

Figure S8

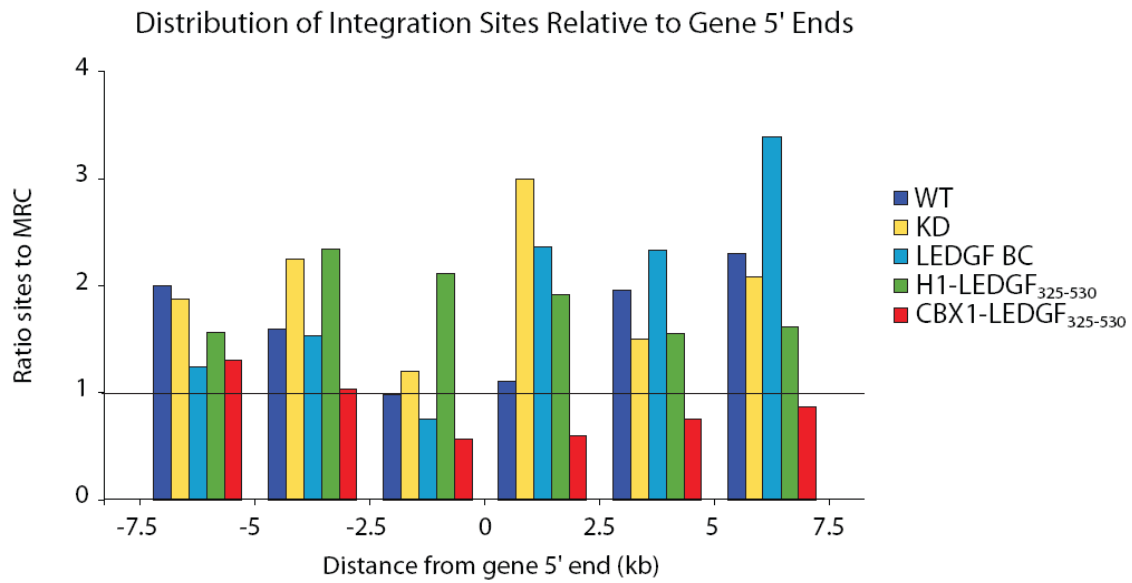


Figure S8. Distribution of integration sites relative to transcription start sites. EIAV integration sites in WT, KD and LEDGF₃₂₅₋₅₃₀-fusion cell lines were grouped by distance to the nearest gene 5' end (negative numbers mean the integration site is upstream of the transcription start site). The proportion of sites in each 2.5kb window is shown, normalized to the proportion of matched random control (MRC) sites in each window.