

Figure S2. General characterisation of Hi-C datasets. (A) Contacts vs distance plots for HiC dataset. For each Hi-C dataset we generated two replicates and in the first five panels we compare the two replicates with a merged dataset of the two replicates for: Kc167 WT cells, BG3 WT cells, BG3 cells with BEAF-32 single knockdown, BG3 cells with Cp190 Chro double knockdown and BG3 cells with BEAF-32 Dref double knockdown. The plots confirm that there are negligible differences between the two replicates and the merged dataset in each condition. In the last panel, we plot the merge datasets for all five conditions. The plot shows that the three knockdowns in BG3 display different behaviours to WT. The inset plot shows the p-value of the paired Mann Whitney U Test and shows that all differences between the WT and knockdowns are statistically significant. (B) Genome-wide contact map of the three knockdowns (BG3 cells with BEAF-32 single knockdown, BG3 cells with Cp190 Chro double knockdown and BG3 cells with BEAF-32 Dref double knockdown) at 100 kb resolution. Each element in the matrix represents the log₂ of the number of contacts between the two corresponding bins. (C) log₂ ratio between the normalised number of contacts on chromosome 2L in: (i) BEAF-32 knockdown and WT cells, (ii) Cp190 Chro double knockdown and WT cells, (iii) Cp190 Chro double knockdown and BEAF-32 knockdown cells, (iv) BEAF-32 Dref double knockdown and WT cells, (v) BEAF-32 Dref double knockdown and BEAF-32 knockdown cells and (vi) BEAF-32 Dref double knockdown and Cp190 Chro double knockdown cells. Red colours indicate less contacts in the first condition and blue colours more contacts in the first condition. (D) Histograms of the log₂ ratio between the normalised number of contacts genome wide in the six cases in panel (C). The vertical lines mark -1 and 1 indicating a two-fold difference between the two conditions. (E) Percentages of contacts at 100 kb bins that show at least two-fold difference between the two conditions. We also performed a Fisher's exact text and confirm that the differences in these percentages are statistically different (p-value < 0.001 in all cases).