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Supplementary Information for

Human retroviral antisense mRNAs are retained in the nuclei of infected cells for viral persistence.

Guangyong Ma, Jun-ichirou Yasunaga, Kazuya Shimura, Keiko Takemoto, Miho Watanabe, Masayuki Amano, Hirotomo Nakata, Benquan Liu, Xiaorui Zuo and Masao Matsuoka

Guangyong Ma
E-mail: gma@cpu.edu.cn
Masao Matsuoka
E-mail: mamatsu@kumamoto-u.ac.jp

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Supplementary Materials and Methods

Transfections. $2x10^5$ HeLa cells were seeded in a 12-well plate and transfected with 1 μg of various plasmids by TransIT-LT1 (Mirus Bio) the second day. The transfection of Jurkat cells was performed by electroporation using Neon (ThermoFisher Scientific). Briefly, $4x10^5$ Jurkat cells were transfected with 1 μg of various plasmids by electroporation following the recommended protocol. RNA-FISH, ChIP or poly (A) tail assays were performed 24 hours post transfection.

Establishment of stable lines from Kit225. The HTLV-1 uninfected T cell line Kit225 was cultured in RPMI supplemented with 10% FBS and 100 U/ml IL-2. All pME vectors were linearized and transfected into Kit225 cells using Amaxa nucleofector. Three days later, 600 μg/ml of G418 was added for selection for two weeks.

Quantitative PCR (qPCR). RNA was extracted using the RNeasy Mini kit (Qiagen) with an on-column DNase digest. cDNA was synthesized using SuperScript III reverse transcriptase (ThermoFisher Scientific). qPCR was performed using SYBR green (Roche) on a StepOnePlus (Thermo Fisher Scientific). Primer sequences are TGGCTGTGTTCGCCTCCCTT and GGGAGCTGAGAACCTTCCAC for CCR4, ATGGCGGCCTCAGG and TTCTAAGGATAGCAAACCGT for HBZ, AACCCGTTGAACCCCATT and CCATCCAATCGGTAGTAGCG for 18S rRNA, AGACCACCAACACCATGGCC and CCGAACATAGTCCCCCAGAG for Tax, GAACCATTAGGAGTAGCACCCACCA and AGGAACAAAGCTCCTATTCCCACTG for HIV-1 ASP RNA,

AAGAGCTCATCAGAACAGTCAGACT and TTCTTCTTCTATTCCTTCGGGCCTG for Tat, ACGCCGAATATAATCCCAAG and CCAGTCTGGACTGTTCTTCA for TBP, and ACAGCCTCAAGATCATCAGC and GATGGCATGGACTGTGGTCA for GAPDH.

RNA-FISH. The RNAscope RNA-FISH kit was purchased from Advanced Cell Diagnostics. All procedures were performed following the protocol of the manufacturer. Cultured cells were prepared on slides by cytospin before fixation and probe hybridization. Probes used in this study are HTLV-1 HBZ (#432901), HTLV-1 HBZ intron (#472861), HTLV-1 Tax (#472871), HIV-1 ASP (#572111), HIV-1 Env (#532341), PPIB (#701031) and DapB (#701011). Slides of RNA-FISH were observed under an FV1000 fluorescent confocal microscope (Olympus).

RNA-FISH data analysis. For each slide, nine random areas were selected and photos were taken for analysis by ImageJ software. In Fig. 1A-C and Fig. 3A-B, the numbers of nuclear and cytoplasmic RNA spots were counted, and the proportion of spots that were nuclear was calculated. In Fig. 2B, D, E and Fig. 4A-B, it was impossible to count the number of RNA spots; instead, the number of cells with predominant nuclear, cytoplasmic or mixed localization of RNA spots was counted and their respective proportion is shown.

RNA-seq. Conventional RNA-seq was performed by Macrogen Japan using the TruSeq RNA Sample Prep Kit v2 on an Illumina platform. Stranded RNA-seq with pre-removal

of Ribosomal RNAs using a Ribo-Zero Gold Kit was performed by Takara Japan on an Illumina platform. All data was analyzed on a CLC workbench platform (Qiagen).

ChIP-qPCR. ChIP was performed using EpiQuik (Epigentek) following the manufacturer's protocol. Briefly, HeLa cells cultured in a 6-well plate were transfected with HBZ RNA expression vectors that used either SRα or the HTLV-1 3' LTR as the promoter. 24 hours later, cells were fixed and subjected to sonication on a Covaris M220 Focuses-ultrasonicator. Then the sonicated chromatin was added to the EpiQuik 96-well plate to incubate with various antibodies. The eluted and purified chromatin was analyzed by quantitative PCR (qPCR) using SYBR green (Roche) on a StepOnePlus (Thermo Fisher Scientific). Primers for HBZ were TAAAGGACAAGGAGGAGGAG and GCTTTCTCCCCTGGAGGGCC. ChIP-grade antibodies used were anti-RNA Pol II (clone 8WG16, Merck Millipore), anti-Ser2P RNA Pol II (clone 3E10, Merck Millipore), anti-Ser5P RNA Pol II (clone 4H8, Merck Millipore), anti-PAF1 (clone ab20662, Abcam), anti-CPSF73 (A301-091A, Bethyl Laboratories) and anti-CstF64 (A301-092A, Bethyl Laboratories).

Poly (A) tail assay. The Poly(A) Tail-length Assay Kit (764551KT) was purchased from ThermoFisher Scientific. RNA was extracted using the RNeasy Mini kit (Qiagen), and one microgram of total RNA was used in cDNA synthesis. PCR was performed to amplify both poly (A) tail and gene-specific products using a two-step protocol recommended by the manufacturer. Six microliters of the PCR products were run on a 2% agarose gel. The primer sequences are AGGTCGAGGGTCCACGAACAA and

CTCGCCACTTTGATTTTATTCTTCCA for endogenous HBZ (Fig. 1E and Fig. 4D), AGGAGGCTCGCATCTCTCCTTCA and AGAGTTGAGCAAGCAGGGTCAGGCA for endogenous Tax (Fig. 1E and Fig. 4D), CAGGAGAAGGAGGATTTAATGGGAGAGGTT and TGTGAAATTTGTGATGCTATTGCT for pME-HBZ-SpA (Fig. 2A), CAGGAGAAGGAGGATTTAATGGGAGAGGTT and AAGTTTCTCGCCACTTTGATTTTATTC for pME-HBZ-HpA mutants (Fig. 2A, C), GCGAGCCCTCAGATGCTGCATATAA and GAAGCACTCAAGGCAAGCTTTATTG for HIV-1 sense RNAs (Fig. 4D, H) and CCATAATCCCTGATGATCTTTGCTT and TTCGGGTTTATTACAGGGACAGCA for HIV-1 ASP RNA (Fig. 4D, H).

ChIRP-PCR. The Magna ChIRP RNA Interactome kit was purchased from Merck Millipore. Briefly, 3~5 x10^7 cells (100 mg) were collected and fixed in 1% glutaraldehyde for 10 minutes before proceeding to DNA shearing on a Covaris M220 Focuses ultrasonicator. Probes for HTLV-1 HBZ RNA (Supplementary Table 2) or HIV-1 ASP RNA (Supplementary Table 3) were designed using the Stellaris FISH Probe Designer and synthesized by ThermoFisher Scientific. The sequences of primers to amplify CCR4 promoter are CTCAGCTACTTGGGAGACTAAGGCA and TCACTCTGTCACCCAGACTGGTGTT. The sequences of primers to amplify HIV-1 LTR are CAGGGGTCAGATATCCACTGACCTT and AAGCTGGTGTTCTCTCCTTTATTGG (product U3-1), AGTGTTAGAGTGGAGGTTTGACAGC and

GAAAGTCCCTTGTAGCAAGCTCGAT (product U3-2), TGCCTGTACTGGGTCTCTCTGGTTA and GCACTCAAGGCAAGCTTTATTGAGG (product R) and CCGTCTGTTGTGTGACTCTGGTAACTAGA and GGCTTTACTTTCGCTTTCAAGTCCCTGTT (product U5G).

HIV-1 infection of T cells. The production of HIV-1 virions was performed as previously reported (1). $4x10^6$ HEK293T cells in 10 ml DMEM containing 10% FBS were seeded in a 10-cm dish and transfected the next day with 10 μg pNL4-3. 48 hours later, supernatants were collected and centrifuged at 25000 rpm for 2 hours at 4°C. Then the supernatant was removed and the pellet was resuspended in 500 μL RPMI and stocked at -80°C. $2x10^5$ T cells in 500 μL RPMI containing 10% FBS were seeded in a 24-well plate and infected with 100 μL HIV-1 virion stock in the presence of 1 μg/ml polybrene. 24 hours later, infected cells were subjected to RNA-FISH analysis.
For HIV-1 infection of primary cells, PBMCs from a healthy donor were subjected to CD4 T cell isolation by MACS cell separation using human CD4 microbeads (Miltenyi Biotec). Isolated CD4 T cells were stimulated by anti-CD3 (clone UCHT1, Biolegend) and anti-CD28 (clone CD28.2, Biolegend)) antibodies in the presence of 50 U/ml IL-2 for three days before HIV-1 infection. In Fig. 5C, the second day after HIV-1 infection, CD4 T cells were transduced by VSV-G packaged lentiviruses encoding *ASP* RNA or empty control and incubated for two days before subject to RNA-FISH analysis.

HTLV-1 infection of T cells. MT-2 cells were irradiated by X-ray (150Gy) and cocultured with Jurkat or Kit225 at 1:3 in appropriate media. Irradiated MT-2 cells were

also cultured alone as a control to monitor killing efficiency of the irradiation. One week later, infected Jurkat or Kit225 were subjected to RNA-FISH analysis.

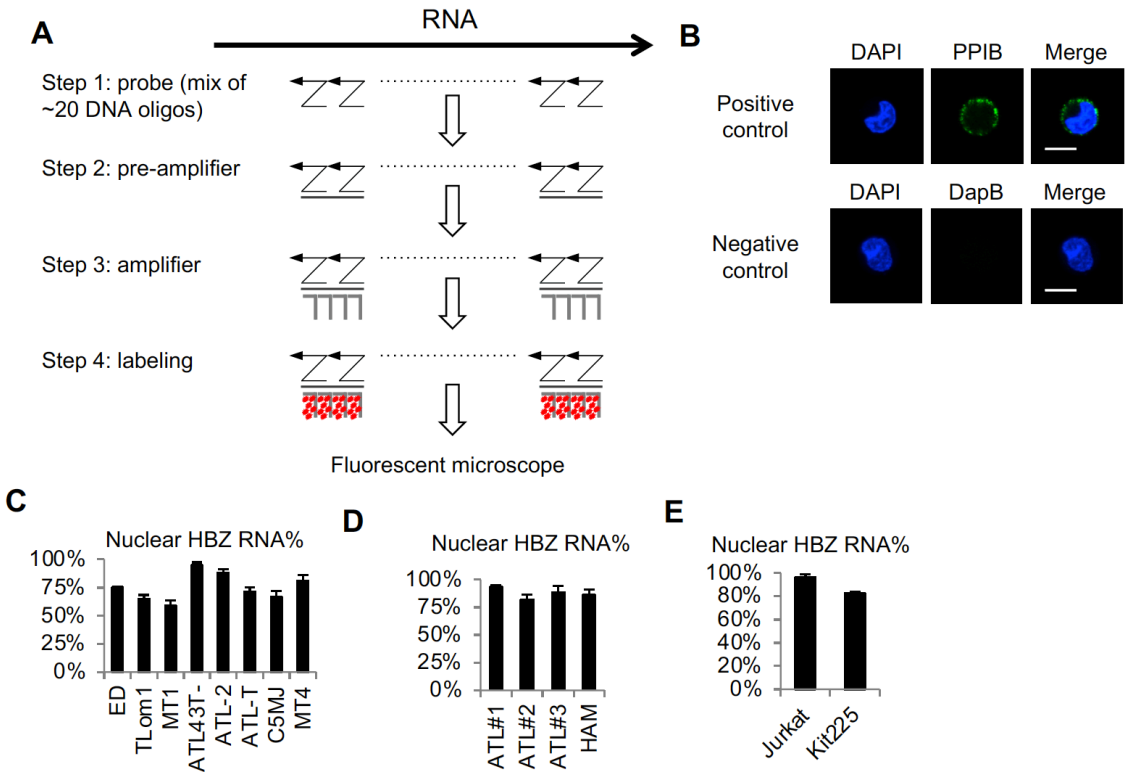
Antisense oligos. Antisense oligos (ASO) against HBZ or ASP RNA were designed and synthesized by Qiagen, and a final concentration of 50 nM was used. ASOs were transfected by Lipofectamine 2000 (ThermoFisher Scientific) or TransIT-X2 (Mirus Bio). The sequences of ASOs against HBZ RNA are CACTTGCGCTCACGGC (#2) and AGGCAAGCATCGAAAC (#4). The sequences of ASOs against HIV-1 ASP RNA are TCTATGAAACTTACGG (#1) and CAATAGTAGTAGCGGG (#2). The sequence of the negative control ASO is AACACGTCTATACGC (NC).

Flow cytometry. 24 hours after transfection with ASOs, HIV-1 infected BH11 cells were fixed in 1% formalin and analyzed for BFP expression on a FACSverse (BD Biosciences). Data was processed using the FlowJo software (BD Biosciences).

3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. ATL-43T- or MT4 cells were resuspended at 3-5x10^4 /ml and transfected with ASOs. 24 hours later, 100 µl of the cell suspension was seeded into a 96-well plate and 10 µL of MTT was added. Cells were kept in the dark in a humidified incubator at 37°C with 5% CO_2. 2 hours later, cells were lysed with 100 µL of lysis buffer (Nacalai Japan) and further incubated in the dark at room temperature for 15 minutes. Then the plate was measured for absorbance at 595 nm on a plate reader (Berthold).

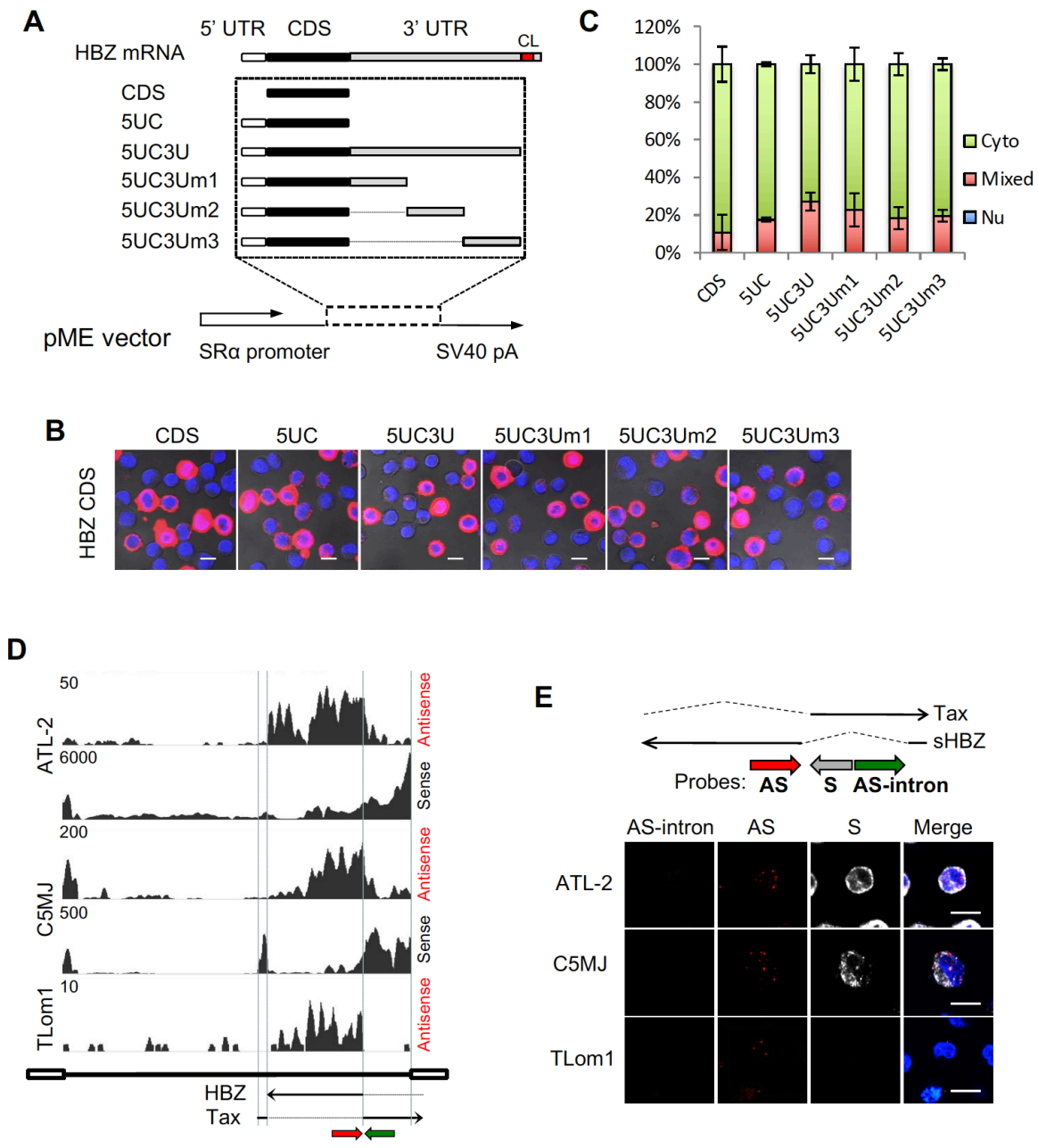
Western blot. 24 hours after transfection of ASOs, 10^6 ATL-43T- or MT4 cells were resuspended in 100 μL lysis buffer (1% NP40, 0.1 % sodium deoxycholate, 150 mM sodium chloride, 20 mM Tris) supplemented with protease inhibitor cocktail (Nacalai Japan) and kept on ice for 30 minutes. The lysates were pelleted down and the supernatants were removed and mixed with 6x sample buffer (Nacalai Japan) and denatured at 100°C for 5 minutes. The denatured protein lysates were run on a 15% SuperSep gel (Wako Japan) and transferred to a nitrocellulose membrane (BioRad) for probing with HBZ or tubulin (clone DM1A, Sigma) antibodies. Mouse anti-HBZ monoclonal antibody (clone 1A10) was generated by immunizing C57BL/6 mouse with HBZ peptide (CKQIAEYLKRKEEEKARRRRRAEKKAADVARRKQEEQE).

Fig. S1.



A, Scheme showing how the highly sensitive RNA-FISH works. Step 1, probe hybridization with target RNA; step 2, pre-amplifier-probe binding; step 3, amplifier-pre-amplifier binding; step 4, amplifier-dye binding. **B**, Positive (PPIB) and negative (DapB) controls for RNA-FISH. **C**, The total number of nuclear and cytoplasmic *HBZ* RNA spots in nine fields was counted under a confocal fluorescence microscope. The percentage of HBZ RNA that is nuclear in each cell line of Fig. 1A is shown. **D**, The percentage of HBZ RNA that is nuclear in each primary case of Fig. 1B is shown. **E**, The percentage of HBZ RNA that is nuclear in *de novo* HTLV-1 infected cells of Fig. 1C is shown.

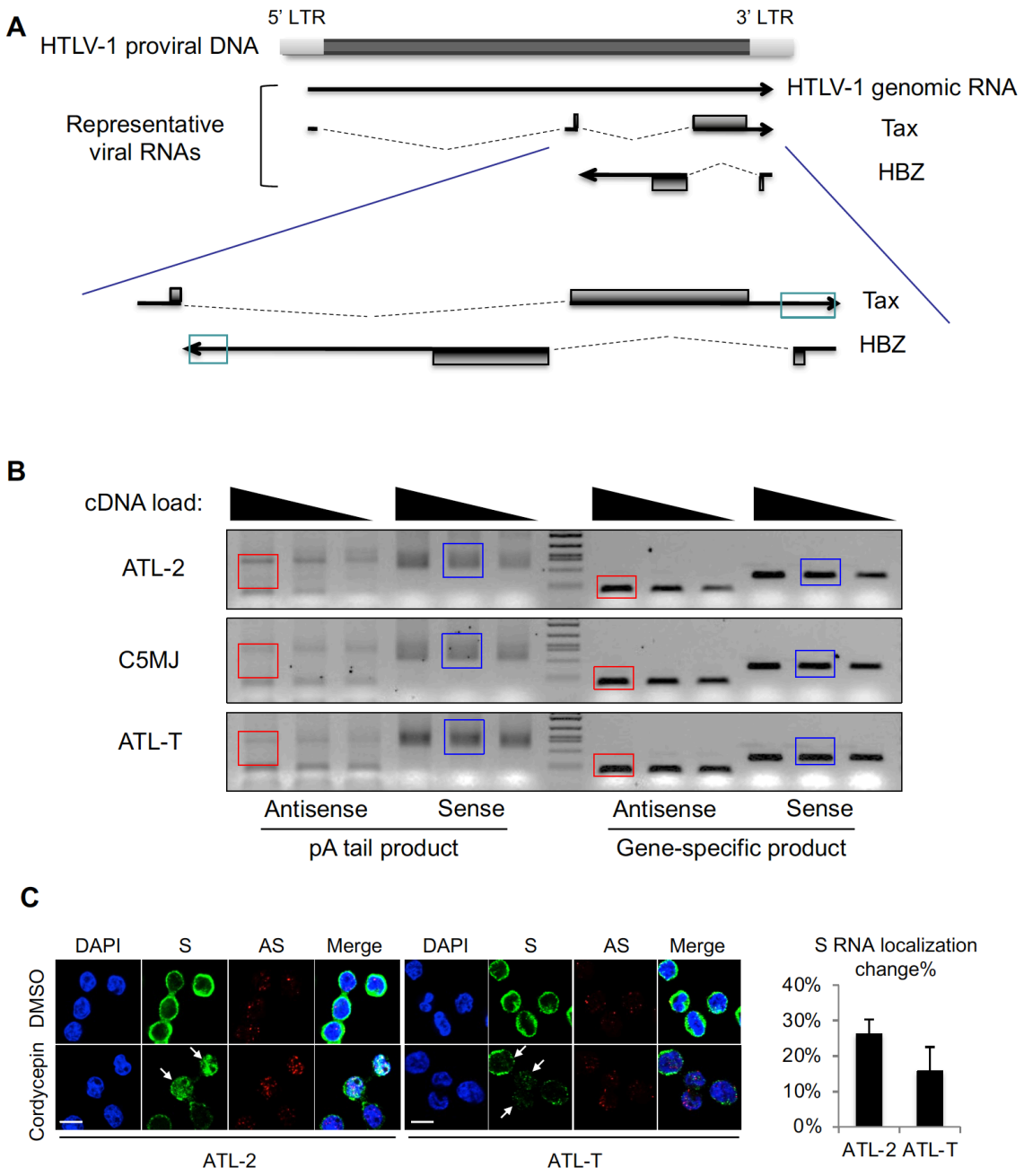
Fig. S2.



A, The complete or truncated *HBZ* sequence was cloned into a pME vector, which uses an SRα promoter and an SV40 polyadenylation signal. CL indicates the cleavage site. **B**, The above plasmids were transfected into HeLa cells, and representative RNA-FISH results are shown. *HBZ* RNA (red) is predominantly localized in the cytoplasm. Bar=10μm. **C**, The percentage of cells from **B** with predominantly cytoplasmic, nuclear

or mixed localization patterns of *HBZ* RNA. **D**, Stranded RNA-seq results of HTLV-1 infected cell lines, including two Tax-positive (ATL-2 and C5MJ) lines and a Tax-negative (TL-Om1) line. The positions of probe mixes used for detection of HTLV-1 antisense mRNA *HBZ* (red arrow) and sense mRNAs (green arrow) are marked. **E**, A new RNA-FISH probe, AS-intron, targeting the intron region of *HBZ* RNA was used in three HTLV-1 infected cell lines. Probe AS stains the *HBZ* exon in red while AS-intron stains the *HBZ* intron in green. Probe S stains HTLV-1 sense mRNAs in white. Bar=10μm.

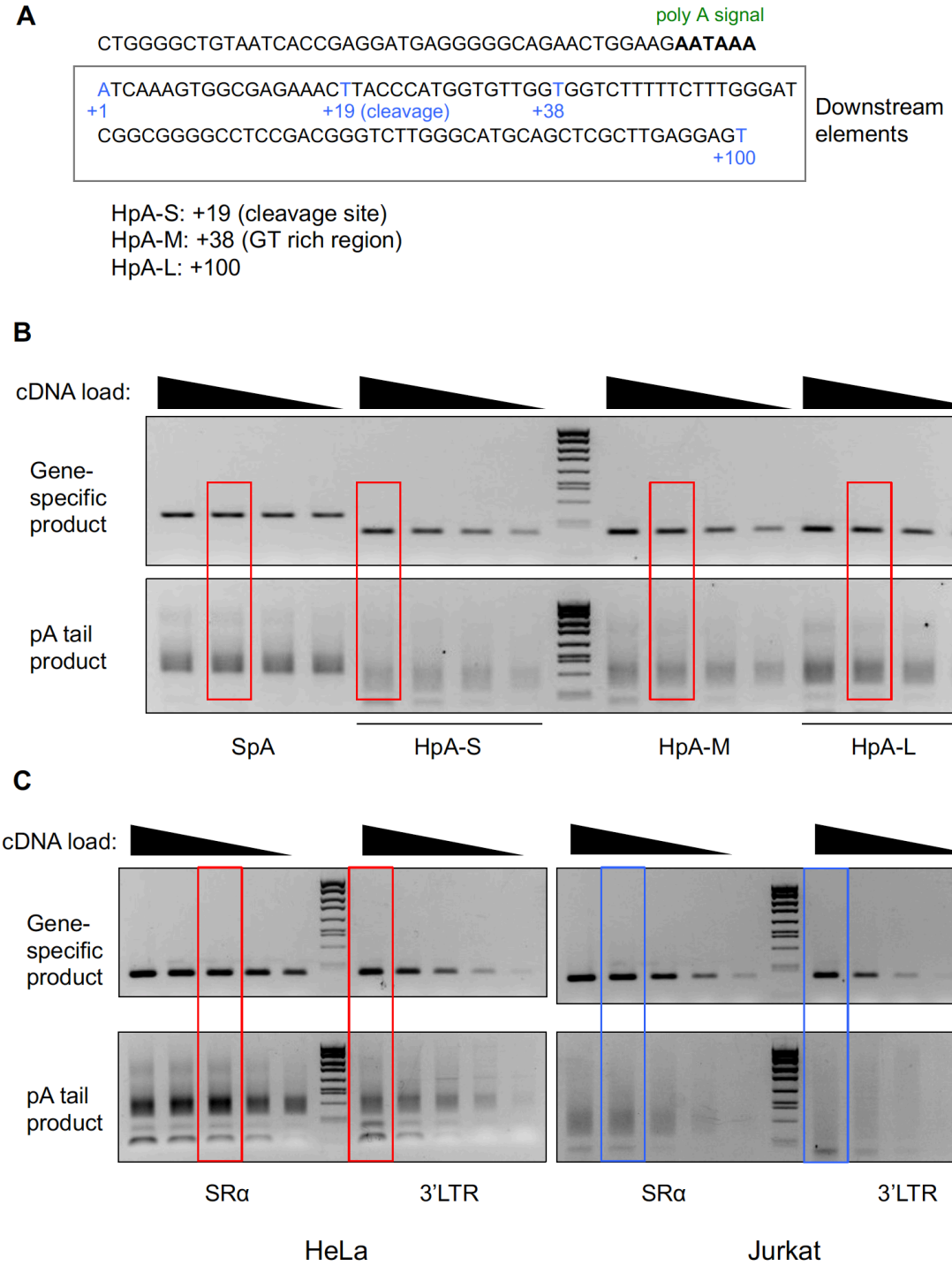
Fig. S3.



A, Scheme showing the regions amplified in the pA tail assay for Tax or HBZ, marked in aqua squares. **B**, Optimization of the pA tail assay. The pA tail assay is a semi-quantitative PCR-based assay. While other PCR parameters were the same, the amount of cDNA was pre-optimized in order to obtain equivalent amounts of gene-specific products

for HTLV-1 antisense and sense mRNAs. The experimental conditions of the selected lanes (red and blue boxes) having the equivalent amounts of gene-specific products were used in a new experiment, and the results are presented in Fig. 1E. **C**, Two Tax-positive HTLV-1 infected cell lines were treated with DMSO or cordycepin (100 μM) for 24 hours before RNA-FISH. The result indicates that sense mRNAs (green) underwent dramatic localization change upon treatment of cordycepin (shown by arrows) whereas antisense mRNA *HBZ* (red) did not. The percentage of cells with sense mRNAs undergoing localization change is shown in the right panel. Bar=10 μm.

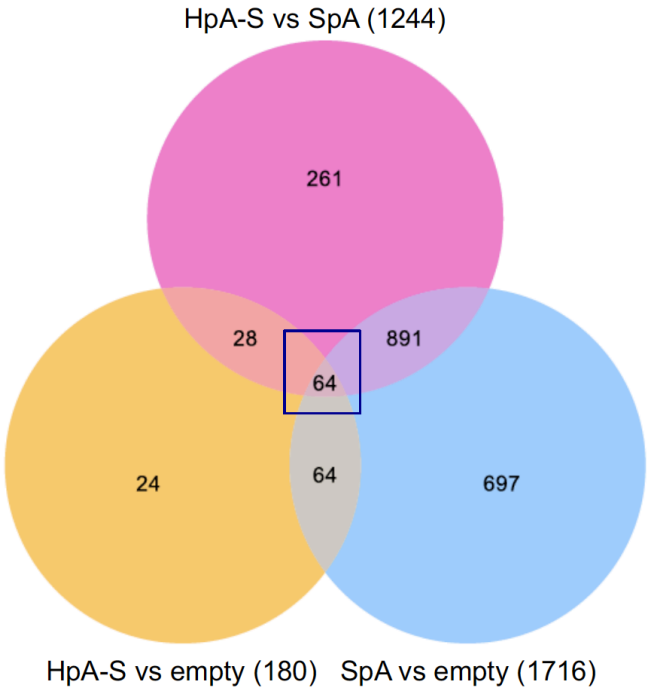
Fig. S4.



A, The complete sequence of the HBZ pA signal used for cloning. The HpA signal reported by Cavanagh et al. (2) corresponds to HpA-M in Fig. 2A, and was not competent enough in our assay systems, so we extended it to 100 bp downstream of the AATAAA

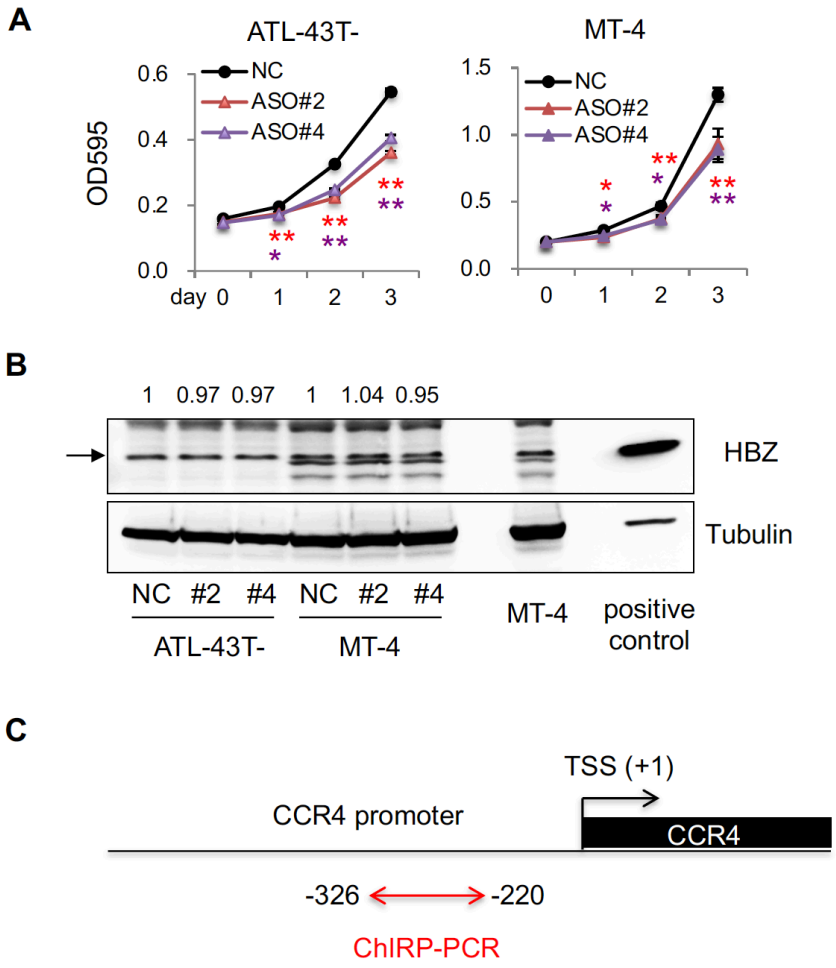
sequence to generate HpA-L, which was fully competent. **B**, Optimization of the pA tail assay. The amount of cDNA was pre-optimized to obtain equivalent amounts of gene-specific products for all four HBZ expression vectors. The experimental conditions of the selected lanes were used in a new experiment, and the results are presented in Fig. 2A. **C**, Optimization of the pA tail assay. The amount of cDNA was pre-optimized to obtain equivalent amounts of gene-specific products for the HBZ expression vectors using different promoters. The experimental conditions of the selected lanes were used in a new experiment, and the results are presented in Fig. 2C.

Fig. S5.



RNA-seq results were obtained from four Kit225 lines and three comparisons were done, which indicate 180 genes having >twofold change in the HpA-S line compared with empty control (orange), 1716 genes having >twofold change in SpA line compared with empty control (blue) and 1244 genes having >twofold change in HpA-S line compared with SpA (red). The overlap of these three comparisons contains 64 genes whose expressions were changed by HBZ RNA, but were regulated differently in HpA-S or SpA lines.

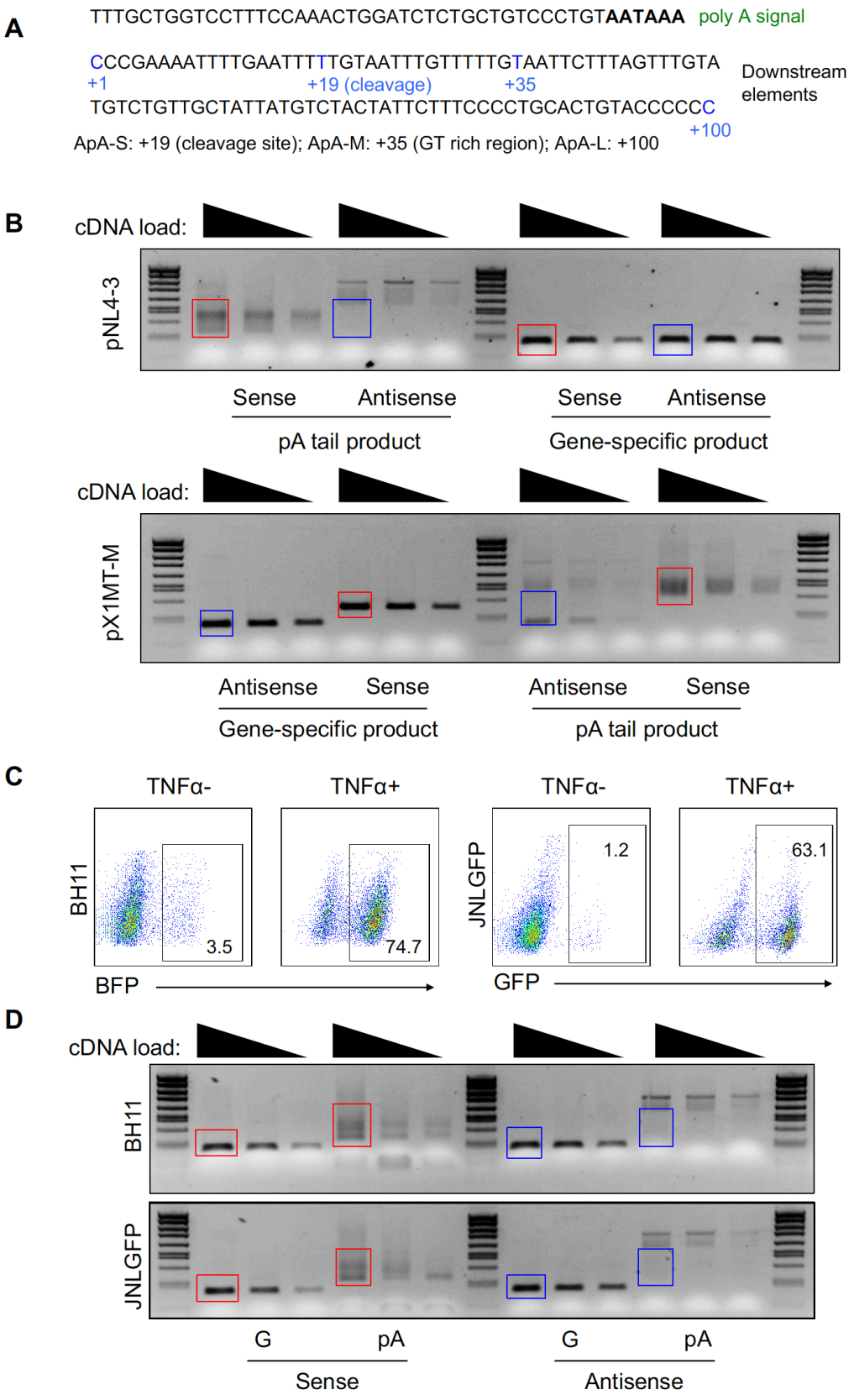
Fig. S6.



A, ATL-43T- or MT-4 cells were transfected with negative control or HBZ-knockdown ASOs, and cell growth was quantified by MTT assay every day. The statistical analyses were performed by student's t-test. *, $p<0.05$. **, $p<0.01$. The red asterisks indicate statistical differences of ASO#2 vs. NC whereas the purple asterisks indicate statistical differences of ASO#4 vs. NC. Note that HBZ-knockdown ASOs led to reduced cell proliferation as early as 24 h post transfection. **B**, 24 hours after transfection with ASOs, ATL-43T- or MT-4 cells were harvested for protein lysate preparation and subsequent Western blot. HEK293T cells transfected with an HBZ-expressing vector were used as the positive control. **C**, A scheme illustrating the promoter and transcription start site

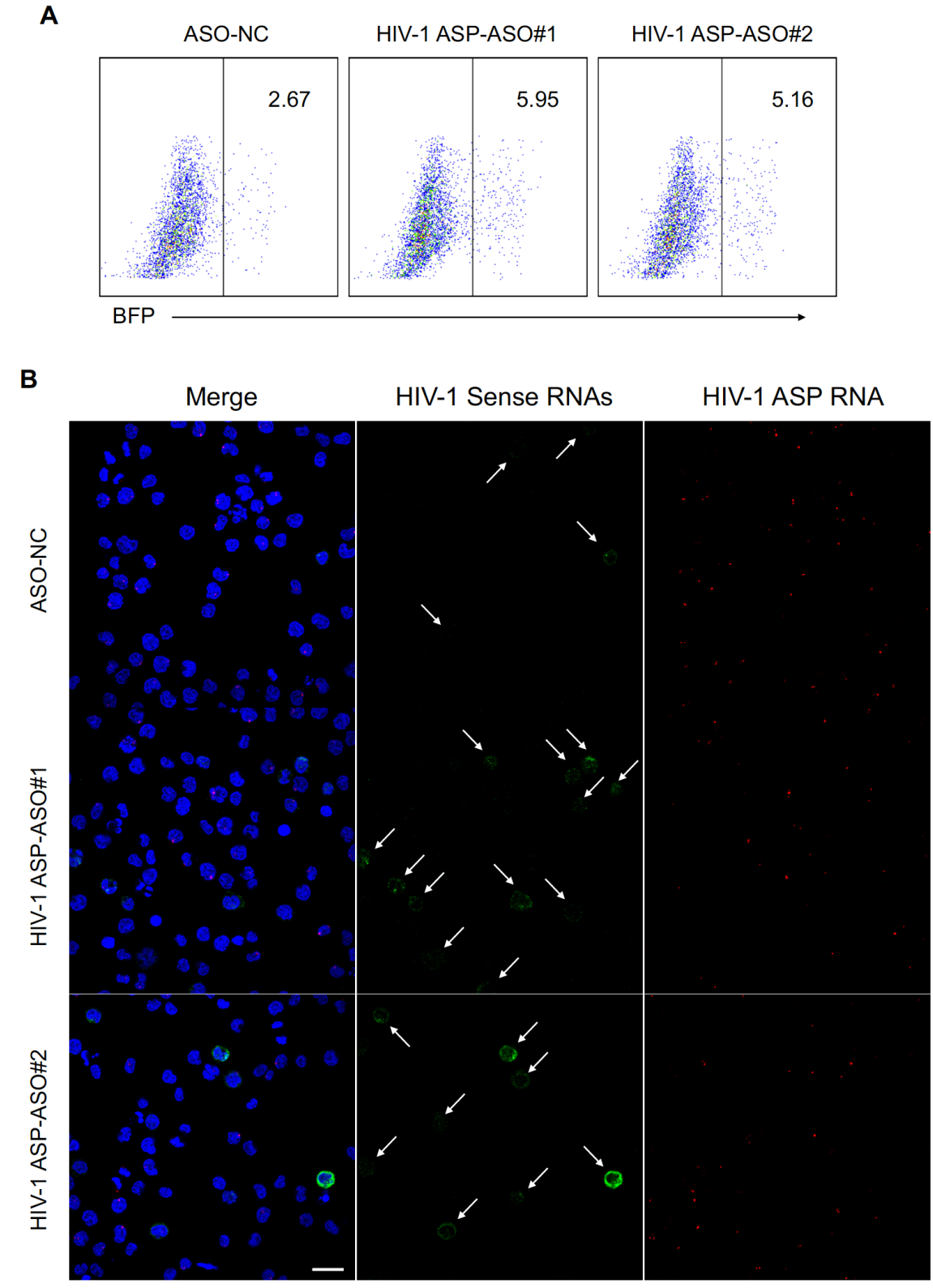
(TSS) of CCR4. ChIRP-PCR was performed to amplify the -326 to -220 bp region upstream of the TSS site (3).

Fig. S7.


A
TTTGCTGGTCCTTTCCAAACTGGATCTCTGCTGTCCCTGTAATAAA poly A signal
CCCGAAAATTTTGAATTTTTGTAATTTGTTTTTGTAATTCTTTAGTTTGTA
+1
+19 (cleavage)
+35
Downstream elements
TGTCTGTTGCTATTATGTCTACTATTCTTTCCCCTGCACTGTACCCCCC
+100
ApA-S: +19 (cleavage site); ApA-M: +35 (GT rich region); ApA-L: +100
B
cDNA load:
pNL4-3
Sense
Antisense
Sense
Antisense
pA tail product
Gene-specific product
cDNA load:
pX1MT-M
Antisense
Sense
Antisense
Sense
Gene-specific product
pA tail product
C
TNFα-
TNFα+
TNFα-
TNFα+
BH11
3.5
74.7
JNLGFP
1.2
63.1
BFP
GFP
D
cDNA load:
BH11
JNLGFP
G
pA
G
pA
Sense
Antisense

A, The complete sequence of the ASP pA signal used for cloning. Various lengths of downstream elements are cloned in order to compare the competency of the ASP pA signal. **B**, Optimization of the pA tail assay. The amount of cDNA was pre-optimized to obtain equivalent amounts of gene-specific products for HTLV-1 or HIV-1 antisense and sense mRNAs. The experimental conditions of the selected lanes were used in a new experiment, and the results are presented in Fig. 4D. **C**, Left panels, BFP expression of BH11 treated with or without TNFα (10 ng/ml) for 24 hours. Right panels, GFP expression of JNLGFP treated with or without TNFα (10 ng/ml) for 24 hours. **D**, Optimization of the pA tail assay. The amount of cDNA was pre-optimized to obtain equivalent amounts of gene-specific products for BH11 or JNLGFP antisense and sense mRNAs. The experimental conditions of the selected lanes were used in a new experiment, and the results are presented in Fig. 4H.

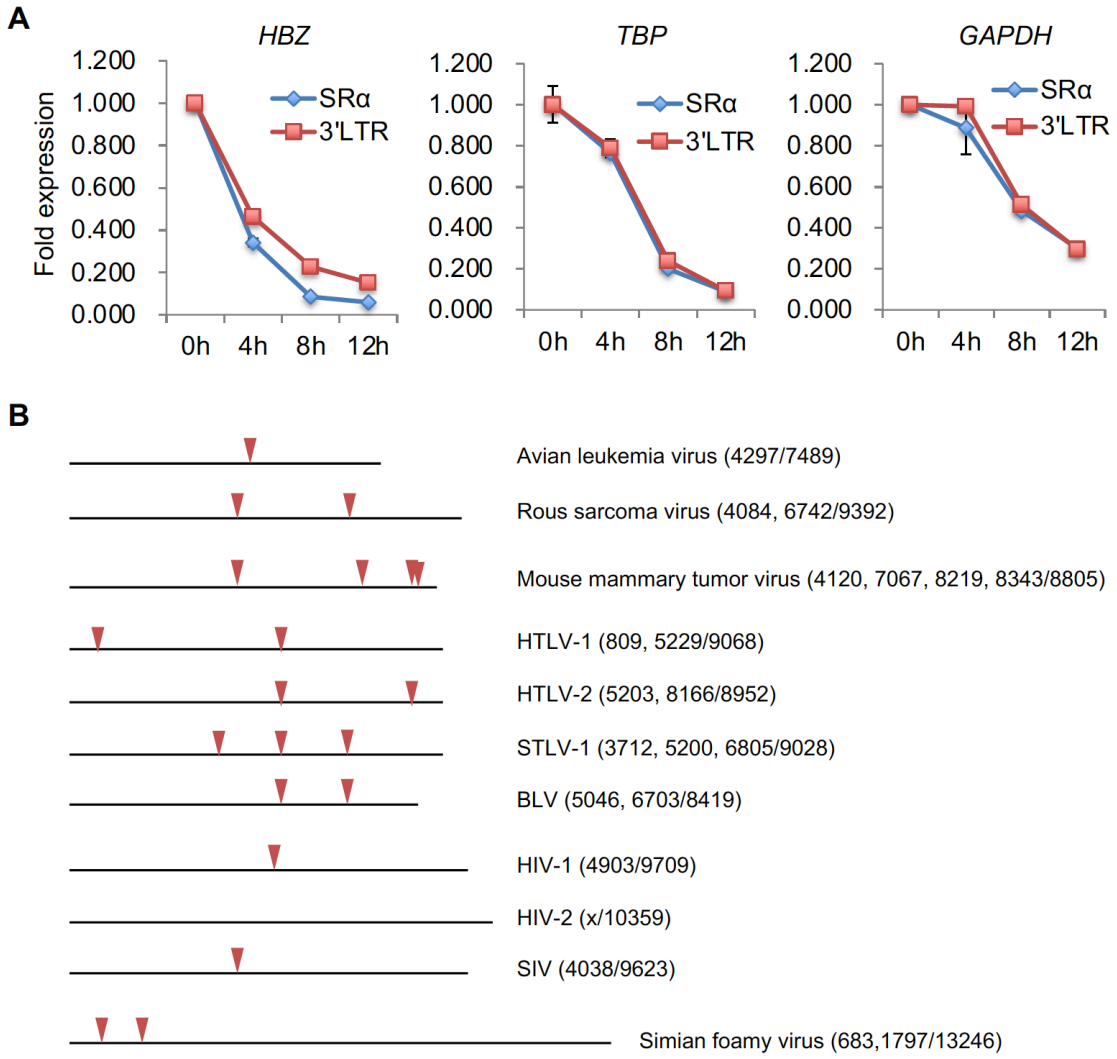
Fig. S8.



A, Representative flow cytometry results of Fig. 5B, left panel. **B**, Representative RNA-

FISH results of BH11 cells transfected with negative control (NC) ASO or ASO that target HIV-1 *ASP* RNA (ASO-HIV-1 ASP #1 and #2). White arrows indicate cells with HIV-1 sense RNAs detected (green). Summarized results are shown in Fig. 5B, middle and right panels. Bar= 20 μm.

Fig. S9.



A, After transfection with HBZ expression vectors that used either SRα or the HTLV-1 3'LTR as the promoter, HeLa cells were treated with actinomycin D (1.5 μg/ml) and harvested at different time points for RNA extraction and qPCR quantification. TBP and GAPDH were used as two internal controls. **B**, The conserved motif AATAAA, which indicates the presence of a potential polyadenylation signal, is present in the antisense strand of most retroviruses. Numbers in parentheses: location(s) of AATAAA/genome size (bp).

Table S1. 15 genes showing opposite regulations in HpA-S vs. SpA lines among the 64 genes (Fig. S6) differentially regulated by HpA-S and SpA lines

	TTG HBZ (HpA-S vs SpA)		TTG HBZ (HpA-S vs empty)		TTG HBZ (SpA vs empty)	
Name	Fold change	FDR p-value	Fold change	FDR p-value	Fold change	FDR p-value
AC002116.1	-14.5423471	1.30E-10	-5.58426163	0.00785332	2.60221651	0.00044953
HIST2H2AA3	-2.11255184	6.20E-06	-4.95894975	0	-2.34744502	2.51E-12
AC009237.16	-13.96075572	0	-3.14936932	0.0361065	4.43120513	2.86E-14
KCTD3	-34.96226834	0	-2.71188711	0.00004035	12.89065889	0
ATP8A2	-4.03299919	0	-1.9999653	4.92E-09	2.01651167	1.21E-12
FAM129B	-3.25049211	1.74E-11	-1.94205869	0.02452283	1.67362792	0.00492462
IL4I1	-4.05800004	0	-1.914829	0.0016784	2.11916265	5.28E-09
GPR132	-2.8251254	4.07E-14	-1.76432526	0.00694383	1.60120302	0.00136432
PTPRG	-3.53768885	0	-1.62467265	0.00526023	2.17744149	4.76E-13
CXCL10	-4.54284551	0	-1.55169639	0.02966258	2.92760714	0
CCR4	6.12387805	0	1.75979784	0.00003964	-3.47970585	0
RPS10-NUDT3	5.14046842	8.33E-10	1.99669357	0.03002666	-2.57394824	0.00654959
CARD11	6.40494963	0	2.75145585	3.08E-13	-2.32766822	0.00001446
CD36	19.93057588	0	3.93977216	0	-5.05859871	0
SERPINB9	33.92080965	6.82E-10	4.65419419	2.03E-07	-7.27737057	0.00746081

Table S2. ChIRP probes for HTLV-1 HBZ RNA

Probes	Sequence
HBZ-probe-1	tgacacaggcaagcatcgaa
HBZ-probe-2	aggatagcaaaccgtcaagc
HBZ-probe-3	tctttttttcgcttcctctt
HBZ-probe-4	tctagtatagccatcaatcc
HBZ-probe-5	ttaacctctcccatcaaatc
HBZ-probe-6	ccccattactctcttataaa
HBZ-probe-7	caaactggaatcacccttgt
HBZ-probe-8	ttcccatgtctcaatactac
HBZ-probe-9	gaaagagcctcctacatgag
HBZ-probe-10	cttttccttgtcacctgttc
HBZ-probe-11	cgttaccatttaactggacc
HBZ-probe-12	acttgcattgtctgtatcga
HBZ-probe-13	actctaacctagaccacatc
HBZ-probe-14	tcgacgctccaggatatgac
HBZ-probe-15	tggaagtttcagcacgatgt
HBZ-probe-16	attcagcctcttattcagac
HBZ-probe-17	ccctaacctagtaagttact
HBZ-probe-18	tctcctcataccactctaaa

Table S3. ChIRP probes for HIV-1 ASP RNA.

Probes	Sequence
ASP RNA-probe-1	gacagggcttggaaaggatt
ASP RNA-probe-2	tcctacagtattggagtcag
ASP RNA-probe-3	tagcacttatctgggacgat
ASP RNA-probe-4	gggatattcaccattatcgt
ASP RNA-probe-5	ggcaagtttgtggaattggt
ASP RNA-probe-6	ggatggagtgggacagagaa
ASP RNA-probe-7	aaaggatcaacagctcctgg
ASP RNA-probe-8	atttgctgagggctattgag
ASP RNA-probe-9	gaataggagctttgttcctt
ASP RNA-probe-10	gaggcgatatgagggacaat
ASP RNA-probe-11	tcccatcagtggacaaatta
ASP RNA-probe-12	acttggagtactgaagggtc
ASP RNA-probe-13	ttaagcaatcctcaggaggg
ASP RNA-probe-14	gtacagctgaacacatctgt
ASP RNA-probe-15	atcaggccagtagtatcaac
ASP RNA-probe-16	gttgtaacacctcagtcatt
ASP RNA-probe-17	taccaatagtagtagcggga
ASP RNA-probe-18	ggtagaacagatgcatgagg
ASP RNA-probe-19	taatgtttgggccacacatg
ASP RNA-probe-20	aattgtgggtcacagtctat
ASP RNA-probe-21	gcagaagacagtggcaatga
ASP RNA-probe-22	ctcatcaagcttctctatca
ASP RNA-probe-23	tgctttcattgccaagtttg
ASP RNA-probe-24	ggagagcaagaaatggagcc
ASP RNA-probe-25	atacttgggcaggagtggaa
ASP RNA-probe-26	acactagagcttttagagga
ASP RNA-probe-27	agataaagccacctttgcct
ASP RNA-probe-28	ttaggacgtatagttagtcc
ASP RNA-probe-29	gtctccatagaatggaggaa
ASP RNA-probe-30	aagttcagaagtacacatcc
ASP RNA-probe-31	gtgatgattgtgtggcaagt
ASP RNA-probe-32	aaaggtgaaggggcagtagt

SI References

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3. Sugata K, Yasunaga J, Kinosada H, Mitobe Y, Furuta R, Mahgoub M, Onishi C, Nakashima K, Ohshima K, Matsuoka M. 2016. HTLV-1 Viral Factor HBZ Induces CCR4 to Promote T-cell Migration and Proliferation. Cancer Res 76:5068-79.