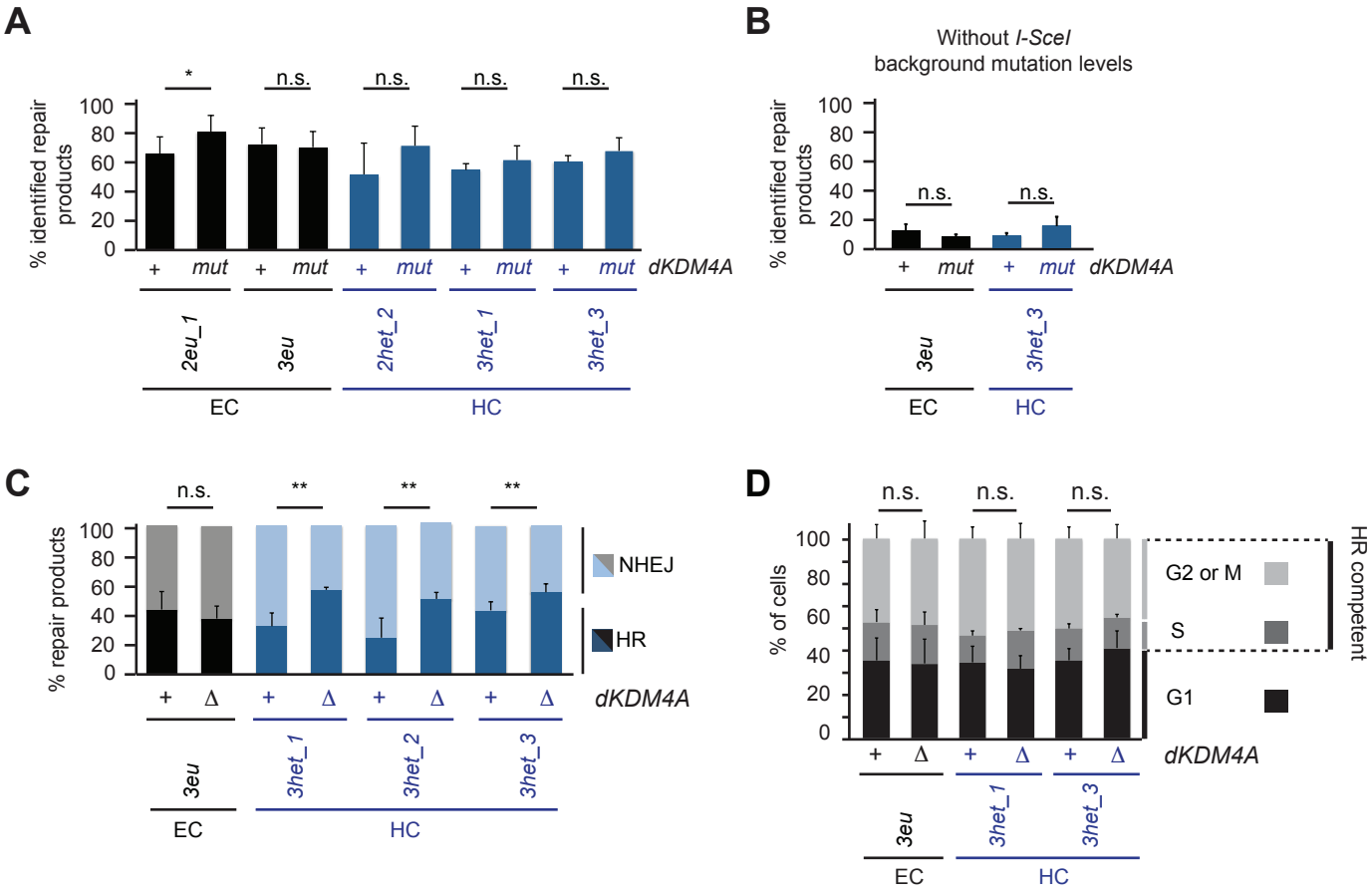
Supplemental figure 5



	FoldChange (dKDM4A RNAi vs control RNAi)	padj	FoldChange in 1st instar (deletion/ insertion vs WT)	padj
mu2	0.990277695330394	0.997879	1.04340742146436	0.999034
spnA	1.05421043673324	0.997879	0.969202680544619	0.999034
CtIP	0.974959516625972	0.997879	0.985430069528658	0.999034
tosca	1.00821463400451	0.997879	1.00344337032336	0.999034
Blm	0.926381405058853	0.997879	0.943003283873478	0.999034
lrbp	1.03863841432886	0.997879	0.9838109379101	0.999034
Ku80	1.04410785633905	0.997879	0.875328712750564	0.999034
lig4	1.08838871263183	0.997879	0.770517003983855	0.593783

Supplemental figure 5.
A) Quantification of the percentage of total identified repair products (indels + HR) in the DR-*white* PCR products using the TIDE-algorithm. Averages + STDEV are shown of n ≥ 5 DR-*white*/*I-SceI* larvae per condition. n.s. = p-value ≥ 0.05, * = p-value < 0.05, ** = p-value <0.01 (t-test, unpaired). B) Quantification of the percentage of identified background mutations in the DR-*white* PCR products using the TIDE-algorithm in control wild type and dKDM4A mutant larvae without *I-SceI* transgene expression. Averages + STDEV are shown of n = 3 DR-*white* larvae per condition. n.s. = p-value ≥ 0.05, * = p-value < 0.05, ** = p-value <0.01 (t-test, unpaired). C) TIDE algorithm-dependent extraction of the percentage of HR products (dark colored bars) and insertions and deletions (NHEJ) (light colored bars) from the total pool of DR-*white* 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 the dKDM4A homozygous mutation. n ≥ 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). D) Cell cycle analysis using *FUCCI* expressing larval tissue with indicated genotypes. Cell cycle phase of individual cells was determined based on expression of mRFP1-CycB1-266 or GFP-E2F-230; G2 or mitotic cells (G2 or M, RFP + GFP positive), S phase (S, RFP positive, GFP negative) and G1 phase (G1, RFP negative, GFP positive). n.s. = p-value ≥ 0.05, * = p-value <0.05, ** = p-value <0.01 (t-test, unpaired). Averages + STDEV are plotted for n = 3 tissues/condition with ≥ 99 cells/tissue. E) Relative changes in mRNA levels of indicated repair genes in dKDM4A depleted cells (Colmenares et al., Dev. Cell, 2017) and dKDM4A mutant flies (Crona et al., Dev. Biol, 2013).