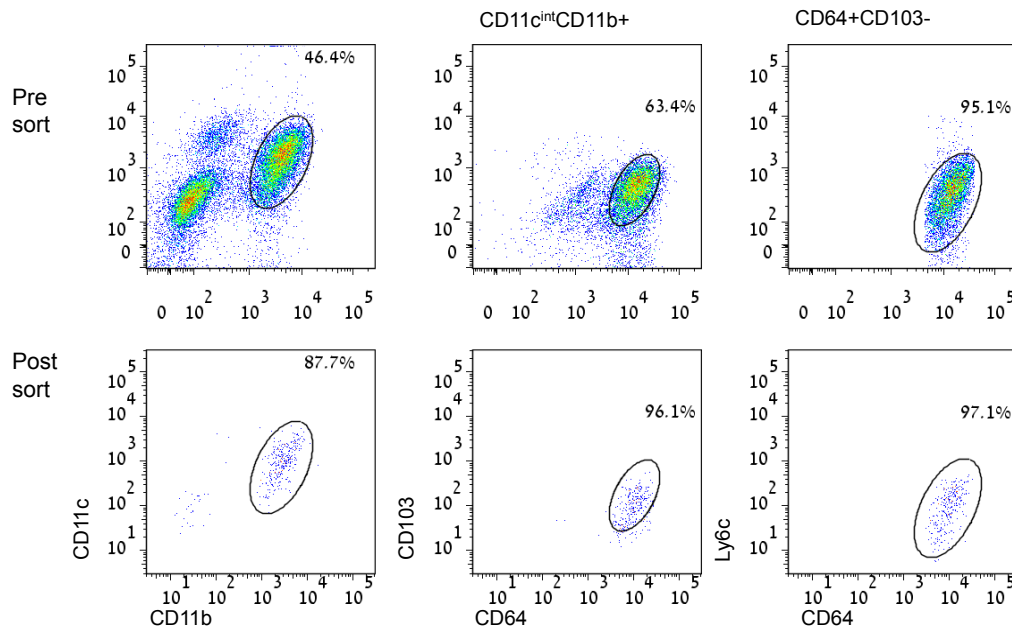
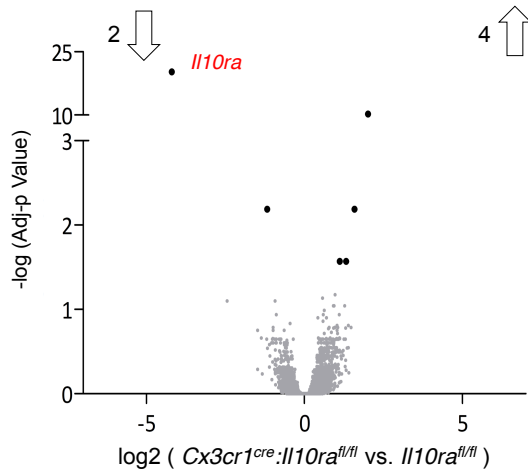


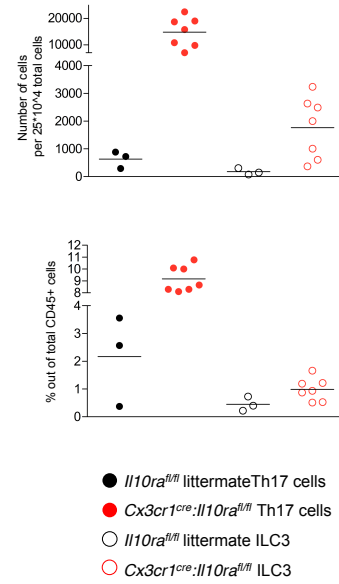
A



B



C



Supp Figure 1

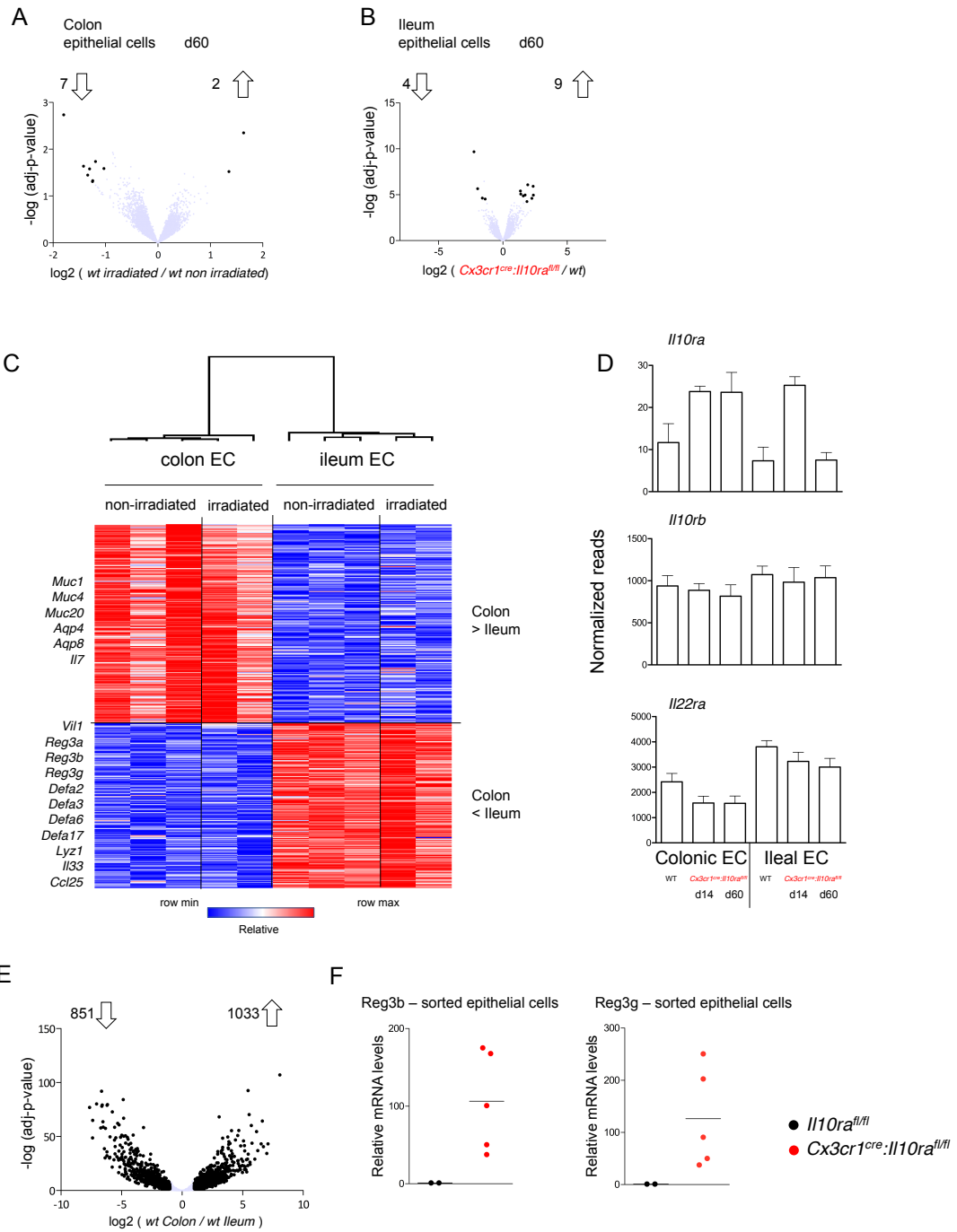
Supplementary Figure 1. Gating strategies and transcriptome analysis of animals exposed to antibiotics

This figure includes data related to main text Figures 1 and 3

(A) Gating strategy for sorting colonic lamina propria macrophages

(B) Volcano plot of statistical significance ($-\log_{10}$ p-value) against \log_2 ratio of macrophages sorted from the colonic lamina propria of *Cx3cr1^{cre}:Il10ra^{fl/fl}* and *Il10ra^{fl/fl}* co-housed littermates continuously treated with broad spectrum antibiotics given upon weaning, based on RNA-seq data. Significantly up or down regulated genes (fold change > 2, adj-p value < 0.05) are in black. Cre transgene positive mice were collected from 2 independent experiments (n=2 in each), littermates are from one experiment (n=3).

(C) Quantification of flow cytometry analysis presented in Fig1F.



Supp Figure 2

Supplementary Figure 2. Transcriptome analysis of epithelial cells of *Villin^{cre}:R26-tdTomato* mice.

This figure includes data related to main text Figure 2

(A-B) Volcano plot of statistical significance ($-\log_{10}$ p-value) against log 2 ratio based on RNA-seq data between A - colonic epithelial cells sorted from [*Cx3cr1^{gfp/+}* > *Villin^{cre}:r26-tdTomato*] BM chimeras and *Villin^{cre}:r26-tdTomato* mice or B – ileal epithelial cells sorted from [*Cx3cr1^{cre}Il10ra^{fl/fl}* > *Villin^{cre}:r26-tdTomato*] BM chimeras and *Villin^{cre}:r26-tdTomato* mice.

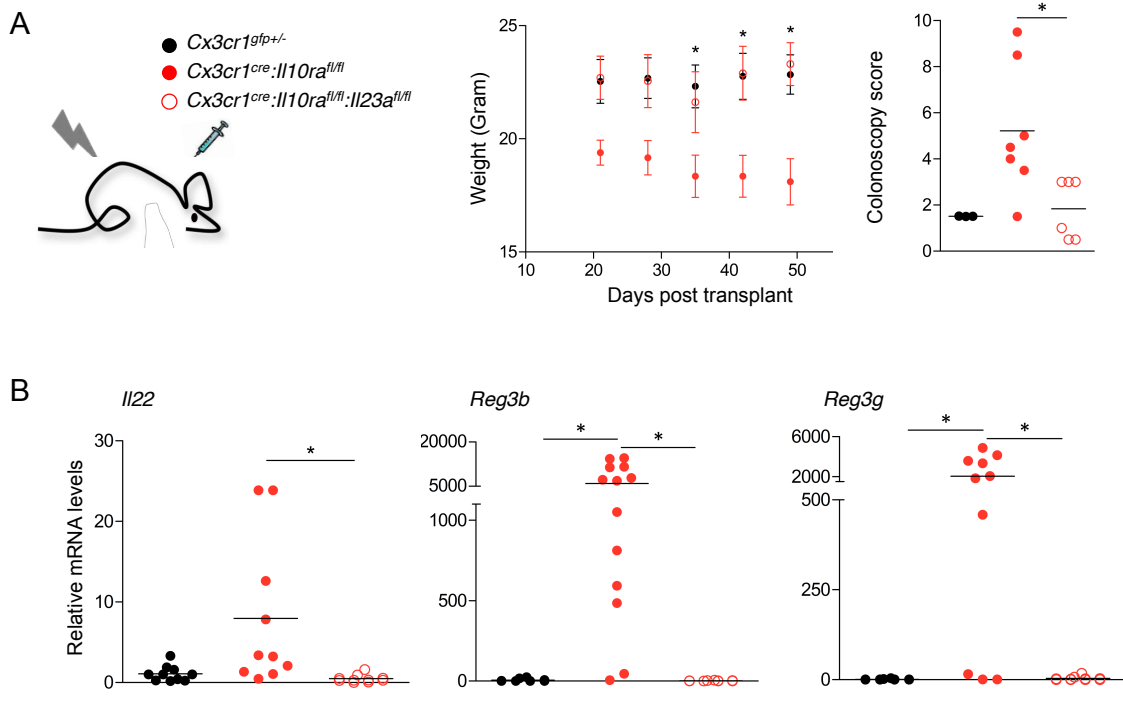
Significantly up or down regulated genes (fold change > 2, adj-p value < 0.05) are in black.

(C) Heat map displaying RNA-seq data of sorted colonic and ileal epithelial cells from [*Cx3cr1^{gfp/+}* > *Villin^{cre}:r26-tdTomato*] BM chimeras and *Villin^{cre}:r26-tdTomato* mice. Presented are 1884 genes significantly differentially expressed (fold change > 2, adj-p value < 0.05) between colon and ileum. Normalized read number were log transformed and clustered by a Pearson correlation test and number of partition clusters was set to two. Samples were hierarchically clustered by a Pearson correlation test.

(D) RNA-seq normalized read numbers of indicated genes expressed by colonic and ileal epithelial cells extracted from *Villin^{cre}:r26-tdTomato* mice and [*Cx3cr1^{cre}Il10ra^{fl/fl}* > *Villin^{cre}:r26-tdTomato*] BM chimeras at indicated time points.

(E) Volcano plot of statistical significance ($-\log_{10}$ p-value) against log 2 ratio between colonic and ileal epithelial cells sorted from *Villin^{cre}:r26-tdTomato* mice based on RNA-seq data. Significantly up or down regulated genes (fold change > 2, adj-p value < 0.05) are in black.

(F) qRT-PCR analysis of *reg3b* and *reg3g* expression in sorted colonic epithelial cells (CD45-fraction) of *Cx3cr1^{cre}:Il10ra^{fl/fl}* mice and littermate controls



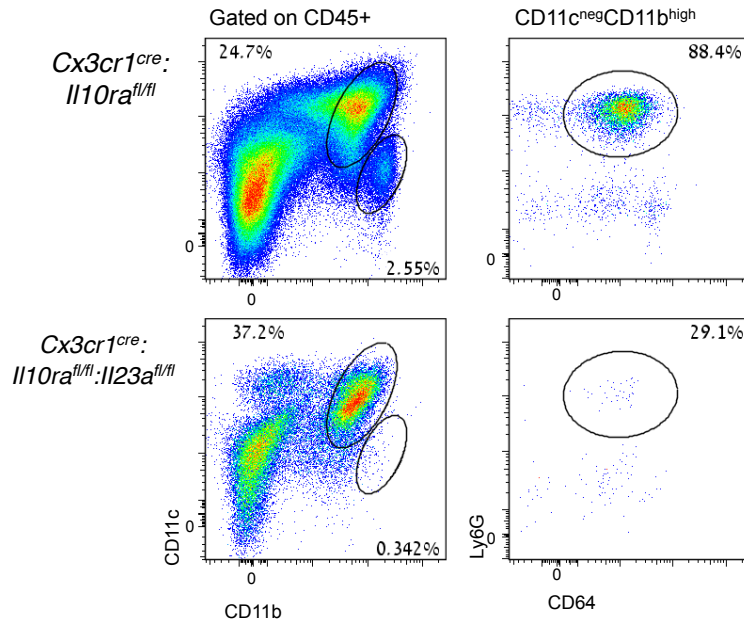
Supplementary Figure 3. Lack of neutrophil infiltrates in the *lamina propria* of *Cx3cr1^{cre}:Il10ra^{fl/fl}:Il23a^{fl/fl}* mice.

This figure includes data related to main text Figure 6

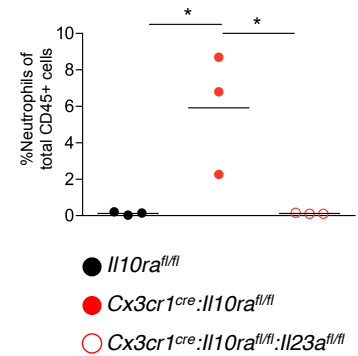
(A) Representative plots of flow cytometry analysis of the colonic *lamina propria* of indicated mouse strains.

(B) Quantification of flow cytometry analysis according to gating strategy indicated in A. data are from one experiment.

A



B



Supplementary Figure 4. Macrophage-derived Il23a is critical for colitis induction in BM chimeras model.

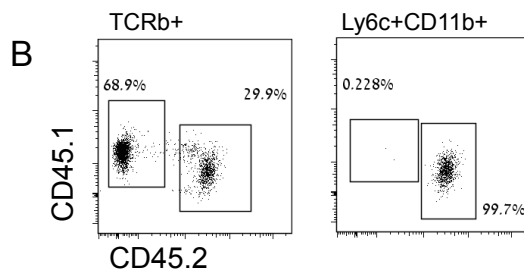
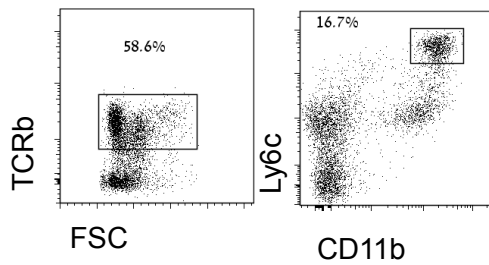
This figure includes data related to main text Figure 3

(A) Weight and colonoscopic analysis of [*Cx3cr1*^{cre}:*Il10ra*^{fl/fl} > WT], [*Cx3cr1*^{gfp/+} > WT] or [*Cx3cr1*^{cre}:*Il10ra*^{fl/fl}:*Il23a*^{fl/fl} > WT] BM chimeras. Colonoscopy was performed 6 weeks post-transplant.

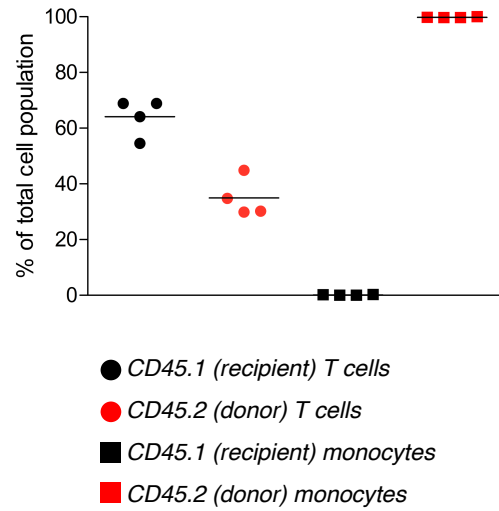
(B) qRT-PCR analysis of *il22*, *reg3b* and *reg3g* expression in colonic whole tissue RNA extracts of indicated BM chimeric mice.

Data are collected from 2 independent experiments, n>=3 in each.

A [CD45.2->CD45.1] BM chimeras
– blood analysis



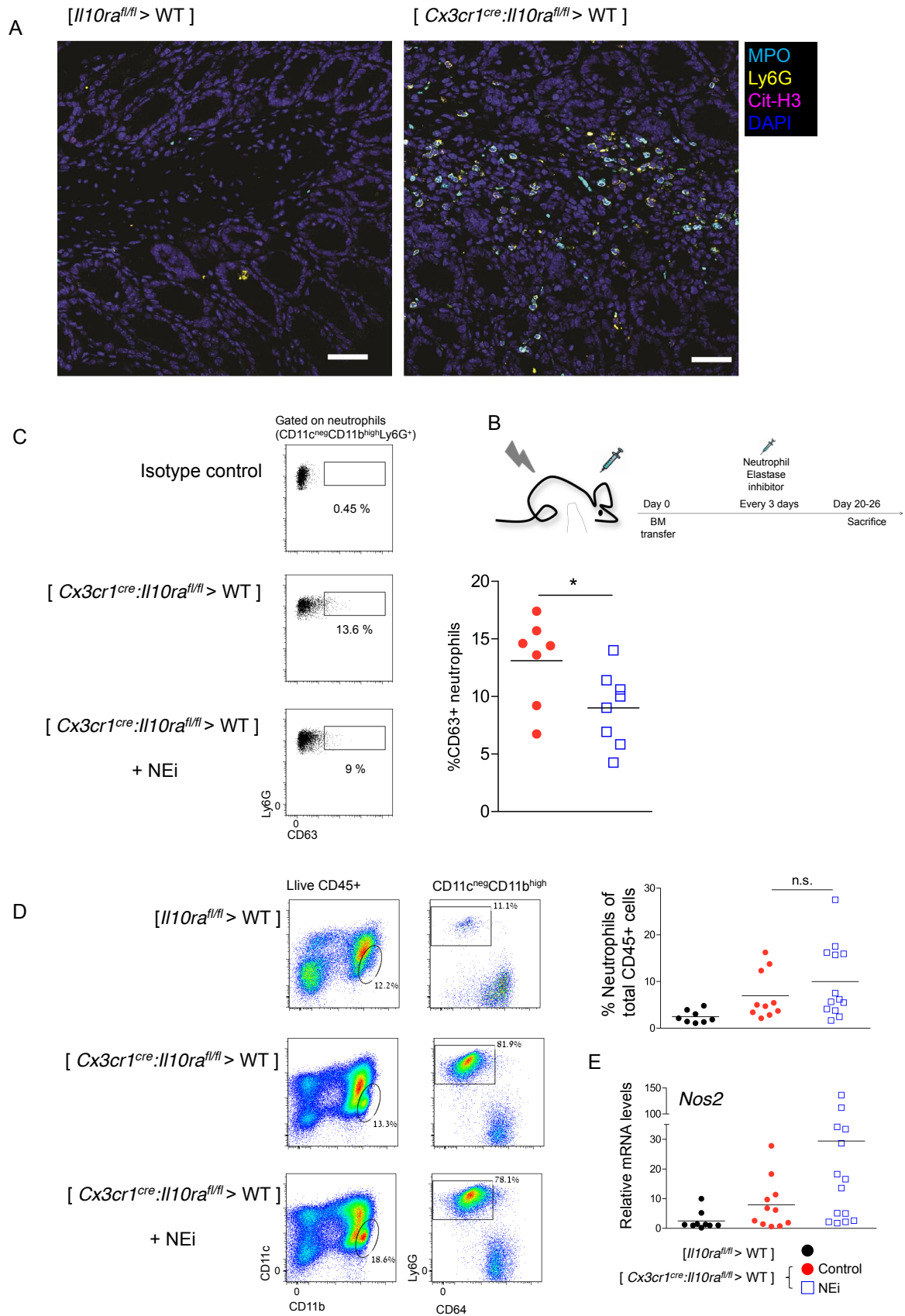
C



Supplementary Figure 5. Chimerism of blood monocytes and T cells.

(A-B) Representative flow cytometry analysis of blood withdrawn from [CD45.2>CD45.1] BM chimeras one month post transfer.

(C) Quantification of flow cytometry analysis presented in A-B.



Supp Figure 6

Supplementary Figure 6. Analysis of neutrophil elastase inhibitor (NEi) treated BM chimeras

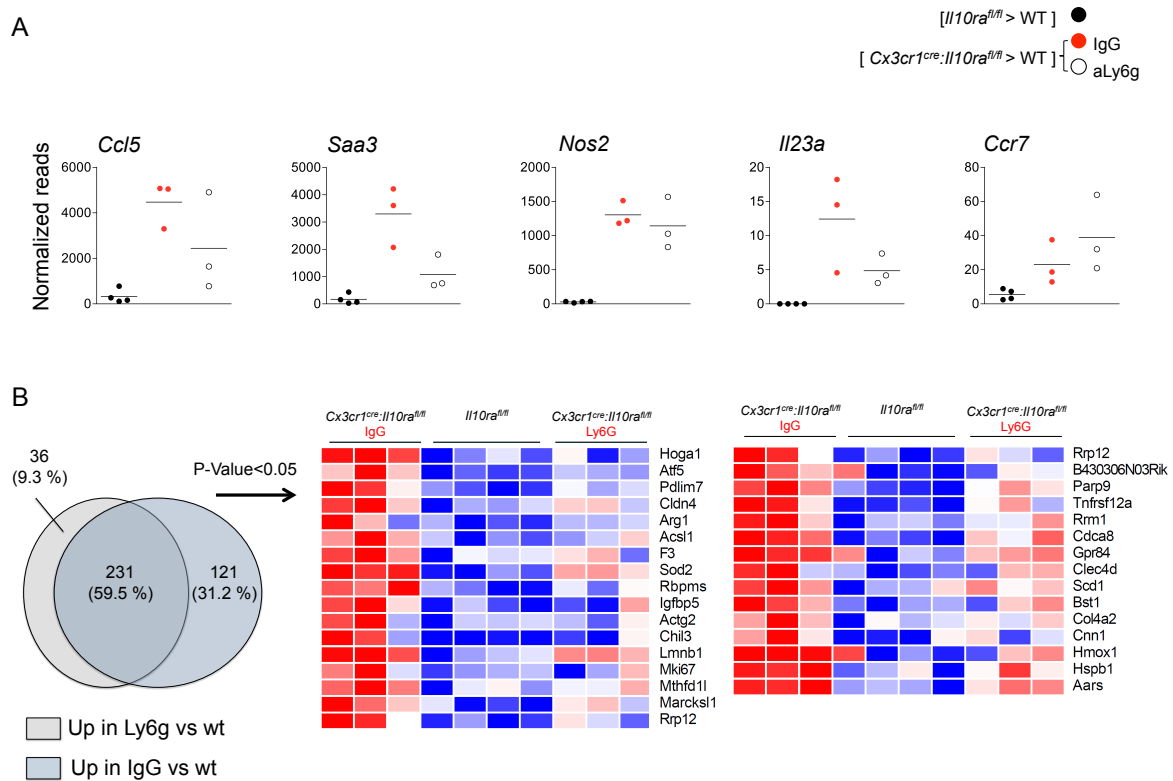
(A) Representative immunofluorescence images of the colonic tissue of [*Il10ra^{fl/fl}* > WT] or [*Cx3cr1^{cre}:Il10ra^{fl/fl}* > WT] BM chimeras.

(B) Schematic of NEi treatment

(C) Representative plots of flow cytometry analysis of the colonic *lamina propria* of [*Il10ra^{fl/fl}* > WT] or [*Cx3cr1^{cre}:Il10ra^{fl/fl}* > WT] BM chimeras left untreated or treated with NEi (left).

Quantification of flow cytometry analysis (right). qRT-PCR analysis of *Nos2* expression in whole tissue extracts of colons of indicated BM chimeric mice (right).

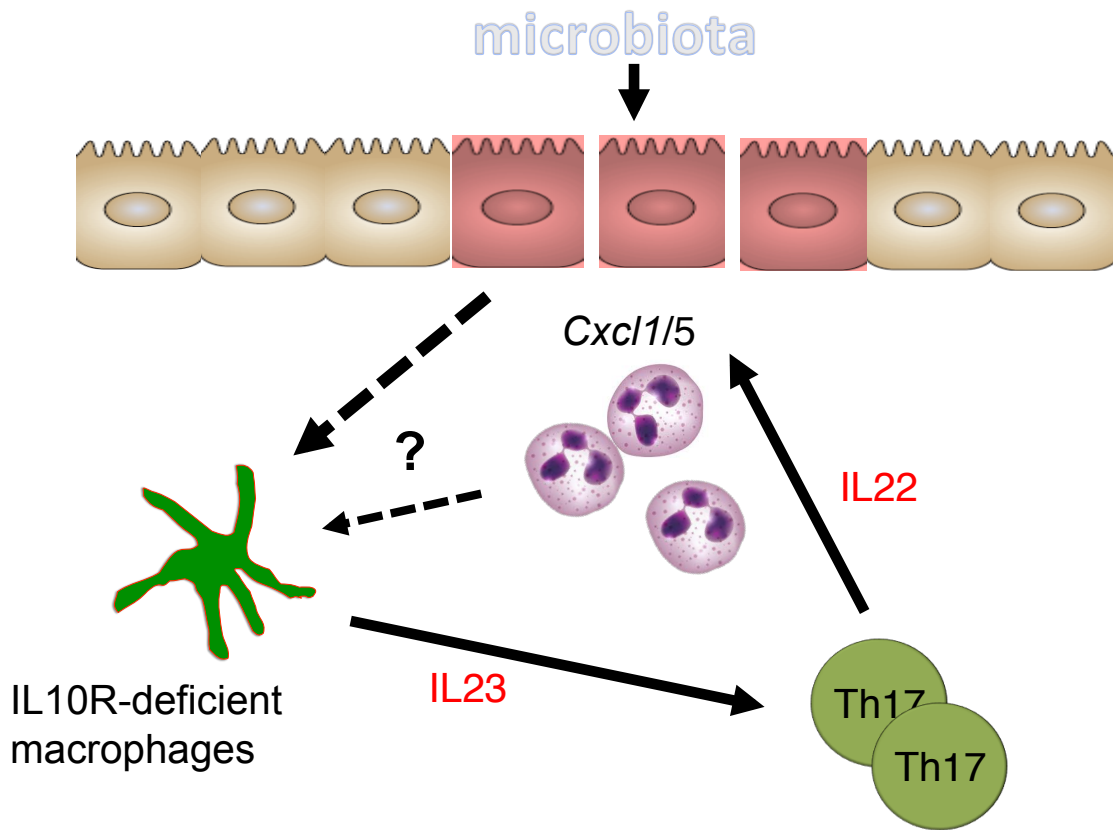
(D) Representative plots of flow cytometry analysis of CD63 staining of neutrophils extracted from the colonic *lamina propria* of [*Cx3cr1^{cre}:Il10ra^{fl/fl}* > WT] BM chimeras left untreated or treated with NEi (left). Quantification of flow cytometry analysis (right).



Supplementary Figure 7. Analysis of transcriptomes of macrophages retrieved from BM chimeras treated with control IgG or neutrophil-depleting anti-Ly6G antibody.

(A) RNA-seq normalized read numbers for single genes of interest are plotted separately, each dot represents one mouse.

(B) Venn diagram and heatmap of RNAseq data of colonic macrophages extracted from [*Cx3cr1^{cre}:Il10ra^{fl/fl}* > WT] BM chimeras treated with IgG control or anti Ly6G antibody. Normalized reads number were log transformed. Presented are genes of interest, significantly up-regulated in anti Ly6g treated vs WT control and unaltered in IgG treated vs WT.



Supplementary Figure 8. Summary schematic illustrating the finding of this study.

In response to a microbial stimulus IL10R-deficient macrophage secrete IL-23 that induces Th17 cells to produce IL-22. IL-22 in turn activates epithelial cells to produce chemokines that recruit neutrophils that cause tissue damage. Our results suggest that the full pro-inflammatory signature of macrophages is a secondary effect induced by epithelial response or the tissue damage.