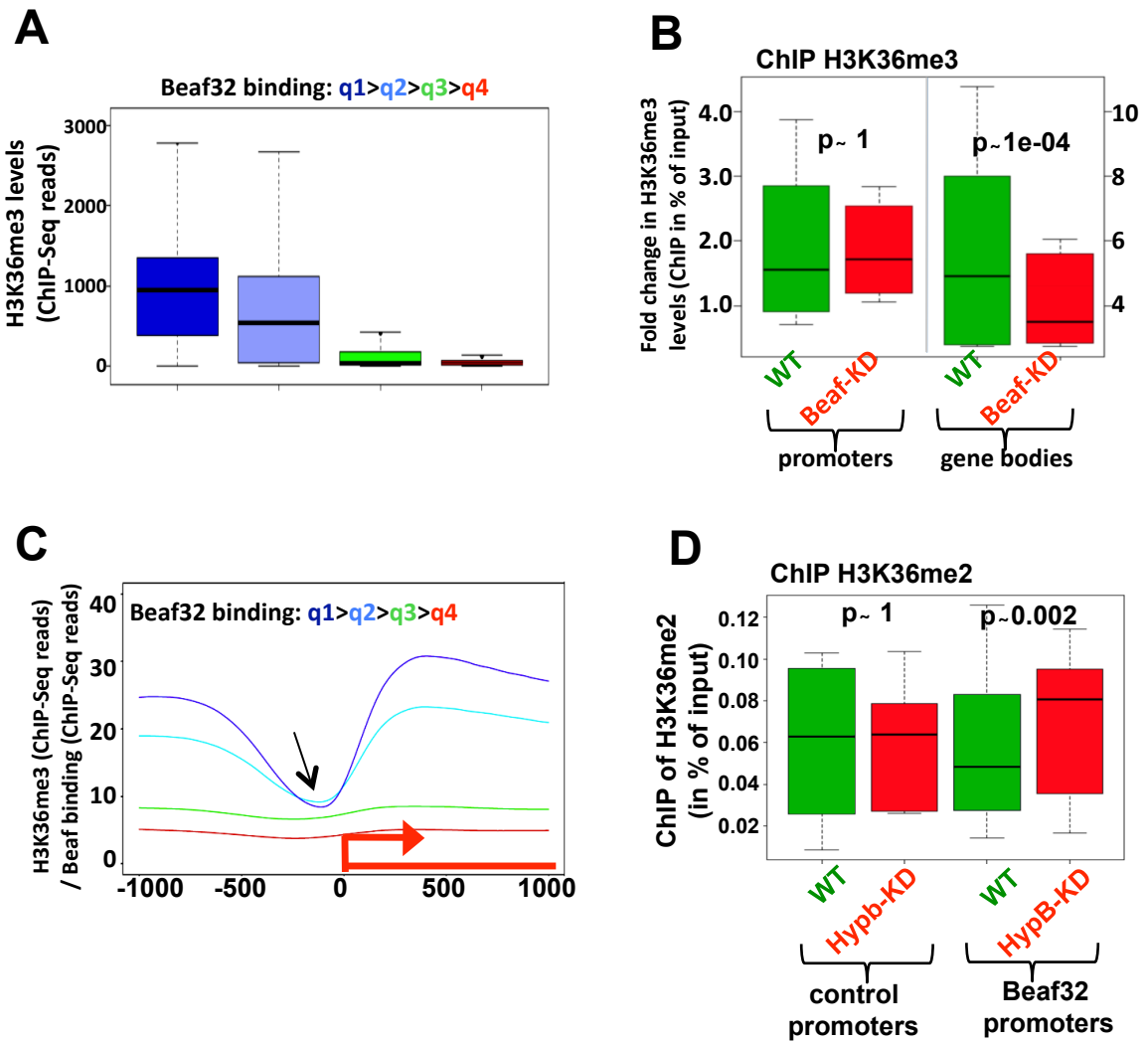
A
Beaf32 binding: q1>q2>q3>q4
H3K36me3 levels (ChIP-Seq reads)
3000
2000
1000
0
B
ChIP H3K36me3
Fold change in H3K36me3 levels (ChIP in % of input)
4.0
3.0
2.0
1.0
10
8
6
4
p~ 1
p~1e-04
WT
Beaf-KD
WT
Beaf-KD
promoters
gene bodies
C
Beaf32 binding: q1>q2>q3>q4
H3K36me3 (ChIP-Seq reads) / Beaf binding (ChIP-Seq reads)
40
30
20
10
0
-1000
-500
0
500
1000
D
ChIP H3K36me2
ChIP of H3K36me2 (in % of input)
0.12
0.10
0.08
0.06
0.04
0.02
p~ 1
p~0.002
WT
Hypb-KD
WT
HypB-KD
control promoters
Beaf32 promoters

Figure S6. Beaf32 binding correlates with H3K36me3 levels

A. Box plot showing the enrichment in H3K36 trimethylated levels according to the ranking of genes by quartiles of Beaf32 binding (~3650 genes/quartile; from 'q1'/highest to 'q4'/lowest-levels). y-axis, ChIP-Seq reads for H3K36me3.

B. Box plot showing the results of ChIP performed in Beaf32-KD (red boxes) compared to WT-control (mock-depleted) cells (green boxes) in percent of input (y-axis) with anti- H3K36me3 antibodies or IgG control for promoters harboring a Beaf32 site (see Methods for a list of genes; see Figure 5A for similar analysis of the same Beaf32 bound promoters as compared to control promoters). ChIP data were analyzed by qPCR analyses in triplicates and for three independent measures normalized to three control loci.

C. Averaged profiles of H3K36me3 levels (y-axis; in ChIP-Seq reads) according to quartiles of Beaf32 binding (see panel A). The arrow indicates the relatively low levels of H3K36me3 in promoter regions as compared to gene bodies.

D. Box plot showing the results of ChIP performed in Hypb-KD (red boxes) compared to WT-control (mock-depleted) cells (green boxes) in percent of input (y-axis) with anti- H3K36me2 antibodies or IgG control, for 16 promoters harboring a Beaf32 site or not (see Methods for a list of genes). ChIP data were analyzed by qPCR analyses in triplicates and for two independent measures normalized to three control loci. Note that the increase in H3K36me2 levels upon Hypb-KD supports its role in triggering the transition from H3K36me2 to H3K36me3 (Bell et al., 2007).