

Figure S1:

1. (Left panel) Ranked correlation matrix of genes and 42 transposable elements (TE) families, which are differentially expressed between *proliferative* (MITF-High) and *invasive* (MITF-Low) primary melanoma cultures. Genes and TE families are manually annotated. Colour codes on the left side of the heat map panel represent the unsupervised clusters of most variable genes and TEs across the samples. On the right, selected genes are listed that are positively or negatively correlated with LTR5\_Hs expression across the melanoma primary cultures.
2. Bar plot shows the pairwise ‘Spearman’ rank correlation of LTR5\_Hs expression with those most variable genes across primary melanoma cultures that were either significantly correlated or anti-correlated (p-value < 1e-05, cor.test).
3. Distribution of ChIP-seq signal of the H3K4Me3 histone mark occupancy, corresponding to active promoters averaged over LTR5\_Hs loci in MITF-High (*proliferative*) vs. MITF-Low (*invasive*) state of primary melanoma cultures.
4. Distribution of ChIP-seq signal of the H3K27Ac histone mark occupancy (lower panel) averaged over LTR5\_Hs loci in MITF-High (*proliferative*) vs. MITF-Low (*invasive*) state of primary melanoma cultures.
5. Heatmap displays the expression (log2 TPM) of DEGs upon KD-Rec in A375 cells vs. KD-Scr.

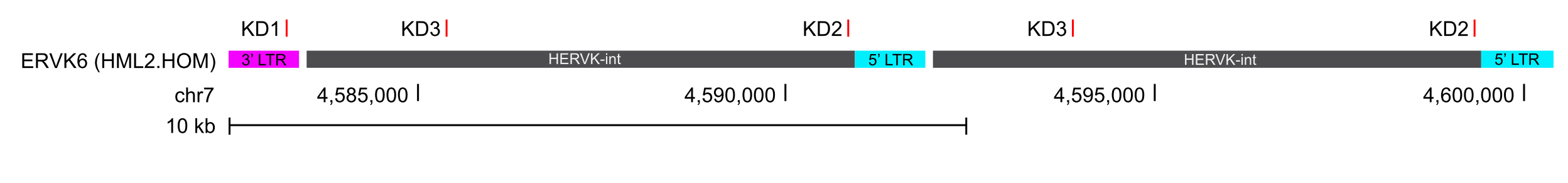


Figure S2:

Schematic of the positions targeted by the knockdown (KD1,2,3) constructs on the ERVK6(HML2.HOM) locus. ERVK6 is a tandemly organized HERV-K(HML2) provirus, possessing three LTRs. The genomic coordinates of the locus on chr7 are indicated. Both proviruses are type 2, and encode identical Rec proteins (UniProt). Note that due to the high conservation of Rec sequences in the human genome [15], the KD Rec was targeted multiple loci in the human genome.

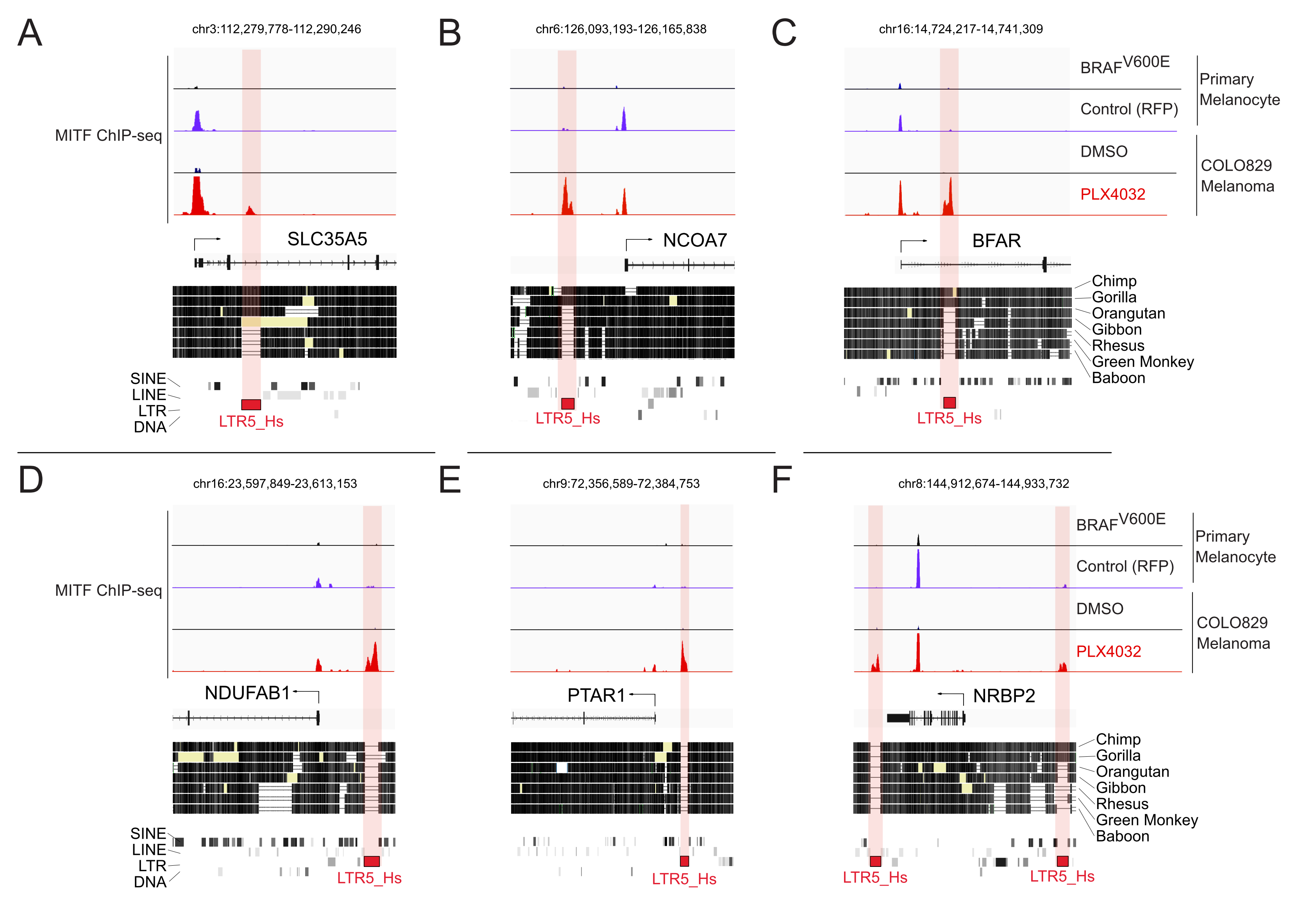


Figure S3:

(A-F) Integrative genome browser tracks showing the MITF ChIP-seq signals at the following human genomic loci: SLC35A5, NCOA7, BFAR, NDUFAB1, PTAR1 and NRBP2. Phylogenetic conservation of the respective loci is demonstrated on the middle panels. Schematic structures of the solo LTR5\_Hs sequences are shown at the bottom in *repeatmasker* track.