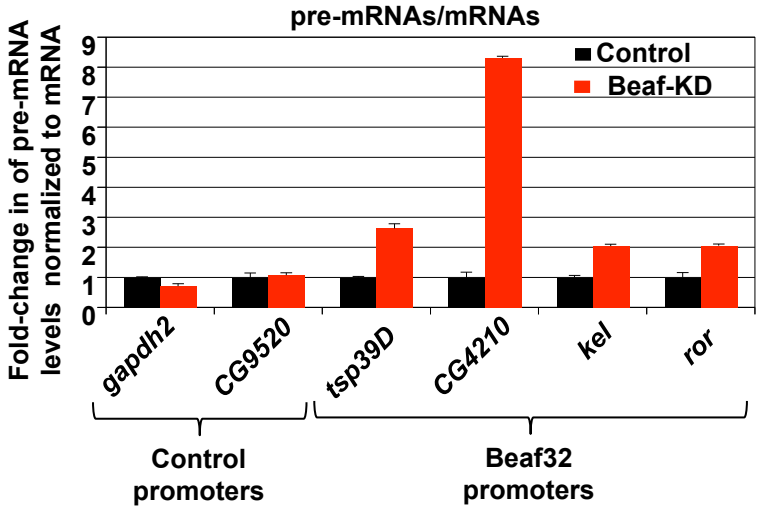
A


pre-mRNAs/mRNAs
Fold-change in of pre-mRNA levels normalized to mRNA
0
1
2
3
4
5
6
7
8
9
Control
Beaf-KD
gapdh2
CG9520
tsp39D
CG4210
kel
ror
Control promoters
Beaf32 promoters

B

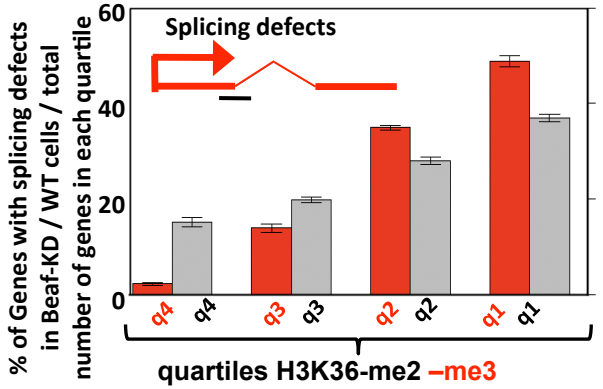

% of Genes with splicing defects in Beaf-KD / WT cells / total number of genes in each quartile
0
20
40
60
Splicing defects
q4
q4
q3
q3
q2
q2
q1
q1
quartiles H3K36-me2 –me3

Figure S7. RNA splicing defects upon depletion of Beaf32 or dMes-4

A. Graph showing examples of RTqPCR measurements (in triplicate) using oligos that span exon-intron junctions to quantify the levels for immature RNAs in Beaf32-KD (red bars) compared to WT cells (black bars) after normalization to the levels of mature RNAs for the indicated genes that harbor a Beaf32 binding site or not (see also Figure E9B for a similar analysis to 16 Beaf32-bound or unbound genes in Beaf32-KD; see Methods for a list). y-axis, fold change normalized to mature RNA levels.

B. Histogram showing the percentage of genes with significant splicing defects as quantified by measuring 'retained introns' by counting RNASeq reads in introns normalized to RNASeq read counts in exons in three independent Beaf32-KD compared to WT cells (see Methods)(Hu et al., 2013), as a function of the H3K36-me2 or -me3 quartiles (see also Figure 5C).