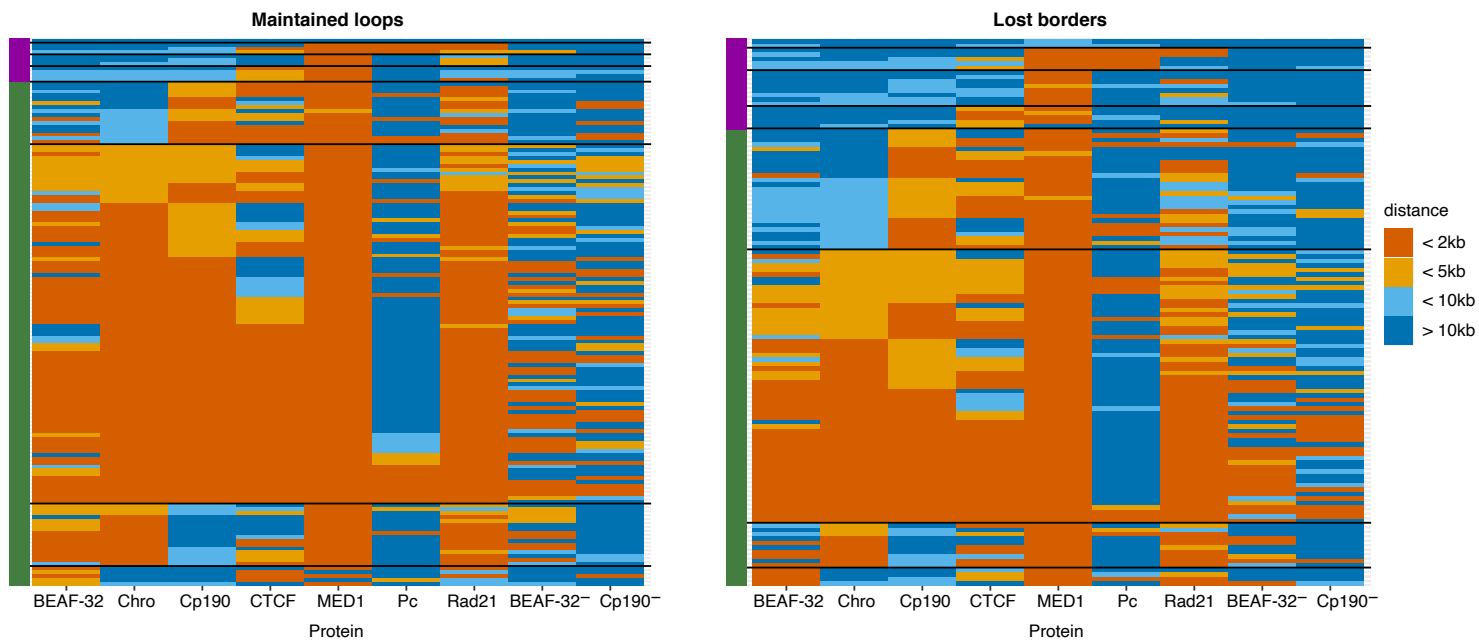
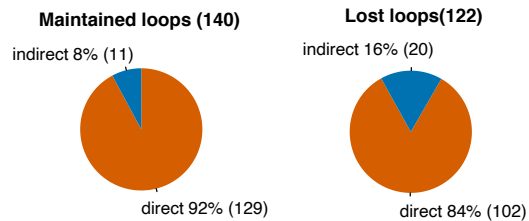


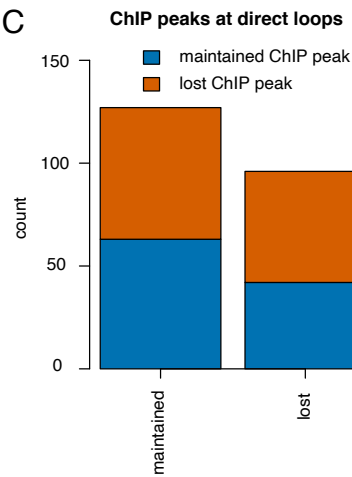
A



B



C



D

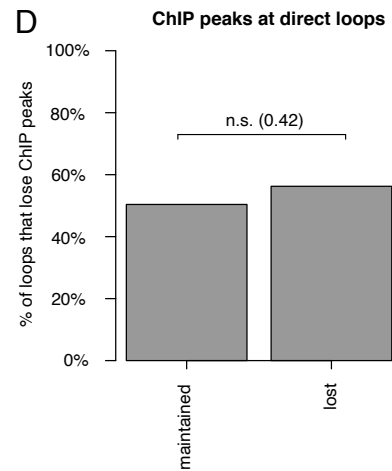


Figure S13. Direct and indirect chromatin loops. We considered separately the cases of maintained and lost chromatin loops. (A) Heatmaps plotting the distance of the closest ChIP peak from a maintained or lost loop for: BEAF-32 (WT and BEAF-32 knockdown), Chro (WT), Cp190 (WT and Cp190 knockdown), CTCF (WT), MED1 (WT), Pc (WT) and Rad21 (WT). Green bar on the side of each heatmap marks direct loops (loops that show binding of BEAF-32, Chro and/or Cp190 in WT cells), while purple indirect loops (all other borders). (B) Percentage of maintained and lost chromatin loops that have direct binding of BEAF-32, Cp190 and Chro. (C) number of chromatin loops that have BEAF-32 or Cp190 ChIP in WT cells and lose those peaks in BEAF-32 and Cp190 single knockdowns. (D) Percentage of chromatin loops that have BEAF-32 or Cp190 ChIP in WT and lose them in the in BEAF-32 and Cp190 single knockdowns. We performed a Fisher's exact test and the corresponding p-value is displayed above the barplots.