



Supplementary Figure S3. Regulation of TP73 by BATF3 and IRF4.

(A) H3K27ac enrichment, BATF3/IRF4 binding regions of ENCODE data (ChIP-seq; SRX2646182 and SRX1998451) (74) analyzed by using the ChIP-Atlas (73), Chromatin accessibility (ATAC-seq) and transcription (RNA-seq) of Trp73 in HBZ-transduced murine CD4⁺ T cells.

(B and C) CHIP-qPCR in healthy human donor CD4⁺ T cells (hCD4) and ATL cell lines for BATF3 (B) and IRF4 (C) in the open region found in Fig. 3C (hg19 genome region of chr1:3593076-3594185) (n=3).

(D and E) Promoter assays of the open region in Jurkat cells. The IRF4/AP-1 motifs identified within the open region (hg19 genome region of chr1:3593076-3594185) were subjected to promoter assays with IRF4 and/or BATF3 induction for the promoters of TAp73 (D) and DNp73 (E) (n=3). A schematic of the assay construct is shown above the corresponding bar plot.

(F) EZH2 transcriptional changes in Jurkat cells during 24 hours after HBZ transduction (n=3).

Results are plotted as mean \pm SD, using one-way ANOVA with Dunnet (B-E) or Student's t test (F). *p < 0.05, **p < 0.01, ***p < 0.001; ns, not significant.