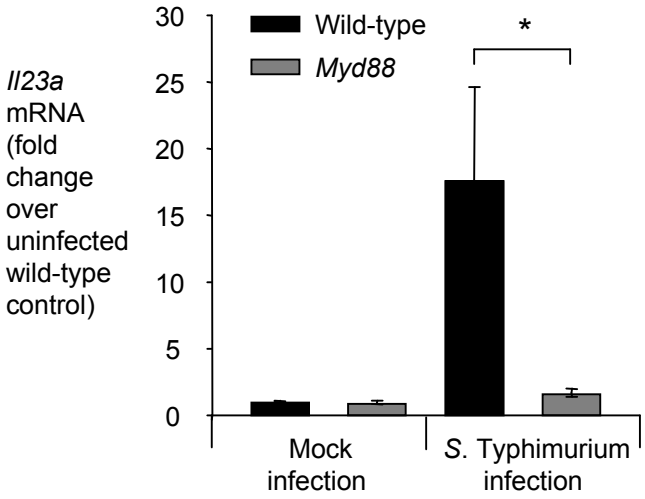
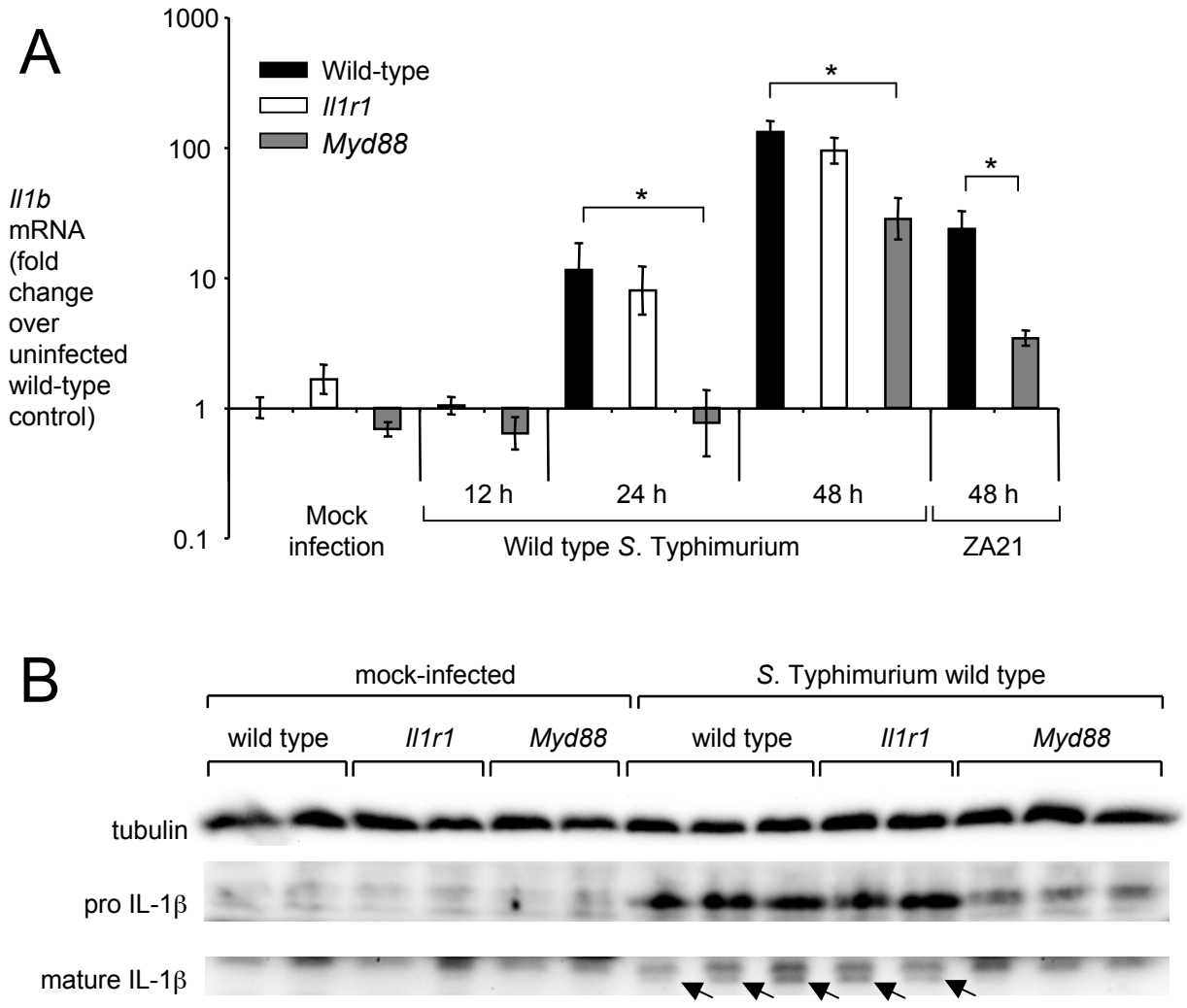
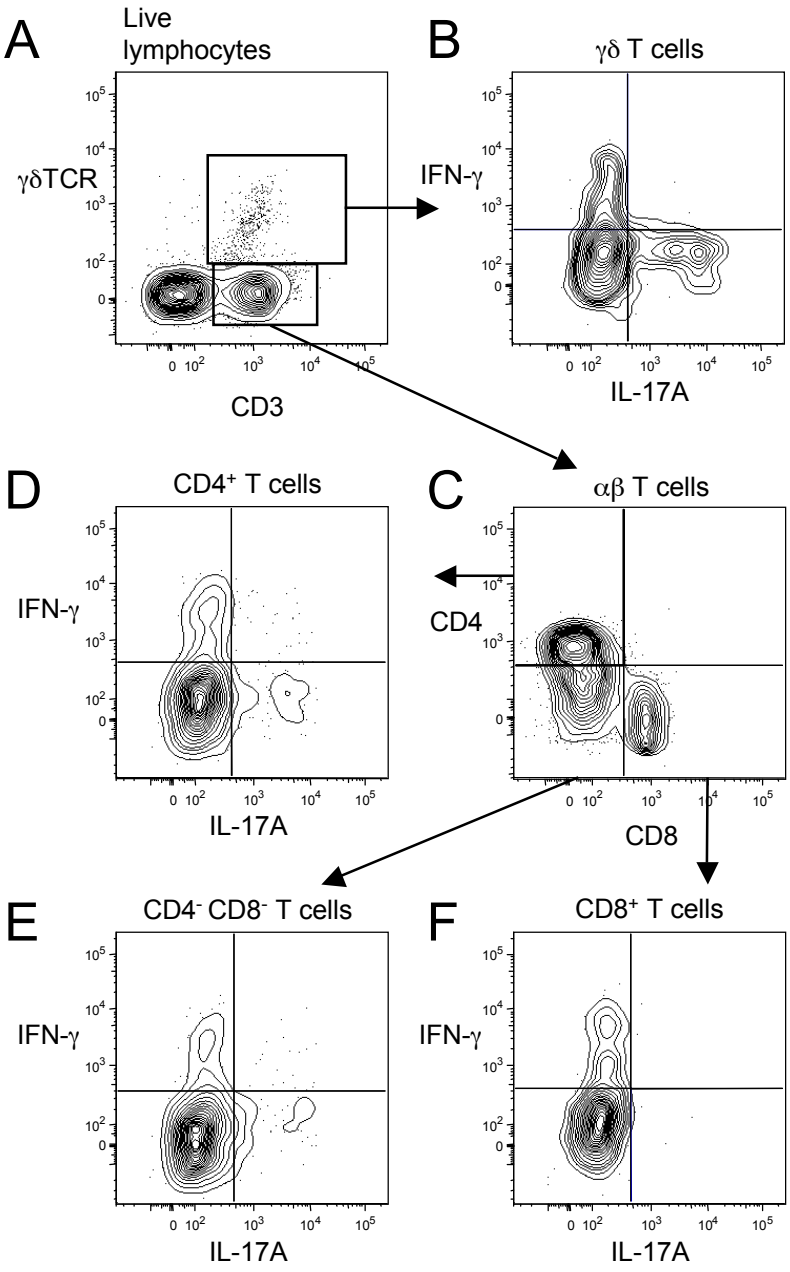


Supplementary Figure 1: Relative *Il23a* transcript levels determined after stimulation of splenocytes from C57BL/6 mice (wild-type, black bars) or MyD88-deficient mice (*Myd88*, grey bars) with *S.* Typhimurium or medium control using quantitative real-time PCR. Bars represent geometric means ± standard error of three independent experiments.



Supplementary Figure 2: IL-1β expression in the mouse colitis model. (A) Relative *Il1b* transcript levels in the cecal mucosa were determined by quantitative real-time PCR using the mouse colitis model. C57BL/6 mice (wild-type, black bars), MyD88-deficient mice (*Myd88*, grey bars) or IL-1 receptor-deficient mice (*Il1r1*, white bars) were inoculated with wild type *S.* Typhimurium, a non-invasive *S.* Typhimurium mutant (ZA21) or sterile medium (mock infection) and RNA extracted from the cecal mucosa at the indicated time points. Bars for mock-infected animals represent the combined geometric means ± standard error from samples collected at 12, 24 and 48 hours after inoculation. All other bars represent geometric means ± standard error from at least four different animals. (B) Detection of pro-IL-1β (middle panel) and IL-1β (arrows, bottom panel) by Western blot in protein extracts from the cecal mucosa of C57BL/6 mice (wild-type), MyD88-deficient mice (*Myd88*) or IL-1 receptor-deficient mice (*Il1r1*) 48 hours after mock-infection or infection with wild type *S.* Typhimurium. Expression of tubulin was detected by Western blot as a loading control (top panel). Each lane contains protein extracted from the cecal mucosa of a different animal.



Supplementary Figure 3: Gating strategy for analysis of cytokine expression in intestinal T cell populations by flow cytometry. Forward scatter and side scatter characteristics of intestinal cells used to set a lymphocyte gate. Dead cells were excluded based on Dead/Live Aqua staining. Live lymphocytes (A) were gated into γδ T cells ($CD3^+$ γδ TCR^+)(B) and αβ T cells ($CD3^+$ γδ TCR^-)(C) populations. The αβ T cell population (C) was further subdivided into $CD4^+CD8^-$ T cells (D), $CD4^-CD8^-$ T cells (E) and $CD4^-CD8^+$ T cells (F). $CD4^+CD8^-$ T cells (D), $CD4^-CD8^-$ T cells (E), $CD4^-CD8^+$ T cells (F) and γδ T cells (B) were then analyzed for expression of IL-17A and IFN-γ. Gates were based on Fluorescence-Minus-One controls.