Supplemental Figures:

Figure S1: (A) qPCR of MeRIP control transcripts using DiCER as known m6A modified transcript and C19ORF66 as another known SOX escapee. (B) qPCR of GFP mRNA levels of the transfected GFP reporters in HEK293T cells showing no significant difference between the two reporters. (C) qPCR of GFP-WTSRE and GFP-mutSRE reporters transfected into Latent and 24 hour Lytically reactivated iSLK cells showing no significant difference between the reporter expression.

Figure S2: (A) qPCR of GFP reporters using the SREs of other known escapees as indicated. These reporters were transfected into 293T-ΔYTHDC2 cells with either Mock or SOX plasmids transfected as well. (B) YTHDC2 expression was knocked down in iSLK.219 cells and Western blots were performed to assess knocked down efficiency as well as its effect on ORF50 and ORF59[61]. YTHDC2 depletion had no effect on these viral genes. (C) iSLK.219 were treated with an siRNA control or targeting YTHDC2. Latent cells fluoresce green because of a GFP marker on the viral genome and red when reactivated because of a RFP marker under the PAN promoter. Knock down of YTHDC2 does not affect viral reactivation. (D) qPCR of endogenous transcripts in either latent or lytically reactivated iSLK.219 cells that had been treated with siYTHDC2 prior to reactivation.

Figure S3: Precise PureCLIP peak position on the IL-6 3’UTR sequence and predicted secondary structure.

Table S1: Primer dataset. Contains sequencing and qPCR primers used.

Table S2: M6A-eCLIP IP iSLK-Lat Crosslink Site dataset. Crosslink sites were identified using the tool PureCLIP. Input samples were used as a background control for crosslink site identification. The score is the log posterior probability ratio of the first and second likely state. The fold change is the fold change of IP read starts vs. input read starts.

Table S3: M6A-eCLIP IP iSLK-Lyt Crosslink Site dataset. Crosslink sites were identified using the tool PureCLIP. Input samples were used as a background control for crosslink site identification. The score is the log posterior probability ratio of the first and second likely state. The fold change is the fold change of IP read starts vs. input read starts.

Table S4: Full list of peaks within KSHV transcripts in induced and uninduced samples. Bolded transcript name represents transcripts that were identified in previous KSHV and m6A characterizations.