Fig S4: Many types of aberrant transcripts are upregulated in Δxap5. Percentage of (A) sense non-coding transcripts (SNC) and (B) intergenic transcripts that are up- and down-regulated in Δxap5. Venn diagrams showing the overlap between (C) up- and (D) down-regulated SNC transcripts and (E) up- and (F) down-regulated intergenic transcripts in the indicated mutants. Transposon-associated and antisense (AS) sequences are upregulated in Δxap5. (G) Strand-specific RT-PCR confirmation of upregulation of AS transcripts at representative loci; representative of two independent experiments (H) Quantitative RT-PCR confirmation of upregulation of wtf loci. Lowercase letters denote statistically significantly different groups (one-way ANOVA with Bonferroni’s multiple comparison test, p<0.05); the values are the mean±s.e.m of three independent experiments, each with three biological replicates (n=3). Abundance of sense and antisense transcripts are not correlated in Δxap5. (I-L) Representative loci with different patterns of regulation of sense and AS transcripts. In 41% of the loci with significantly upregulated AS transcripts, sense transcripts are significantly (p≤0.01) downregulated, as shown for the (I) fet4 and (J) SPAC1142.04 loci. 21% of the loci with upregulated AS transcripts do not show significant alterations in levels of sense transcripts, as shown for the (K) swr1 and (L) rad26 loci. dm = Δxap5Δpht1 double mutant. Statistical significance of differential expression was determined using the negative binomial exact test (p≤0.01, fold change≥2). Panels A-F and I-L are based on three biological replicates.