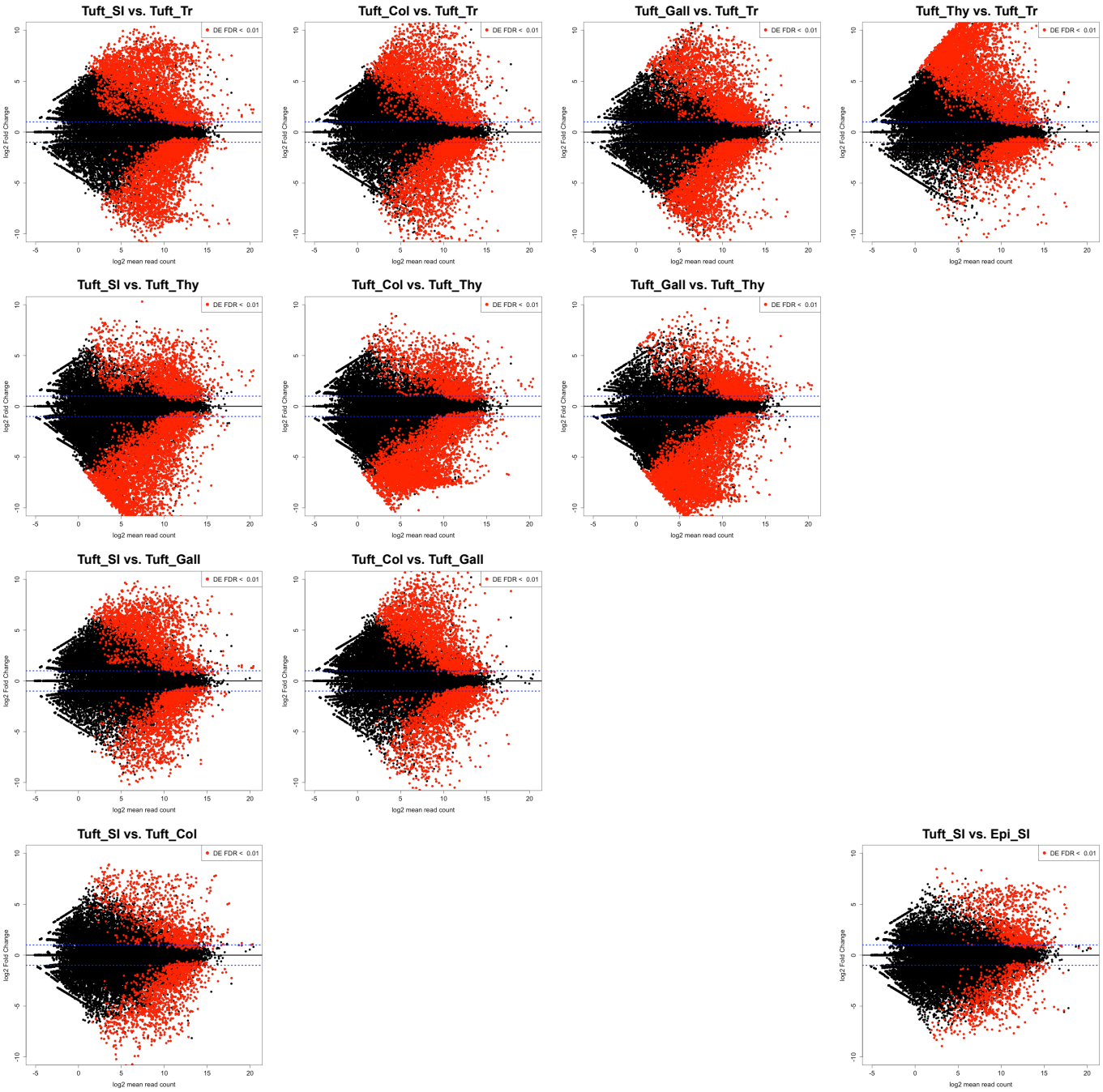

Figure S1 | Related to Figure 1
Volcano plots showing pairwise comparisons of differentially expressed genes in the cell subsets analyzed by mRNA sequencing. Y axis = log2 fold change; X axis = log2 mean read count. Red dots represent genes with FDR < 0.01. SI = small intestine; Col = colon; Gall = gall bladder; Thy = thymus; Tr = trachea

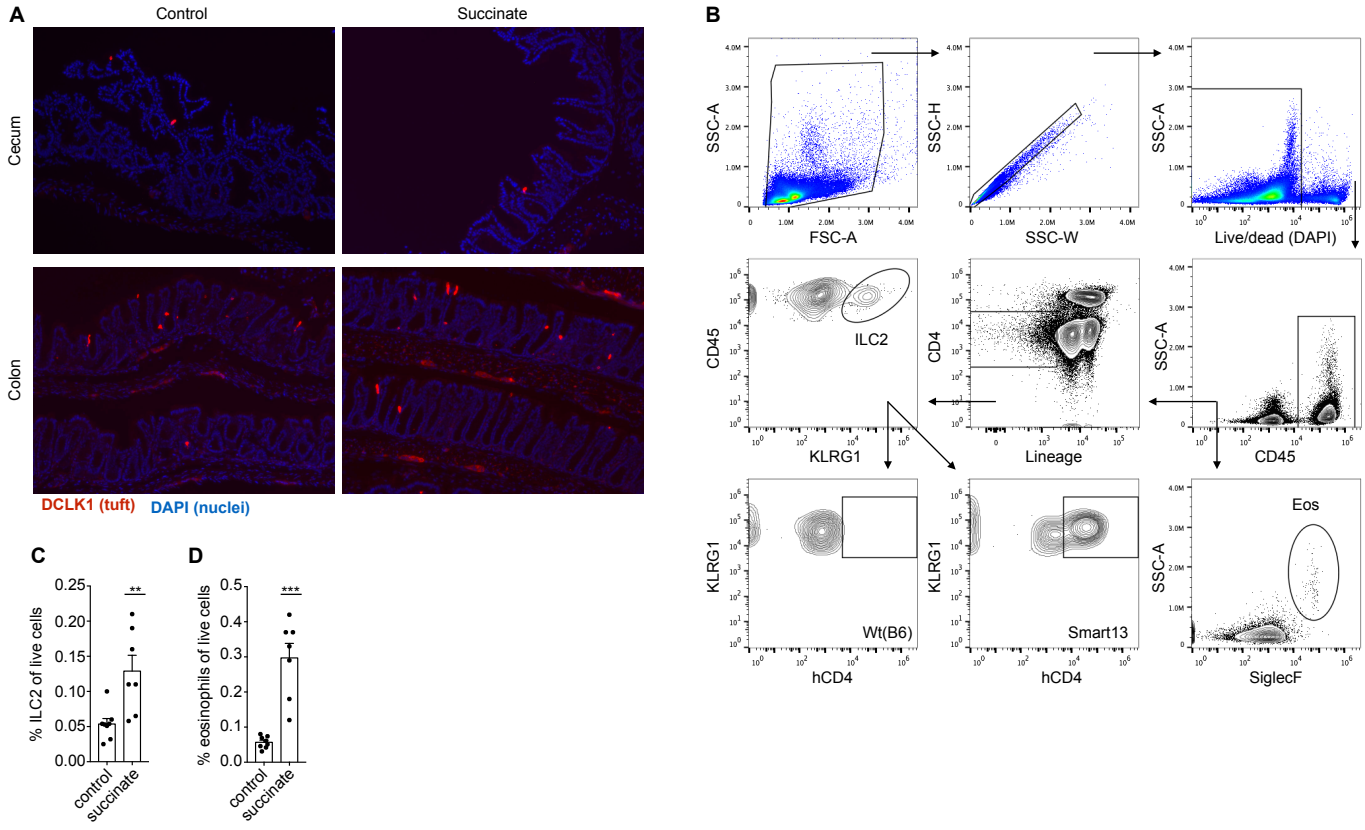

Figure S2 | Related to Figure 2
(A) Indicated tissues from control or succinate-treated (150 mM; 7 days) wild-type mice were stained for tuft cells (anti-DCLK1; red) and nuclei (DAPI; blue). **(B)** Gating strategy for identification of ILC2s and eosinophils in the mesenteric lymph nodes (MLN). IL-13 production was assessed by staining for human CD4 in Smart13 reporter mice. **(C-D)** MLN from control or succinate-treated (150 mM; 7 days) wild-type mice were analyzed by flow cytometry to assess the frequency of ILC2s **(C)** and eosinophils **(D)** among all live cells. Data in A-B are representative of at least three experiments. Data in C-D are pooled from two experiments and bar graphs depict mean + SEM. Each symbol represents an individual mouse.**, $p < 0.01$; ***, $p < 0.001$ by Mann-Whitney.

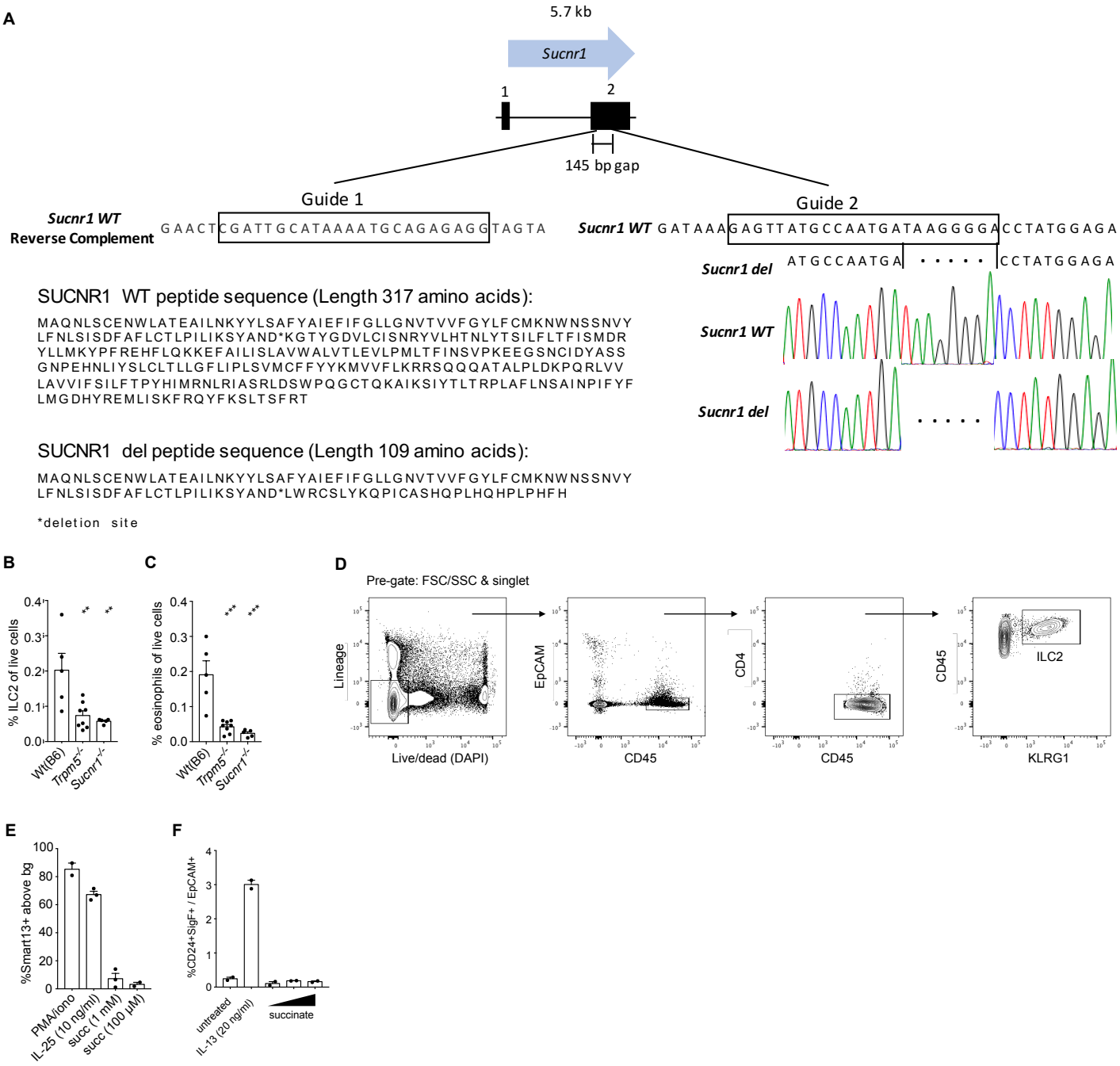

Figure S3 | Related to Figure 3

(A) Diagram depicting the location of guide RNAs used to target *Sucnr1* for disruption by CRISPR/Cas9. Guide 1 failed to induce any mutations. In the founder used to establish the *Sucnr1*$^{-/-}$ line reported in this study, an 8 base-pair deletion was detected at the binding site for guide 2. The resulting frame shift inserts a premature stop codon that truncates the C-terminal 208 amino acids of SUCNR1. **(B-C)** Mice of indicated genotypes were treated with 150 mM succinate for 7 days and mesenteric lymph nodes were harvested to quantify the frequency of ILC2s **(B)** and eosinophils **(C)** among all live cells by flow cytometry. **(D)** Gating strategy to identify ILC2s in the lamina propria of the small intestine. **(E)** ILC2s were stimulated in vitro as indicated for 6 hours and IL-13 production was quantified by flow cytometry using Smart13 reporter expression. **(F)** Epithelial organoids from murine small intestine were cultured for 7 days under indicated conditions. Succinate concentrations = 100 µM, 1mM, and 10 mM. Tuft cell frequency (CD24+SigF+EpCAM+ cells) was quantified by flow cytometry. Data are representative of one (E) or two (D, F) experiments or are are pooled from three experiments (B-C). Bar graphs depict mean + SEM. Each symbol represents an individual mouse (B-C) or technical replicate (E-F). *, $p < 0.05$ **, $p < 0.01$; ***, $p < 0.001$ by one-way ANOVA with comparison to Wt(B6).

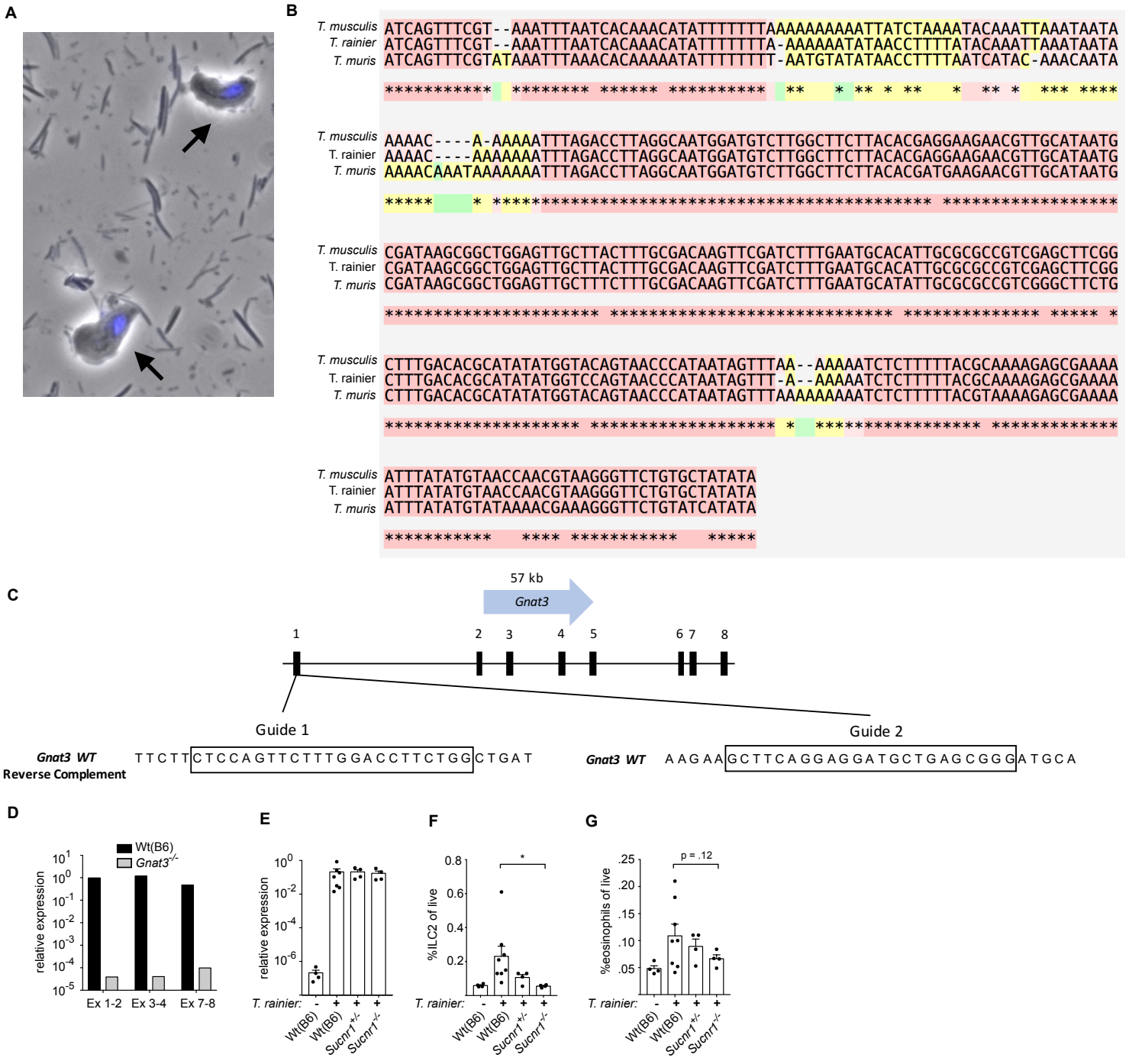

Figure S4 | Related to Figure 4

(A) Representative images of *T. rainier* (arrows) with DAPI (blue) staining of nuclei. **(B)** Alignment of internal transcribed spacer sequence of *T. rainier* with published sequences for *T. muris* and *T. musculis*. **(C)** Diagram depicting the location of guide RNAs used to target *Gnat3* for disruption by CRISPR/Cas9. In the founder used to establish the *Gnat3*$^{-/-}$ line reported in this study, the region between guide 1 and guide 2 was deleted. **(D)** Functional deletion of *Gnat3* was confirmed by qPCR using primer pairs spaced across the entire mRNA. **(E)** *Tritrichomonas* colonization of indicated mice was quantified by qPCR using DNA generated from cecal contents. **(F-G)** Mice of indicated genotypes were colonized with *T. rainier* for 7 days and mesenteric lymph nodes were harvested and the frequency of ILC2s **(F)** and eosinophils **(G)** among all live cells was assessed by flow cytometry. Data are representative of three (B) two (A) or one (D) experiment or pooled (E-G) from two experiments. Bar graphs depict mean + SEM. Each symbol represents an individual mouse. *, $p < 0.05$ by one-way ANOVA with comparison to colonized Wt(B6).