



Fractions of “active” cells with high gene set enrichment scores for inflammation-related processes in immune cells from *Red2Onco* mice and *Confetti* control. Immune cells from *Red2-Kras^{G12D}* (R2KR) and *Red2-PIK3CA^{H1047R}* (R2P3) mice do not display high signatures of inflammation compared to those of *Confetti* (CONF). The gene sets for (A-D) were collected from the following references: up-regulated 340 genes among 712 ulcerative colitis (UC) severity genes in Haberman et al., 2019 for (A); up-regulated 84 genes that are shared between mouse and human UC in Czarnewski et al., 2019 for (B); 55 genes belonging to chemokine-mediated signaling pathway (GO: 0070098) for (C); 101 genes belonging to T cell receptor signaling pathway (KEGG: hsa04660) for (D). Data are presented as mean \pm SEM from biological replicates (n=2 for *Confetti* and *Red2-PIK3CA^{H1047R}*; n=3 for *Red2-Kras^{G12D}*). p-values from unpaired two-sided t-test. N.S., not statistically significant (p > 0.05).