



**Figure S8. Additional chromatin features enrichment at TAD borders.** (A) Profiles of architectural proteins (JIL-1, mod(mdg4), su(Hw), Zw5, fs(1)h, SA, SMC1 and Nipped-B) around direct maintained and lost TAD borders. The right panel plots clustering of the signal at maintained and lost TAD borders (see Materials and Methods). (B) Profiles of accessibility (H1 and DNase-I) and transcription (MED1 and Pof) at maintained and lost TAD borders. In addition, we plot RNA-seq signal in WT, BEAF-32 knockdown and Cp190 and Chro double knockdown. (C) Profiles of histone modifications (H2Bubi, H3K18ac, H3K23ac, H3K27me1, H3K36me1, H3K4me2, H3K79me1, H3K79me2, H3K79me3, H4K16ac, H4K20me1, H4K8ac, H3K36me3 and H3K27me3) at direct maintained and lost TAD borders. In the clustering analysis, we marked with red histone modifications associated with dense chromatin and with green histone modifications associated to open chromatin. Histone modifications that have been reported to be associated with both open and dense chromatin were marked by black.