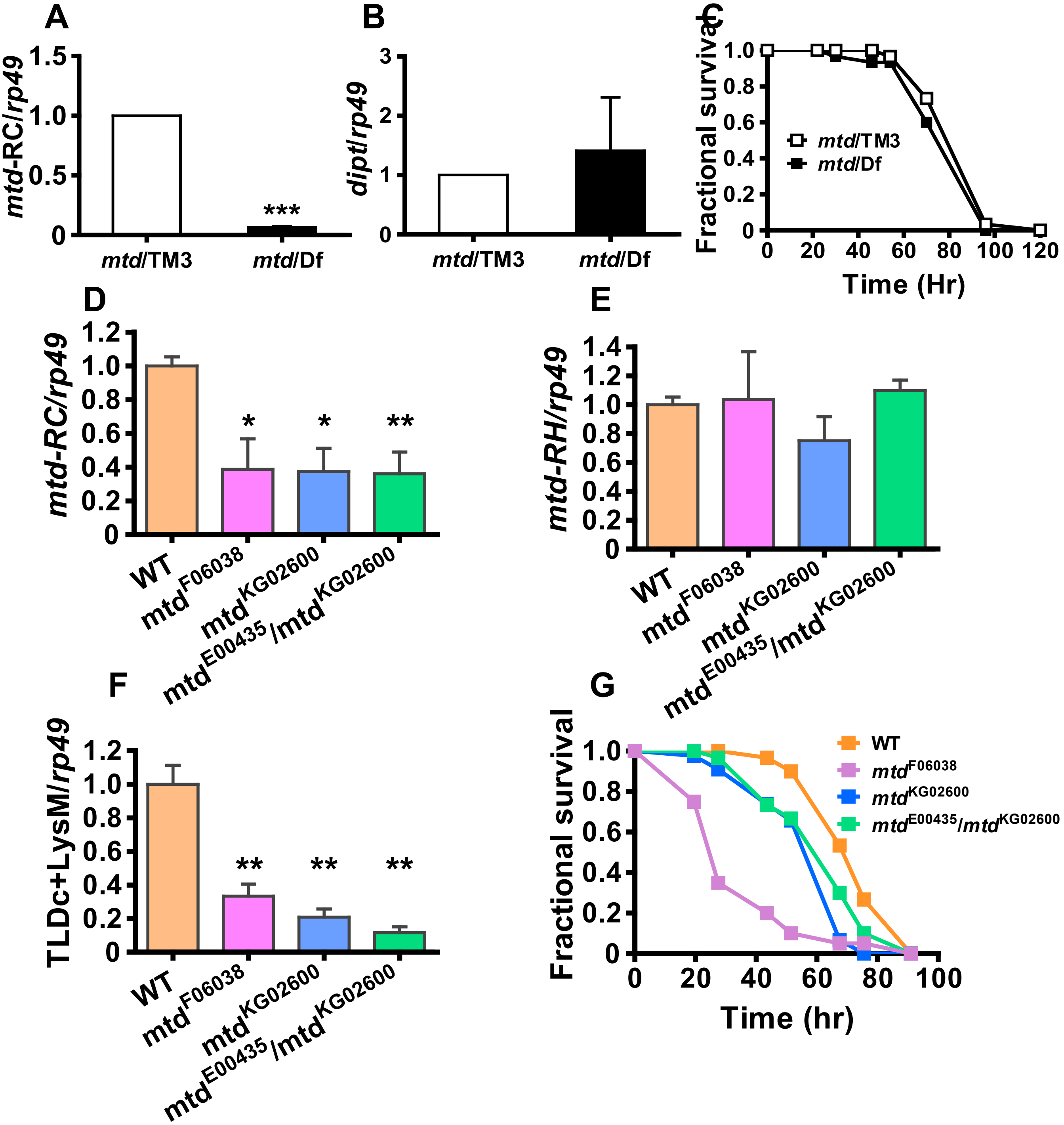

Figure S3. The *mtd*^{EY04695} mutant phenotype is not recapitulated in mutants with decreased levels of *mtd*-RC. qRT-PCR quantification of *mtd*-RC levels (A) and *dipt* levels (B) in *mtd*^{EY04695}/TM3 and *mtd*^{EY04695}/Df(3R)3-4 flies. (C) Fractional survival over time of *mtd*^{EY04695}/TM3 and *mtd*^{EY04695}/Df(3R)3-4 flies. The susceptibility of the hemizygous mutant was not distinguishable from that of control flies ($p > 0.05$)**.** qRT-PCR quantification of (D) *mtd*-RC, (E) *mtd*-RH, and (F) long transcripts (TLDc+LysM) in *yw* flies (WT) as well as the indicated *mtd* transposon-insertion mutants (insertion sites shown in Fig 6A). * indicates $p < 0.05$; ** indicates $p < 0.01$; *** indicates $p < 0.001$. (G) Fractional survival over time of orally infected *yw* flies and transposon insertion mutants. There is a statistically significant difference between survival of control flies and *mtd*^{F06038} ($p < 0.0001$), *mtd*^{KG02600} ($p < 0.0001$) and *mtd*^{E00435}/*mtd*^{KG02600} ($p = 0.018$) mutants.