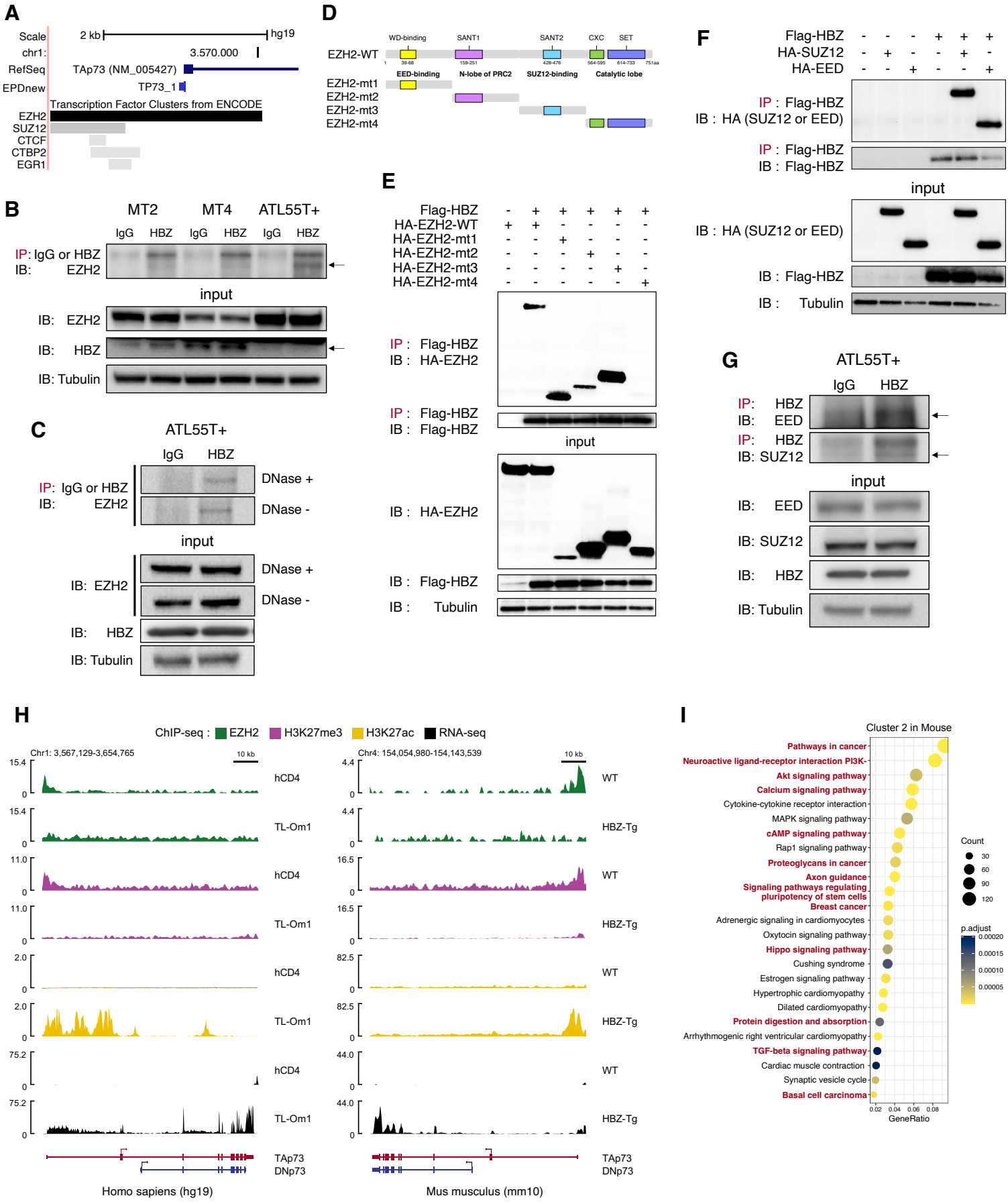

Supplementary Figure S2. HBZ protein alters epigenetic regulation of TAp73 by EZH2.
(A) A snapshot of the UCSC genome browser around the TAp73 promoter (registered as TP73_1 in the EPDnew [Eukaryotic Promoter Database]) in hg19. Enriched transcription factors from the ENCODE are shown as barplots.
(B) Immunoprecipitation (IP) of endogenous HBZ protein and EZH2 in HTLV-1-infected cells. IP was performed with anti-HBZ antibody and analyzed by SDS-PAGE and immunoblotting (IB).

Supplementary Figure S2. HBZ protein alters epigenetic regulation of TAp73 by EZH2. (Continued)
(C) IP of endogenous HBZ and EZH2 with or without DNase I.
(D and E) IP to examine binding sites of HBZ protein to EZH2. A schematic diagram showing the EZH2 mutants and the domains of the EZH2 protein (D). IP of wild-type (WT) or mutant EZH2 with HBZ protein (anti-Flag antibody) in HEK293T cells (E).
(F) IP of SUZ12 or EED with HBZ protein (anti-Flag antibody) in HEK293T cells
(G) IP of SUZ12 or EED with endogenous HBZ protein (anti-HBZ antibody) in ATL55T+ cells.
(H) EZH2, H3K27me3 and H3K27ac enrichments (ChIP-seq) and transcripts (RNA-seq) around TP73 in human CD4+ T cells from healthy donors (hCD4) and TL-Om1 cells (left), and around Trp73 in WT or HBZ-Tg mouse CD4+ T cells (right).
(I) Results of KEGG pathway analysis using the mouse cluster 2 genes (Fig. 2H). Shared pathways between human and mouse cells are highlighted in red. Statistical values and gene counts calculated by the clusterProfiler are shown.