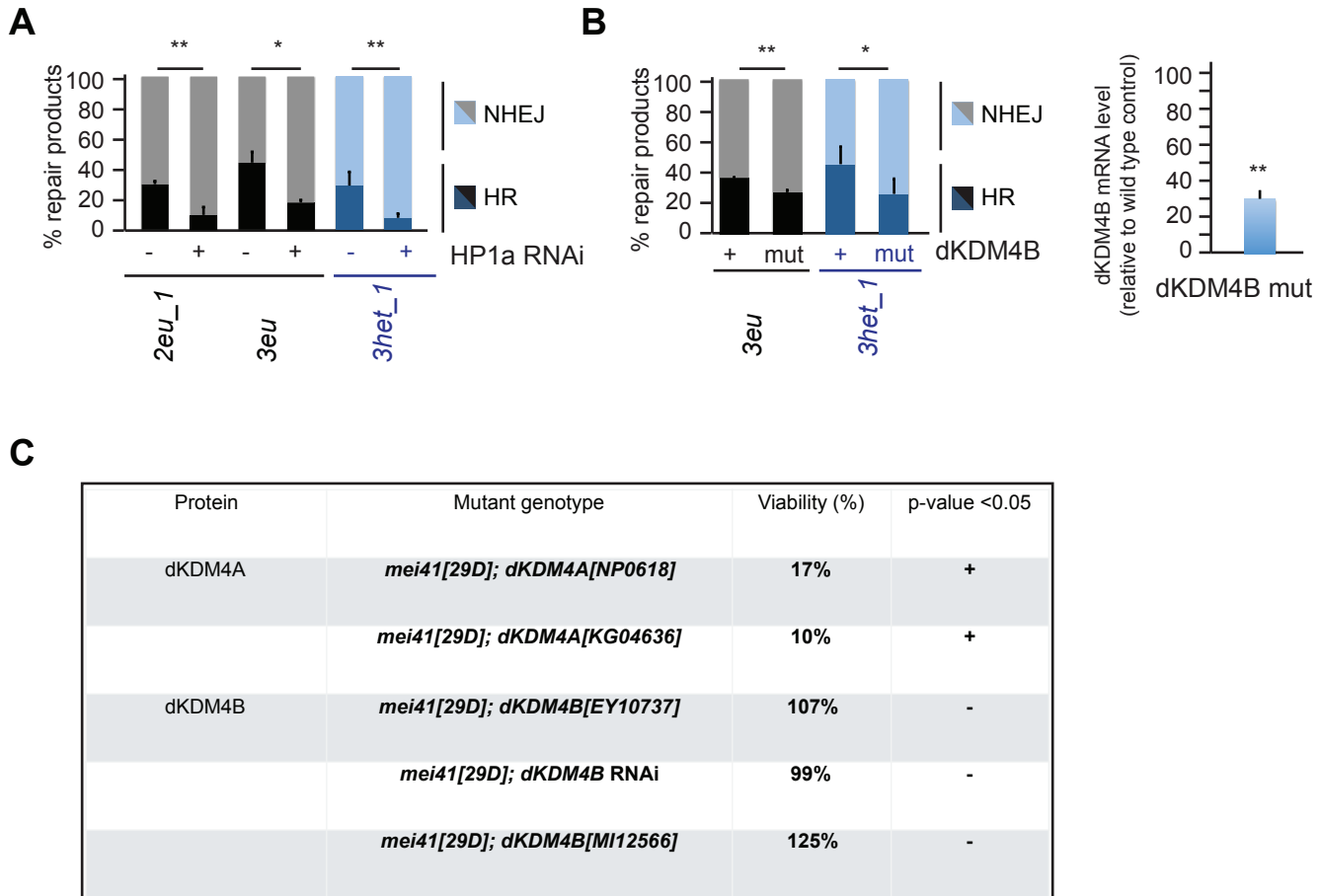


Supplemental figure 6



Supplemental figure 6.

A, B) TIDE algorithm-dependent analysis of the percentage of HR products (dark bars) and insertions and deletions (NHEJ) (light bars) from the total pool of DNA repair products identified using Sanger Sequencing. PCR was performed on genomic DNA from larvae with indicated DR-*white* insertions in the presence or absence of HP1a RNAi (A) or *dKDM4B* homozygous MI12566 mutant (B) $n \geq 3$ DR-*white*/I-SceI larvae per condition + STDEV. n.s. = p-value ≥ 0.05 , * = p-value < 0.05 , ** = p-value < 0.01 (t-test, unpaired). B, right) qRT-PCR analysis for *dKDM4B* mRNA levels in mutant. C) Quantification of the number of offspring resulting from crosses between *dKDM4A* and *dKDM4B* mutant flies and ATR (*mei-41*) mutants. p-value was determined using t-test, unpaired. Numbers indicate percentage of offspring.