Ninova et al., Figure S1

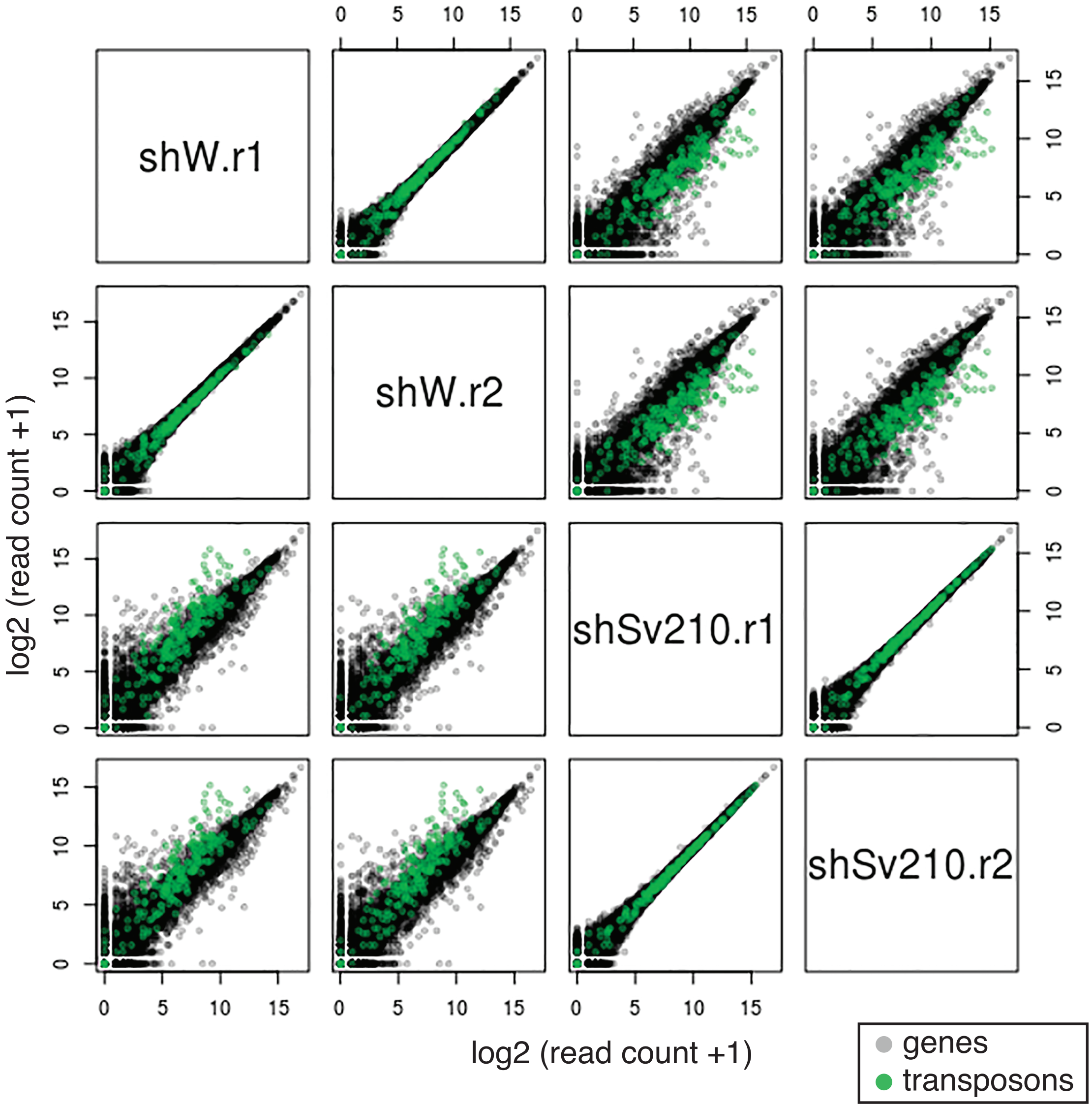


Figure S1. Related to Figure 1A. All-vs-all correlation plots between RNA-seq libraries. Data points represent log2-transformed read counts to exonic regions of genes (uniquely mapping reads) or genomic regions corresponding to RepeatMasker-annotated TE families (including repetitive reads corrected for mappability).

Ninova et al., Figure S2

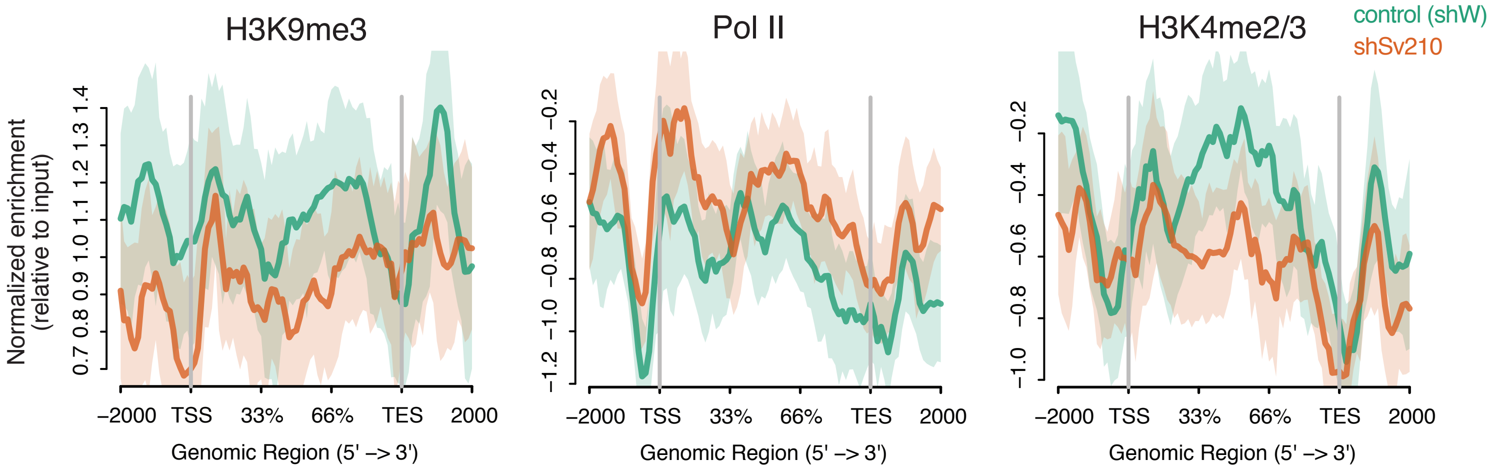


Figure S2. Related to Figure 3C. Average profiles of H3K9me3, H3K4me2/3 and RNA pol II over gene bodies of heterochromatic genes upregulated upon Su(var)2-10 GLKD in indicated conditions.

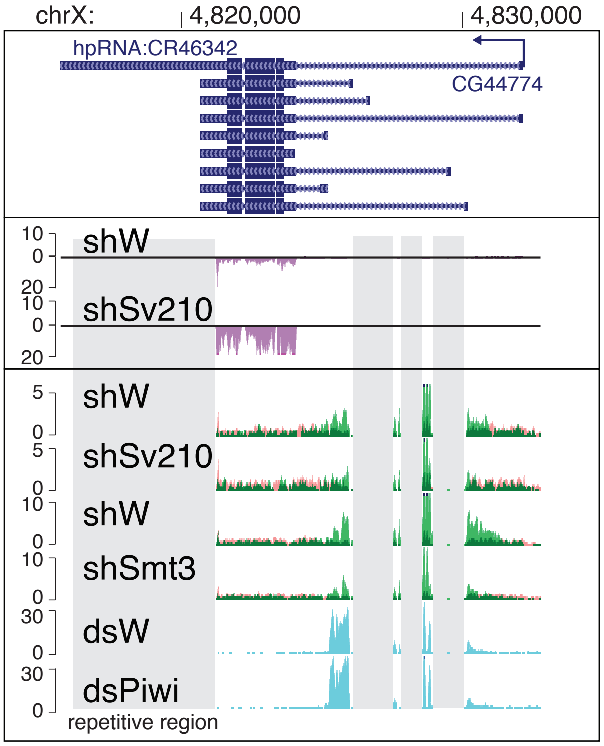
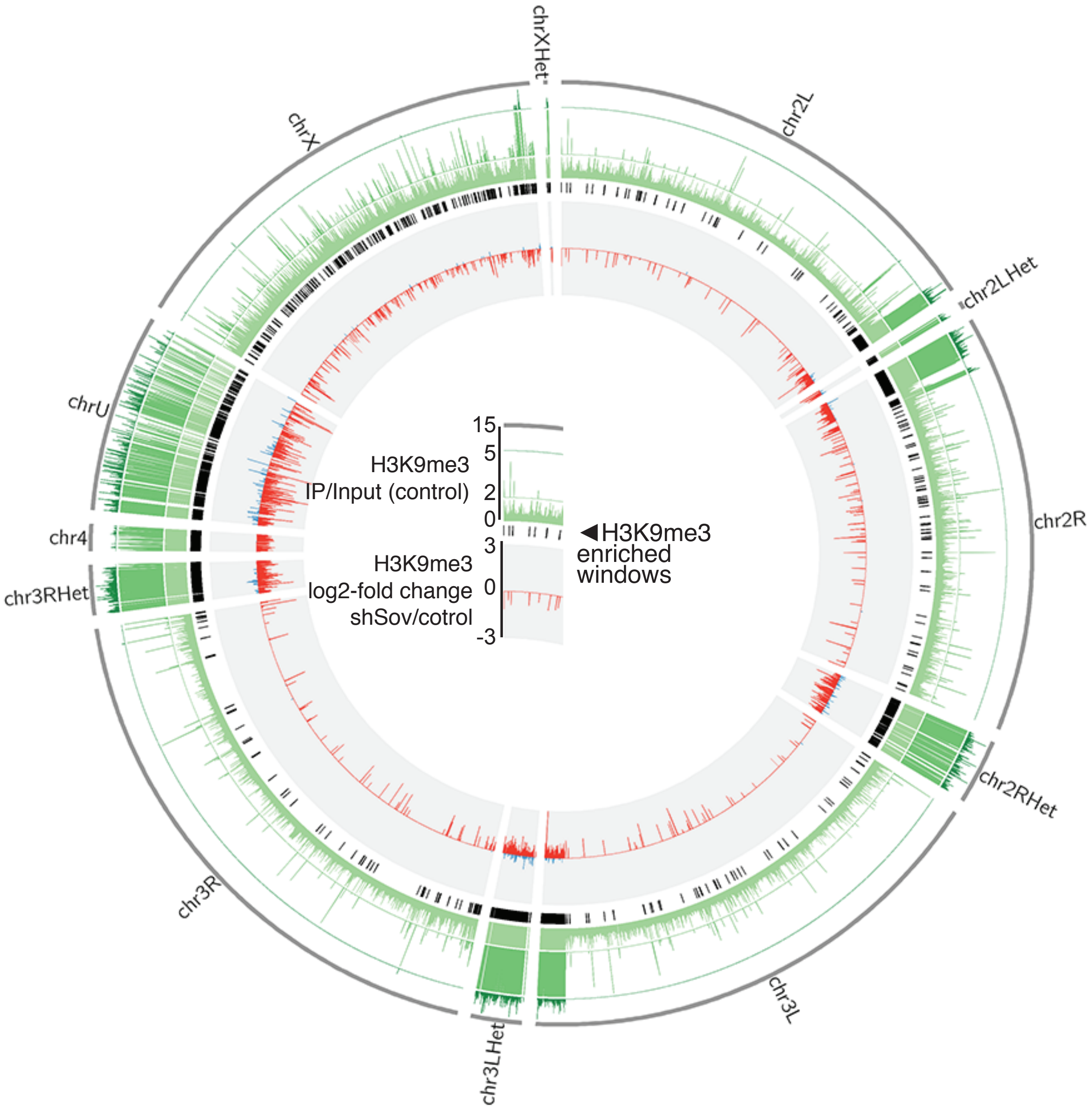

chrX:
4,820,000
4,830,000
hpRNA:CR46342
CG44774
10
0
20
shW
10
0
20
shSv210
5
0
shW
5
0
shSv210
10
0
shW
10
0
shSmt3
30
0
dsW
30
0
dsPiwi
repetitive region

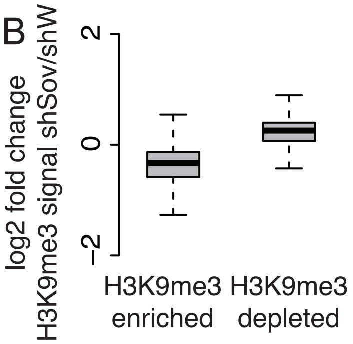
Figure S3. Loss of H3K9me3 islands at euchromatic genes leads to ectopic gene expression. Related to Figure 5. Regulation of testis-biased endo-siRNA locus *CG44774/CG4068/esi-2* through a Su(var)2-10-dependent H3K9me3 mark. UCSC browser tracks show the RNA-seq and H3K9me3 ChIP-seq signals in the indicated conditions. The *CG44774* gene is marked by a Su(var)2-10- and SUMO-dependent, but Piwi-independent, H3K9me3 peak and is expressed at low levels in the ovary. Su(var)2-10 GLKD leads to H3K9me3 loss and transcript up-regulation. Areas shaded in grey represent repetitive regions where reads did not align uniquely.

Ninova et al., Figure S4

A



B



C

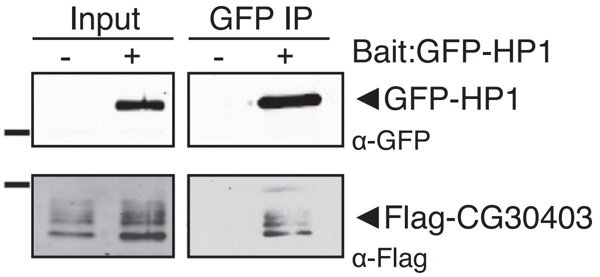


Figure S4. Sov regulates genome-wide H3K9me3 profiles. Related to Figure 6. (A) Circle plot of the H3K9me3 genome-wide distribution and fold changes upon Sov GLKD. Outer circle shows the enrichment of H3K9me3 (IP/Input) for 5-kb genomic windows in control ovaries. Black tiles indicate 5-kb windows enriched in H3K9me3 (>2 IP/Input signal ratio). Inner circle shows the fold change of H3K9me3 signal between Sov KD and control ovaries for H3K9me3-enriched regions. (B) Boxplot of the log2-transformed fold change of H3K9me3 signal upon Sov GLKD relative to control ovaries for 5-kb genomic windows enriched or depleted of H3K9me3 signal (>2 fold enrichment cutoff). (C) CG30403 interacts with HP1. Flag-CG30403 and GFP-HP1a were co-expressed in S2 cells. Western blot shows results from co-immunoprecipitation using GFP-HP1 as a bait.

Ninova et al., Figure S5

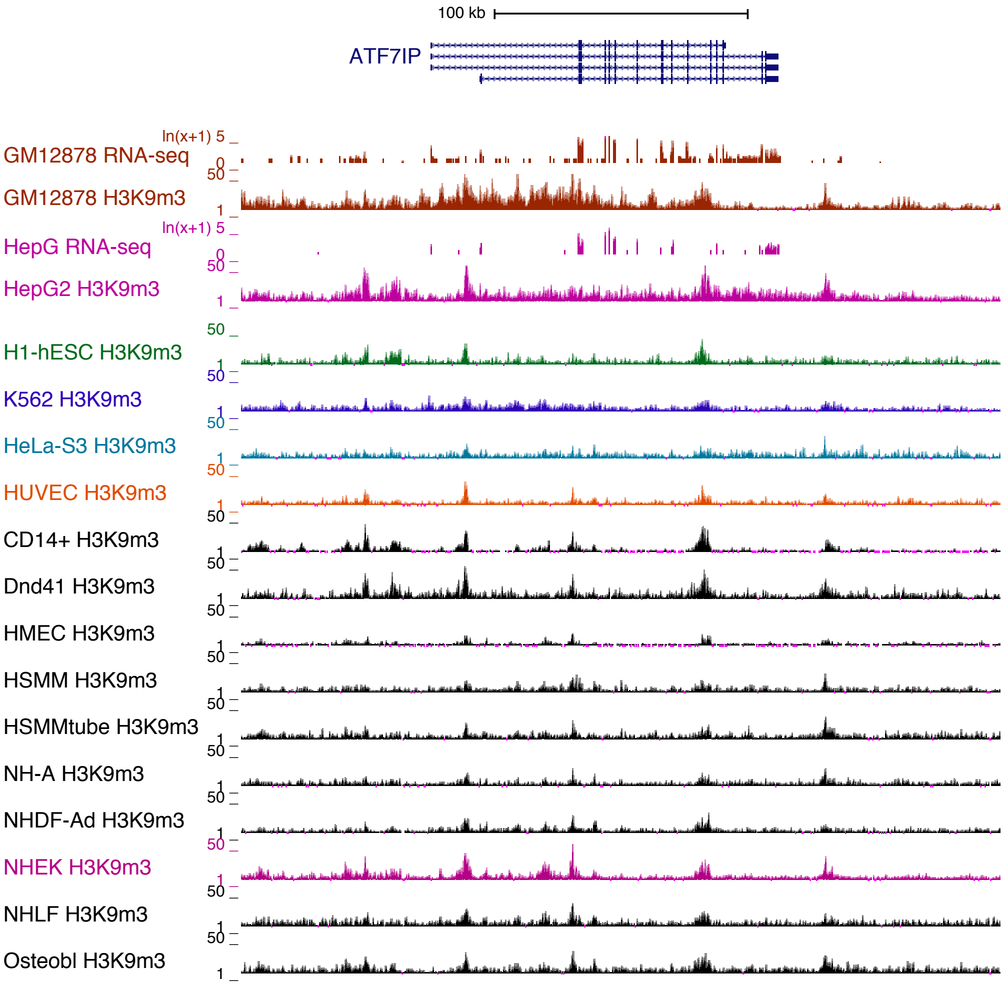


Figure S5. H3K9me3 mark on ATF7IP. Related to Figure 6. UCSC ENCODE tracks of H3K9me3 enrichment over ATF7IP (Wde homolog) in various human cell lines (hg19). RNA-seq tracks show that ATF7IP is expressed in lines with high H3K9me3 enrichment.