Figure S4

a

BRD4 occupancy around integration sites (50 bp)

b

c

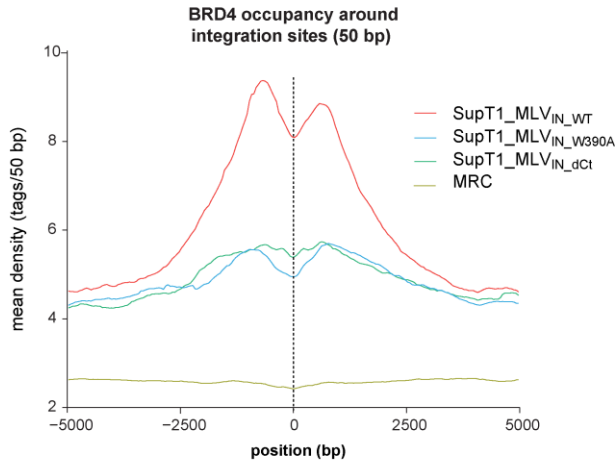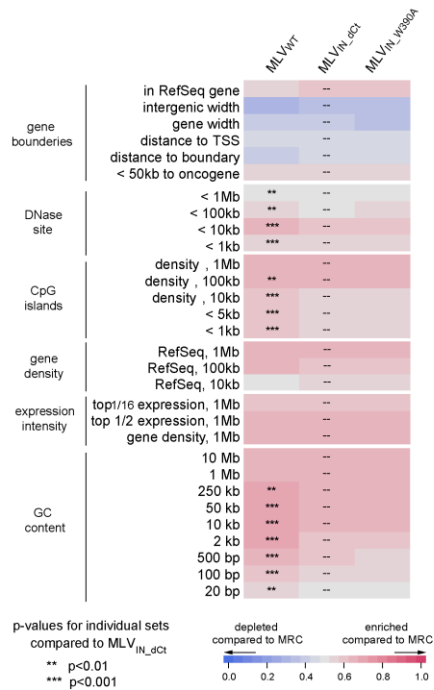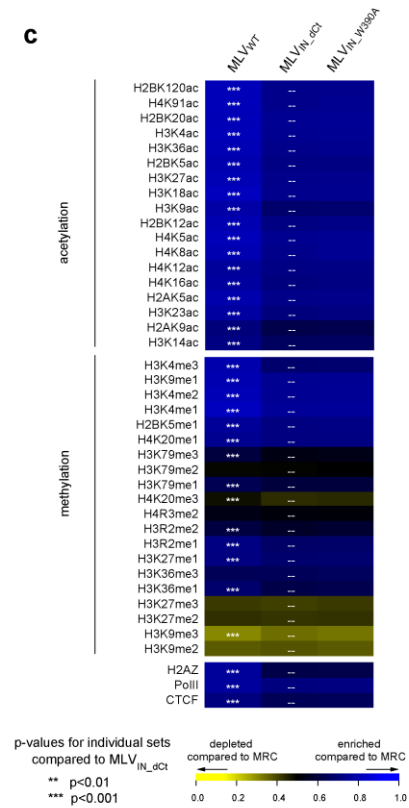**Figure S4: Loss of the BET interaction uncouples MLV integration from BET hot spots**

(a) Mean background-subtracted ChIP-seq read density for BRD4 generated in CD4+ T-cells in 50bp bins for a 10kb window around MLV_{IN_WT}, MLV_{IN_W390A} and MLV_{IN_dCt} integration sites obtained in SupT1 cells.

(b-c) Heat map summarizing the relation between vector integration site frequency and genomic (b) or epigenetic (c) features in SupT1 cells. Evaluated vectors are indicated above the columns. Features analyzed are shown to the left of the corresponding row of the heat map. Tile colors indicate whether a particular feature is favored or disfavored for integration of the respective data sets relative to their MRCs, as detailed in the colored ROC area scale at the bottom of each panel. p-values (*) show significance of departures from MLV_{IN_dCt} integration sites in SupT1 cells. (**$p<0.01$; ***$p<0.001$, Wald statistics referred to $\chi2$ distribution).