a Fecal 16s sequencing-PCoA plot

b Taxa summary bar plots

c Linear discriminant analysis using LEfSe

d Body weight

e Colon length

f Colon histology

Supplementary information, Fig. S14 Depletion of altered microbiota alleviates the severer colitis in $Irf1^{KO}$ mice.

a-c. Fecal 16s rDNA sequencing analysis of $Irf1^{KO}$ mice and their littermates.
a. PCoA plot generated from unweighted UniFrac distance matrix displaying the distinct clustering pattern for the intestinal bacteria communities of $Irf1^{KO}$ mice ($n = 9$) and of their littermates ($n = 7$).
b. Relative abundance of taxonomic groups averaged across $Irf1^{KO}$ mice ($n = 9$) and their littermates ($n = 7$) at the family level.
c. Composition differences of the intestinal microbiota in $Irf1^{KO}$ mice and their littermates, determined by linear discriminant analysis using LEfSe.
$Irf1^{KO}$ ($n = 9$) and their littermates $Irf1^{WT}$ ($n = 7$) mice were used in 16s rDNA sequencing experiments and were representative of 2 independent 16s rDNA sequencing experiments.

d-f. ABx-treated and untreated $Irf1^{KO}$ mice and their littermates were induced with 2.5% DSS. Colitis was monitored by body weight loss (**d**), colon shortening (**e**), and H&E staining of colon tissues (**f**). For H&E staining (f): Left, representative pictures. Scale bars, 50µm. Right, quantification of corresponding histology scores. 5 views per mice.
Data (**d-f**) are representative of 3 independent experiments. Data are shown as means ± SEM. Body weight changes (**d**) was analyzed by two-way ANOVA. Colon length (**e**) and histology scores (**f**) were analyzed by one-way ANOVA. **$P < 0.01$, ****$P < 0.0001$, ns, not significant.