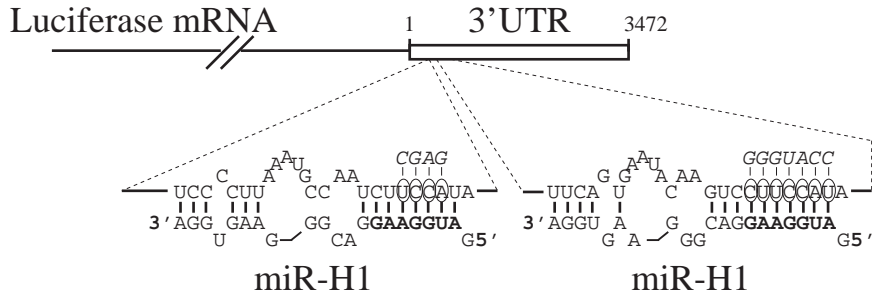
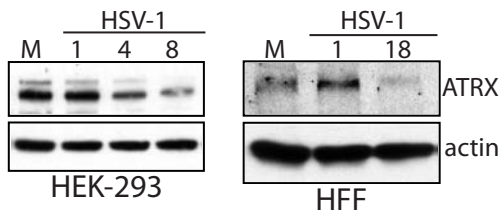


Supplemental Figure 1.



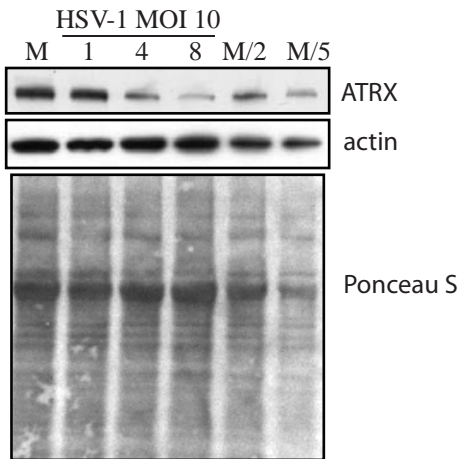
Supplemental Figure 1. Schematic representation of Luciferase mRNA fused to 3' UTR of the ATRX gene and targeting by miR-H1. The mRNA coding sequence and 3' UTR are shown as a solid line and an unfilled box, respectively. The numbers indicate the first and the last nucleotide of the 3' UTR sequence. Below are shown expanded views of miR-H1 (lower sequence) binding to sequences within the 3' UTR predicted by RNAhybrid. The seed sequence of miR-H1 is shown in bold. The nucleotides within the 3' UTR that were mutated are shown in small ovals, and introduced nucleotides are given above the 3' UTR.

Supplemental Figure 2.



Supplemental Figure 2. HEK-293 or HFF cells were mock-infected (M) or infected with HSV-1 an MOI of 10. Samples for the analysis were collected at different hours after infection, indicated above the top panels, and the proteins were analyzed by Western blotting using antibodies against the proteins indicated to the right. M: mock infected cells.

Supplemental Figure 3.



Supplemental Figure 3. HEK-293 were mock-infected (M) or infected with HSV-1 an MOI of 10. Samples for the analysis were collected at different hours after infection, indicated above the top panels, and the proteins were analyzed by staining with Ponceau S and Western blotting using antibodies against the proteins indicated to the right. M: mock infected cells, M/2 and M/5: serial dilutions of M sample two and five fold, respectively.