

Weak intron Competent Polycomb Heterochromatin Heterochr. in eu. Basal New Borders Whole Genome Lost Borders Maintained Borders 20 1.0 og₂(obs/exp) 0.0 -1.0 -2.0 Basal Active TSS Active intron Weak intron Competent Polycomb Heterochromatin Heterochr. in eu Chromatin states at direct borders common to BG3_{BEAF-32} and BG3_{Cp190}-Chro-in 5 kb windows TSS proximal Elongation Enhancer Active TSS Active intron Weak intron Competent Polycomb Heterochromatin Heterochr. in eu. Basal New Borders Whole Genome LostBorders 2.0 1.0 log_(obs/exp) 0.0 -1.0 -2.0 Basal Active TSS Neak intron Polycomb Heterochromatin Active intron Competent Heterochr. in eu.

TSS proximal

Elongation

Active TSS

Active intron

Enhancer

Pol-II pausing at all genes in 5 kb of direct borders common to BG3BEAF-32 - and BG3Cp190- Chro-



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 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: log₂(observed/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. (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 bordewn. We performed a Mann-Whitney *U* test (p-value: n.s. ≥ 0.05 , * p-value < 0.05, * p-value < 0.