ampulla and fimbria) fallopian tubes (scRNA-seq). First tab: Abbreviations. Second tab: Cellular composition for each cell cluster for pre- and post-menopausal fallopian tubes (ampulla and fimbria combined). Third tab: Cellular composition for each cell cluster for pre- and post-menopausal fallopian tubes by patients and anatomical site. Cellular composition for each cell cluster for pre-menopausal fallopian tubes by anatomical site (ampulla, isthmus, and fimbria). Fourth tab: Cellular composition for each cell cluster for pre-menopausal fallopian tubes by anatomical site (ampulla, isthmus, and fimbria). Fifth tab: Cellular composition for each cell cluster for post-menopausal fallopian tubes by anatomical site (ampulla, isthmus, and fimbria).

Supplementary Data 3 -(related to Figure 2): Canonical marker genes used to annotate cell types in the fallopian tube (scRNA-seq). First tab: Abbreviations. Second tab: Canonical cell marker genes for the human fallopian tube. Third tab: Marker genes for fallopian tube epithelial and PEG cells.

Supplementary Data 4 -(related to Figure 2): Top 100 differentially expressed genes from each cell cluster identified in the pre-menopausal fallopian tube (scRNA-seq). First tab: Abbreviations. Second to fourteenth tab: Top 100 differentially expressed genes in pre-menopausal fallopian tubes by cell clusters in alphabetical order (B/P1, CE, LE, MA, MN, MP, NK, PV1-2, SE1-3, SM, ST1- 3, and T cell clusters).

Supplementary Data 5 -(related to Figure 2): Total cell numbers and relative percentages of individual cell clusters found in the pre-menopausal fallopian tube by patient (scRNAseq). First tab: Abbreviations. Second tab: Total cell numbers and relative percentages of pre-menopausal fallopian tube cell clusters by patient, with SE3 pre highlighted (ampulla and fimbria combined).

Supplementary Data 6 -(related to Figure 2): Label transfer statistics between scRNA-seq and scATAC-seq standalone clusters. First tab: Abbreviations. Second tab: Label transfer statistics summary for each sample. Third tab: Cell type composition by cell clusters for pre- and post-menopausal samples.

Supplementary Data 7 -(related to Figure 3): Transcription factor activities in premenopausal fallopian tubes by cell type. First tab: Abbreviations. Second tab: Pre-menopausal transcription factor activities by cell clusters.

Supplementary Data 8 -(related to Figure 3- 4): Differential gene expression in pre- and post-menopausal SE cells. First tab: Abbreviations. Second tab: Differentially expressed genes/ upregulated in pre-menopausal SE cells. Third tab: Differentially expressed genes/ upregulated in post-menopausal SE cells.

Supplementary Data 9 -(related to Figure 4):): Differential transcription factor activities in pre- and post-menopausal fallopian tubes by cell clusters. First tab: Abbreviations. Second to twelfths tab: Differential transcription factor activities in pre- and post-menopausal fallopian tubes by cell clusters in alphabetical order (B/P1, CE, LE, MA, MN, MP, PV1-2, SE1-2, SM, ST1- 3, and T/NK).

Supplementary Data 10 -(related to Figure 4): Top 100 overexpressed genes and selected, associated gene ontology for each SE cluster. First tab: Abbreviations. Second to sixth tab: Top 100 overexpressed genes for each secretory epithelial subtype (SE1- pre, SE2-pre, SE3-pre, SE-post and SE-post specific). Seventh tab: Selected gene ontology enrichment terms for each secretory epithelial subtype.

Supplementary Data 11 -(related to Figure 5 and Table S9): Genes up regulated in pre- and post-menopausal stromal clusters and gene ontology enrichment analysis. First tab: Abbreviations. Second to sixth tab: Genes upregulated in pre-and post-menopausal ST1-3. Seventh tab: Selected gene ontology terms for pre- and post-menopausal ST1, ST2 and ST3 cell clusters.

Supplementary Data 12 -(related to Figure 5): Differentially expressed genes in SE cells during the secretory and proliferative phase using pseudo-bulk analysis. First tab: Abbreviations. Second tab: Differentially expressed genes/ upregulated in pre-menopausal SE cells during the proliferative menstrual cycle phase. Third tab: Differentially expressed genes/ upregulated in pre-menopausal SE cells during the secretory menstrual cycle phase.

Supplementary Data 13 -(related to Figure 6): Gene markers upregulated in post- and premenopausal SE cells. First tab: Abbreviations.