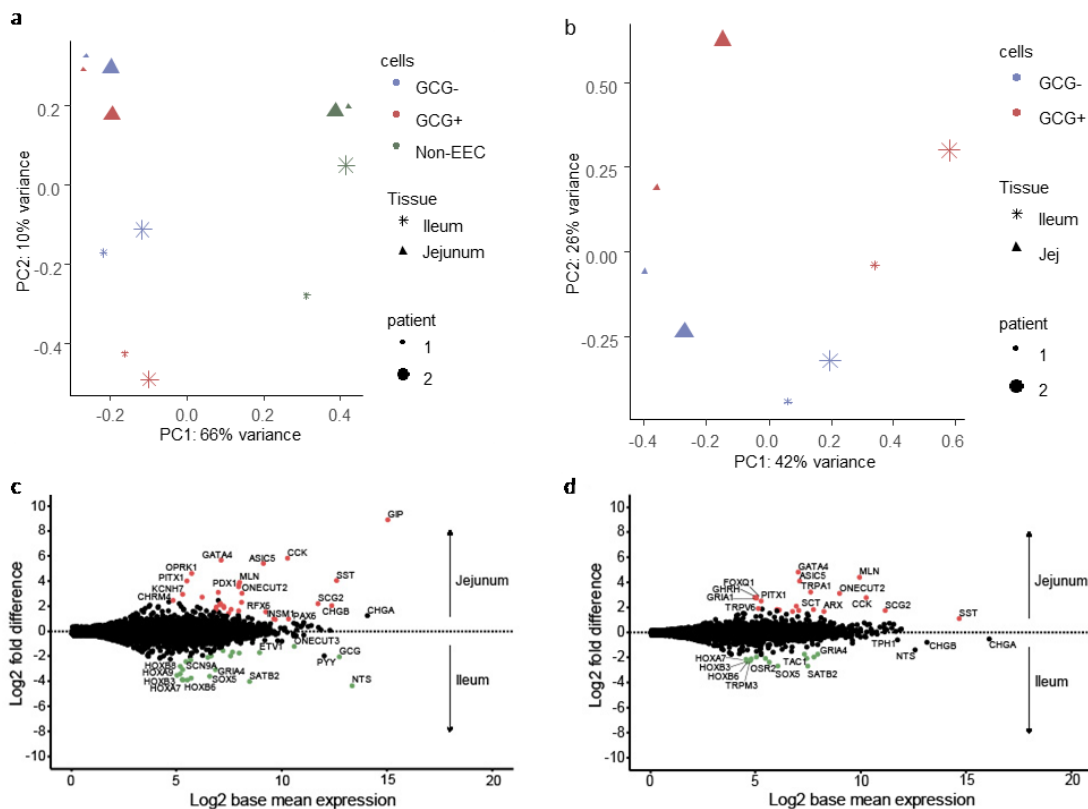


Supplementary Figure 2. Comparison between EECs from human jejunum and ileum



(a) Principal component analysis (PCA) plot of matched human jejunum vs ileum samples, labelled by cell population, anatomical location and patient (n=3 cell populations from both anatomical regions from each of 2 participants) of the 500 top variable genes when using a DESEQ2 model. PCA separated EECs from negative cells on the first component and the anatomical location of GCG+ and GCG- cells on the second component. (b) PCA plot for the same samples as in (a), but excluding the non-enteroendocrine (Neg) samples from the DESEQ2 model and the PCA analysis. PCA showed separation of ileal from jejunal samples on the first component and GCG+ from GCG- on the second component. Samples from the different participants are depicted by different sized symbols.

(c,d) Enrichment vs expression plots for GCG+ (c), and GCG- (d), cell populations. Enrichment is presented as the log<sub>2</sub> fold difference between the cell populations indicated, and expression is presented as the log<sub>2</sub> base mean normalised expression extracted from the DESEQ2 model. Red – enriched (adjusted  $P \leq .1$  in DESEQ2 model) in jejunum; Green – enriched in ileum.

*GIP*, *CCK*, *SST*, *MLN*, *SCT*, *GHRH*, *ASIC5*, and *TRPA1* were notably higher in jejunal than ileal EECs (GCG+ or GCG-), whereas *GCG*, *NTS* and *TAC1* were higher in ileum than jejunum.