Supplementary Figures.

Figure legends.

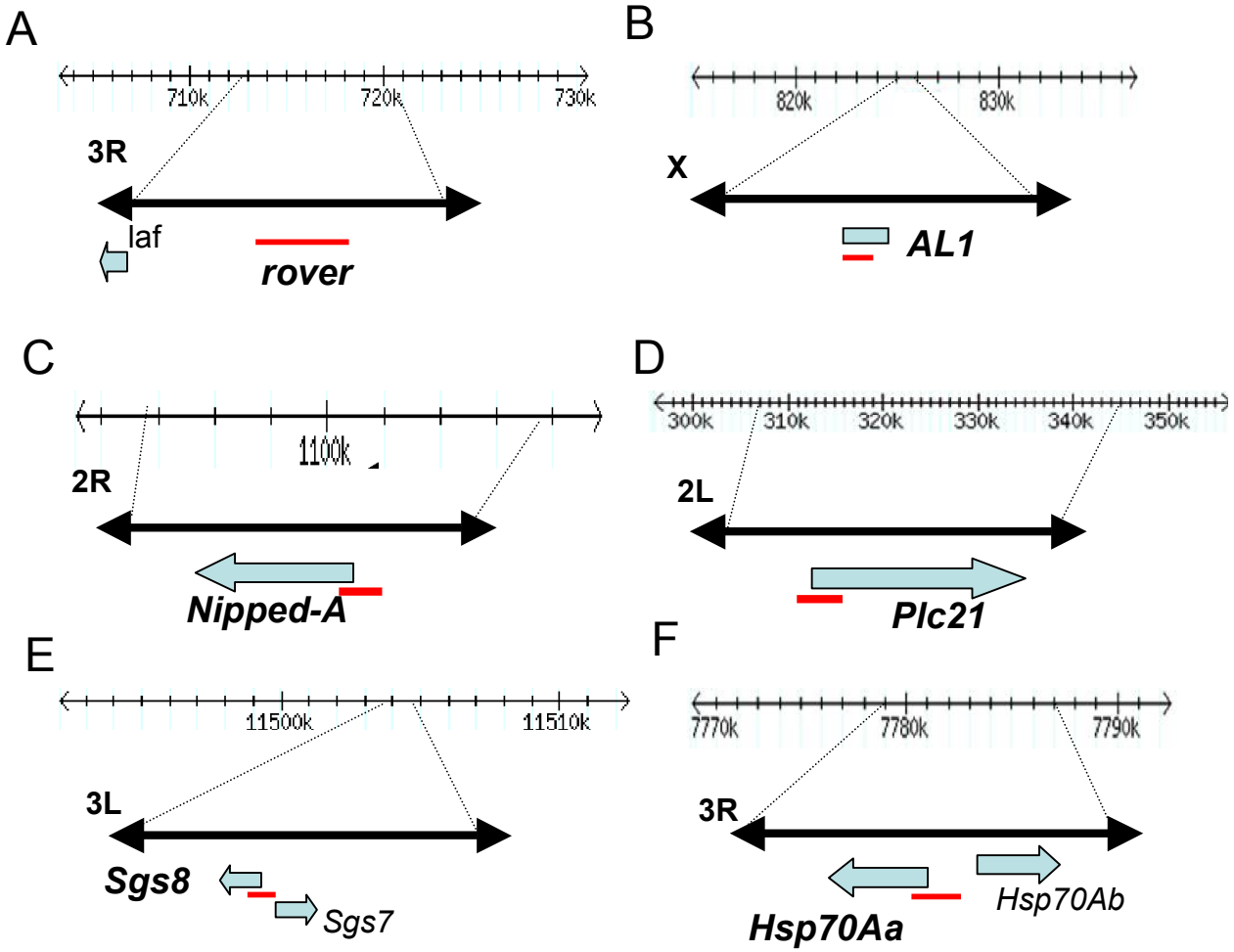
Supp. Figure 1. Specific DNA regions analyzed by ChIP before and after UV irradiation. The red line indicates the analyzed region by q-PCR. Also the chromosome arm and location of the amplified region is indicated as it is reported in flybase. In the case of structural genes the amplified sequences are located around the transcription initiation site. A) *rover* retro-transposon. B) *AL1* element. C) *Nipped* gene. D) *Pcl2* gene. E) *Sgs* 8 gene, in this particular case also the 3´region was analyzed. F) Hsp70Aa gene, in this case also the +200 to +400 sequence was analyzed. The sequences of the primers used for the analysis of these chromosomal regions are indicated in the experimental procedures section.

Supp. Figure 2. Presence of nucleosomes after UV irradiation in different chromatin regions. A, B and C) ChIP analysis of three different chromatin regions analyzed in this work, from wt flies before and after UV irradiation using an anti-core H3 antibody. Not significant changes are detected; indicating that H3 is maintained in the chromatin after UV induced DNA damage. D) ChIP analysis of the *rover* region using an anti-H3K9-Ac antibody. Note that before UV irradiation the H3K9-Ac levels are low, however after UV irradiation there is an increase in the H3K9-Ac levels in *rover*. The *rp49* promoter is highly acetylated and its levels do not change after UV irradiation. ChiP signals quantified by means of quantitative polymerase chain reaction, are presented as mean percent of input chromatin precipitated at each region; error bars indicate +/- SD.

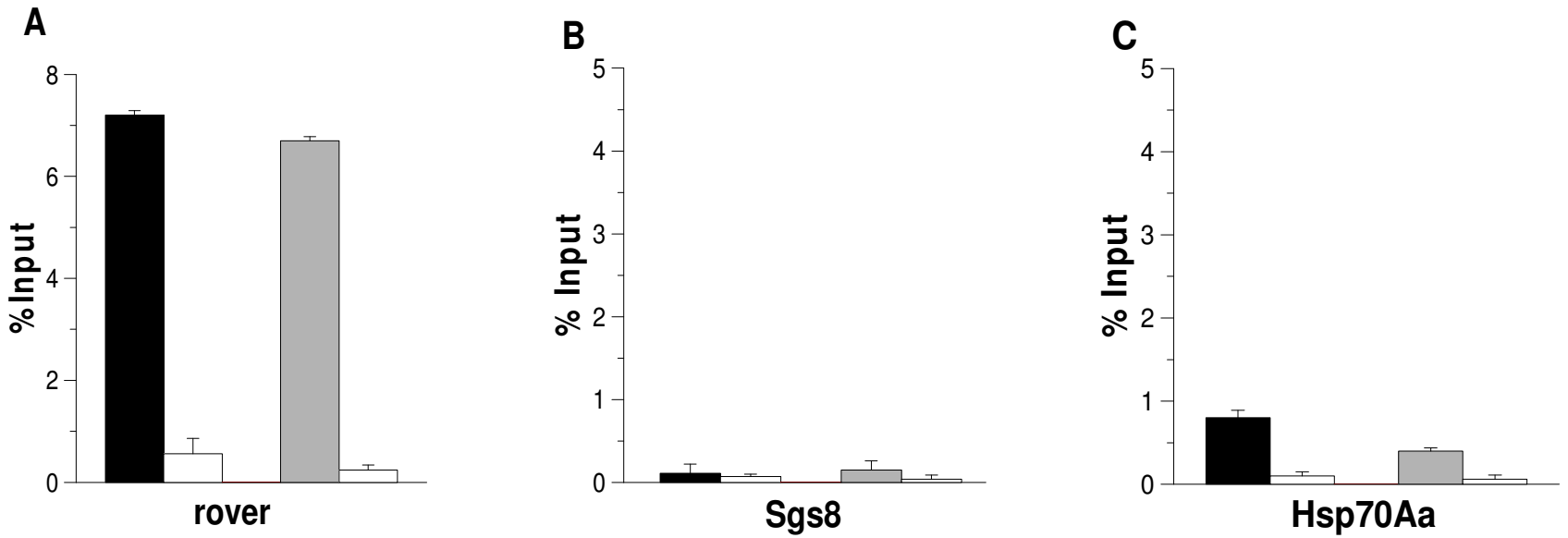
Supp. Figure 3. Location of the *Kdm4B*^{03531} transposoble element insertion in the *Kdm4B* gene. The chromosomal organization and transcripts of the *dKdm4B* gene are indicated from the flybase gene annotation. The *Kdm4B*^{03531} allele is caused by an insertion of the *P{PZ}* element in the 5´UTR of the largest mRNA *Kdm4B* isoform.

Sup. Figure 4. Recovery of the H3K9me3 levels in the rover element after UV irradiation. Third instar larvae were irradiated at 200J/m^2 and then salivary glands were dissected and fixed for ChIP experiments at different times as it is indicated in the figure. ChIP was performed as indicated in the experimental procedures section and analyzed by q-PCR. Note that after 3hr post irradiation the levels of H3K9me3 are maintained low. However after 15h, these levels increase again. ChiP signals quantified by means of quantitative polymerase chain reaction, are presented as mean percent of input chromatin precipitated at each region; error bars indicate +/- SD.

Supp. Figure 1.

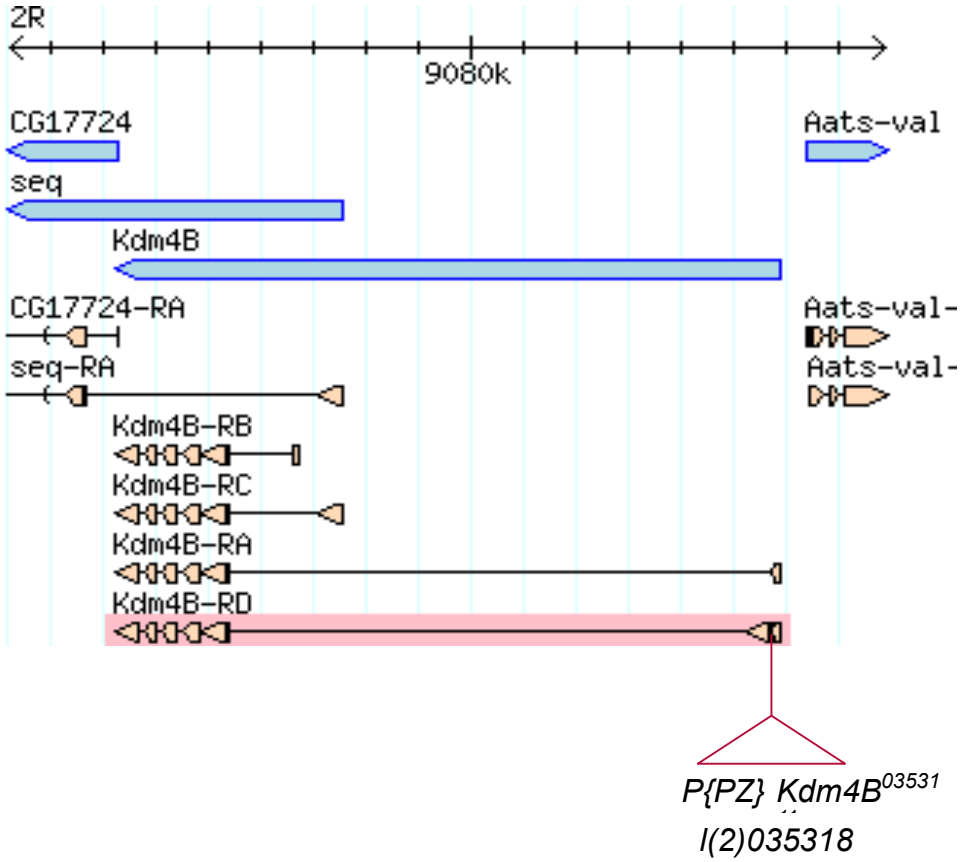


ChIPs: anti-H3



ChIPs: anti-H3K9Ac

Supp. Figure 3



Supp. Figure 4