



- bulk RNA-seq epithelial cells tumor
- bulk RNA-seq epithelial cells normal
- scRNA-seq Barrett's epithelial, Patient A
- scRNA-seq Barrett's epithelial, Patient D
- scRNA-seq normal epithelial, Patient E
- scRNA-seq normal epithelial, Patient F

Supplementary Figure 1. Comparison of scRNA-seq and cell type-specific RNA-seq of non-cancer epithelial esophagus cells.

Random samples of 100 single-cells each from four different patients with Barrett's esophagus (A and D) or without Barrett's esophagus (E and F) were selected from (Owen et al., 2018) and a matrix of counts was generated by adding the raw counts from the bulk RNA-seq of epithelial cells from flow-sorted samples. RCA clustering shows high projection scores onto epithelial tissues for both, single-cells as well for FACS-sorted samples.