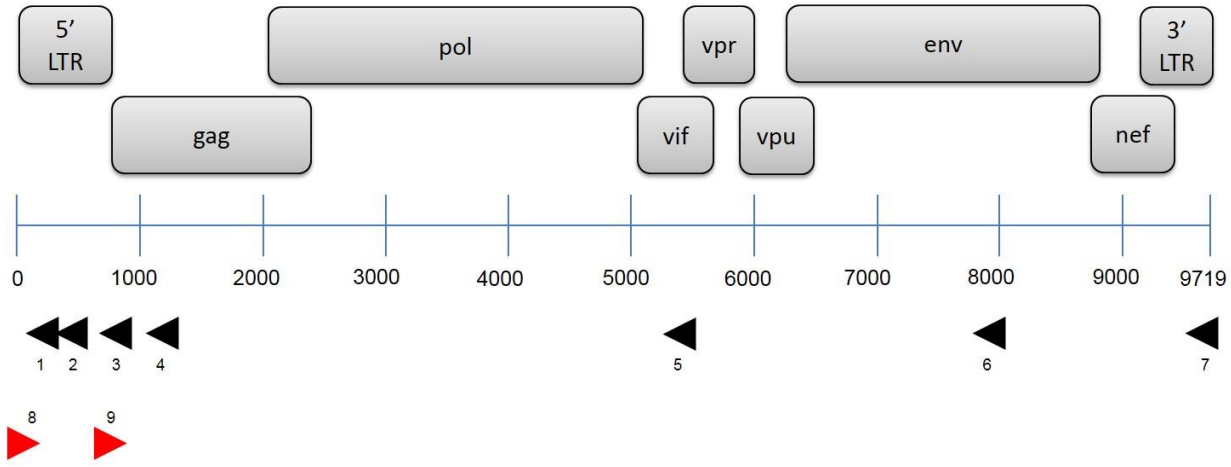


Supplemental Figure 1: A diagram of the location of primers used in this study. The arrows represent all HIV-1 primers used in this study. The black arrows represent the reverse primers. #1, 2, 4, 5, 6, and 7 were used in RT reactions. "TAR" and "TAR-*gag*" RT-qPCR used primers #1 and 8. "Genomic" RT-qPCR used primers #3 and 9.

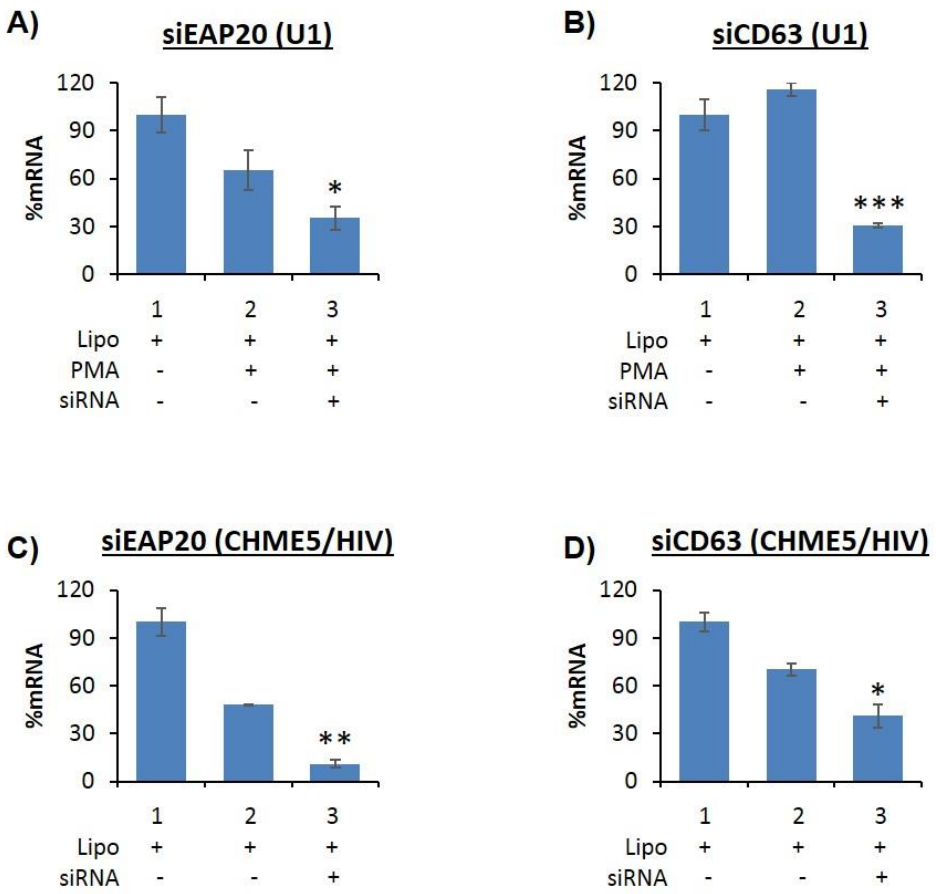
Primer/Probe name	Primer/Probe Sequence	Location in HIV-1 genome
8: TARfII-F	5'- GGT CTC TCT GGT TAG ACC AGA TCT G -3'	1-25
1: TAR+59R*	5'- CAA CAG ACG GGC ACA CAC TAC -3'	99-119
2: LTR+341-R*	5'- ACC CAT CTC TCT CCT TCT AGC C -3'	320-341
9: GAG1-F	5'- TCA GCC CAG AAG TAA TAC CCA TGT -3'	835-849
3: GAG2-R	5'- CAC TGT GTT TAG CAT GGT GTT T -3'	886-909
4: Gag 1625R*	5'- GCT GGT AGG GCT ATA CAT TCT TAC -3'	1155-1178
5: Vpr-R208*	5'- TAA ACG GCA GTT GTT GCA GA -3'	5293-5312
6: Env-2187R*	5'-TGG GAT AAG GGT CTG AAA CG-3'	7917-7936
7: 5T25*	5'- TTT TTT TTT TTT TTT TTT TTT TTT TTG AAG -3'	9178+
NF-κB1-2F	5'-TTC CGC TGG GGA CTT TCC -3'	
EAP20-F	5'-TTC CTG GGC TAC TAC GAT GG-3'	
EAP20-R	5'-ATG CTG GAC TGT TTG TGC AG-3'	
CD63-F	5' CCC TTG GAA TTG CTT TTG TCG 3'	
CD63-R	5' CGT AGC CAC TTC TGA TAC TCT TC-3'	

*primers used in RT reaction

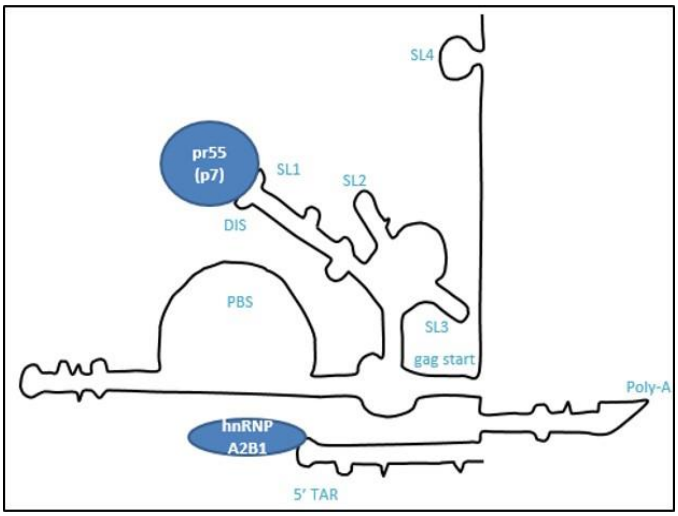
Supplemental Figure 2: Primer sequences used in this study. All primer names, sequences, and exact locations in the HIV-1 genome (when applicable) used throughout this study are shown. Numbers correspond to numbers in **Sup. Fig. 1**. Primers marked with "*" were used in RT reactions.

WIHS Patient Number	Group	Race	Age
30306305	ART Responder	White	34
30306608	ART Responder	White	33
30409062	ART Responder	African American	45
30403086	ART Responder	Hispanic	35

Supplemental Figure 3: Patient demographics. Patient samples used in **Fig. 8** were obtained from WIHS. Their patient number, group, race, and age are shown in the figure.



Supplemental Figure 4: siRNA knockdown of ESCRT. U1 cells were seeded then transfected with siRNA the next day. After one day, the supernatant was removed and replaced with fresh media with PMA. After 3 days the cells and supernatant were harvested. The cells were lysed and DNA and RNA were isolated. The RNA was subjected to RT with oligo-dT primers. RT-qPCR was performed with primers specific for EAP20 **(A)** and CD63 **(B)** (two of the targets of siRNA). The percent of the control (Lipo+, PMA-) was found. Student's T-test was performed between the Lipo+ PMA+ cells and the siRNA-treated cells. GAPDH RT-qPCR was performed on the DNA for normalization. CHME5/HIV cells were seeded and transfected with siRNA the next day. After one day, the supernatant was removed and replaced with exosome-free DMEM. After 3 days the cells and supernatant were harvested. The cells were lysed and DNA and RNA were isolated. The RNA was subjected to RT with Oligo-dT primers, and RT-qPCR was performed with primers specific for the EAP20 **(C)** and CD63 **(D)** (two of the targets of siRNA). Percentage of the negative control (Lipo-) were found. Student's T-test was performed between the Lipo+ cells and the siRNA-treated cells. GAPDH RT-qPCR was performed on the DNA for normalization.



Supplemental Figure 5: Diagram of TAR-*gag* and its binding partners. The hnRNPA2B1 binds to the TAR region (either methylated or unmethylated) and pr55 Gag (through p7) binds to the DIS/SL1 region of HIV-1 RNA. The complex is potentially packaged into exosomes released from infected cells.