

## **Supplementary Information**

### **HIV-1 proviral genome engineering with CRISPR-Cas9 for mechanistic studies**

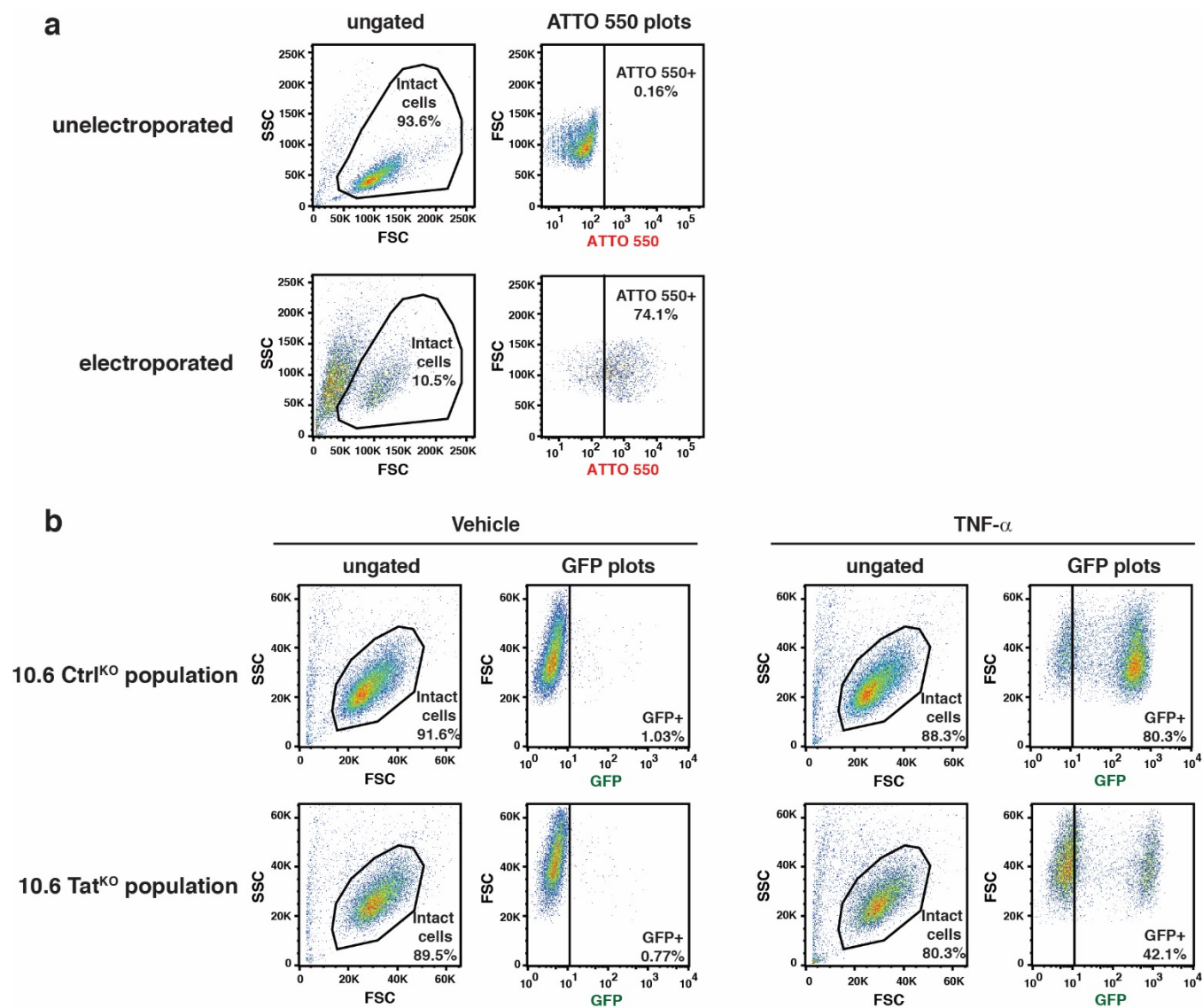
Usman Hyder<sup>†</sup>, Ashutosh Shukla<sup>†‡</sup>, Ashwini Challa and Iván D'Orso<sup>\*</sup>

Department of Microbiology, The University of Texas Southwestern Medical Center, Dallas, TX 75390, USA;

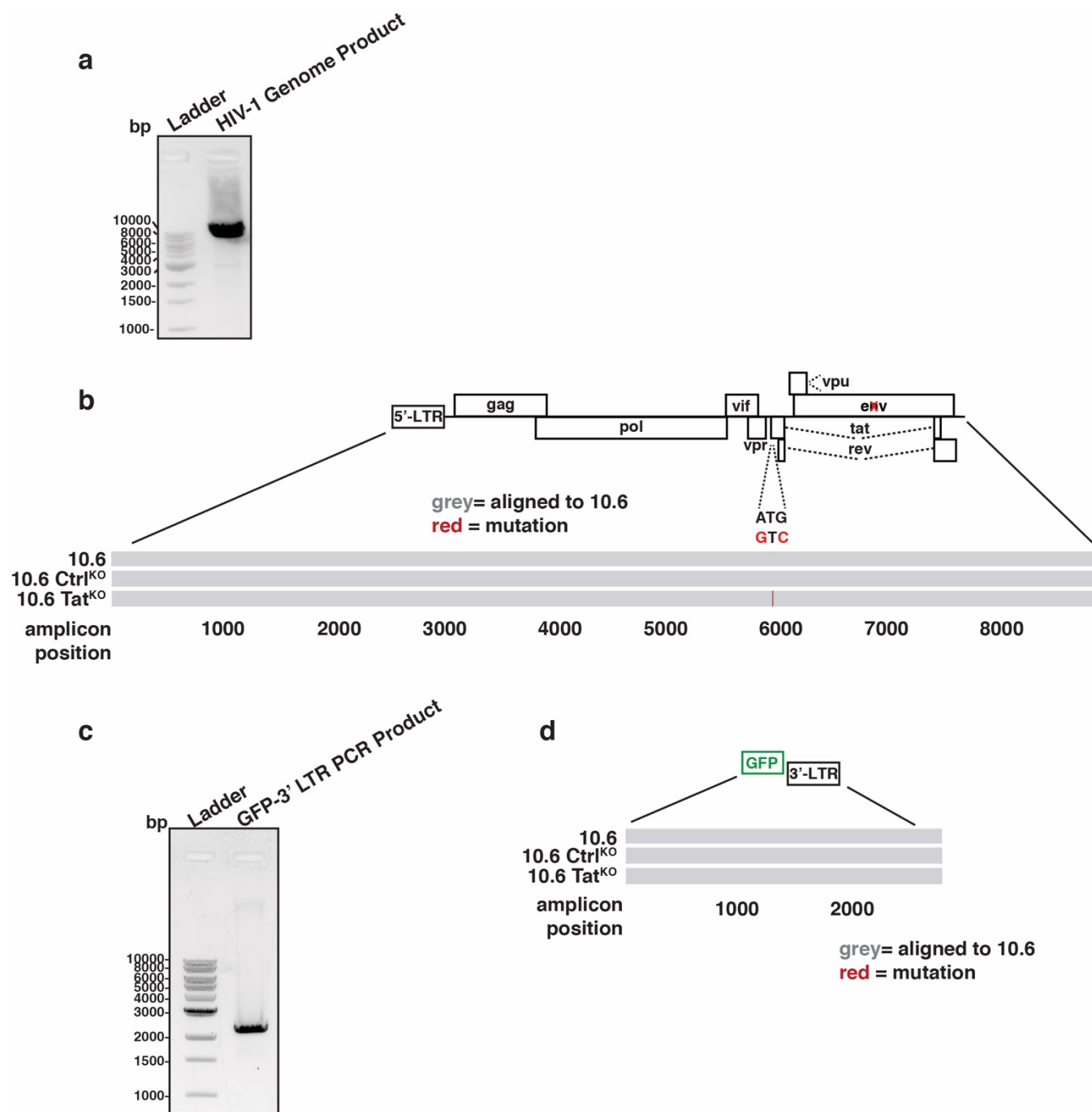
<sup>†</sup>These authors contributed equally

<sup>‡</sup> Current address: Division of Digestive and Liver Diseases, The University of Texas Southwestern Medical Center, Dallas, TX 75390, USA;

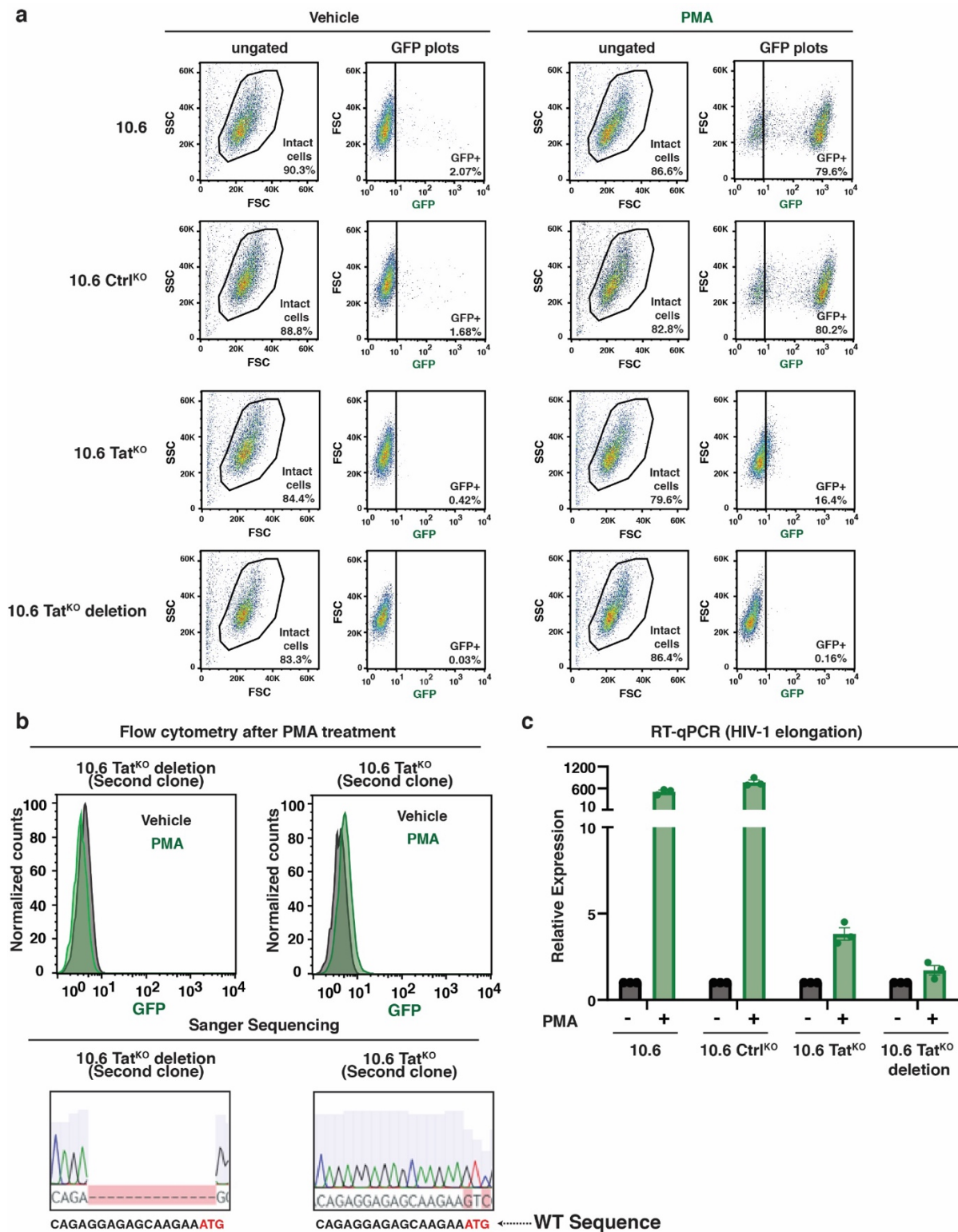
<sup>\*</sup>For correspondence: [ivan.dorso@utsouthwestern.edu](mailto:ivan.dorso@utsouthwestern.edu)



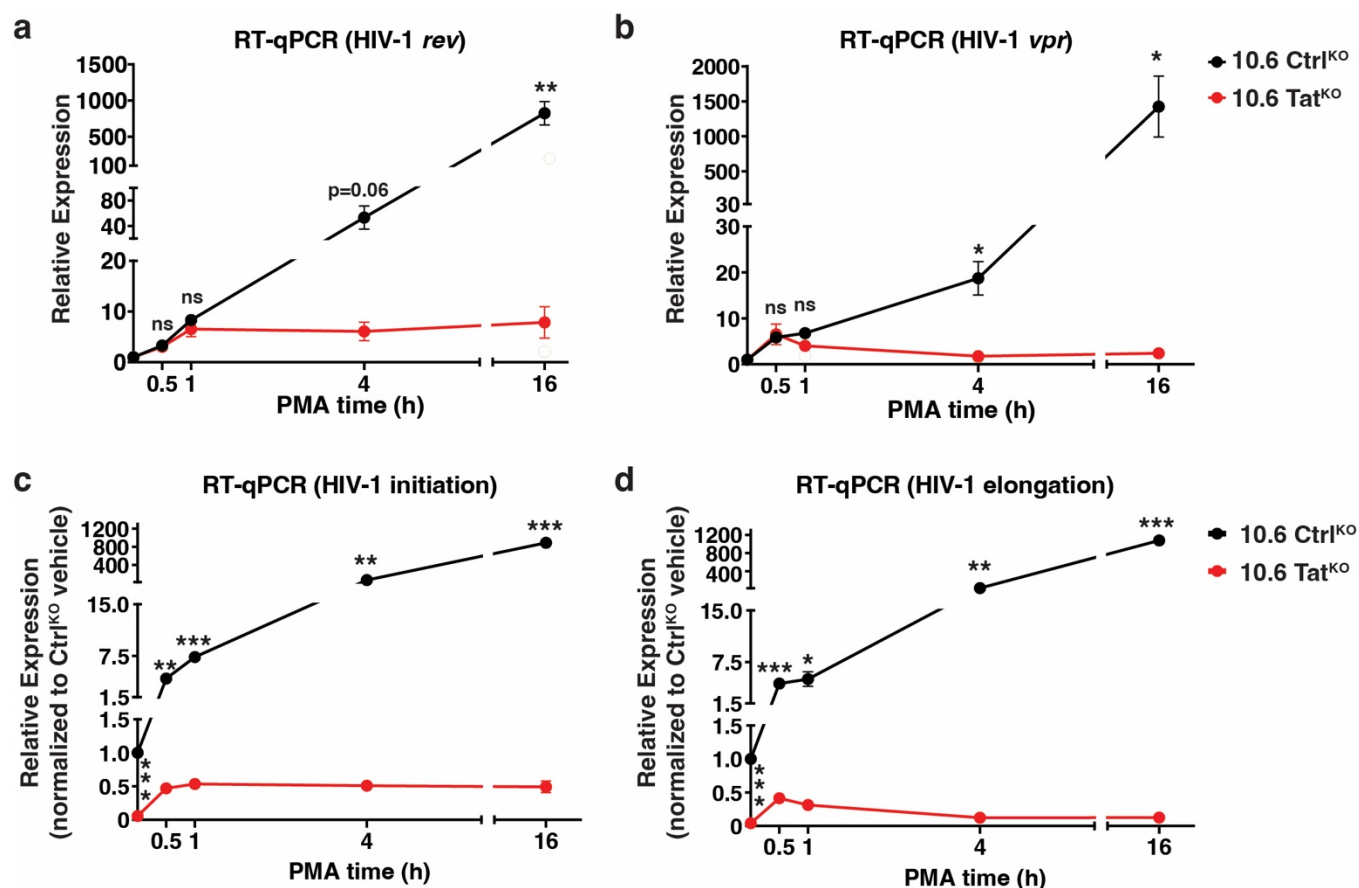
**Supplementary Figure S1. J-Lat 10.6 Tat<sup>KO</sup> cells can be made using a CRISPR-Cas9-based approach.**  
 (a) Raw flow cytometry plots (ungated cells and ATTO 550+ cells) for data in Figure 3a. (b) Raw flow cytometry plots (ungated cells and GFP+ cells) for data in Figure 3b.



**Supplementary Figure S2. HIV-1 genome sequencing in 10.6 Ctrl<sup>KO</sup> and 10.6 Tat<sup>KO</sup> clones.** (a) Agarose gel showing the HIV-1 genome PCR product. Parental 10.6 cells are shown as an example. (b) Amplicon sequencing of the HIV-1 genome PCR products showing alignment between DNA obtained from 10.6, 10.6 Ctrl<sup>KO</sup>, and 10.6 Tat<sup>KO</sup> cells. (c) Agarose gel showing the GFP-3' LTR PCR product. 10.6 parental cells are shown as an example. (d) Amplicon sequencing of the GFP-3' LTR PCR products showing alignment between DNA obtained from 10.6, 10.6 Ctrl<sup>KO</sup>, and 10.6 Tat<sup>KO</sup> clones.



**Supplementary Figure S3. Precise provirus genomic mutations and large deletions lead to differences in HIV-1 transcription induction upon cell stimulation.** (a) Raw flow cytometry plots (ungated cells and GFP+ cells) for data in Figures 4a-b. (b) Flow cytometry histograms of the indicated clones treated with vehicle DMSO or PMA. The Sanger sequencing data for each clone is indicated below. (c) RT-qPCR data for HIV-1 elongation in 4 cell lines (10.6, 10.6 Ctrl<sup>KO</sup>, 10.6 Tat<sup>KO</sup>, and 10.6 Tat<sup>KO</sup> deletion) -/+ 16 h PMA. n=3, +/- SEM.



**Supplementary Figure S4. Tat sustains enhanced HIV-1 expression upon cell stimulation.** (a-b) RT-qPCR for HIV-1 *rev* (a) and *vpr* (b) in 10.6 Ctrl<sup>KO</sup> and 10.6 Tat<sup>KO</sup> cell lines across the PMA time course. All data presented in these plots are normalized to the respective vehicle control for that cell line. Statistics are compared between 10.6 Ctrl<sup>KO</sup> and 10.6 Tat<sup>KO</sup> for each time point using an unpaired Student's t-test, n=3, +/- SEM, ns = non-significant, \*  $p < 0.05$ , \*\*  $p < 0.01$ . (c-d) RT-qPCR for HIV-1 initiation (c) and HIV-1 elongation (d) in 10.6 Ctrl<sup>KO</sup> and 10.6 Tat<sup>KO</sup> cell lines across the PMA time course. All data presented in these plots are normalized to the 0 time point of the 10.6 Ctrl<sup>KO</sup> cell line. Statistics are compared between 10.6 Ctrl<sup>KO</sup> and 10.6 Tat<sup>KO</sup> for each time point using a unpaired Student's t-test, n=3, +/- SEM, \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .

**Supplementary Table S1. Oligos used in this paper.**

Number	Name	Sequence (5'-3')	Usage	Modifications
	Tat ATG (10.6) crRNA oligo	CGACAGAGGAGAGCAAGAAA	Annealed to tracrRNA, ATTO™ 550 to create the gRNA	N-terminal AltR1 C-terminal AltR2
	HIV-1 10.6 Positive Donor oligo	G*A*CATAGCAGAATAG GCGTTACTCGACAGAG GAGAGCAAGAAGTCG AGCCAGTAGATCCTAG ACTAGAGCCCTGGAAG CATCC*A*G	HDR donor oligo	N-terminal Alt-R-HDR1 C-terminal Alt-R-HDR2 4 Phosphorothioate bonds (*)
	HIV-1 10.6 Negative Donor oligo	C*T*GGATGCTTCCAGG GCTCTAGTCTAGGATCT ACTGGCTCGACTTCTTG CTCTCCTCTGTCGAGTA ACGCCTATTCTGCTATG *T*C	HDR donor oligo	N-terminal Alt-R-HDR1 C-terminal Alt-R-HDR2 4 Phosphorothioate bonds (*)
3078	HIV-1_Tat_For	AGCCACACAATGAATG GACA	PCR	
3079	HIV-1_Tat_Rev	CAAACCTGGCAATGAA AGCA	PCR; Sanger sequencing	
3931	10.6_up 5' LTR_F	CGTACTGGCTGGAGTA ATAGCT	PCR of HIV-1 genome	
3932	eGFP-N	CGTCGCCGTCCAGCTC GACCAG	PCR of HIV-1 genome	
3933	Frag-26-R-RC	CTGGCTGTGGAAAGAT ACCT	PCR of GFP and 3' LTR	
3934	10.6_down 3' LTR_R	GAATGCCCATTGCTTTG GGAA	PCR of GFP and 3' LTR	
3076	HIV-1_elongation_FWD	GACGGTACAGGCCAGA CAAT	RT-qPCR ChIP-qPCR	
3077	HIV-1_elongation_REV	GATGCCCCAGACTGTG AGTT	RT-qPCR ChIP-qPCR	
1111	HIV-1_initiation_FWD	GCTTAAGCCTCAATAA AGCTTGCCCTGAG	RT-qPCR	
1112	HIV-1_initiation_REV	GTCCTGCGTCGAGAGA GCTCCTCTG	RT-qPCR	
3991	HIV-1_rev_FWD	TTCAGCTACCACCGCTT GAG	RT-qPCR	
3992	HIV-1_rev_REV	TATTTGAGGGCTTCCCA CCC	RT-qPCR	
3372	HIV-1_vpr_FWD	AGCCCCAGAAGACCA AGG	RT-qPCR	
3373	HIV-1_vpr_REV	TTGCCCTAAGCCATGG AG	RT-qPCR	
1868	GAPDH_FWD	GCAAATTCATGGCAC CGT	RT-qPCR	

1869	<i>GAPDH_REV</i>	TCGCCCCACTTGATTTT GG	RT-qPCR	
9	<i>U6_FWD</i>	CTCGCTTCGGCAGCAC ATATAC	RT-qPCR	
10	<i>U6_REV</i>	GGAACGCTTCACGAAT TTGCGTG	RT-qPCR	

**Supplementary Table S2. Antibodies used in this paper.**

<b>Target</b>	<b>Company</b>	<b>Catalog Number</b>	<b>Assay (Dilution/time)</b>
Tat	Abcam	ab43014	Western blot (1:500/ON)
Gag/p24	NIH HIV reagents Program	4121 (Mab to HIV-1 p24 (AG3.0))	Western blot (1:500/ON)
Actin Rhodamine	Bio-Rad	12004163	Western blot (1:10000/1 h)
Goat anti-mouse IgG-HRP	Santa Cruz Biotechnologies	sc-2005	Western blot (1:10000/1 h)
Donkey anti-rabbit IgG-HRP	Santa Cruz Biotechnologies	sc-2313	Western blot (1:10000/1 h)
RPB3 (Pol II)	Millipore	ABE999	ChIP-qPCR (5 µg/ON)