Merged PDF contains:

Supplementary Tables

Supplementary Table 1: Overview of patient characteristics.

Supplementary Table 2: List of antibodies and *in-situ* hybridization probes.

Supplementary Table 3: Primers used in gene expression assays.

Supplementary Table 4: shRNA oligos.

Supplementary Notes

Further Acknowledgements

Supplementary Data Excel File contains:

Summary of Data Sheets

Data sheet: Major Cluster Markers

Data sheet: Goblet sub-cluster Markers

Data sheet: Branch-specific gene expression

Data sheet: DEGs inflamed vs healthy

Data sheet: DEGs uninflamed vs healthy

Data sheet: Undifferentiated cell cluster markers

Data sheet: Enteroendocrine sub-cluster markers

Data sheet: BEST4+/OTOP2+ cell quantitative proteomics

Data sheet: BEST4+/OTOP2+ cell quantitative proteomics, 2+ peptides only

Data sheet: BEST4+/OTOP2+ cell 10x data markers

Data sheet: BEST4+/OTOP2+ cell SmartSeq2 markers

Data sheet: BEST4+/OTOP2+ markers from Li dataset.

Data sheet: BEST4+/OTOP2+ markers from Gao dataset.

Extended Data. Gene cluster markers and differentially expressed genes and proteins. AUC classifier and/or negative binomial likelihood ratio test with Benjamini-Hochberg multiple testing correction (n=2 for *Gao et al*[15] dataset; n=10 for *Li et al*[21] dataset, n=3 per group otherwise) were used for cluster marker and differential gene expression detection. For quantitative proteomics, limma linear model empirical Bayes p-value and Benjamini-Hochberg multiple testing correction was used (BEST4- n=2, BEST4+n=3).