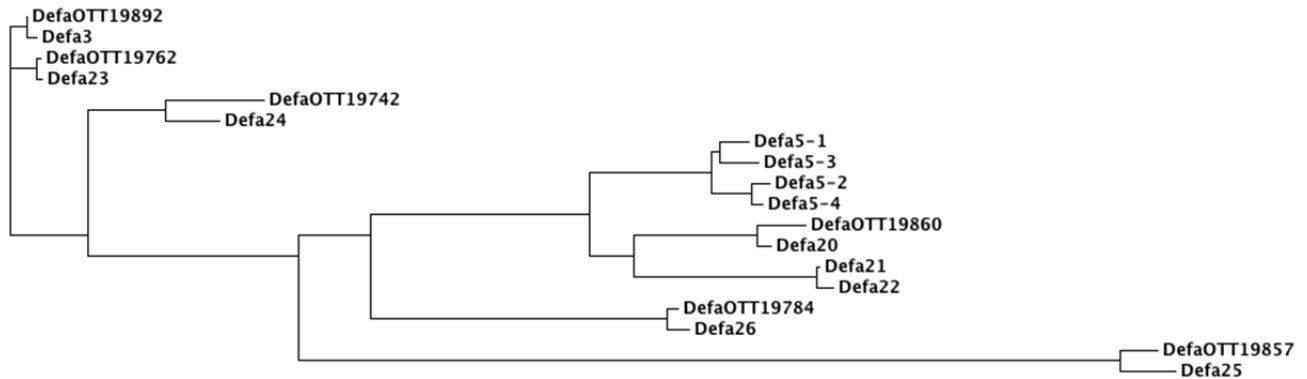
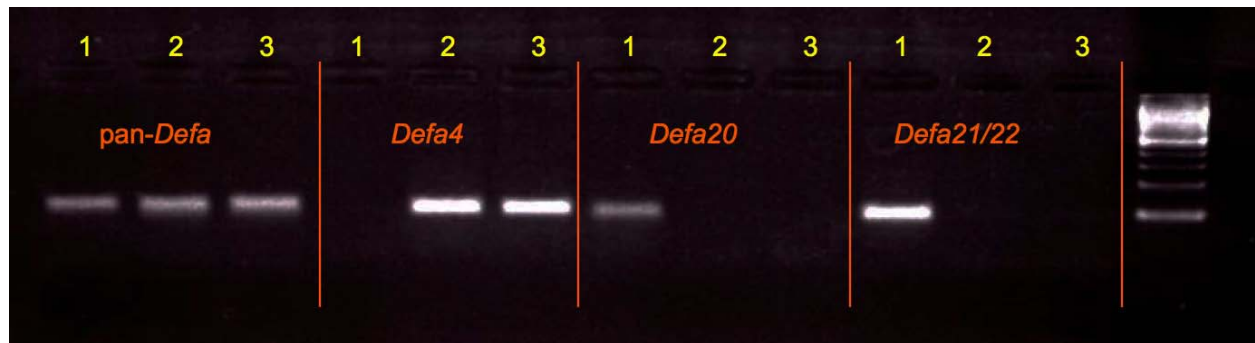


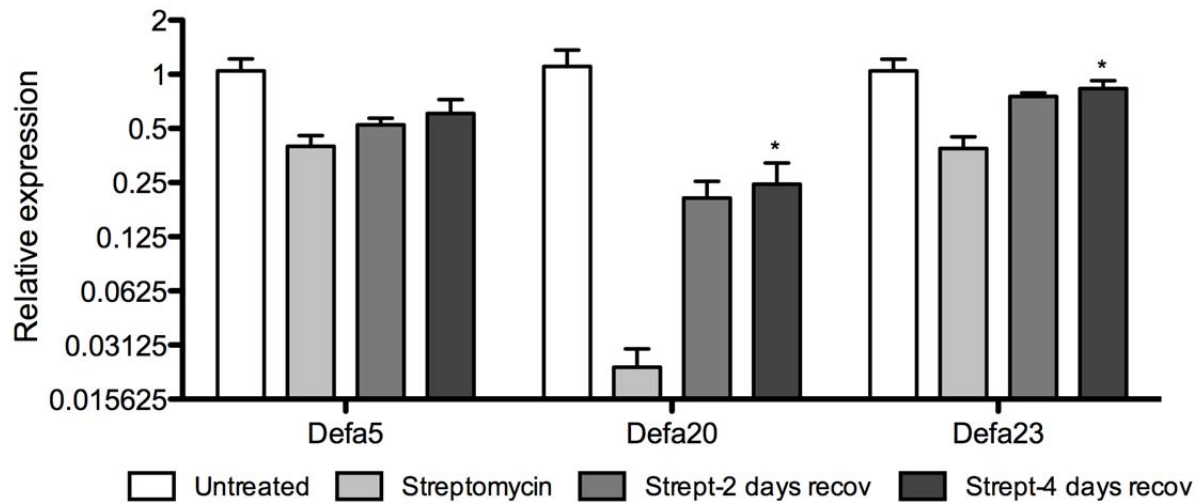
Supplementary Material



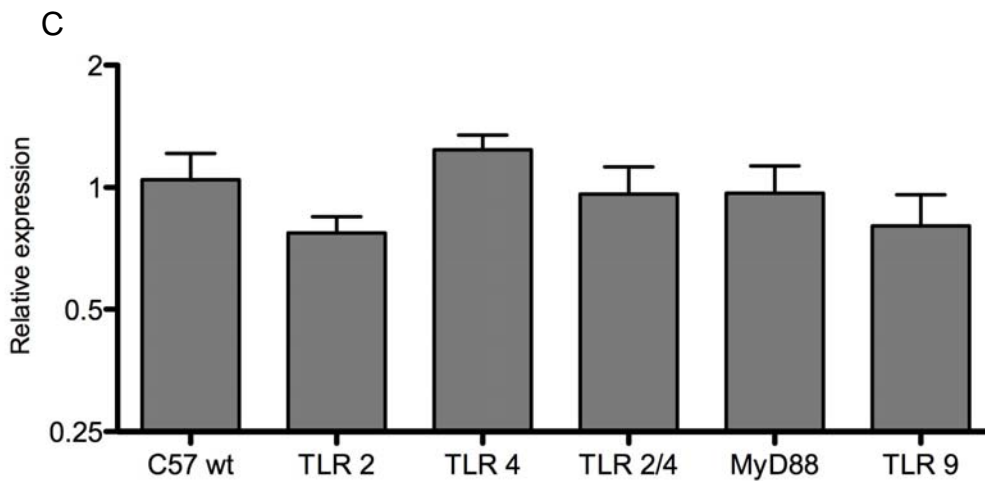
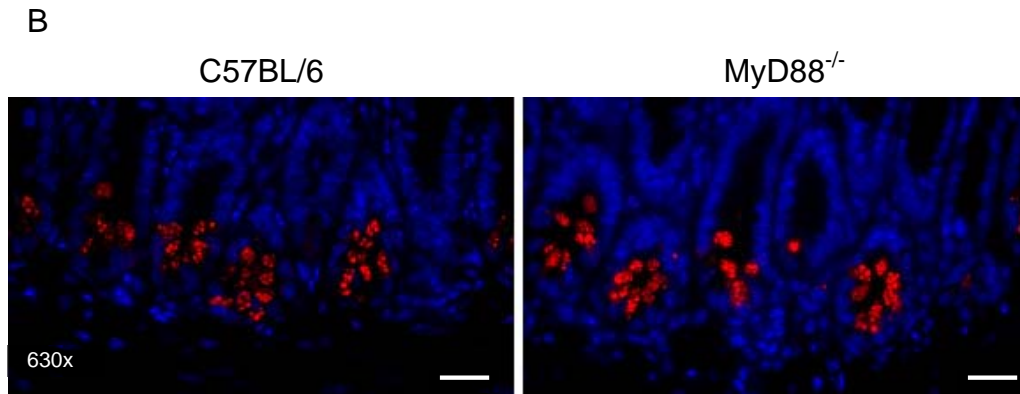
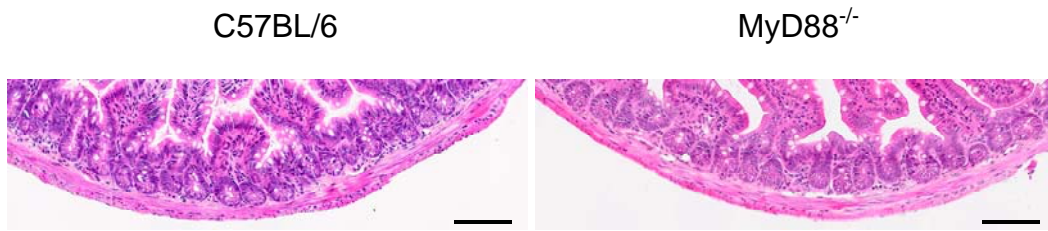
Suppl. Fig. 1. Phylogenetic tree of *Defa* promoters. The 1000 bp upstream of the transcription start site of each gene were aligned and their phylogenetic distance calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).



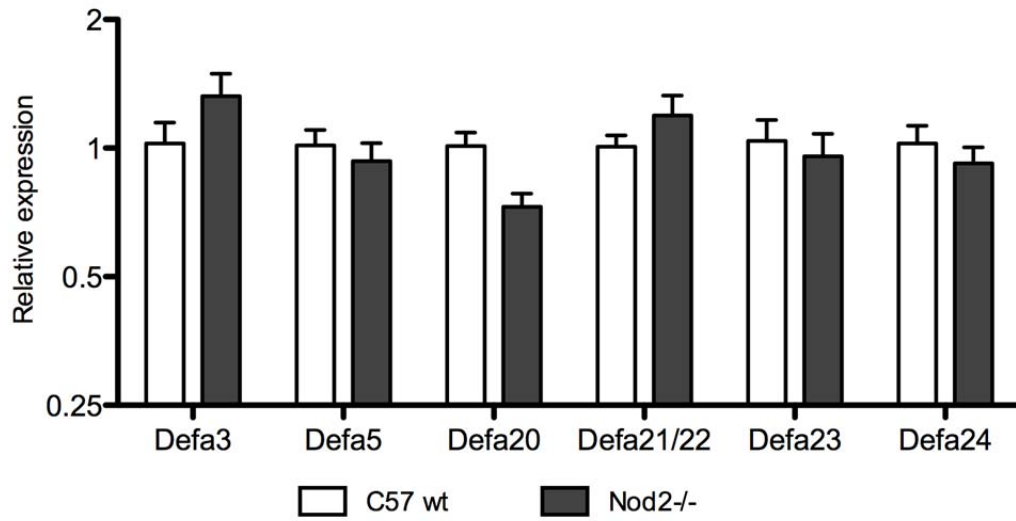
Suppl. Fig. 2. Amplification of *Defa4*, *Defa20* and *Defa21/22* from the ilea of C57BL/6 (1), BalbC (2) or 129SvJ mice (3). Samples are a pool of four animals each. Data by end-point PCR with the corresponding set of primers shown in Table 2. Far right lane is a 100 bp DNA ladder.



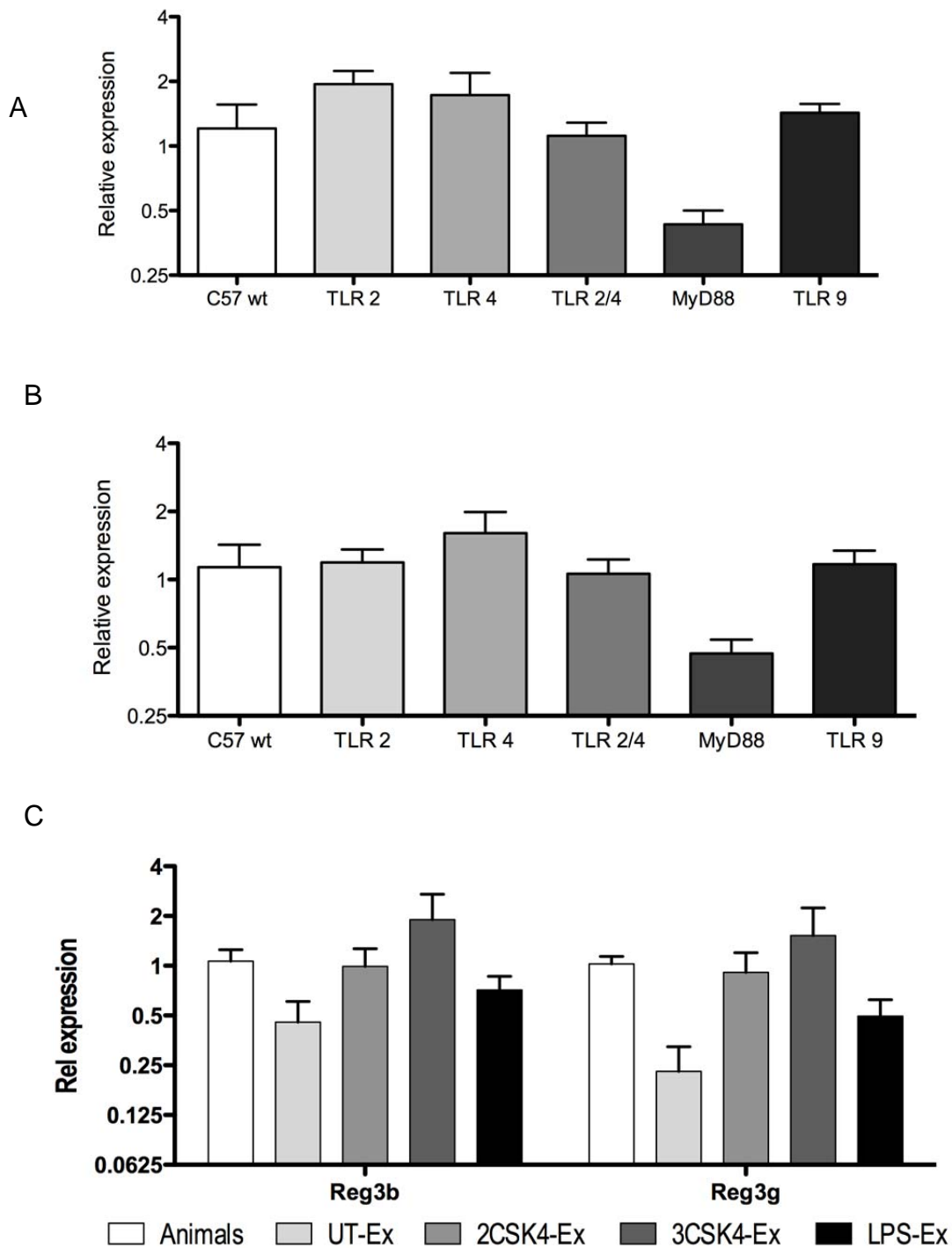
Suppl. Fig. 3. *Defa* gene transcription recovers after suspension of streptomycin treatment. * indicates statistical significance between streptomycin-treated and 4 days recovery groups ($p < 0.05$). Results shown are one representative experiment of two, $n = 4$.



Suppl. Fig. 4. (A) H&E staining of ileal cross-sections from C57BL/6 and MyD88^{-/-} mice (bars are 50 μ m). (B) Paneth cell immunostaining for lysozyme in the ileum of C57BL/6 and MyD88^{-/-} mice (bars are 15 μ m). (C) Transcript levels of lysozyme in the ilea of TLR-deficient mice, qPCR primers are: F: AGCCGATACTGGTGTAAATGATG; R: GCACATTGTATGGCTGCAGTG, this primers set amplifies both lysozyme M and P. **n= 6-9 animals per group.**



Suppl. Fig. 5. NOD2 deficiency does not affect the transcript levels of ileal *Defa* genes; **n= 5**.



Suppl. Fig. 6. (A and B): transcript levels of Reg3 (A) and Reg3 (B) in the ilea of TLR- and MyD88-deficient mice. **(C)** Transcript levels of Reg3 and Reg3 in ileal explants treated with TLR2 and TLR4 agonists (as described in the text and in Fig 6). UT-Ex: untreated explants, 2CSK4-Ex, 3CSK4-Ex and LPS-Ex are the treated explants.