Description of Additional Supplementary Files

Supplementary data 1. Clinical characteristics of POP patients and control samples profiled by sc-RNA seq and validated by staining in this study.

Supplementary data 2. Characterization of cell type in each sample.

Supplementary data 3. Cluster-specific marker genes via differential gene expression analysis.

Supplementary data 4. Differentially expressed genes (DEGs) in POP samples via bulk RNA-seq analysis.

Supplementary data 5. The gene ontology (GO) terms of upregulated and downregulated genes in bulk RNA-seq analysis.

Supplementary data 6. Differentially expressed genes (DEGs) of 11 clusters via scRNA-seq analysis.

Supplementary data 7. Subtype proportion in control and POP samples.

Supplementary data 8. Subtype proportion in each sample.