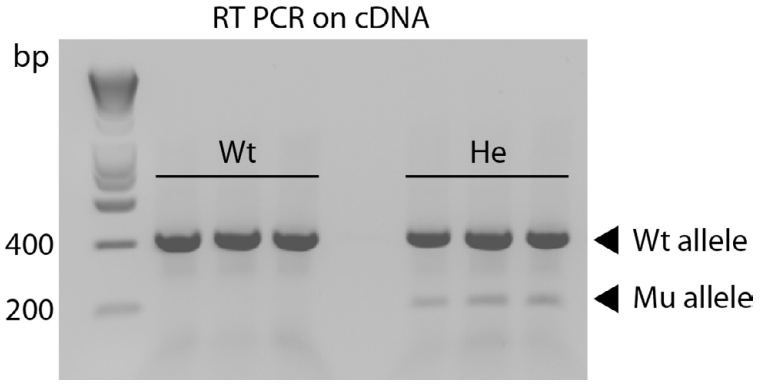

Fig. S1. Mutant transcript stability is lower than wild type transcript stability. To compare the stability of the wild type transcript with that of the mutant transcript, RT PCR was performed on three biological replicates of wild type and heterozygous *myd88* mutants (*n*=20 embryos of 3 dpf per group). The PCR product was digested using MseI, which specifically cuts the mutant transcript (at bp 200 out of 400). The 400 bp wild type transcript and the two 200 bp halves of the mutant transcript were separated by gel electrophoresis, demonstrating that the mutant transcript was less abundant than the wild type transcript.

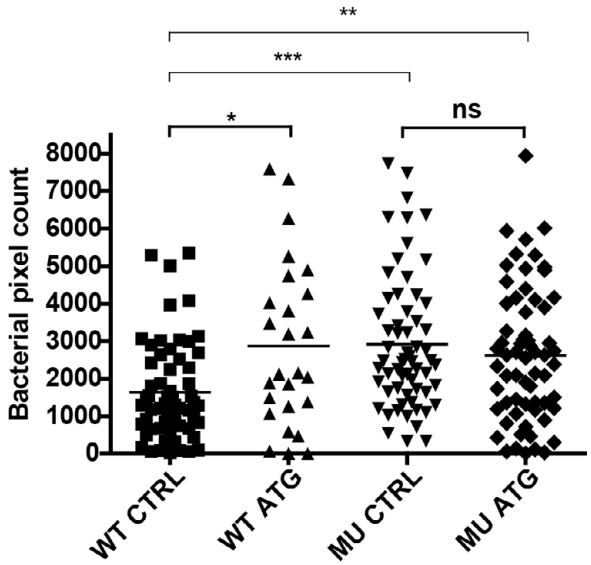

Fig. S2. AUG-morpholino targeting *myd88* does not increase bacterial burdens in *myd88* mutants. At 28 hpf, *myd88*$^{-/-}$ (Mu) and wild type (Wt) embryos injected with either an AUG-morpholino targeting the *myd88* transcript or a 5' mismatch control morpholino were infected with approximately 200 cfu of mCherry-labeled *M. marinum* strain Mma 20 by injection into the blood island and stereo fluorescence images of infected embryos were taken at 3 dpi. Bacterial pixel counts were determined based on stereo fluorescence images. Significant differences (***P<0.001; **P<0.01; *P<0.05) were determined by one-way ANOVA with Tukey's multiple comparison method as a post-hoc test.

Table S1. Primers used for qPCR analysis of gene expression

Gene	Accession #	Forward qPCR primer	Reverse qPCR primer
ppial	AY391451	5'-ACACTGAAACACGGAGGCAAAG-3'	5'-CATCCACAACCTTCCCGAACAC-3'
il1b	NM_212844	5'-GAACAGAATGAAGCACATCAAACC-3'	5'-ACGGCACTGAATCCACCAC-3'
tnfa	NM_212859	5'-AGACCTTAGACTGGAGAGATGAC-3'	5'-CAAAGACACCTGGCTGGCTGTAGAC-3'
il8	EH458432	5'-TGTGTTATTGTTTTCCTGGCATTTC-3'	5'-GCGACAGCGTGGATCTACAG-3'
cxcl-c1c	NM_001115060	5'-TCTTCTGCTGCTGCTTGCGGT-3'	5'-GGTGTCCCTGCGAGCACGAT-3'
mmp9	NM_213123	5'-CATTAAAGATGCCCTGATGTATCCC-3'	5'-AGTGGTGGTCCGTGGTTGAG-3'
ifnphi1	NM_207640	5'-TTAATACACGCAAAGATGAGAACTC-3'	5'-GCCAAGCCATTCGCAAGTAG-3'