./endometrium\_drawing\_heatmap\_luminal\_str.R: scripts for analysis and plotting.

./resources: all data for plotting

human\_ligand\_receptor\_genelist.csv: ligand receptor gene set from database

tfs\_ABCDE220720.csv: transcription factor sets from database

major.harmony.all.rds: Seurat object

major\_pickgenes.txt: ligand-receptor genes overlapped with TAgenes (mi score >0.1) in each celltype

metadata/json\_\*\_hvg.csv: cell id, pseudotime, original group, collection LH time, cell-type and group based on pseudotime.

TAgenes\_subtype/\*\_mi.csv: MI scores for genes in each cell-type

./ heatmap: heatmap plots generated from R script.