



Figure S10. *Chromatin state annotation at maintained, lost and new TAD borders.* We computed the overlap between each maintained, lost and new robust TAD border (see Fig. 1B and Fig. 2A) in the three knockdowns with chromatin states: (A) BEAF-32 single knockdown, (B) Cp190 and Chro double knockdown and (C) BEAF-32 and Dref double knockdown. Top panels: the percentage of the overlap between the different chromatin states and maintained, lost and new robust TAD borders and whole genome. Bottom panels: $\log_2(\text{observed}/\text{expected})$, where observed is the percentage in maintained, lost or new classes and expected is the whole genome distribution. (D) Same as in (A-C) for maintained, lost and new direct borders that were common between BEAF-32 single knockdown and Cp190 and Chro double knockdown. (E) Gene Regulatory Blocks within 2 kb of different categories of direct borders: maintained, lost and new borders common between BEAF-32 single knockdown and Cp190 and Chro double knockdown. We performed a Fisher's exact test (p-value: n.s. ≥ 0.05 , * p-value < 0.05 , ** < 0.01 and *** < 0.001). (F) Pol II pausing at maintained, lost and new direct borders that were common in BEAF-32 single knockdown and Cp190 and Chro double knockdown. We performed a Mann-Whitney U test (p-value: n.s. ≥ 0.05 , * p-value < 0.05 , ** < 0.01 and *** < 0.001).