Fig. S1 : Orientation of genetic elements selected for study in *Salmonella* Enteritidis P125109 genome. Putative promoter regions upstream to individual selected gene are shown as solid bar on the genome as per the orientation of genetic element. Putative promoter regions were cloned into promoterless *GFP-mut2* plasmid pM968.

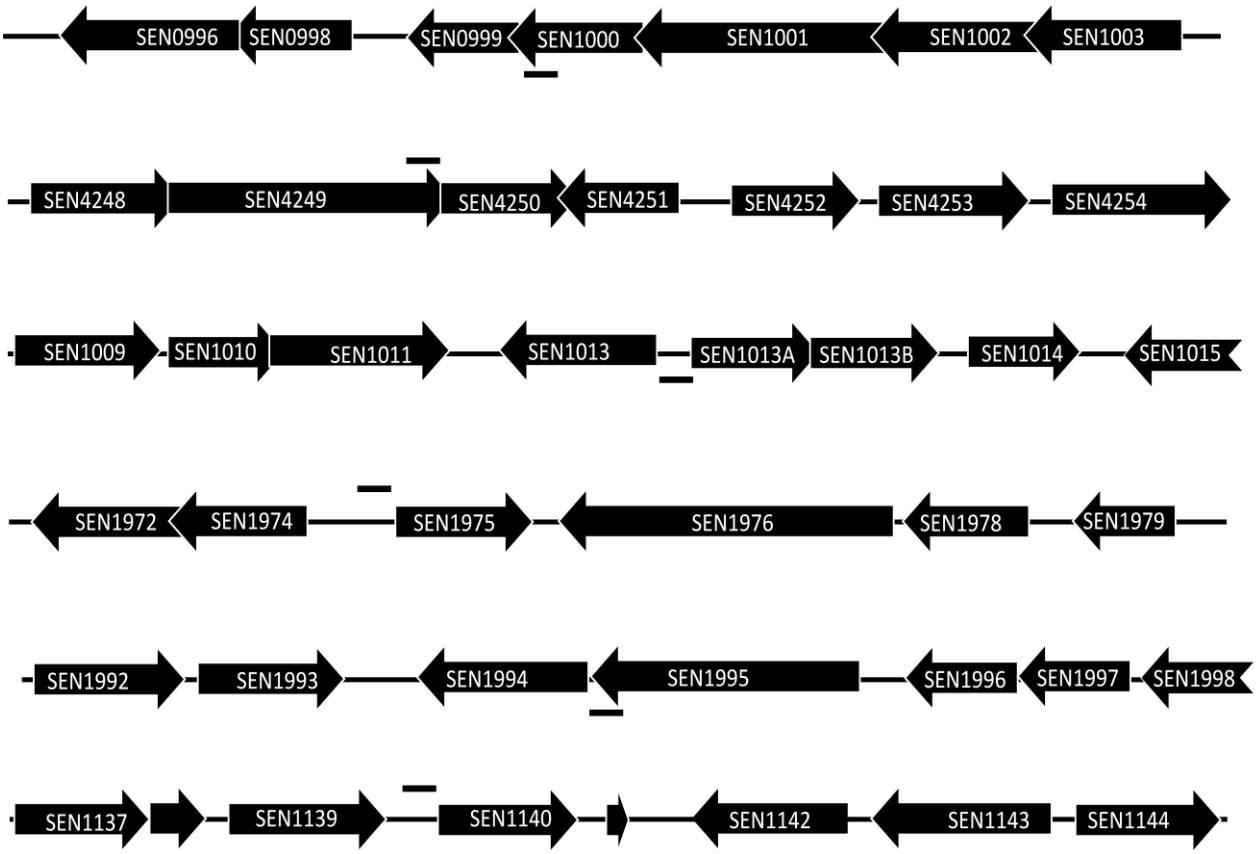

Fig S2: Complementation of *SEN1140* restores the inflammation phenotype: Strain M1511 (*S.* Enteritidis; SPI1¯) and Z292 (*SEN1140* complemented to Z290) were infected to streptomycin pretreated C57B/L6 group of mice. **A.** Cecal inflammation was assessed and presented in 13 point pathoscore scale. P>0.05 T-test. HE stained cecal sections of mice infected with **B.** M1511 (*S.* Enteritidis; SPI1¯) and **C.** Z292 (*SEN1140* complemented to Z290). (L= Lumen; Lp= Lamina propria and S= Submucosal edema). Bar represents 200μm. **D.** Bacterial load at different organ sites of infected mice. Minimum detection limit at 2 days p.i. is indicated as (---) broken line in the graph.

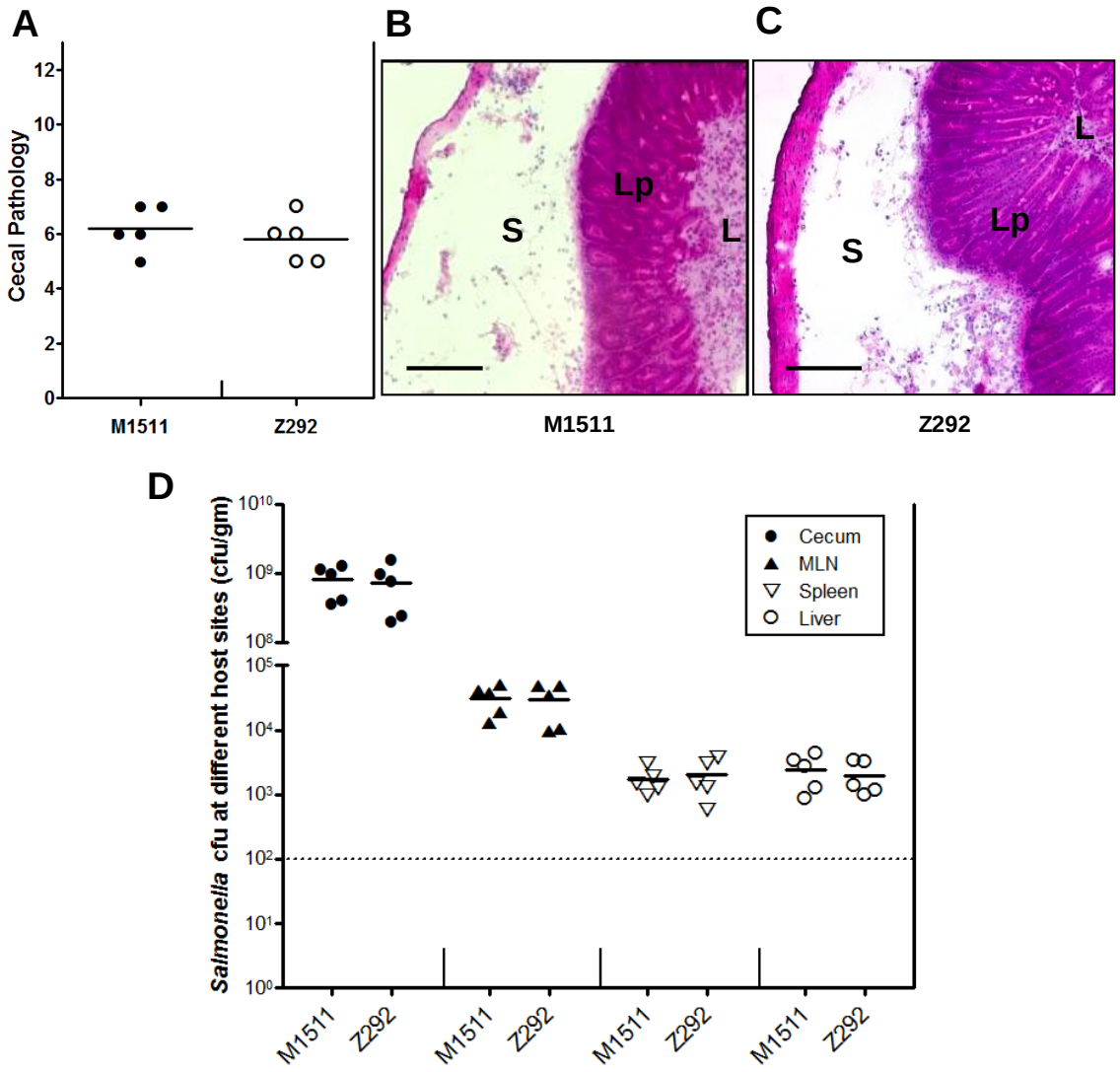

Fig S3: Comparison of cecal inflammation pattern of Z291 (*SEN1140::cat*) and M1525 (SEn-wild type) strains:

Groups of streptomycin pretreated C57B/L6 mice were infected independently with M1525 (*S.* Enteritidis; WT) and Z291 (*SEN1140::cat*). **A.** Bacterial load at different organ sites of infected mice. Minimum detection limit at day 2p.i. is indicated as (---) broken line in the graph, **B.** Cecal inflammation was assessed and presented in 13 point pathoscore scale. P>0.05 T-test; **C.** Group of 7 mice were co-infected with strain M1525 and Z291and the competitive index for colonisation as different host sites was assessed.