



Figure 3. Expression of *IFI16* is increased in multiple colonic epithelial and immune cell lineages in active UC. Analysis of open access UC single-cell RNA-Seq dataset from Smillie et al. (32), consisting of single-cell preparations from colonic mucosal biopsies, $n = 12$ healthy, $n = 18$ active UC, $n = 18$ inactive UC. A: t-SNE plot of epithelial cell populations from healthy, active UC, and inactive UC samples combined. Colored by cell subset assigned in cohort. B: t-SNE plot of immune cell populations from healthy, active UC, and inactive UC samples combined. Colored by cell subset assigned in cohort. C: t-SNE plots of epithelial cell populations from healthy, active UC, and inactive UC samples showing relative expression of *AIM2* (arrowhead, cycling B and T cells in active UC), *IFI16* (arrowhead, active UC *IFI16*⁺ enterocyte cluster), and *CASP1* (arrowhead, active UC *CASP1*⁺ enterocyte cluster). D: t-SNE plots of immune cell populations from healthy, active UC, and inactive UC samples showing relative expression of *AIM2* (arrowhead, cycling B and T cells in active UC), *IFI16* (arrowheads, inflammatory monocytes in active/inactive UC), and *CASP1* (arrowheads, inflammatory monocytes in active/inactive UC). t-SNE plots from A and B are adapted from https://singlecell.broadinstitute.org/single_cell/study/SCP259/intra-and-inter-cellular-rewiring-of-the-human-colon-during-ulcerative-colitis. AIM2, absent in melanoma 2; UC, ulcerative colitis.