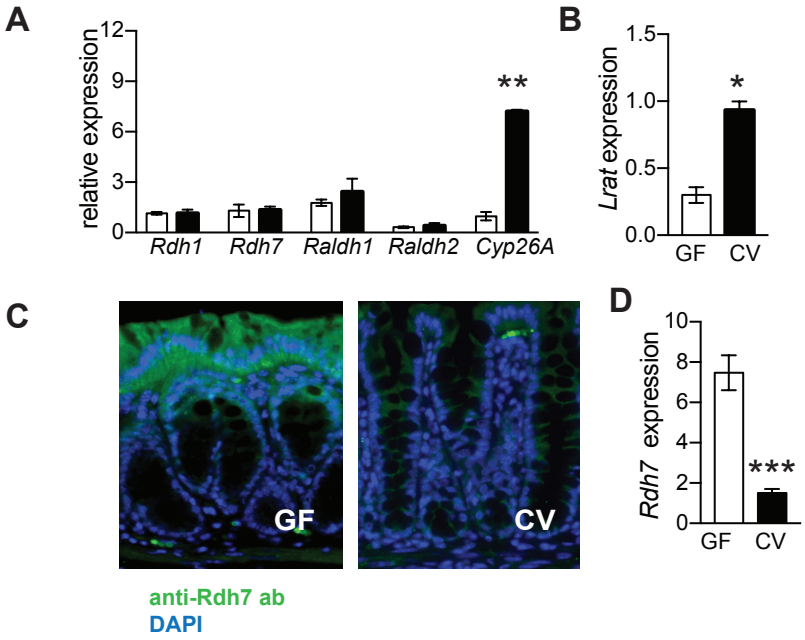

Figure S1. Bacterial regulation of *Rdh7* expression in liver and colon. Related to Figure 2

(A)mRNA quantification of genes involved in Vitamin A metabolism in liver of conventional (CV) and germ-free (GF). (B) mRNA quantification of *Irat* in liver tissue of conventional (CV) and germ-free (GF).
Anti-Rdh7 staining of colon tissues of conventional (CV) and germ-free (GF) mice.
qPCR analysis of *Rdh7* mRNA in colon tissues of conventional (CV) and germ-free (GF) mice.

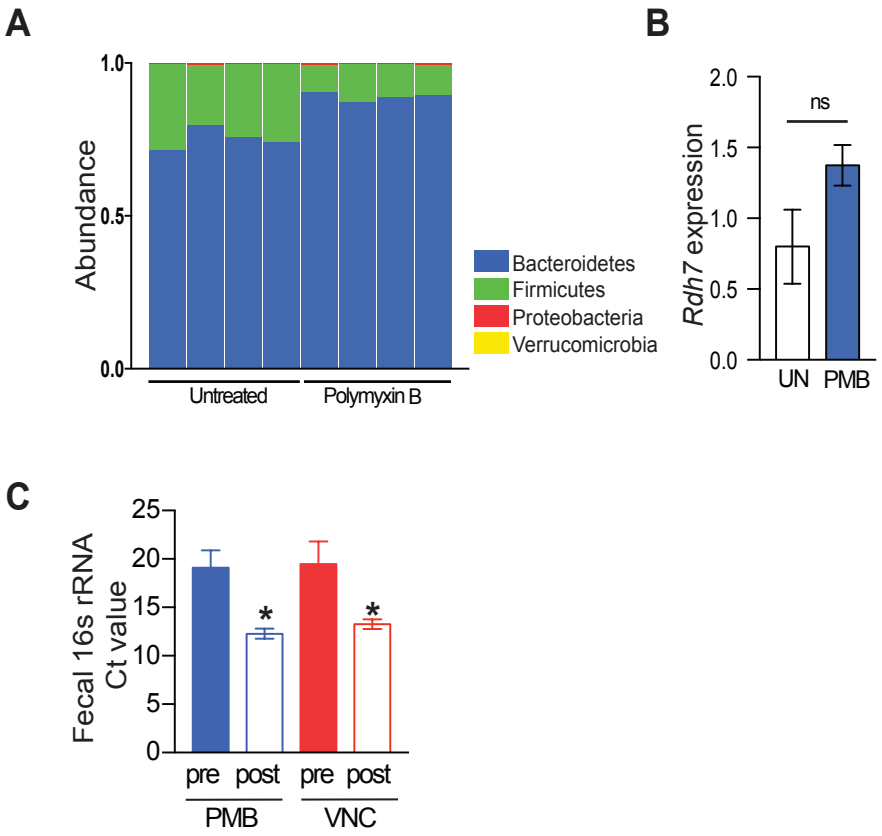

Figure S2. Effect of antibiotics on gut microbiota and *Rdh7* expression. Related to Figure 3

(A) Relative abundance of bacteria at phylum level determined by 16s rRNA analysis of fecal microbiome from untreated and polymyxin B treated mice. Mice were treated with polymyxin B (1000mg/L) in drinking water for four weeks. (B) *Rdh7* mRNA quantification by qPCR in colon tissue mice treated with untreated versus polymyxin B treated mice. (C)16s qPCR to look at bacteria numbers in mice treated with vancomycin and polymyxin B. Figures A-C are representative figures of a single experiment that was done 3 individual times. Student's t-test. Error bars represent SEM. *$P < 0.05$.

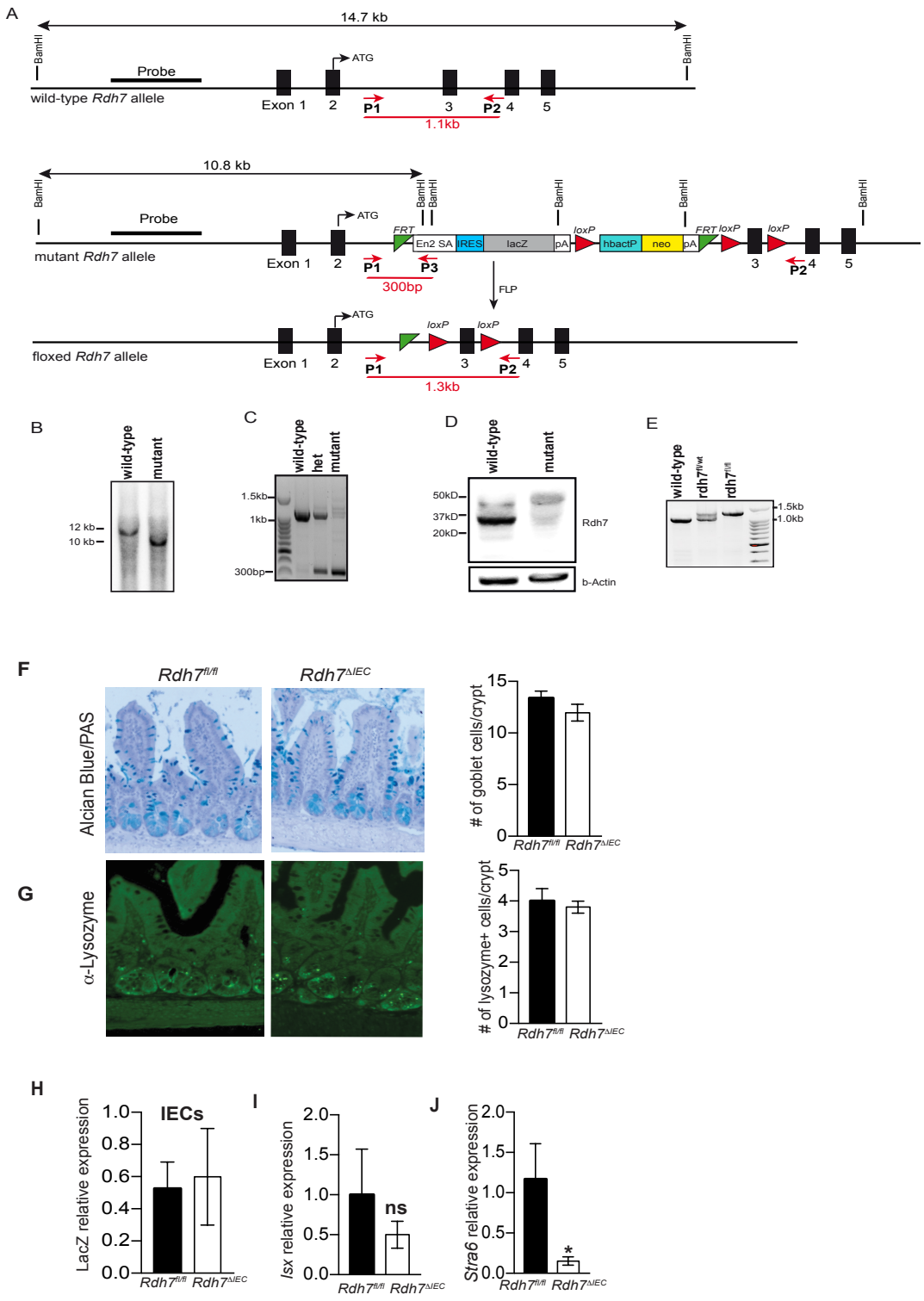

Figure S3. Generation and validation of *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ mouse models. Related to Figure 4

(A) Scheme for generation of Rdh7$^{fl/fl}$ and Rdh7$^{\Delta IEC}$ mouse models (B) Southern Blot confirming correct insertion of trapping vector. (C) PCR results confirming correct insertion. (D) Western Blot results testing for Rdh7 in *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$. (E) Genotyping results for *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$. (F) Alcian Blue staining in paraffin embedded colon tissue to look at goblet cell numbers in *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ mice. Graph on the side shows quantification of goblet cells from Alcian Blue staining. (G) Lysozyme staining in paraffin embedded colon tissue to look at Paneth cell numbers in *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ mice. Graph on the side shows quantification of Paneth cells from Lysozyme staining. (H) *LacZ* mRNA quantification in intestinal epithelial cells (IECs) from *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ (I) *Isx* mRNA quantification in intestinal tissue from Rdh7$^{fl/fl}$ and Rdh7$^{\Delta IEC}$ (J) *Stra6* mRNA quantification in intestinal tissue from *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$. For figures F, G, H-J Student's t-test was performed, Error bars represent SEM. *P <.05.

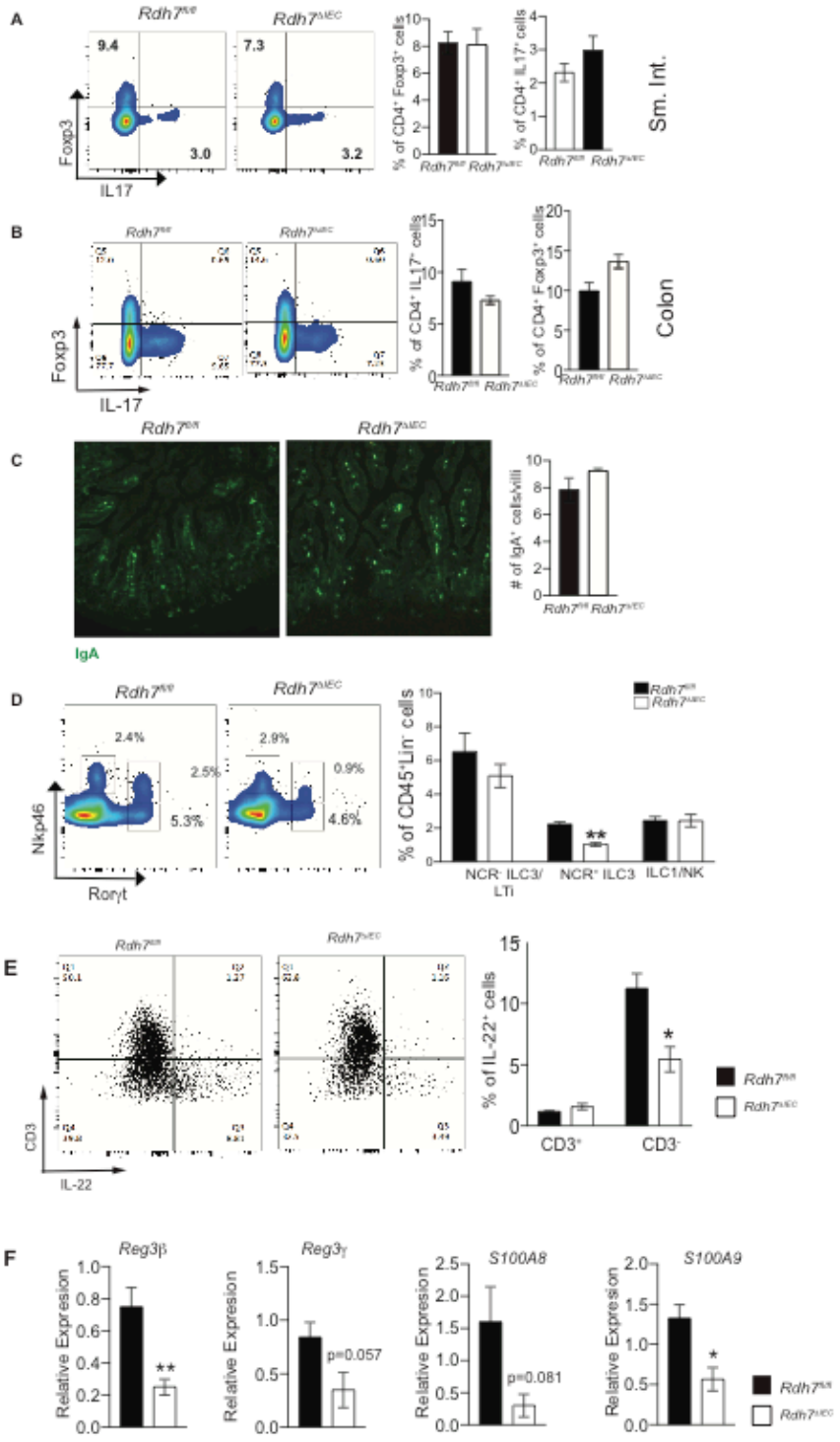

Figure S4. Analysis of gut T and B lymphocytes in *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ mouse models. Related to Figure 5.

(A)Representative flow cytometry plots showing frequency CD45$^+$CD4$^+$ cells. Bar plots show frequencies of T-reg and Th17 cells in the small intestine lamina propria. (B) Representative flow cytometry plots showing frequency CD45$^+$CD4$^+$ cells. Bar plots show frequencies of T-reg and Th17 cells in the colon lamina propria. (C)Immunofluorescent looking at IgA positive cells (green), followed by quantification of IgA$^+$ cells per villi. (D) Representative plots showing live CD45$^+$Lin$^-$(CD3$^-$CD19$^-$CD11b$^-$Gr1$^-$Ly76$^-$) lamina propria lymphocytes and bar plot showing frequencies of Lin$^-$RORγt$^+$NKp46$^-$ (NCR$^-$ILC3/LTi), of Lin$^-$RORγt$^+$NKp46$^+$ (NCR$^+$ILC3s) and of Lin$^-$RORγt$^-$NKp46$^+$(ILC1/NK) lymphocytes. (E) Frequencies of CD3+ IL-22$^+$ and CD3- IL-22$^+$ lymphocyte populations in colon of *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ littermate mice. mRNA quantification of antimicrobials peptides in the intestine controlled by IL-22. (N=4 per group). Student's t-test; Error bars represent SEM. *P < 0.05, **P < 0.01 and ***P < 0.00

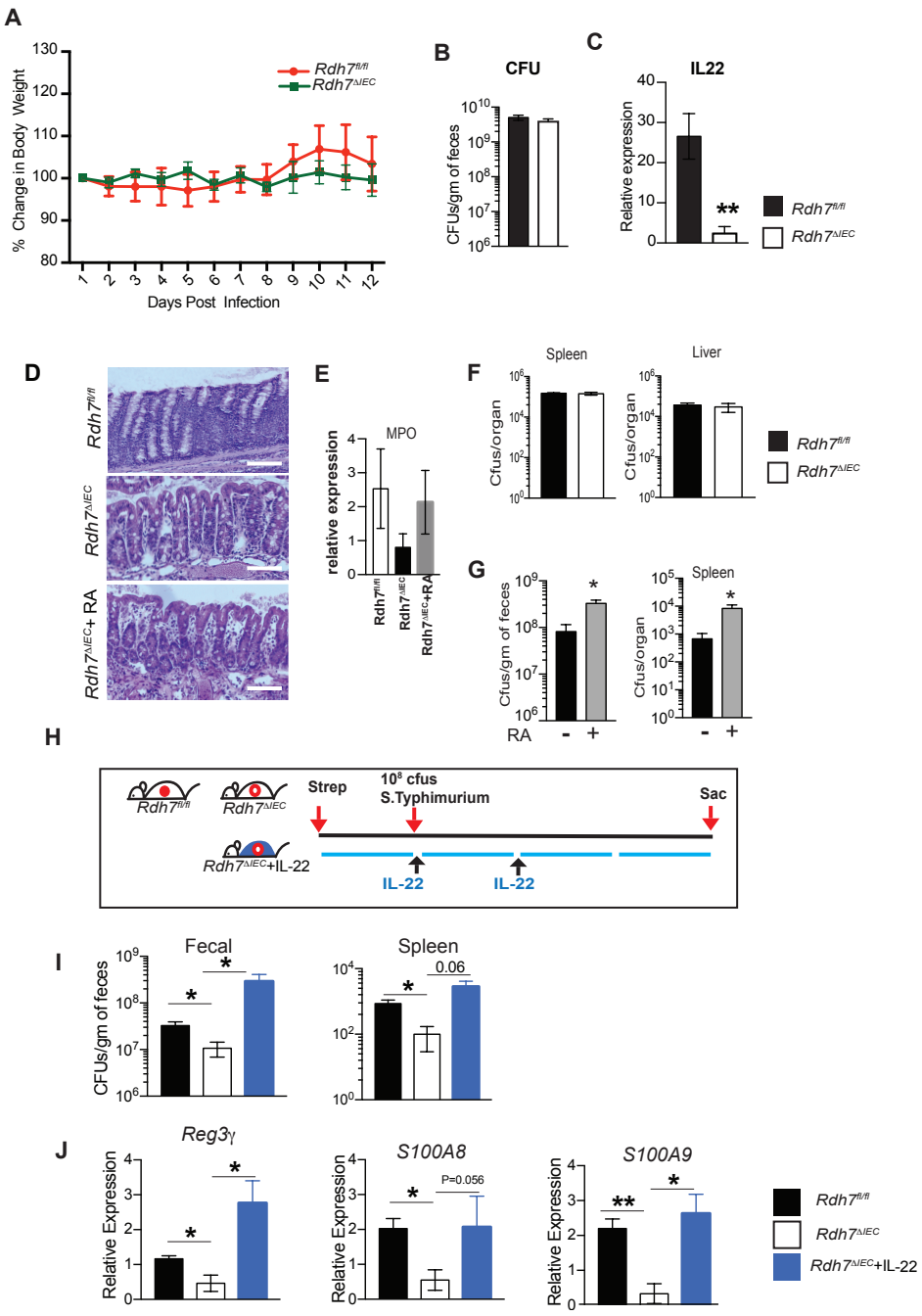

Figure S5. Role of IL-22 and RA in making *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ mice susceptible to enteric pathogens. Related to Figure 6.

(A) Change in body weight percentage in mice that were orally given 2x10^9 CFU of *C.rodentium* and sacrificed 12 days post infection. Body weight was taken and recorded daily. (B) Colony forming units/mL (CFU/mL) were determined onthe last day of the experiment. (C) Quantification of *Il-22* mRNA in colonic tissue. (D) H&E stained colon sections of *Rdh7*$^{fl/fl}$ and *Rdh7*$^{\Delta IEC}$ and *Rdh7*$^{\Delta IEC}$ +RA during *Salmonella* infection. These images are at 10x magnification. (E) *Mpo* mRNA expression to look at neutrophil activity. (F)Quantification of bacterial burden in spleen and liver from systemic *S.* Typhimurium (Given intraperitoneally) in *Rdh7*$^{fl/fl}$, *Rdh7*$^{\Delta IEC}$ mice at 24 hours post infection. (G) Quantification of *S.* Typhimurium bacterial burden in feces from streptomycin treated C57 wild-type and C57 wild-type +RA mice at 72 hours post infection. (H) Diagram illustrating *S.*Typhimurium infection and IL-22 treatment timeline. (I) Quantification of *S.* Typhimurium bacterial burden in fecal content and spleen from streptomycin treated *Rdh7*$^{fl/fl}$, *Rdh7*$^{\Delta IEC}$ and *Rdh7*$^{\Delta IEC}$+IL-22 mice at 72 hours post infection.(J)mRNA quantification from colon tissue of IL-22 dependent antimicrobials, in the colon of *Rdh7*$^{fl/fl}$, *Rdh7*$^{\Delta IEC}$ and *Rdh7*$^{\Delta IEC}$+IL-22 mice 72 hours post infection with *S.* Typhimurium. Representative data of a single experiments that were performed three times (N=4 per group). Student's test; Error bars represent SEM. **P* < 0.05, ***P* < 0.01.

retinoid	mass	DP, V	Q1, m/z	EP, V	CE, V	Q3, m/z	XP, V
*at*RA	300.2	80	301.2	10	17	205.1	10
*at*RA-d5	305.2	80	306.2	10	17	208.1	10
ROH	286.2	60	269.2	10	25	93	10
ROH-d8	294.2	60	277.2	10	25	98	10
RE palmitate	524.5	60	269.2	10	25	93	10
RE palmitate-d4	528.5	60	273.2	10	25	94	10

Supplemental Table 1 MS/MS parameters used for retinoid quantification. Related to figure 1.

CE- collision energy, DP, declustering potential, EP entrance potential, Q1 precursor ion, Q3 product ion, XP exit potential.

Gene	Forward	Reverse
Rdh7	5' GTGTCTTTGTGTGGTGGTGGTTAC 3'	5' CCACAGCTTCTCTATGCTGTGTGA 3'
Raldh1	5' GAATTCTGCCAAGGGATTCA 3'	5' GGGGTCAGAGGATTTCCAAGAACATA 3'
Raldh2	5' AATCCAGCCACAGGAGAGCAAGTG 3'	5' CACGGTGTTACCACAGCACAATGC 3'
Cyp26A	5' GCACAAGCAGCGAAAGAAGGTGATT 3'	5' GGAAGAGAGAAGAGATTGCGGGTCA 3'
Lrat	5' AGTTCAAGACTAGCCTGCTCA 3'	5' TACAAGCTGGCCTTCGAC 3'
Reg3β	5' TACTGCCTTAGACCGTGCTTTCTG 3'	5' GACATAGGGCAACTTCACCTCACA 3'
Reg3γ	5' TTCCTGTCCTCCATGATCAAAA 3'	5' CATCCACCTCTGTTGGGTTCA 3'
S100a8	5' TGTCCTCAGTTTGTGCAGAATATAAA 3'	5' TCACCATCGCAAGGAACTCC 3'
S100a9	5' TGTCCTCAGTTTGTGCAGAATATAAA 3'	5' TCACCATCGCAAGGAACTCC 3'
LacZ	5' GCGTGGATGAAGACCAGC 3'	5' CGAAGCCGCCCTGTAAAC 3'
Il-22	5' TTGAGGTGTCCAACTTCCAGCA 3'	5' AGCCGGACGTCTGTGTTGTTA 3'
Gapdh	5' AACTTTGGCATTGTGGAAGG 3'	5' ACACATTGGGGGTAGGAACA 3'
Isx	5'TTCCACTTCACCCATTACCC 3'	5'CTCTTCTCCTGCTTCCTCCA 3'
18-s	5' CATTCGAACGTCTGCCCTATC 3'	5' CCTGCTGCCTTCCTTGGA 3'

Supplemental Table 2 Primers Used for Quantitative PCR. Related to STAR Methods