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Supporting Information

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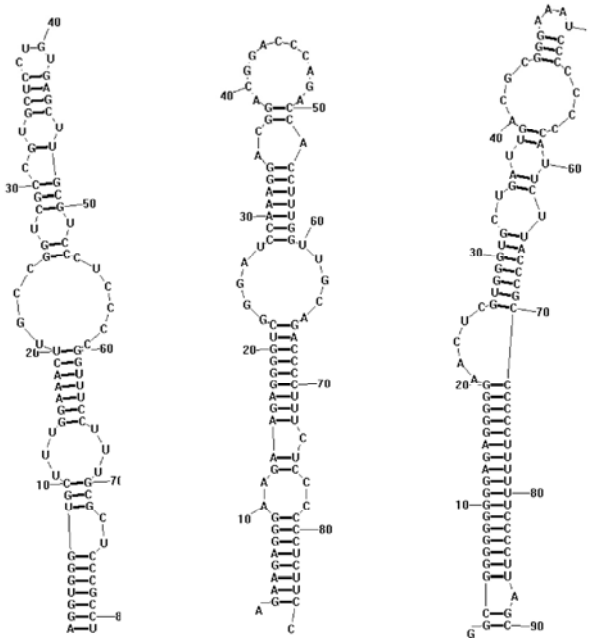

Figure S1 Three potential hairpin structures in non-coding regions of the HSV-1 genome were predicted by computational analysis.

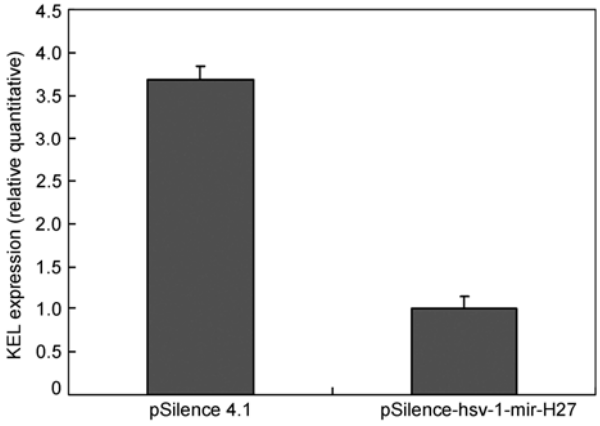

Figure S2 KEL mRNA was inhibited by hsv1-mir-H27. Cells were transfected with 3 μg of pSilence-hsv1-mir-H27 or pSilence 4.1 and harvested 18 h post-transfection. Reverse transcription was performed with Kel-rltm-R or β-actin-R followed by quantitative real-time PCR with Kel-rltm-F and Kel-rltm-R or β-actin-F and β-actin-R primers. Data were normalized based on theβ-actin control and calculated by $\log 2^{-\Delta\Delta C_t}$, n=3.

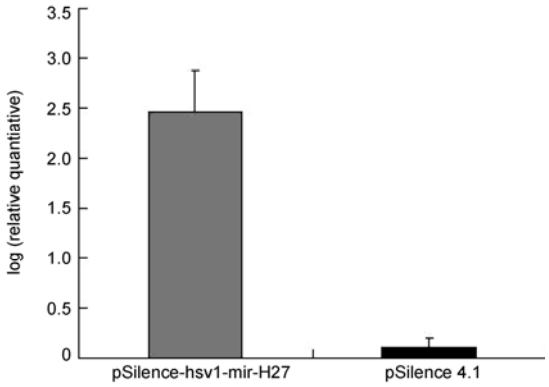

Figure S3 MiRNA hsv1-mir-H27 was highly expressed by pSilence-hsv1-mir-H27. Cells were transfected with 3 μg of pSilence-hsv1-mir-H27 or pSilence 4.1 and harvested 24 h post-transfection. Reverse transcription was performed with mi-loop or u6-loop primers followed by quantitative real-time PCR with mi F and mi R or u6 F and u6 R primers. Data were normalized based on the u6 control and calculated by $\log 2^{-\Delta\Delta C_t}$, n=3.

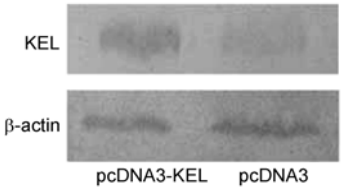

Figure S4 Western blot analysis showing that KEL is expressed in cells transfected with the eukaryotic. Cells were transfected with 3 μg of pcDNA3-KEL or pcDNA3 and harvested 24 h post-transfection. Western blot analysis was conducted with a mouse polyclonal antibody against its N-terminus and normalized to the levels of β-actin detected with a mouse polyclonal antibody Western blot.

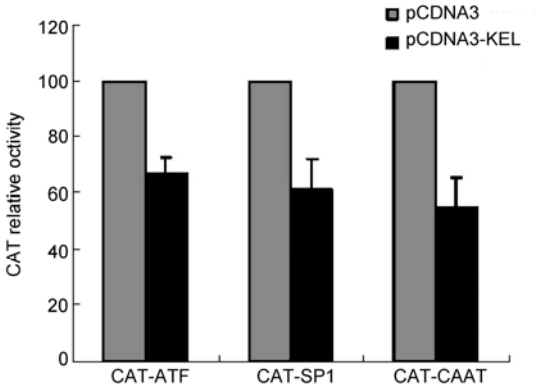

Figure S5 KEL effect on the function of different upstream transcriptional activating elements. One microgram of the CAT reporter gene expression plasmids (pCAT-ATF, pCAT-SP1, or pCAT-CAAT) were co-transfected into cells with 2 μg of pcDNA3-KEL. The CAT relative activity values in each experimental group were calculated by assigning a value of 100 to values resulting from transfection of 1 μg of the CAT reporter gene expression plasmid and relevant amounts of pcDNA3, n=3.

Table S1 Sequences of three potential hairpin structures in the non-coding regions of the HSV-1 genome

Probe numbers	Location	Size (bp)	Sequence
P1	86230-86302	81	5′-AGGUGGGUGCUUUGGAAACUUGCCGGUCGCCGU GCUCCUGUGAGCUUGCGUCCCUCCCCGGUUUCC UUUGCGCUCCCGCCU-3′
P2	2882-2964	83	5′-AGAAGAGGGAAGAAGAGGGGUCGGGAUCCA AAGGACGGACCCAGACCACCUUUGGUUGCAGAC CCCUUUCUCCCCCCUCUUCC-3′
P3	2994-3083	90	5′-GGCGGGGGGGGGGAGAGGGGGAACUCGUGGG UGCUGAUUGACGCGGGAAAUCCCCCCCCAUUCU UACCCGCCCCCCUUUUUUCCCCUUAGC-3′

Table S2 Sequences of three potential miRNA and its probes

Probe numbers	Sequences of probe	Predicted miRNA sequences
Probe.1	5′-GCG ACC GGC AAG TTT CCA AAG CAC CCA CCT-3′	5′-GGG UGC UUU GGA AAC UUG CCG GU-3′
Probe.2	5′-GGA AGA GGG GGG AGA AAG GGG TCT GCA ACC-3′	5′-CAG ACC CCU UUC UCC CCC CUC UU-3′
Probe.3	5′-GGC GGG GGG GGG AGA GGG GGA ACT CGT GGG-3′	5′-CCA CGA GUU CCC CCU CUC CCC C-3′