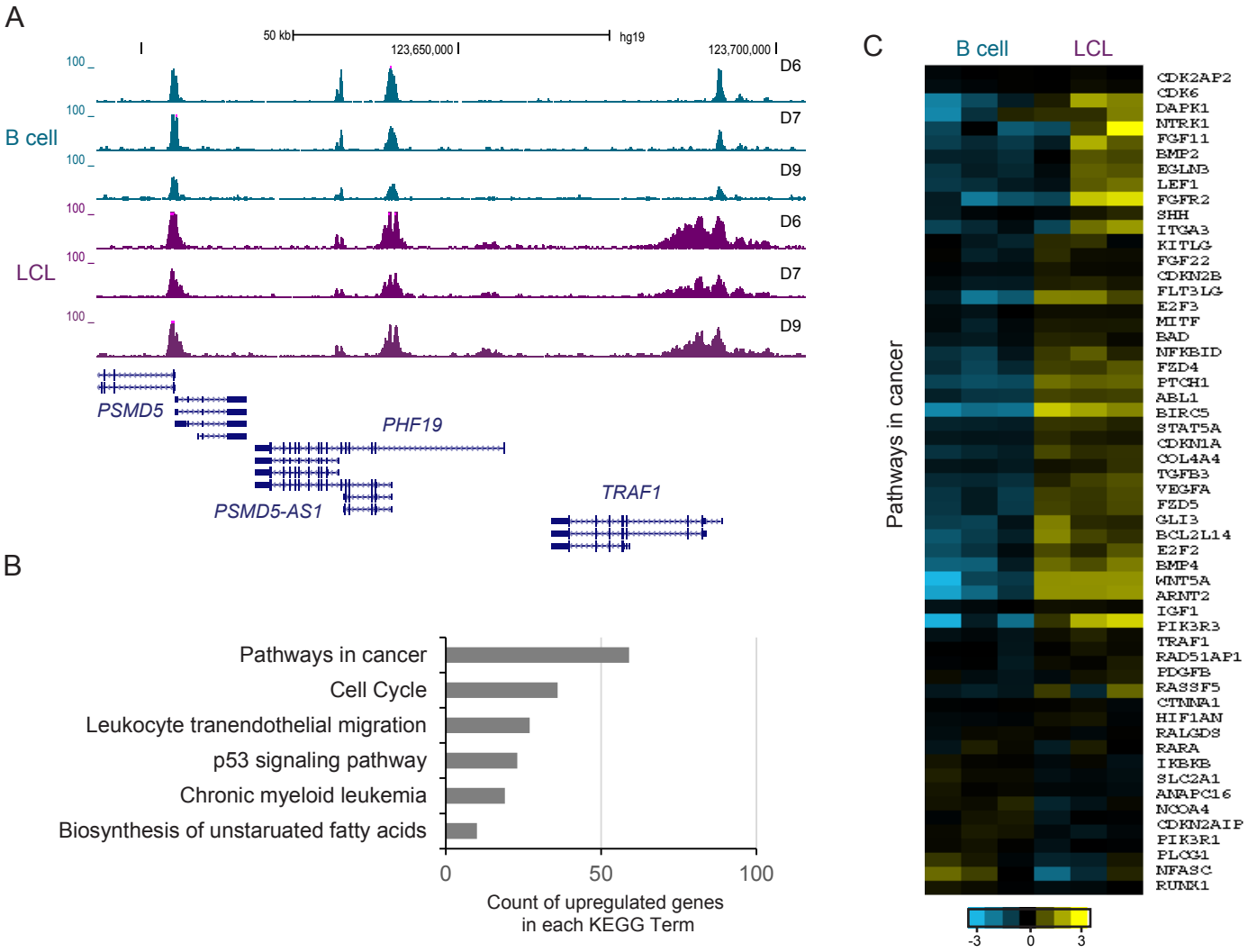

Figure S1: EBV-induced changes at genes. (*A*) Genome browser track of H3K4me3 profiles at *PHF19-TRAF1* and adjacent locus. (Blue box; TSS with decreased H3K4me3 enrichment in LCL, yellow box; TSS with increased H3K4me3 enrichment in LCL.) (*B*) Number of upregulated genes found in each KEGG term (DAVID; P <0.05) (C) Heatmap of normalized read counts at each gene in B cell and LCL for genes in the “Pathway in cancer” KEGG term classification.

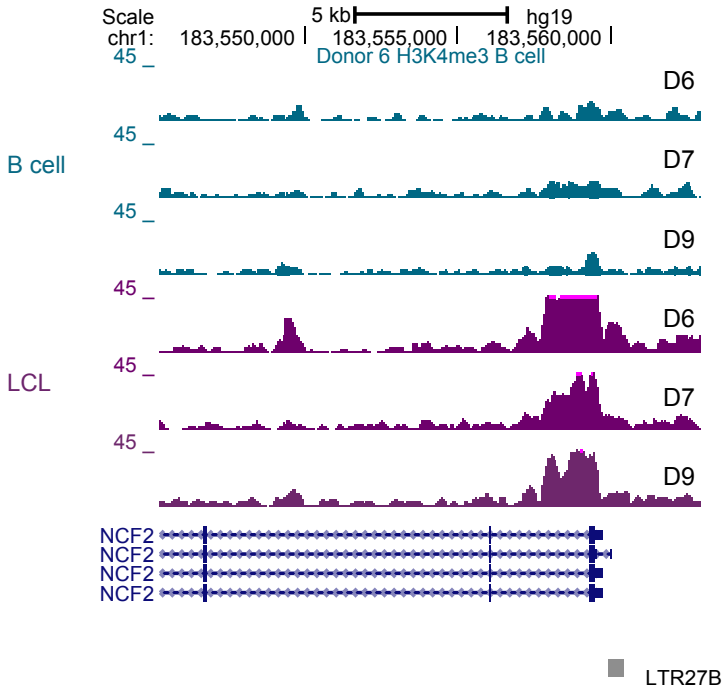

Figure S2: Example of protein-coding gene, *NCF2*, with alternative LTR-driven transcript. Genome browser tracks of H3K4me3 profiles at the NCF2 locus.

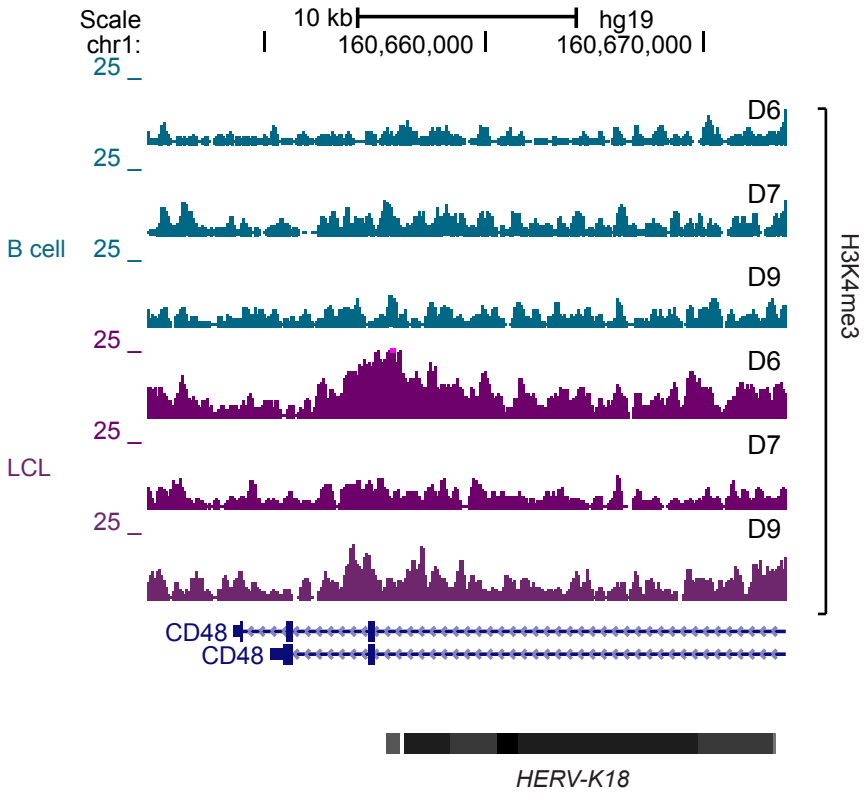

Figure S3: H3K4me3 profile at *HERV-K18* found within *CD48* locus. Genome browser tracks of H3K4me3 profiles at the *HERV-K18* locus which is found within the *CD48* locus.

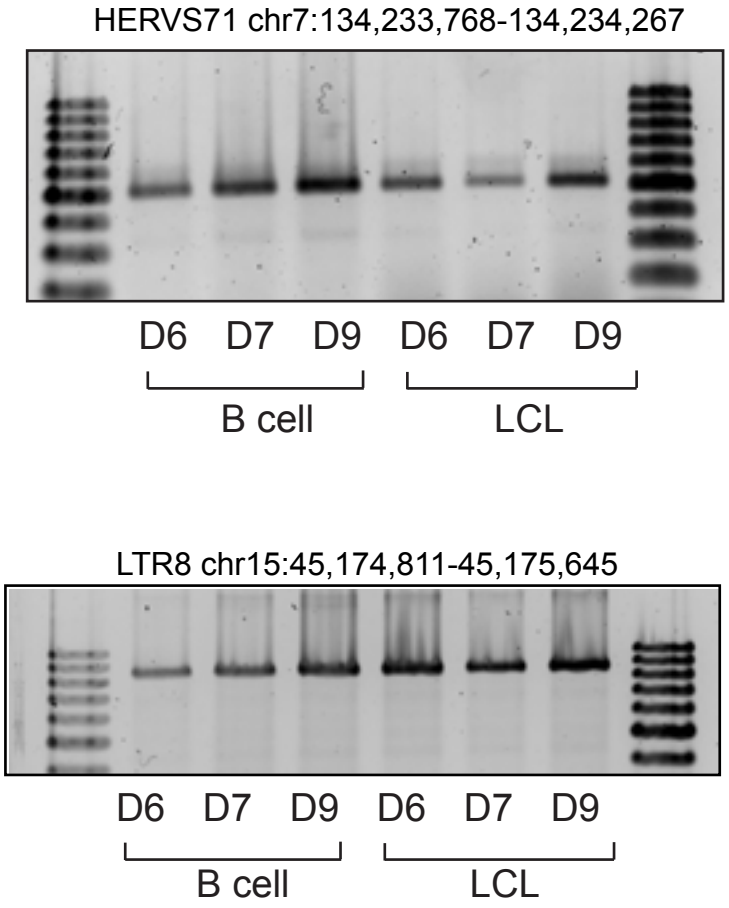

Figure S4: Activated LTRs do not show obvious rearrangements in LCLs. PCR of two LTRs from genomic DNA isolated from B cells and LCLs

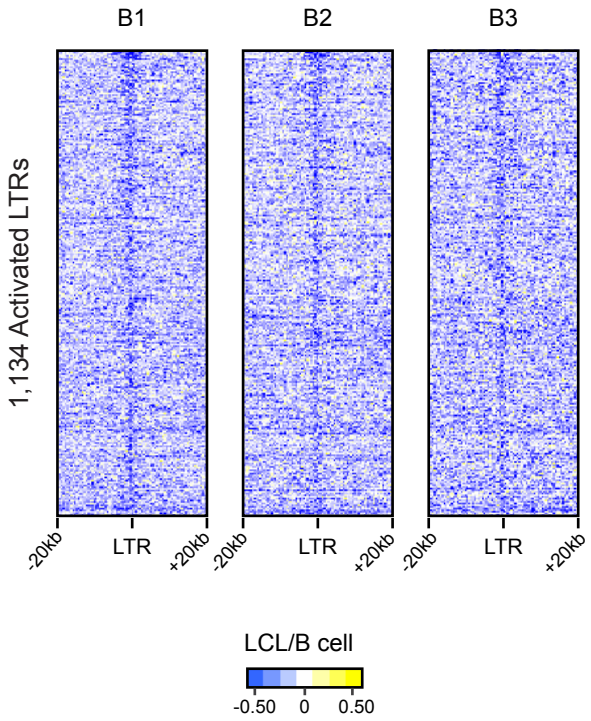

Figure S5: Hypomethylation of activated LTRs occurs locally. Shown are 500bp bins of average CpG methylation in the +/- 20kb region surround the 1,134 activated LTRs. Data from GSE49629.

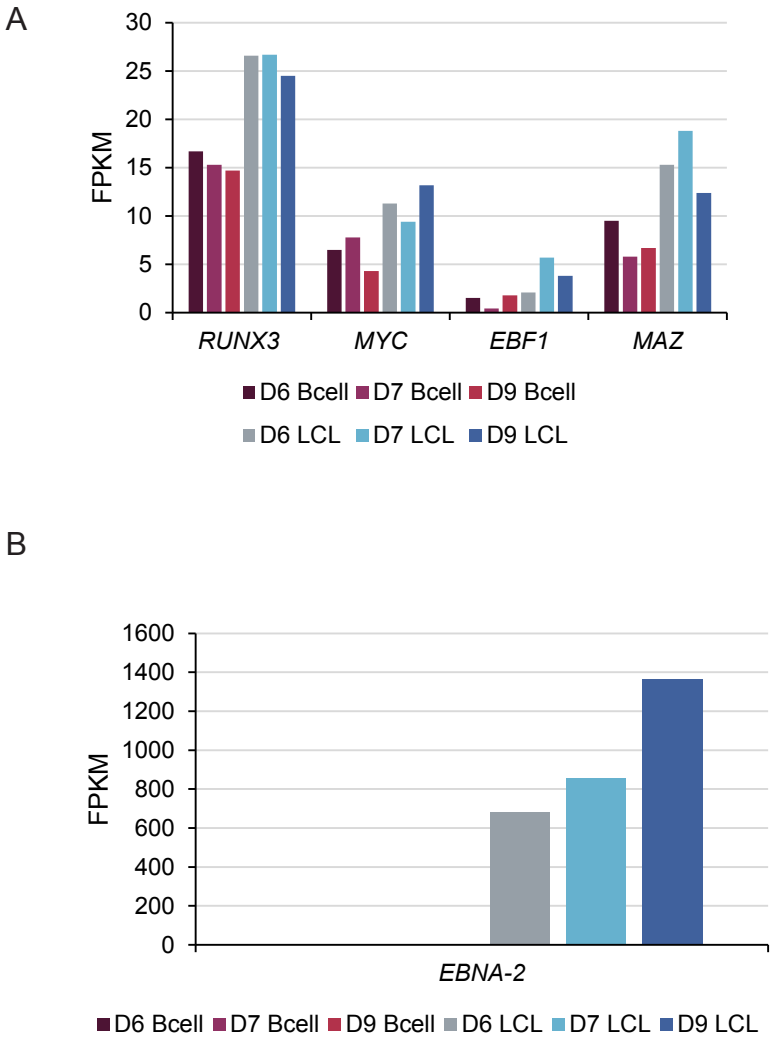

Figure S6: Expression of transcription factors in B cells and LCLs. Shown are FPKM for (*A*) cellular transcription fators and (B) *EBNA-2* , viral encoded transcription factor in B cells and LCLs.

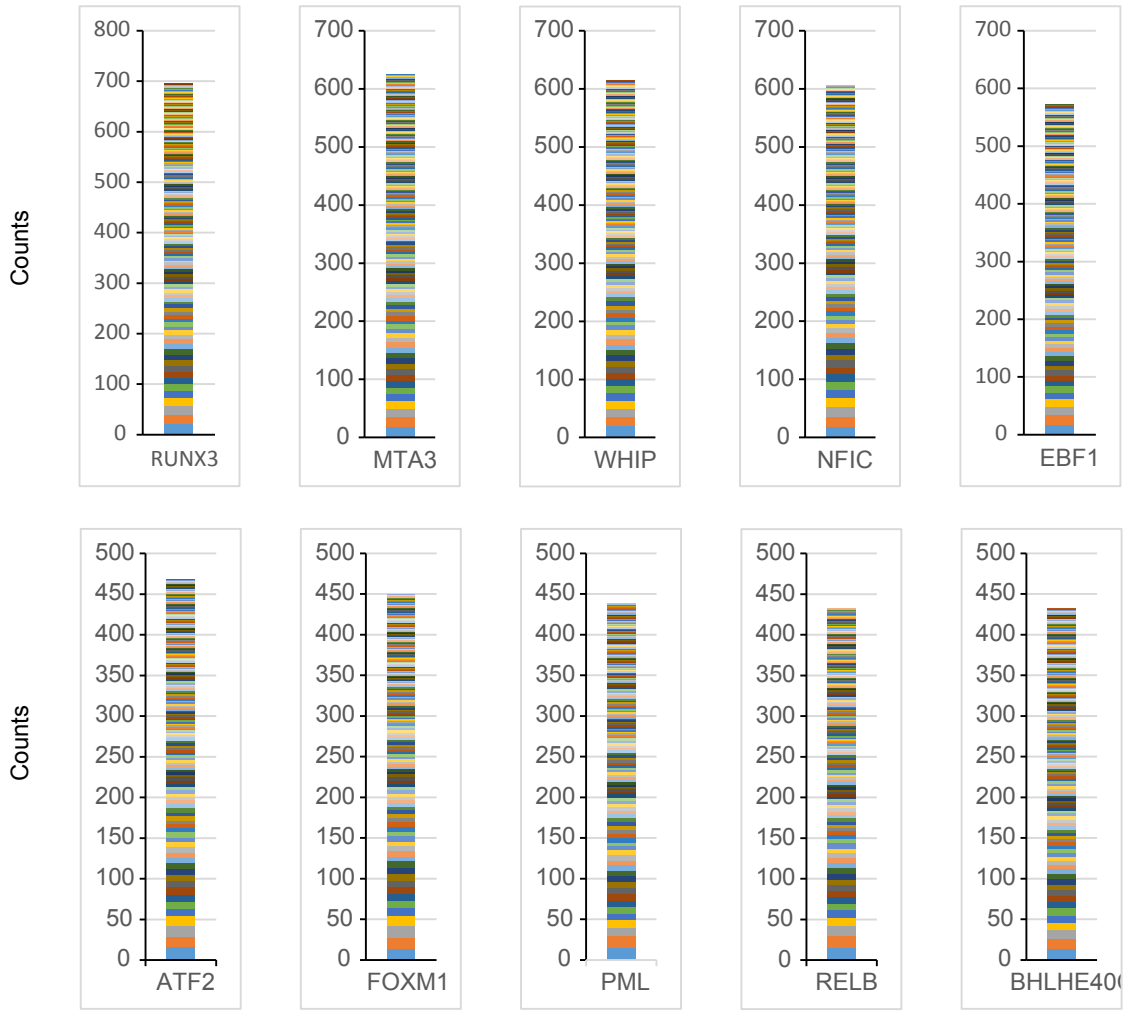

Figure S7: LTR subfamilies bound by specific transcription factors are highly variable. Shown are the counts of LTR subfamiles. Each color is a different subfamily (see Supplemental Table S for exact counts for each subfamily)

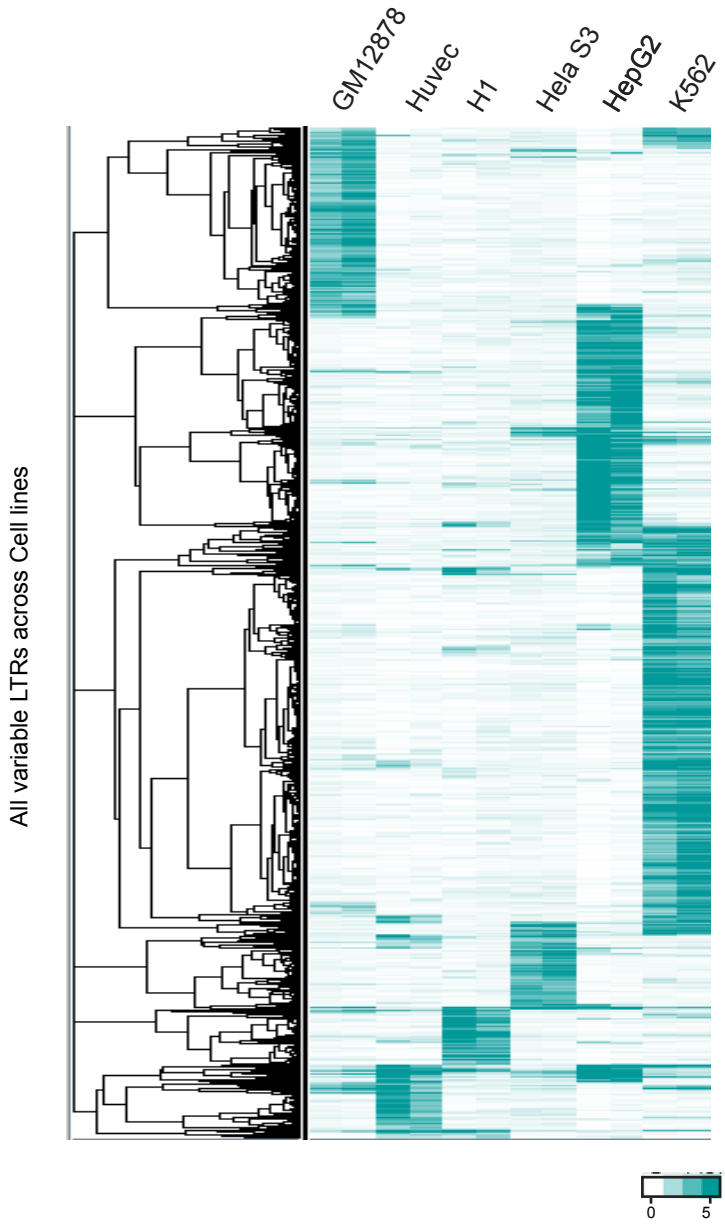

Figure S8: Variable LTR activity in ENCODE cell lines. Heatmap of normalized H3K4me3 levels across ENCODE cell lines. Hierarchical clustering was performed across LTRs that are differentially enriched for H3K4me3.

Figure S9: Variable LTR activity in ENCODE cell lines and Roadmap data. Heatmap of H3K4me3 counts across activated LTRs in ENCODE cell lines, Roadmap data, and our B cell and LCL datasets. Hierarchical clustering was performed across LTRs that are differentially enriched for H3K4me3.

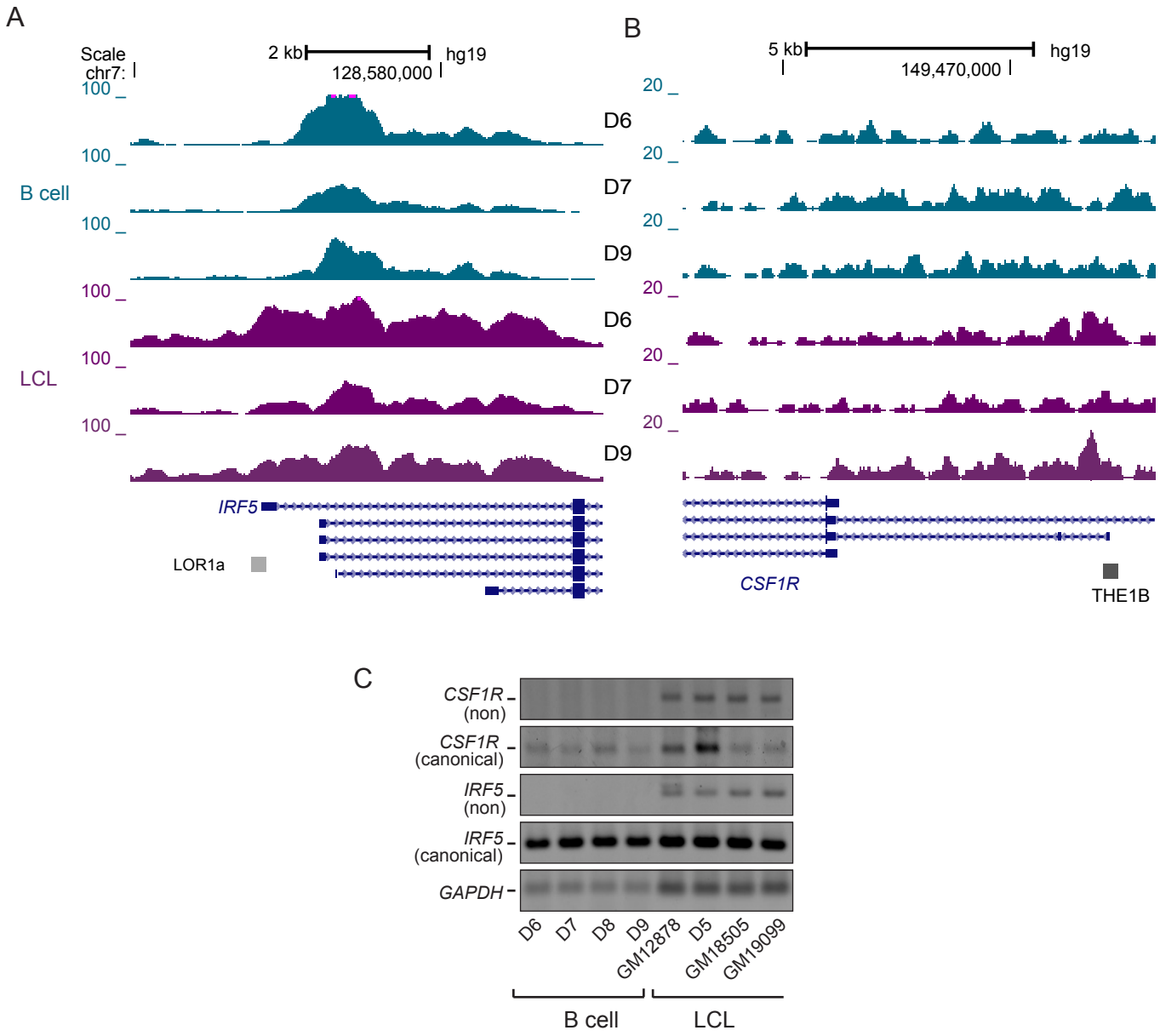

Figure S10: Non-canonical LTR-driven transcripts of *CSF1R* and *IRF5* are expressed in EBV-transformed B cells. Genome browser tracks of (*A*) *IRF5* and (*B*) *CSF1R* locus with H3K4me3 profiles. (*C*). RT-PCR analyzing expression of canonical and non-canonical transcripts in B cells and LCLs.

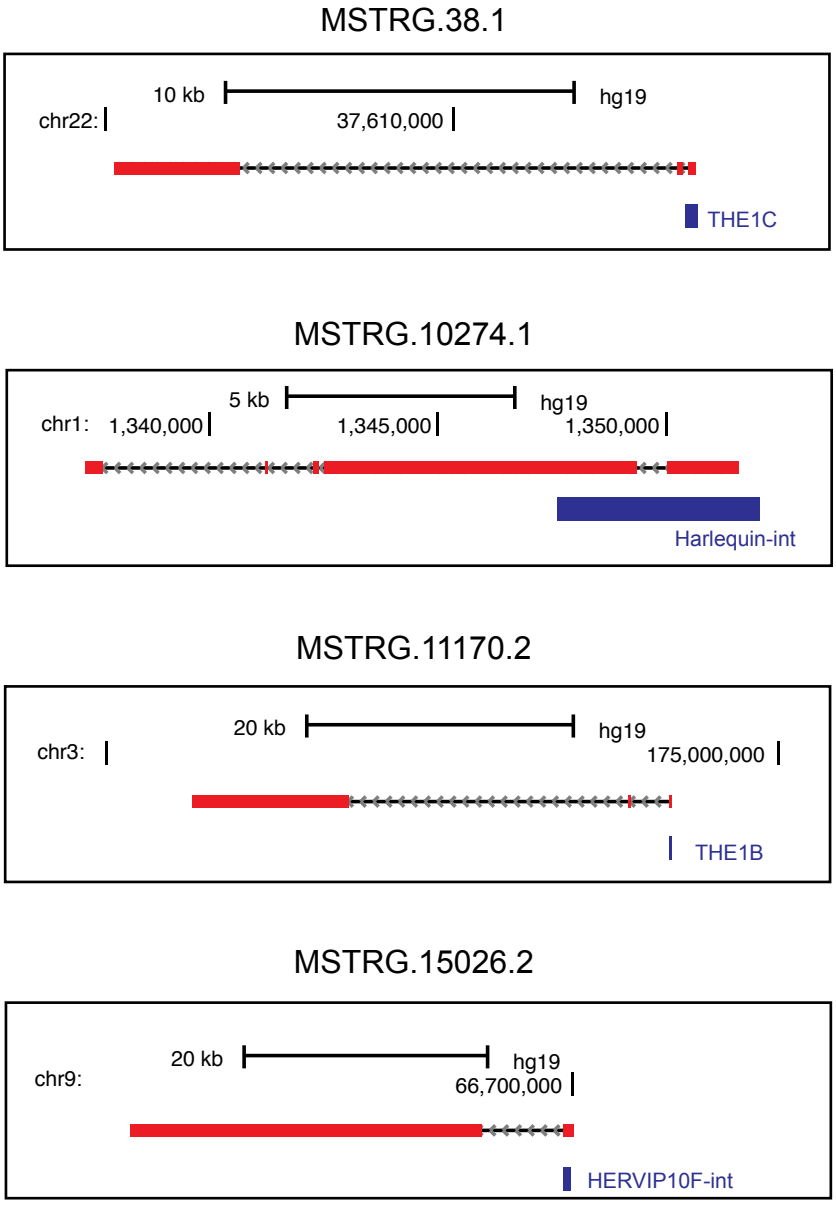

Figure S11: Schematic of transcript structures for novel LTR-driven transcripts. Shown are transcript structures (red) annotated from RNA-seq data from donor B cells and LCLs. Shown in blue are the positions of LTRs

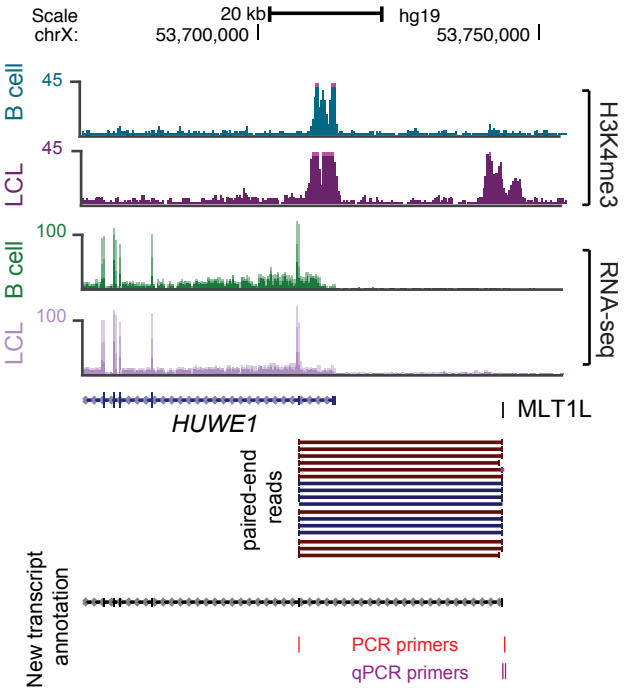

Figure S12: Expanded genome browser tracks of *HUWE1* locus. See Figure 5A legend.

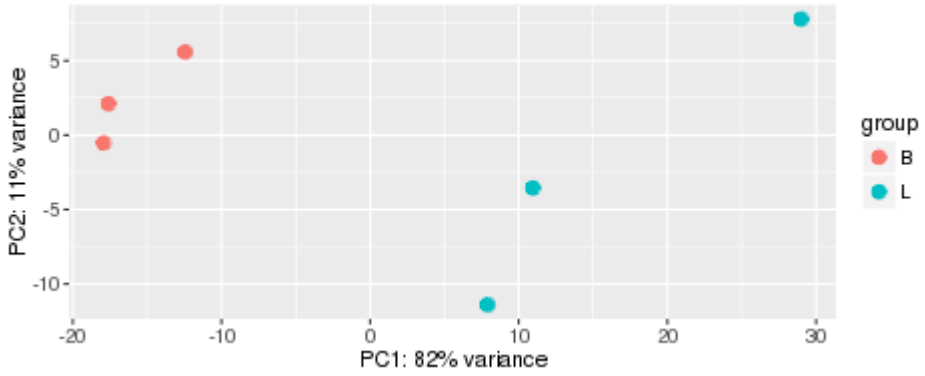

Figure S13: Principal component analysis of ChIP-seq data from DESeq2 normalized read counts at H3K4me3 sites showing PC1 and PC2.