

Additional Figure 1 Legends:

Figure S1: A) J-Lat cells were treated with TNF-alpha or different concentrations of PMA and the % of GFP positive cells were measured. Example dot plot depicting B) UPF1 mRNA, C) UPF2 mRNA and D) SMG6 mRNA expression in mock transfected cells with and without PMA addition using FISH-Flow technique.

Figure S2: J-Lat 10.6 cells were either transfected with siNS or siUPF1 and were uninduced (DMSO) or reactivated (PMA). A) Quantification of UPF1 protein expression by densitometry analysis of Western blots. B) MFI of the vRNA signal were quantified. Asterisks represent statistically significant difference between groups (student's t-test; $p < 0.05$). C) The % of RPL13A mRNA expressing cells were quantified. D) MFI of the PRL13A signal were quantified. E) Relative GAPDH mRNA levels as measured by RT-PCR. For all graphs, error bars represent the standard deviation from three independent experiments.

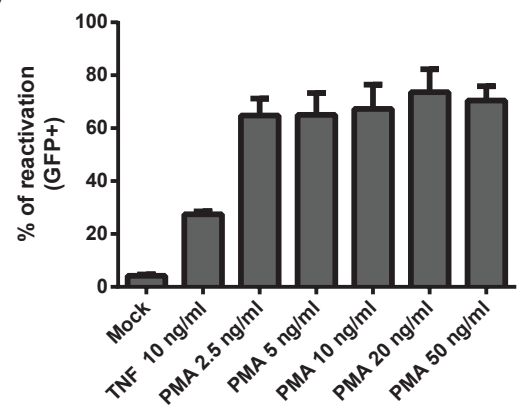
Figure S3: A) Cellular fractionation was performed in siNS or siUPF1 treated conditions, with and without PMA treatment. The fractions were run on SDS-PAGE gels and GAPDH and nucleolin protein levels were detected by Western Blotting to confirm fractionation. B) The relative amounts of vRNA in each fraction were quantified by RT-PCR and normalised to levels of GAPDH mRNA. Error bars represent the standard deviation from three independent experiments. C) J-Lat cells were mock transfected, transfected with FLAG-UPF1, FLAG-UPF2 or HA-SMG6 and reactivated with PMA. The % of vRNA+/GFP- cells was quantified. Error bars represent the standard deviation from three independent experiments.

Figure S4: A) J-Lat cells were mock transfected, transfected with FLAG-UPF1 or with FLAG-UPF1 mutants and reactivated with PMA. Reactivation in the above conditions was quantified and the percentages of reactivation were normalised to the Mock PMA reactivated condition. Error bars represent the standard deviation from three independent experiments with at least 10000 cells counted per treatment. Asterisks represent statistically significant difference between groups. B) J-Lat cells were mock transfected, transfected with FLAG-UPF1, FLAG-UPF2 or HA-SMG6 and reactivated with TNFalpha. Reactivation in the above conditions was quantified and the percentages of reactivation were normalised to the Mock PMA reactivated condition. Error bars represent the standard deviation from three independent experiments with at least 10000 cells counted per treatment.

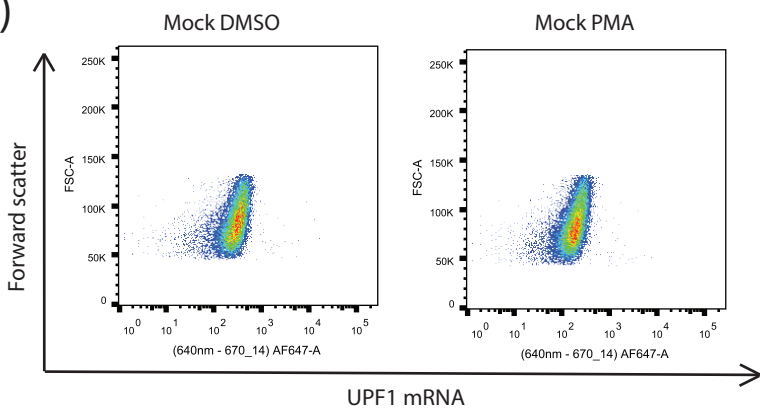
Figure S5: A) Equal amounts of cell lysates from J-Lat 10.6 and primary CD4+ T cells were subjected to Western blotting and probed for UPF1 and actin. B) Primary CD4+ T cells were either transduced with shNS or shUPF1-containing lentiviral particles and either left uninfected or infected with HIV-1. Quantification of UPF1 protein expression by densitometry analysis of Western blots.

Figure S1

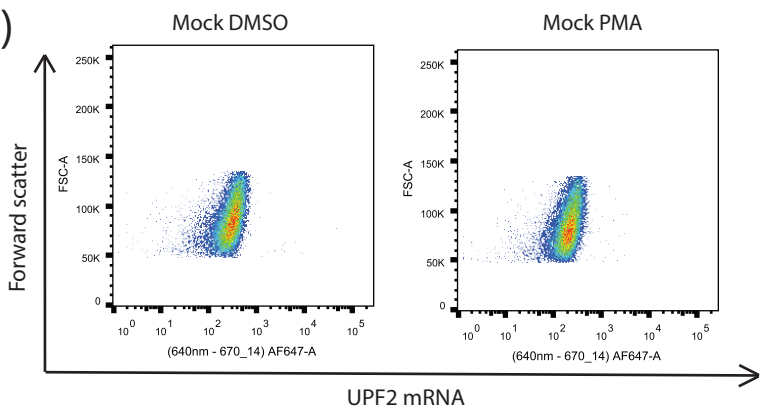
A)



B)



C)



D)

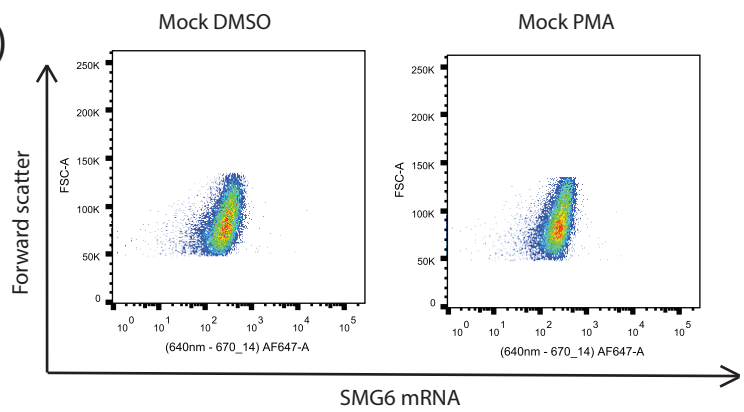


Figure S2

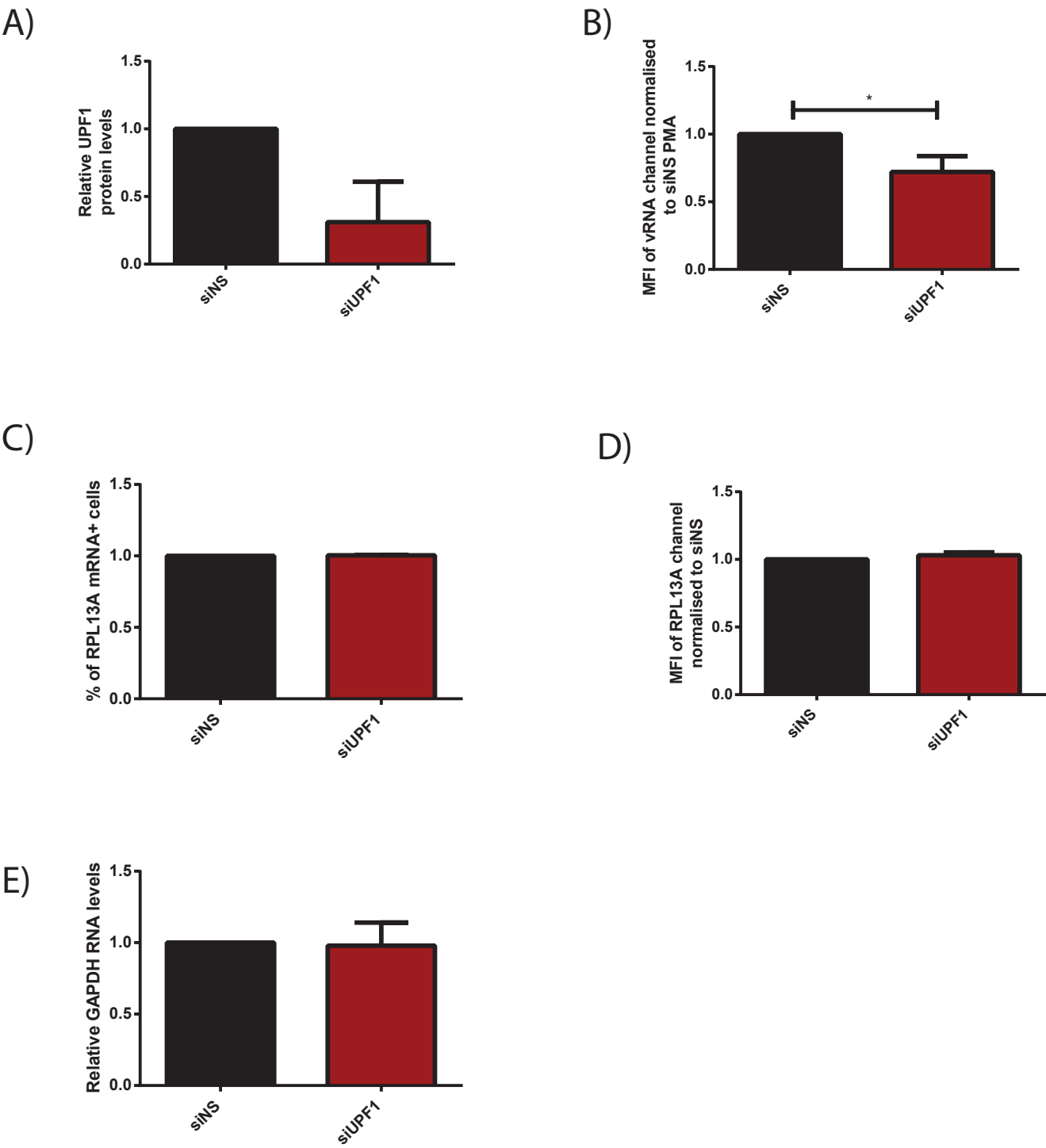
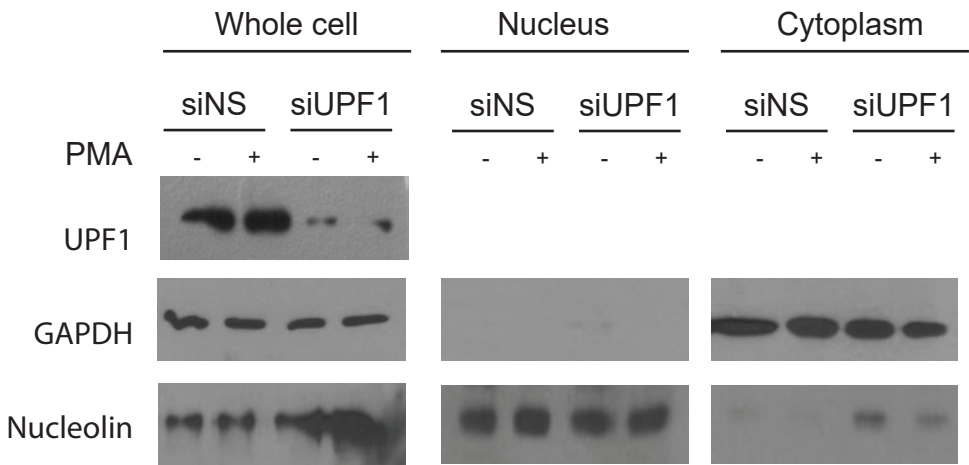
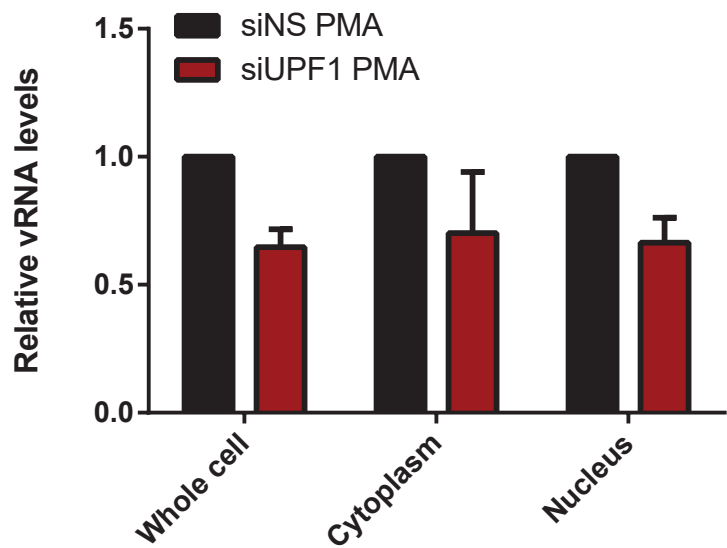


Figure S3

A)



B)



C)

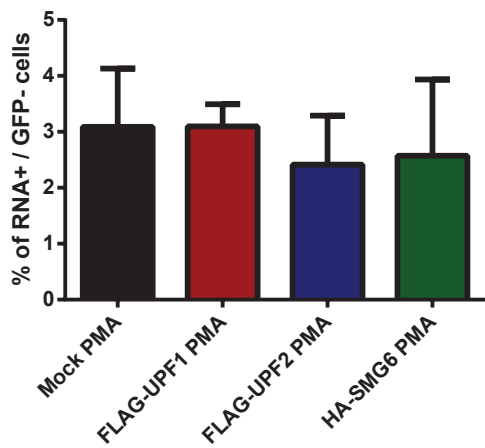


Figure S4

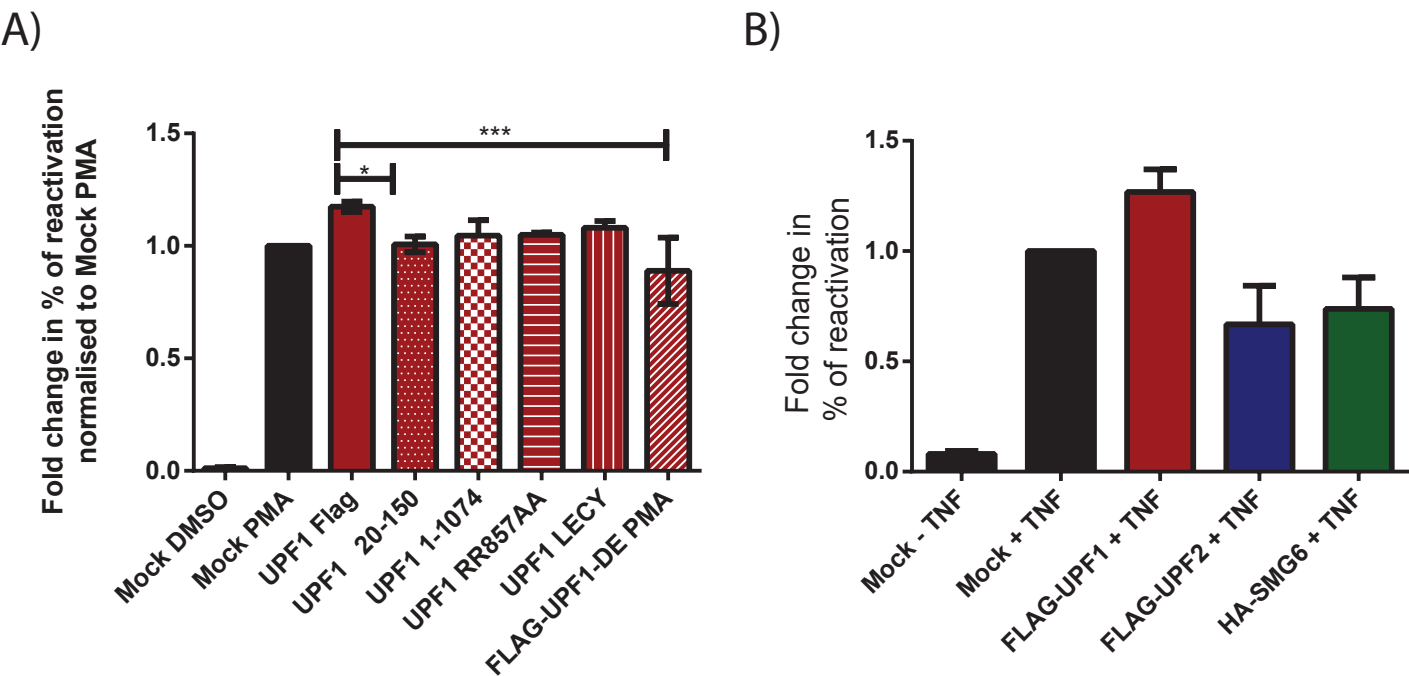


Figure S5

