



### **Figure S10. Influence of IBP/dMes-4 on H3K27me3 deposition**

**A.** Averaged H3K27me3 profiles for control promoters where no significant variations in H3K27me3 levels could be scored between Beaf32-KD and control ('WT') cells as measured by ChIP-Seq (see Methods). Note that such variations were systematically scored over +/- 2 Kbp regions surrounding all *Drosophila* TSSs. See Figure 7B for the complementary list of genes (990 genes) with significant changes in H3K27me3 levels upon Beaf32-KD.

**B.** Histogram representing the percentage of genes with no variation in H3K27me3 levels in Beaf32-KD/WT (y-axis) depending on the presence or absence of a Beaf32 binding site in their promoters. See Figure 7C for a similar analysis of the complementary list of genes.

**C.** Heat map representing the intersection analysis between the list of genes with variations in H3K27me3 levels ('var'; see Figure 7B) or no variation ('ctrl', see Figure E10A) and the list of genes whose promoters were bound by Beaf32 ('Beaf32') or not ('no Beaf32') and/or genes that were differentially expressed ('DE genes') or not (control) genes in Beaf32-KD or dMes4-KD (left and right heat maps, respectively). Each intersection was tested using fisher exact test.

**D.** Fold changes in H3K27me3 levels between Beaf32-KD and dMes4-KD. H3K27me3 levels were measured by qPCR from ChIP experiments performed in three independent triplicates in Beaf32-KD compared to control cells (x-axis) or in dMes4-KD compared to control cells (y-axis). The genes tested include those selected based on variations as scored from our ChIP-seq data (see Methods) as well as those genes tested in other ChIP assays (Figure 6; see Methods for a list).

**E.** Control of primers by quantitative PCR standard curves. The graph shows an example of the standard curve used to quantify gene expression or ChIP analysis by RT-qPCR and q-PCR analyses, respectively, as done for every oligo pair used in this study. The quantification was automatically done using the pyQPCR software to calculate linear regressions and PCR efficiency (calculation details are available at <http://pyqpcr.sourceforge.net/>; see Methods) with triplicate measurements for each of 4 concentrations used to generate a standard curve for either cDNAs (for gene expression measurements) or input DNAs (for ChIP measurements and determination of copy number for gene expression). x-axis: Quantity of DNA (in Log scale). y-axis: Ct (threshold cycle) of qPCR.