Supplementary data

Suberoyl bis-hydroxamic acid reactivates Kaposi's sarcoma-associated herpesvirus through histone acetylation and induces apoptosis in lymphoma cells

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Sup Fig. 1. Alteration of KSHV-encoded gene expression induced by SBHA. PEL cells were treated with SBHA for 48 hours and RNA samples were subjected to KSHV real-time PCR array to determine expression profiles of KSHV-encoded genes. The copy number of each transcript was normalized to that of GAPDH and the ratio to the value of untreated cells is shown.







Sup Fig. 2. Transcriptome analysis of KSHV-encoded genes in BCBL-1 cells. (A) An overview of coverage of reads mapped to KSHV genome. Read coverage of DMSO (violet), TPA (green) or SBHA (red)-treated BCBL-1 cells mapped to KSHV genome (GenBank accession no. NC_003409) are shown. Maximum coverages in the image of DMSO, TPA and SBHA are 500, 2000, and 15,000, respectively. Coverage of K7 gene is over the maximum reads in each sample. The lowest column indicates coding sequences (CDS) of open reading frame. (B) Read coverage of BCBL-1 cells in K7 (left), vIRFs (center) and latent gene clusters (K12-ORF73, right).



Sup Fig. 3. Notch1 signaling was not activated by SBHA in PEL cells. Western blot analysis for the transmembrane/intracellular region of Notch1 (NTM) and its active form, Notch1 intracellular domain (NICD), is shown. PEL cells were treated with SBHA for 24 or 48 hours. Protein samples from BJAB, Jurkat and MOLT-4 cells were applied as positive control with GAPDH as loading control. The white arrowhead indicates NTM and black arrowheads indicate NICD.