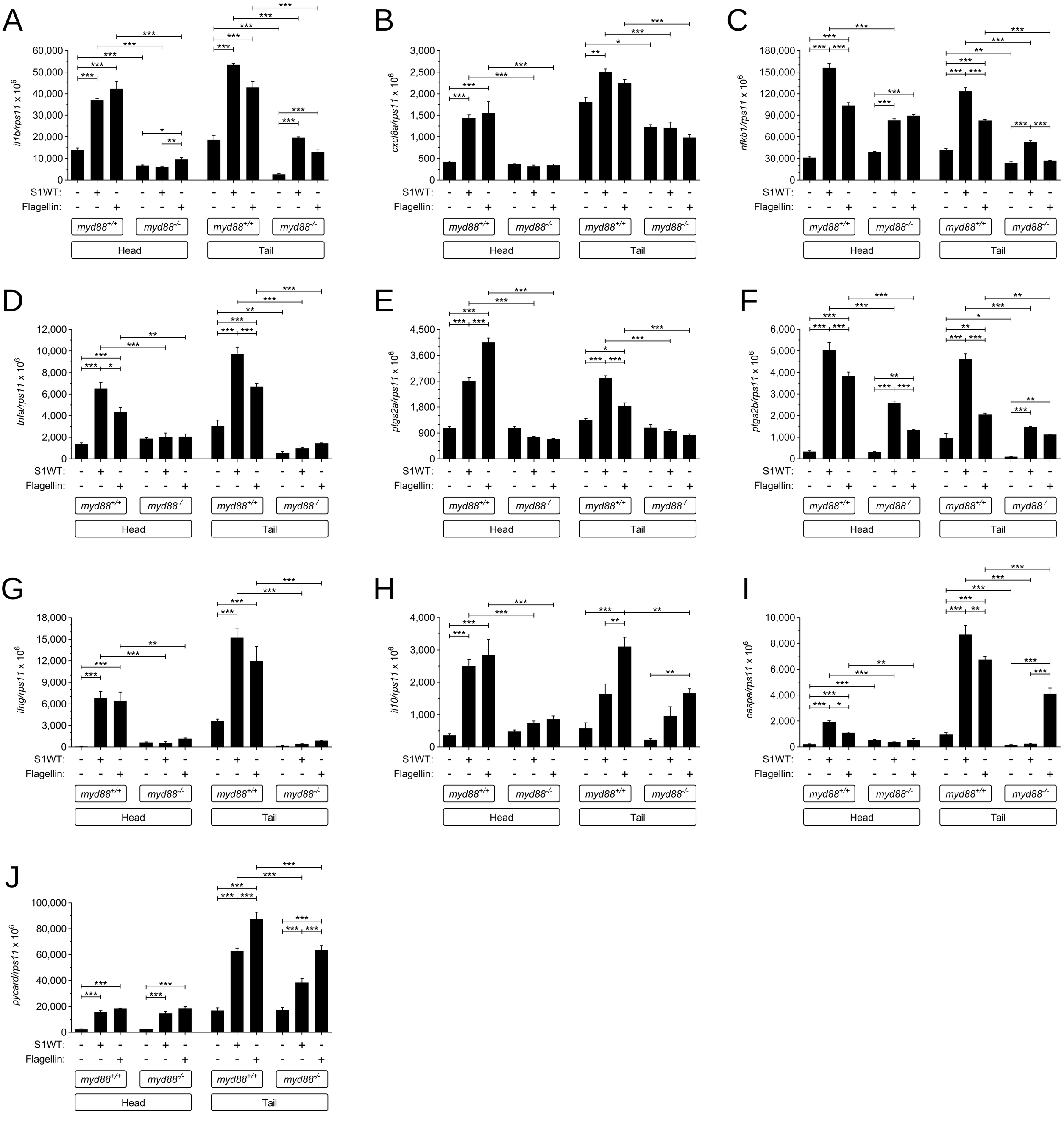
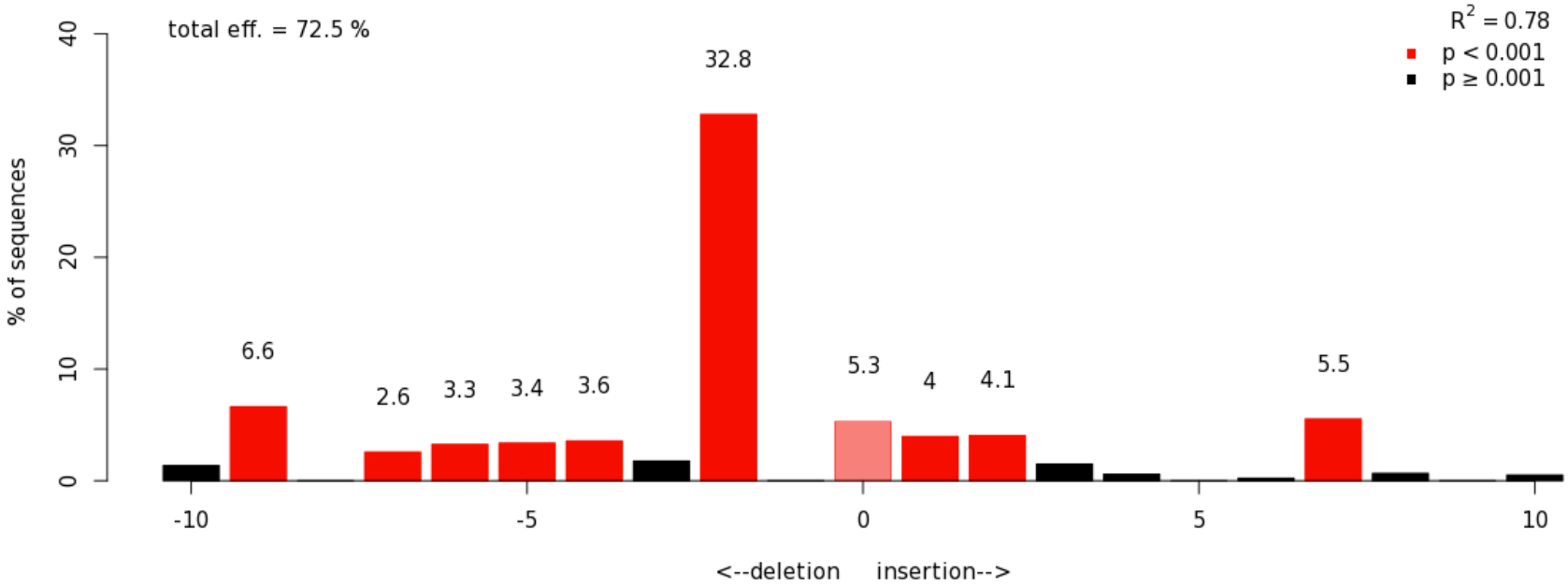


Figure S1 (related to Figure 1). Gene expression analysis of wild type and Myd88-deficient larvae injected with wild type S1. Recombinant S1WT (+) or vehicle (-) were injected in the hindbrain ventricle of 2 dpf wild type and Myd88-deficient larvae, and the transcript levels of the indicated genes were analyzed at 12 hpi by RT-qPCR in larval head and tail. Data are shown as mean ± S.E.M. P values were calculated using one way ANOVA and Tukey multiple range test. ns, not significant, *≤p0.05, **p≤0.01, ***p≤0.001.

A: crIl1b



B: crTlr2

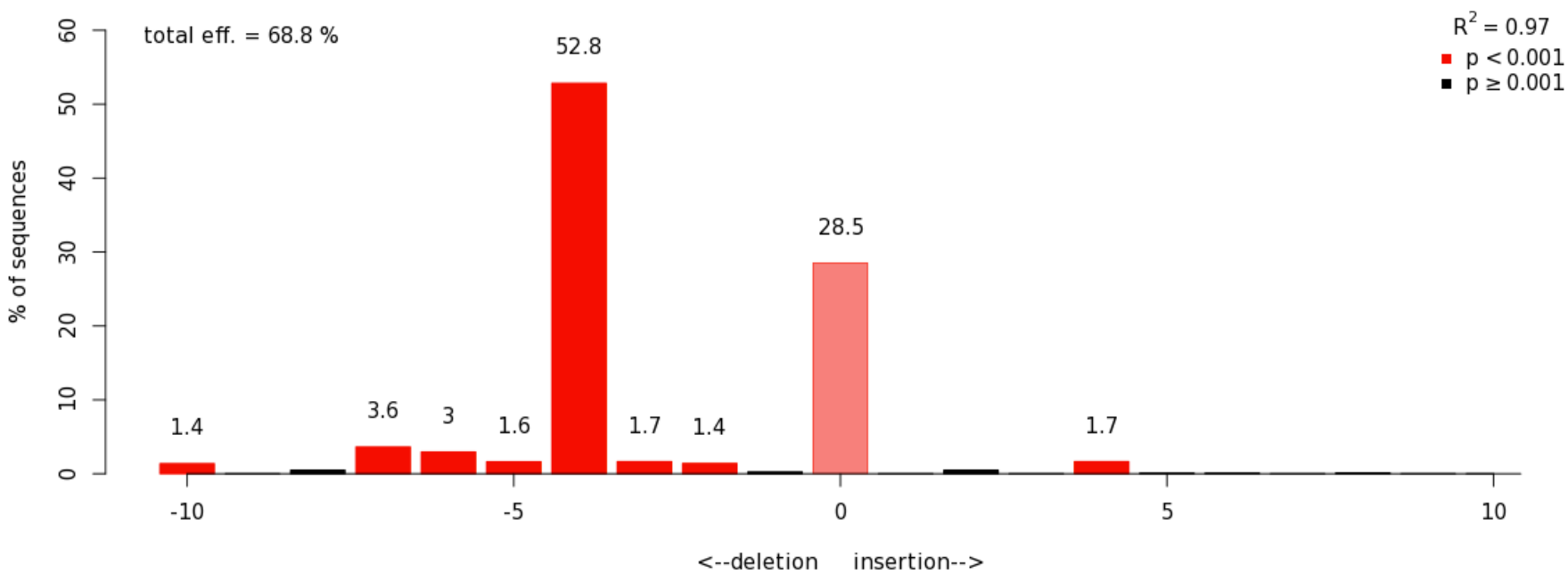


Figure S2 (related to Figures 2 and 3). Analysis of genome editing efficiency in larvae injected with *il1b* (A) and *tlr2* (B) crRNA/Cas 9 complexes and quantification rate of nonhomologous end joining mediated repair showing all insertions and deletions (INDELS) at the target site using TIDE (https://tide.nki.nl).

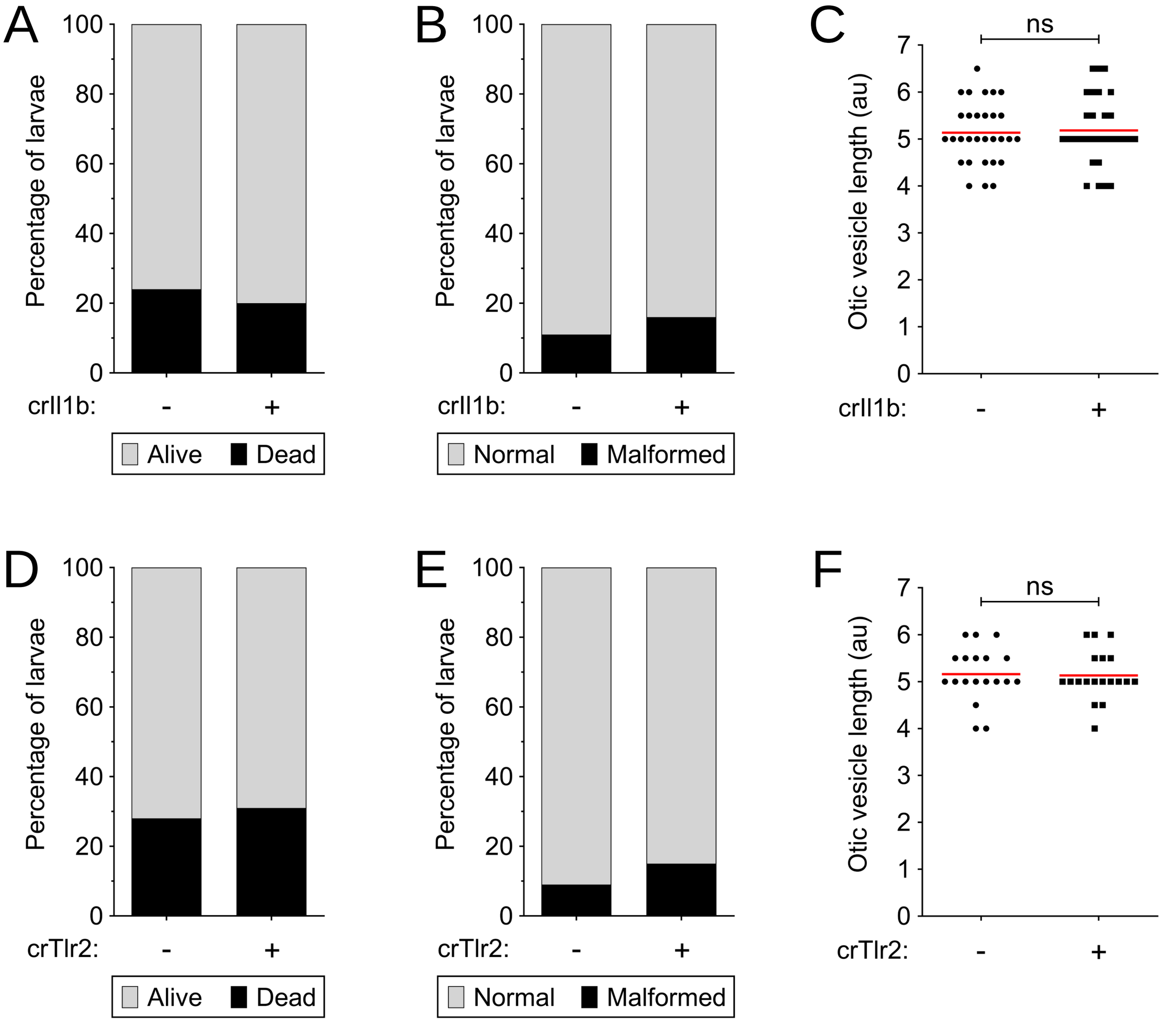


Figure S3 (related to Figures 2 and 3). Il1b and Tlr2 deficiencies do not affect larval development. The precentage of dead/alive (A, D) and malformed embryos (B, E), and the developmental stage (C, F) of Il1b- (A-C) and Tlr2-deficient (D-F) embryos was determined at 24 hpf. au, arbitrary units.

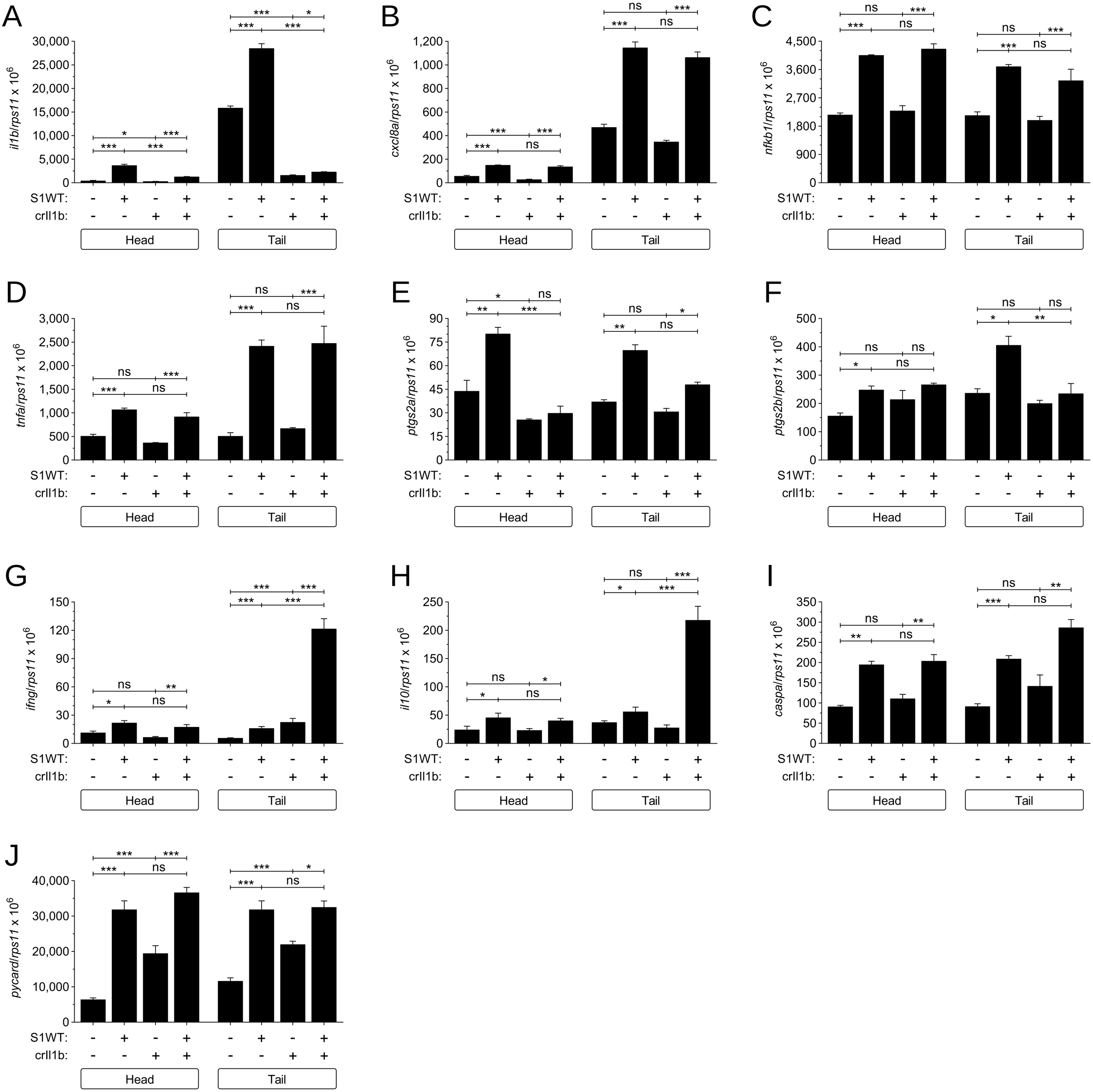


Figure S4 (related to Figure 2). Gene expression analysis of wild type and Il1b-deficient larvae injected with wild type S1. Recombinant S1WT (+) or vehicle (-) were injected in the hindbrain ventricle of 2 dpf wild type and Il1b-deficient larvae, and the transcript levels of the indicated genes were analyzed at 12 hpi by RT-qPCR in larval head and tail. Data are shown as mean ± S.E.M. P values were calculated using one way ANOVA and Tukey multiple range test. ns, not significant, *≤p0.05, **p≤0.01, ***p≤0.001.

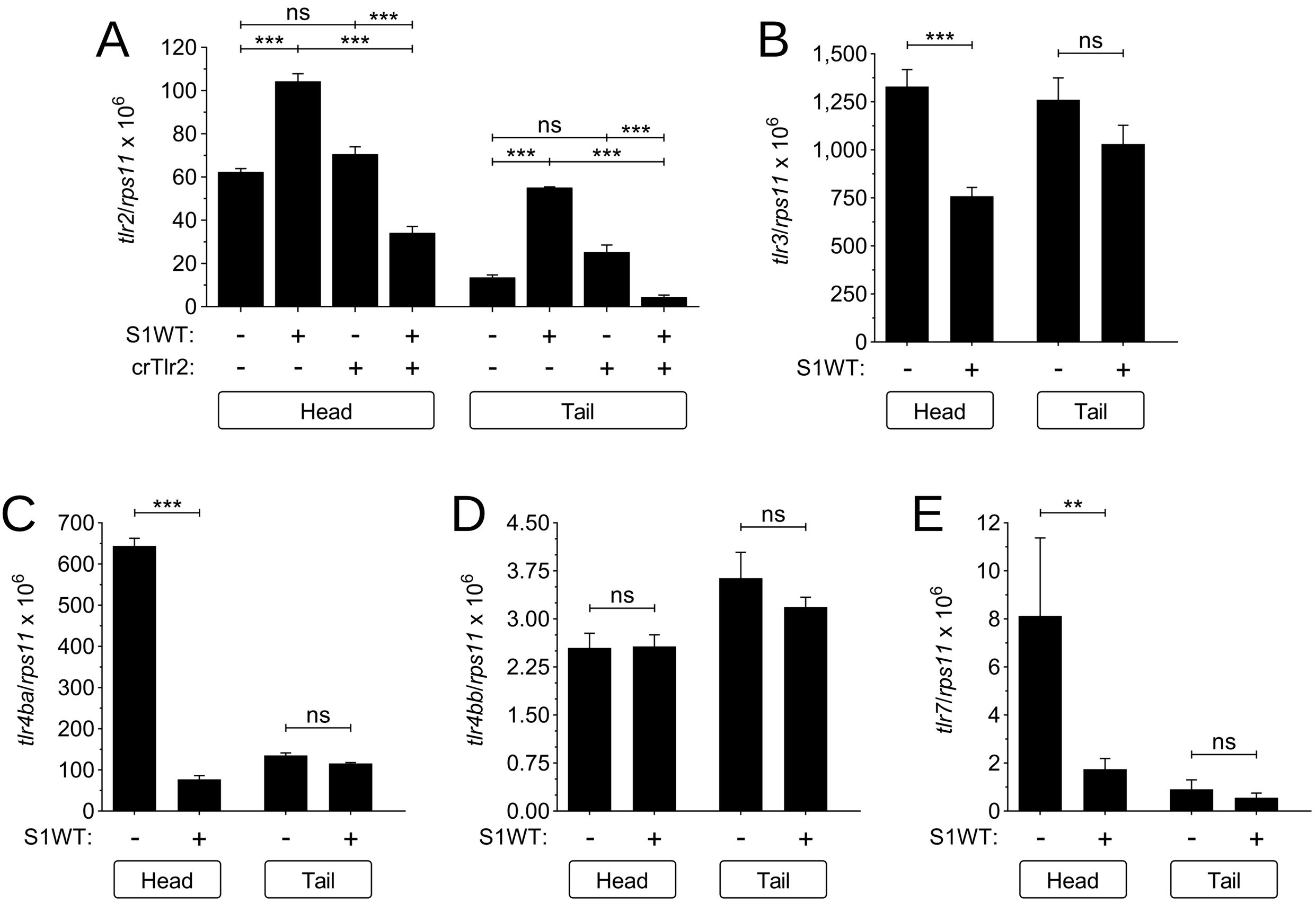


Figure S5 (related to Figure 3). Tlr expression analysis of wild type and Tlr2-deficient larvae injected with wild type S1. Recombinant S1WT (+) or vehicle (-) were injected in the hindbrain ventricle of 2 dpf wild type and Tlr2-deficient larvae, and the transcript levels of the indicated *tlr* genes were analyzed at 12 hpi by RT-qPCR in larval head and tail. Data are shown as mean ± S.E.M. P values were calculated using one way ANOVA and Tukey multiple range test. ns, not significant, **p≤0.01, ***p≤0.001.

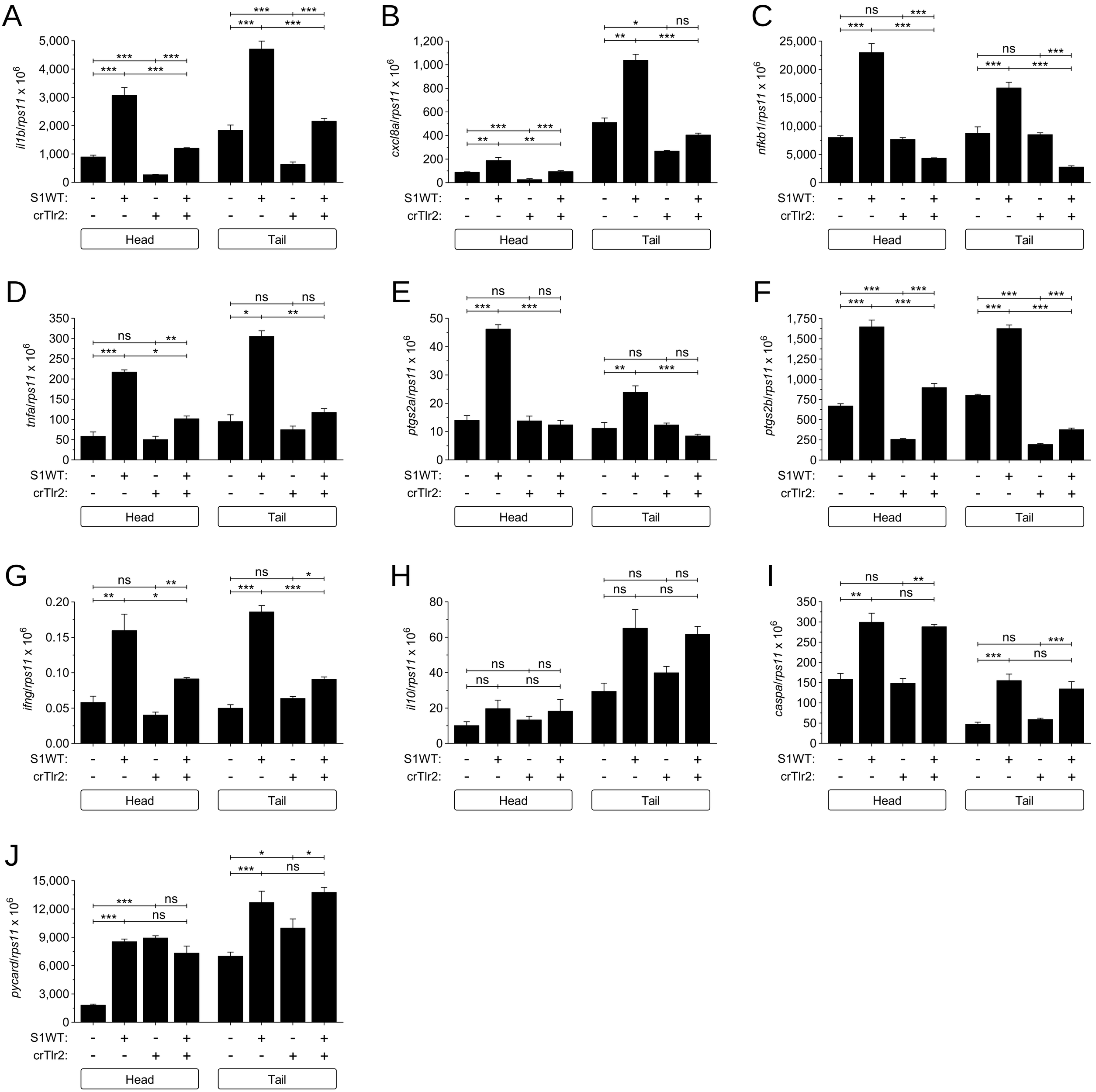


Figure S6 (related to Figure 3). Gene expression analysis of wild type and Tlr2-deficient larvae injected with wild type S1. Recombinant S1WT (+) or vehicle (-) were injected in the hindbrain ventricle of 2 dpf wild type and Tlr2-deficient larvae, and the transcript levels of the indicated genes were analyzed at 12 hpi by RT-qPCR in larval head and tail. Data are shown as mean ± S.E.M. P values were calculated using one way ANOVA and Tukey multiple range test. ns, not significant, *≤p0.05, **p≤0.01, ***p≤0.001.