Supplemental material

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Gut

Supplementary Methods

Bioinformatic analysis of single-cell data

All commands for the reanalysis of the single cell sequencing dataset are available at https://gist.github.com/beardymcjohnface/27f3190fc48cf4a140994f83c3047494.

Briefly, single cell sequencing data, consisting of raw read counts of all genes and cells, were downloaded from the Gene Expression Omnibus for the accession GSE92332 [7]. Raw counts were converted to Counts Per Million (CPM). The log2 of the mean CPM and the fraction of cells expressing a gene were calculated for the genes of interest across the different cell types and visualised in R. Next, subsets were generated consisting of cells expressing each EEC marker gene (CPM > 100). The log2 of mean CPM and fraction of cells expressing the genes of interest were recalculated for each subset and was again visualised in R.