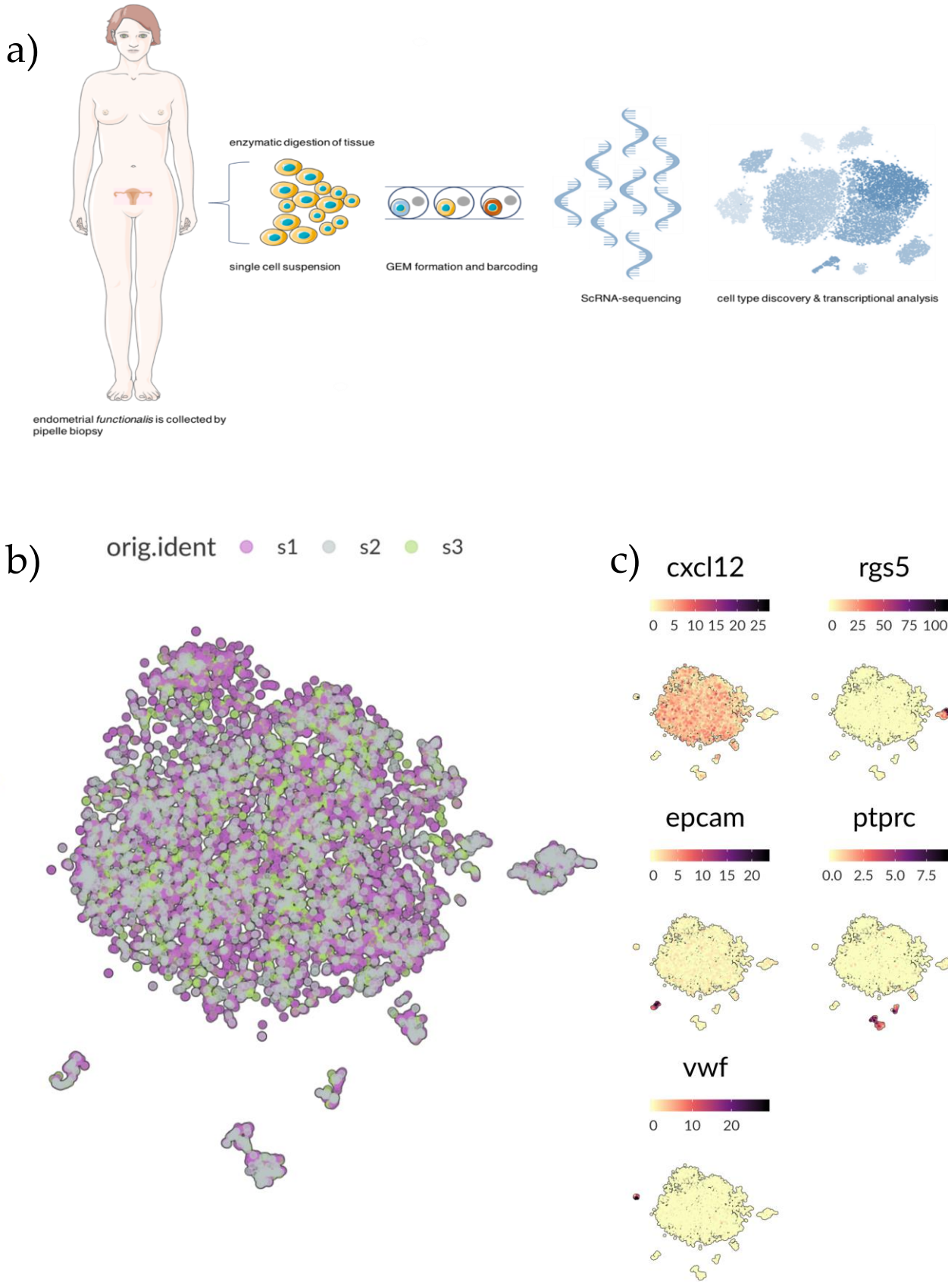
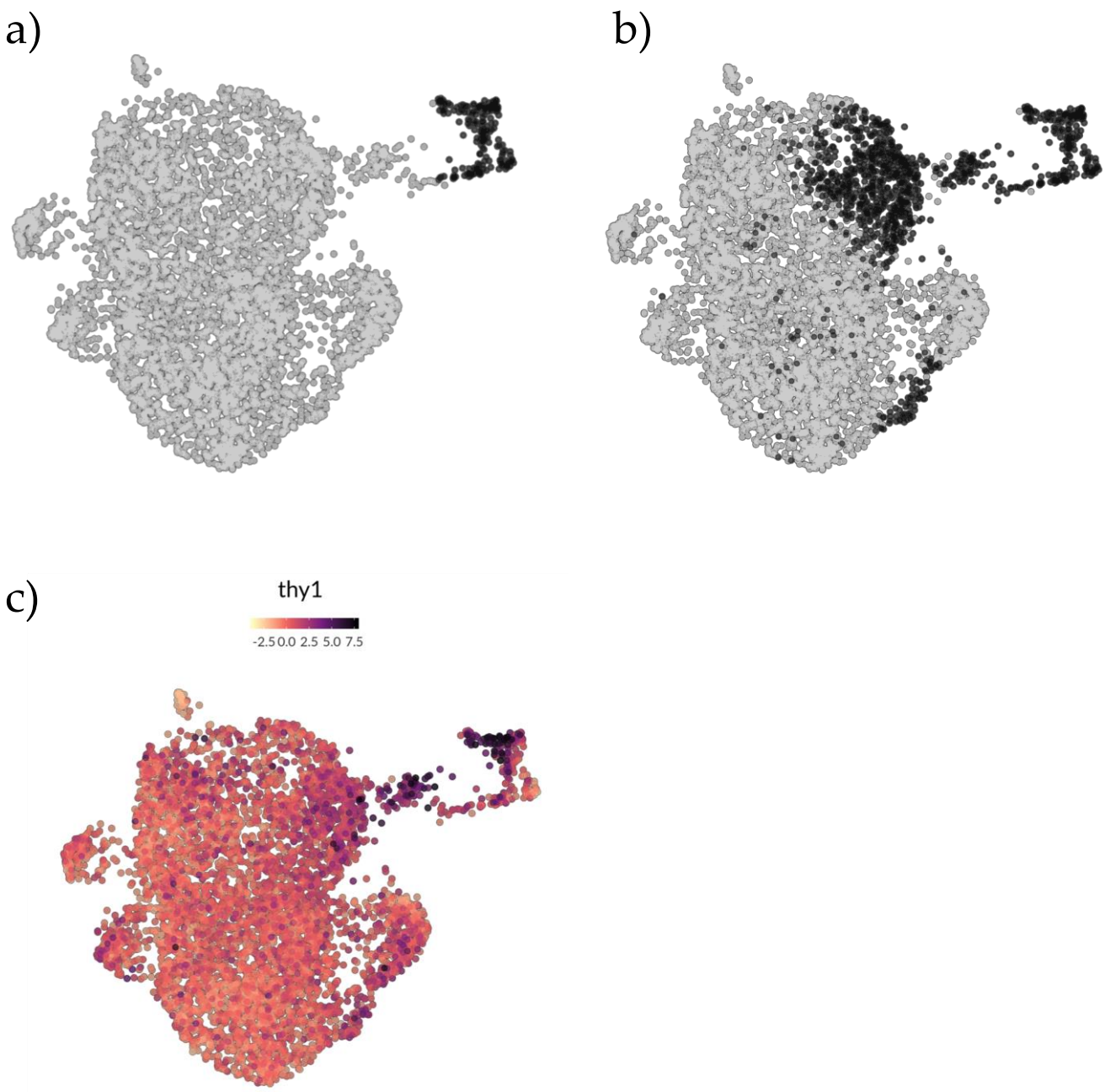
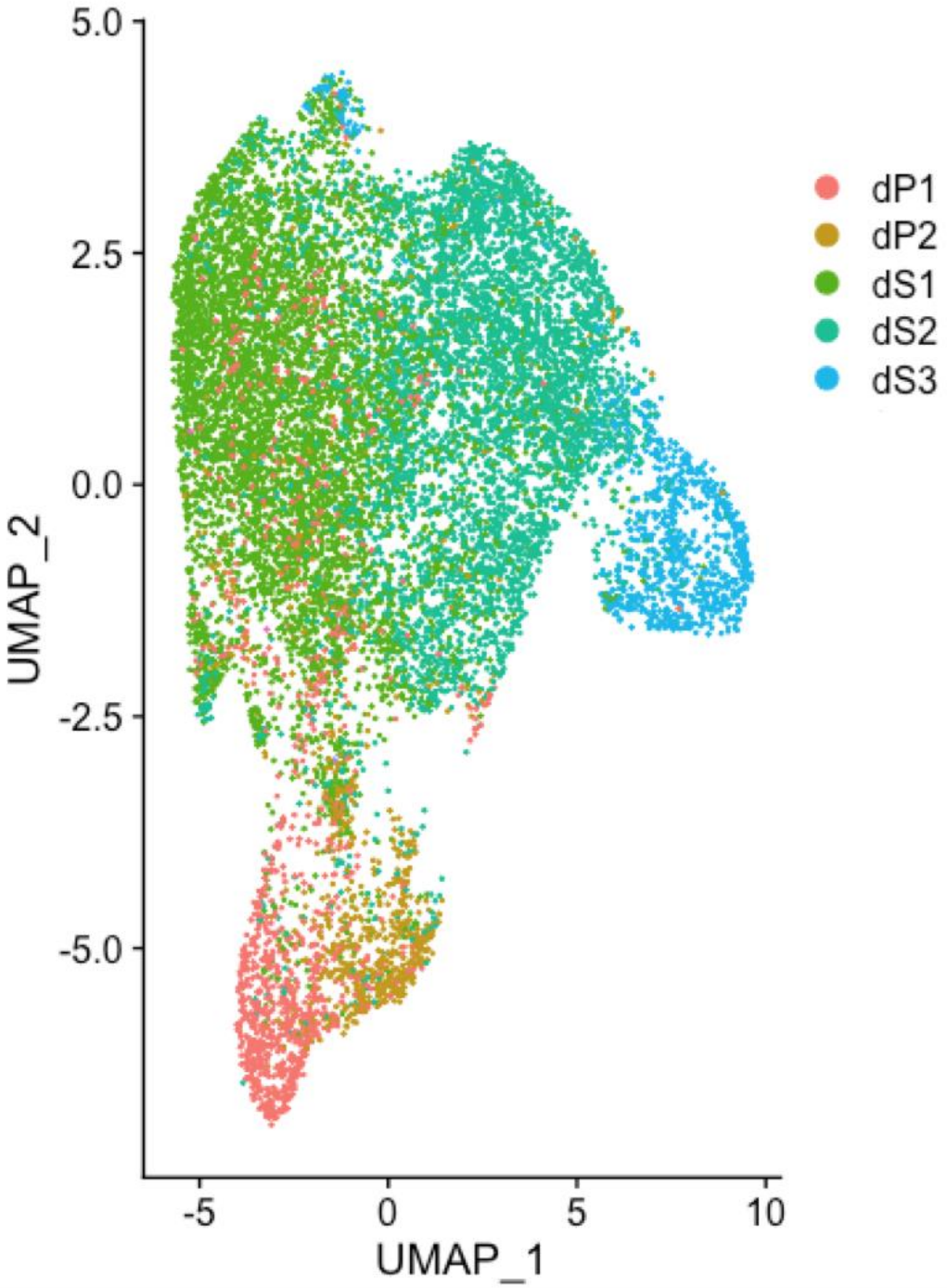


Supplementary Figure S1. Study design and identification of endometrial cell clusters. a) Work flow of scRNA-seq and analysis of endometrial tissue, image created with BioRender.com. Endometrial biopsies (n=3) were collected from three healthy fertile women and enzymatically digested to a single-cell suspension. mRNA from single cells were captured and processed using the 10x genomics chromium work-flow followed by Illumina sequencing. Raw reads were processed to gene counts using Cell rang-er. Gene counts were then used downstream for cell type discovery and analysis. b) tSNE plot visualizing contribution of the three samples (s1, s2 and s3) to the seven identified clusters in the scRNA-sequencing results in proliferative endometrium . c) Gene expression profiles of top marker genes identifying each cell cluster. *CXCL12* shows broad expression in stromal populations, *RGS5* expression identifies pericytes, *EPCAM* identifies epithelial cells, *PTPRC* identifies immune cells and *VWF* identifies endothelial cells.



Supplementary Figure S2. Selection of cells for subanalysis, expression distribution of THY1 and stromal and perivascular cells populations identified by Vento-Tormo et al. a) UMAP plot of scRNA-seq results of endometrial stromal cells and pericytes highlighting cells (in black) expressing pericyte marker *RGS5*. These cells were subset for further analysis. b) UMAP plot of endometrial stromal cells and pericytes highlighting cell types ACTA2+, THY1+ and pericyte 1 and 2 (in black). c) UMAP plot of endometrial stromal cells and pericytes showing increased expression of *THY1* with increasing proximity to the pericyte cluster at the top right.



Supplementary Figure S3. Stromal and perivascular cell populations identified by Vento-Tormo et al. UMAP plot of scRNA-seq data of the maternal *CD45*- decidual fraction from the maternal-fetal interface. Annotation of cell clusters according to original publication by Vento-Tormo et al. which identifies which identifies pericytes (dP1 and dP2) and stromal cells (dS1, dS2 and dS3).