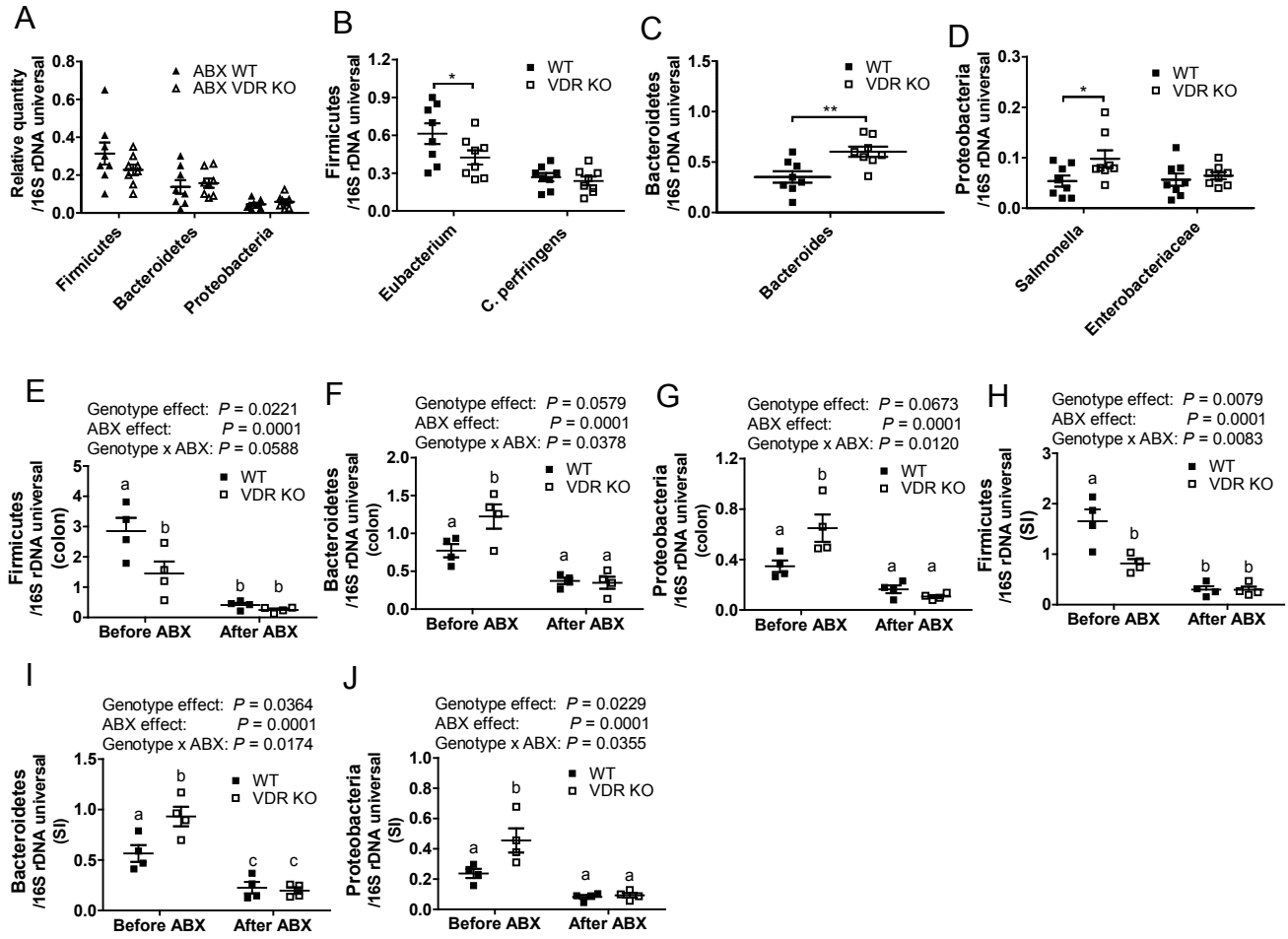
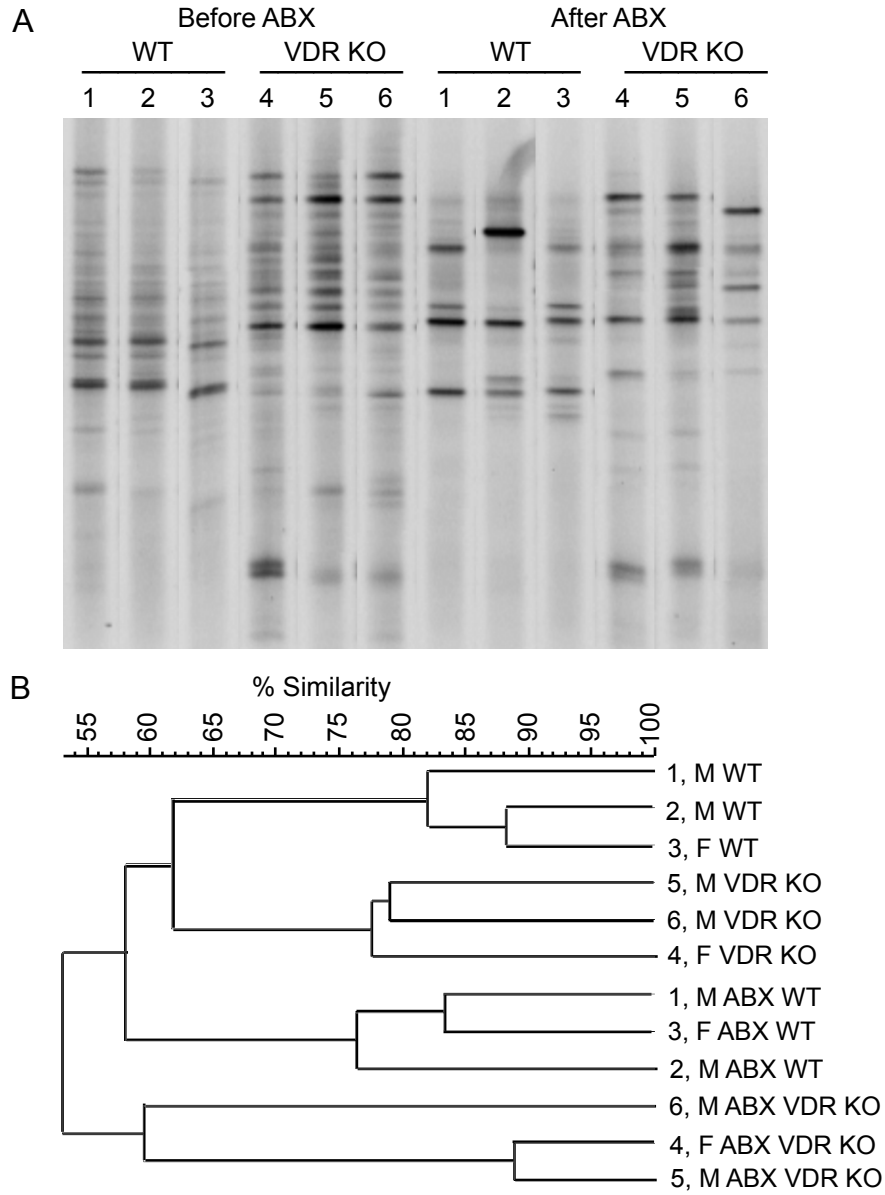


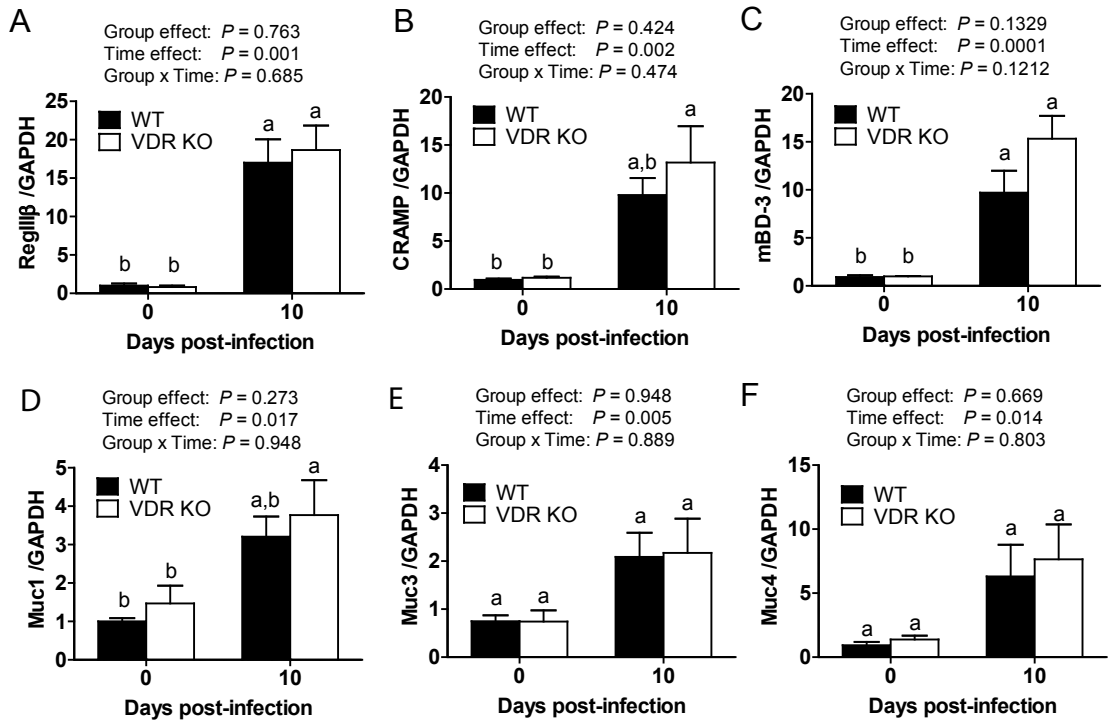
Supplementary Figure 1. Relative amount of bacteria from different phyla and genuses in the feces, colon and SI. (A) The relative quantity of bacteria in the feces of ABX WT and ABX VDR KO mice. (B-D) The relative quantity of (B) Eubacterium and Clostridium perfringens genus, (C) Bacteroides genus and (D) Salmonella and Enterobacteriaceae genus present in the feces of WT and VDR KO mice. (E-G) The relative quantity of bacteria from (E) Firmicutes phylum, (F) Bacteroidetes phylum and (G) Proteobacteria phylum in the colon of untreated or ABX-treated WT and VDR KO mice. (H-J) The relative quantity of bacteria from Firmicutes phylum (H), Bacteroidetes phylum (I) and Proteobacteria phylum (J) in the SI of untreated or ABX-treated WT and VDR KO mice. Data shown is one representative of two independent experiments using n=4-8 mice/group. Values are the mean ± SEM. Means without a common letter differ, P<0.05. Two-tailed Student's t-tests (A-D), Two-way ANOVA with Bonferroni post-hoc tests (E-J), *P<0.05,**P<0.01.

Suppl. Figure 2



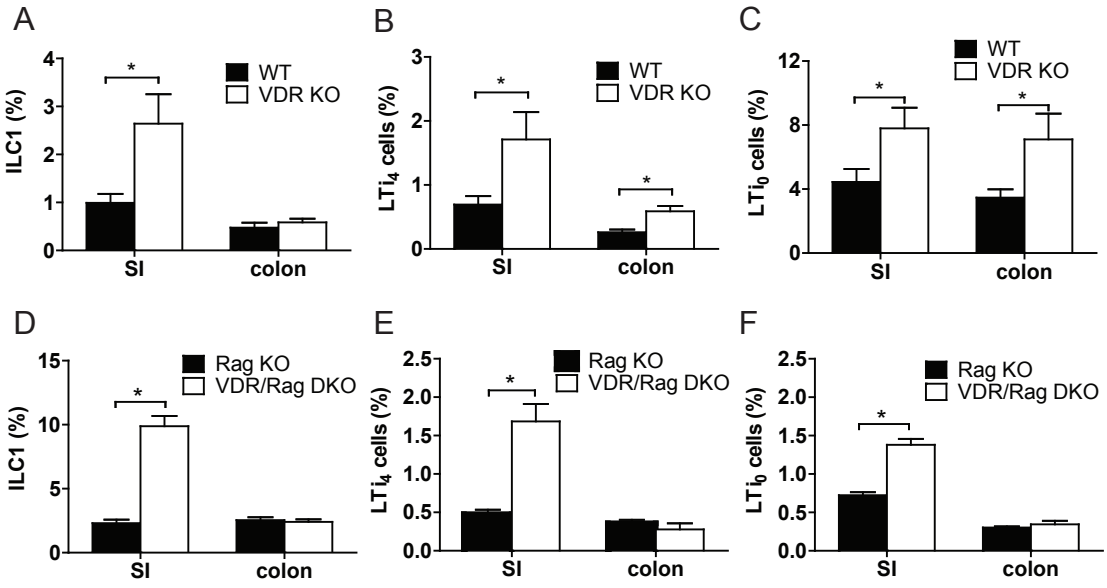
Alterations in denaturing gradiet gell electrophoresis (DGGE) banding patterns of fecal DNA with ABX treatment. (A) DGGE banding patterns of fecal 16S rDNA of WT and VDR KO mice before ABX treatment. Numbersreflect individual mice. There are fewer bands after ABX treatment suggesting a decrease in bacterial diversity. (B) Cluster analysis of the DGGE banding patterns in A. Mice treated with ABX were more similar to each other than to the samples before ABX treatment. Data shown is one representative experiment of two independent experiments. F: females, M: males.

Suppl. Figure 3



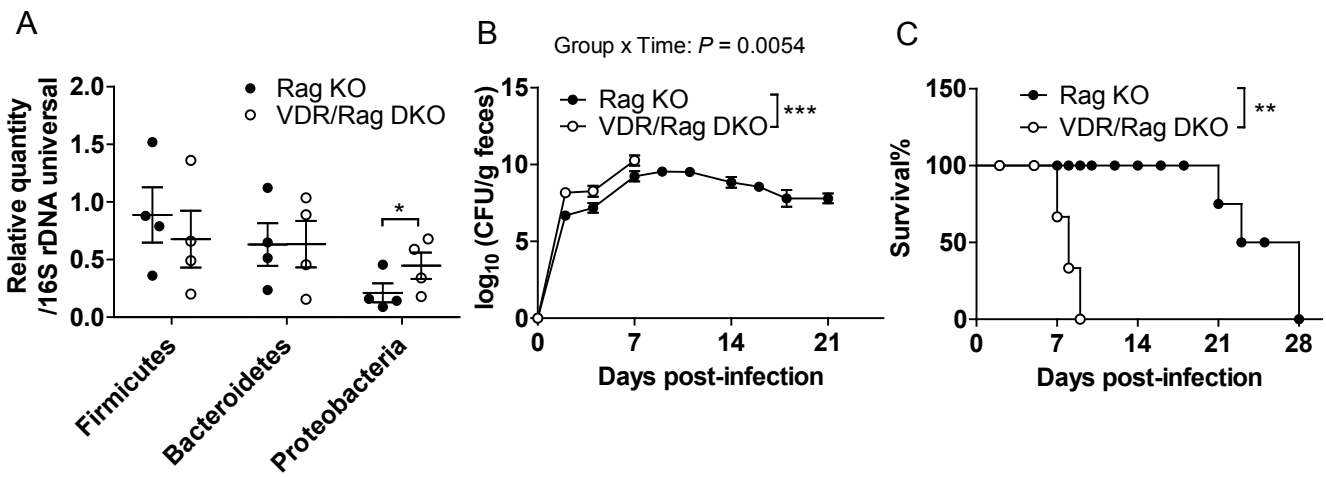
mRNA expression in the colon of WT and VDR KO mice. The relative amount of (A) RegIIIβ, (B) CRAMP, (C) mBD-3, (D) Muc 1, (E) Muc 3, (F) Muc 4 in the colon. Values are the mean ± SEM of two independent experiments. Two-way ANOVA with Bonferroni post-hoc tests (A-F), values without a common letter differ at the indicated time point, $P<0.05$.

Suppl. Figure 4



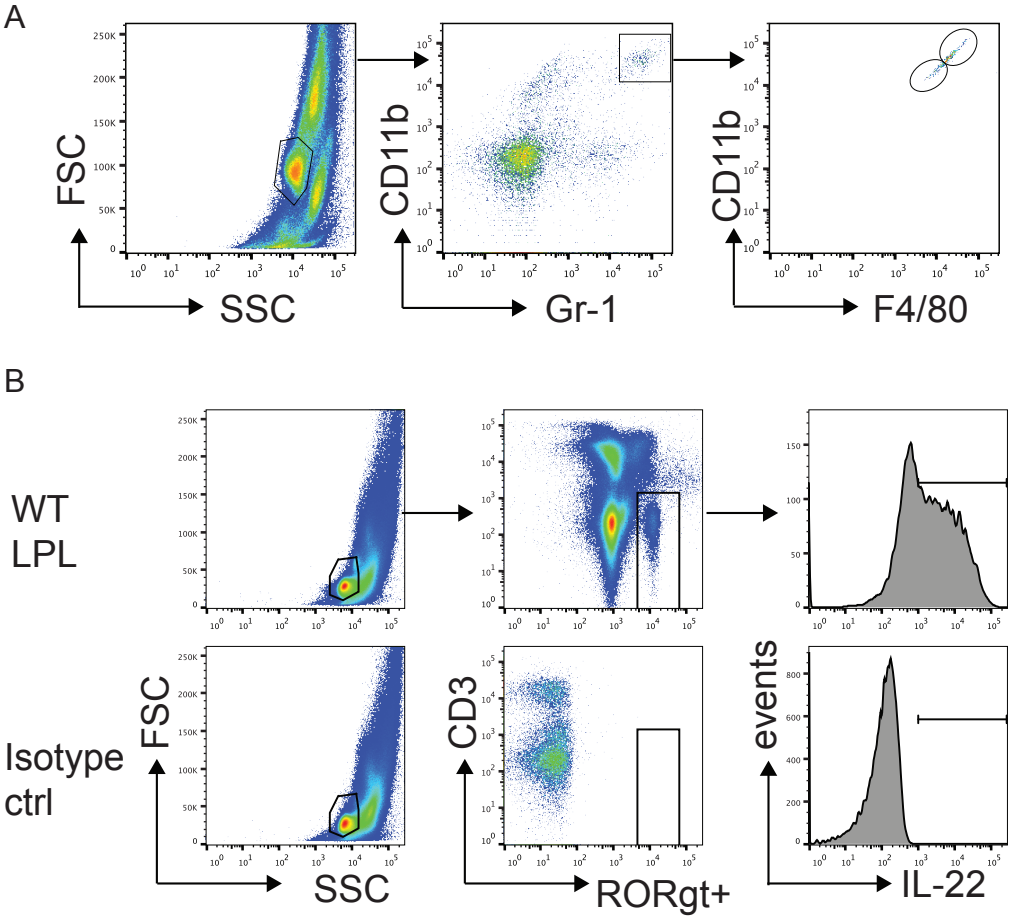
ILC subsets in the SI and colonic LP of WT, VDR KO, Rag KO and VDR/Rag DKO mice. The frequencies of (A, D) ILC1 (CD3-RORγt+NKp46+) cells; (B, E) LTi_4 (CD3-RORγt+NKp46-CD4+) cells, (C,F) LTi_0 (CD3-RORγt+NKp46-CD4-) cells in the SI and colonic LP of (A-C) WT and VDR KO and (D-F) Rag KO and VDR/Rag DKO mice. Data shown is one representative of two independent experiments using n=6-8 mice/group. Two-tailed Student's t tests (A-F), **P*<0.05.

Suppl. Figure 5



VDR/Rag DKO mice are more susceptible to *C. rodentium* than Rag KO mice. (A) The relative quantities of bacteria from Firmicutes, Bacteroidetes and Proteobacteria phyla in the feces. (B) *C. rodentium* shedding in the feces. (C) Survival kinetics following infection with *C. rodentium*. Data shown is one representative of two independent experiments using n=4-10 mice/group. Two-tailed Student's t tests (A), Two-way ANOVA with Bonferroni post-hoc tests (B), log-rank test (C), *P<0.05, **P<0.01, ***P<0.001.

Suppl. Figure 6



FACS gating strategy for Figure 1. (A) Lymphocytes were identified and the CD11b+ and Gr-1high cells were seperated into inflammatory monocytes (F480 high) and neutrophils (F480 low). (B) Lymphocytes in the LP were identified and the CD3-RORgt+ were used to identify ILCs (middle panel). IL-22 secreting ILCs are shown in the right hand panel. The bottom panel shows the isotype control staining for RORgt (middle) and IL-22 (right).

Supplementary Table 1

Gene	Primer sequence (5' to 3')
Bacterial quantification	
Firmicutes	forward: TGAAACTYAAAGGAATTGACG
	reverse: ACCATGCACCACCTGTC
Bacteroidetes	forward: CRAACAGGATTAGATACCCT
	reverse: GGTAAGGTTCCTCGCGTAT
γ-Proteobacteria	forward: TCGTCAGCTCGTGTYGYGA
	reverse: CGTAAGGGCCATGATG
Eubacterium	forward: ACTCCTACGGGAGGCAGC
	reverse: GCTTCTTAGTCAGGTACCGTCAT
Clostridium perfringens	forward: CGCATAACGTTGAAAGATGG
	reverse: CCTTGGTAGGCCGTTACCC
Bacteroides	forward: GGTTCTGAGAGGAGGTCCC
	reverse: GCTGCCTCCCGTAGGAGT
Salmonella	forward: TGTTGTGGTTAATAACCGCA
	reverse: GACTACCAGGGTATCTAATCC
Enterobacteriaceae	forward: GTGCCAGCMGCCGCGGTAA
	reverse: GCCTCAAGGGCACAACCTCCAAG
16S rDNA universal (GC-clamp)	forward: CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCA CGGGGGGCCTACGGGAGGCAGCAG
	reverse: ATTACCGCGGCTGCTGG
Quantitative PCR	
IFN-γ	forward: TGCATCTTGGCTTTGCAGCTCTTCCTCATGGC
	reverse: TGGACCTGTGGGTTGTTGACCTCAAACTTGGC
IL-17A	forward: CAGGGAGAGCTTCATCTGTGT
	reverse: GCTGAGCTTTGAGGGATGAT
IL-6	forward: GCTACCAAACTGGATATAATCAGGT
	reverse: CCAGGTAGCTATGGTACTCCAGAA
RegIIIγ	forward: TTCCTGTCCTCCATGATCAAAA
	reverse: CATCCACCTCTGTTGGGTTCA
RegIIIβ	forward: ATTGCGAGGAAGCTTATGGGAATGGAGTAACAAT
	reverse: CTATAGGGATCCGCAGACATAGGGCAACTTCA
mucin 1 (Muc1)	forward: TGCCAGTGCCGCCGAAAGAG
	reverse: GCCGAAACCTCCTCATAGGGGC
mucin 2 (Muc2)	forward: GCTGACGAGTGGTTGGTGAATG
	reverse: GATGAGGTGGCAGACAGGAGAC
mucin 3 (Muc3)	forward: CGTGGTCAACTGCGAGAATGG
	reverse: CGGCTCTATCTCTACGCTCTCC
mucin 4 (Muc4)	forward: CAGCAGCCAGTGGGGACAG
	reverse: CTCAGACACAGCCAGGGAACTC
Angiogenin-4 (Ang-4)	forward: CTCTGGCTCAGAATGAAAGGTACGA
	reverse: GAAATCTTTAAAGGCTCGGTACCC
β-defensin 3 (mBD-3)	forward: GCTAGGGAGCACTTGTTTGC
	reverse: TTGTTTGAGGAAAGGAGGCA
CRAMP	forward: CTTCAACCAGCAGTCCCTAGACA
	reverse: TCCAGGTCCAGGAGACGGTA
GAPDH	forward: TGAAGGTCGGTGTGAACGGATTTGGC
	reverse: CATGTAGGCCATGAGGTCCACCAC