Protein	Source	D	E	D	x	Identitv(%)
TtAgo	-Thermus thermophilus	avgf d aggr	AQAG <mark>E</mark> RIPQ	lllr d grvp	LHLA D RLVK	17.95
CbAgo	-Clostridium butyricum	FIGL <mark>D</mark> VGTR	PQSG <mark>E</mark> KIAE	VIHR D GFSR	TGYADKICK	22.26
NgAgo	-Natronobacterium gregoryi	FIGI D VSRS	PQLG <mark>E</mark> KLQS	VIHR D GFMN	TAYADQAST	21.34
RsAgo	-Rhodobacter Sphaeroides	VVGM <mark>G</mark> LAEL	ECEY <mark>E</mark> GYSD	RVVF <mark>H</mark> AHRP	IFYSERIAE	14.06
MpAgo	-Marinitoga piezophila	YIGI D LSHD	LELN <mark>E</mark> KMNL	FILR D GRFI	LHIA <mark>N</mark> KVAL	18.34
LrAgo	-Limnothrix rosea	IVGL <mark>D</mark> VSRR	VIDG <mark>E</mark> ILPE	LIHR D GLFP	TYYA <mark>D</mark> KIST	21.09
IbAgo	-Intestinibacter bartlettii	YIGL <mark>D</mark> VCRE	HQSG <mark>E</mark> KIQI	VFHR D GINR	TYYA D LSSI	29.67
CbcAgo	-Clostridium. butyricum CWBI1009	FIGL D VGTR	PQSG <mark>E</mark> KIAE	VIHR D GFSR	TGYA <mark>D</mark> KICK	22.26
CpAgo	-Clostridium perfringens	FVGL D VGTR	PQNG <mark>E</mark> KINT	VIHR D GFSR	TGYADKICK	22.21
SeAgo	-Synechococcus elongates	IIGF D TGTN	VQRG <mark>E</mark> TFSG	LLMR D GLVQ	LHLA D RSSK	18.70
PfAgo	-Pyrococcus furiosus	IIGI D VAPM	EQRG <mark>E</mark> SVDM	lllr d grit	VHYA <mark>H</mark> KFAN	18.30
MjAgo	-Methanocaldococcus jannaschii	IMGL <mark>D</mark> TGLG	PAPG <mark>E</mark> RLHL	lflr d gfiq	IHYA D KFVK	15.77
hAgo2	-Homo sapiens	FLGA <mark>D</mark> VTHP	QHRQ <mark>E</mark> IIQD	IFYR D GVSE	AYYA <mark>H</mark> LVAF	14.97
KpAgo	-Kluyveromyces Polysporus	VLGS <mark>D</mark> VTHY	DGPG <mark>E</mark> EIIT	MYFR d gvsv	VYYADLLCT	13.55
KmAgo	-Kurthia massiliensis	FIGI D VSHE	ILAG <mark>E</mark> KIDD	TIHR D GFWR	IHYA D LSAT	100.00
KmAgo DM	-Kurthia massiliensis double mutant	FIGIAVSHE	ILAG <mark>E</mark> KIDD	TIHRAGFWR	IHYADLSAT	





Supplementary Figure S1. KmAgo harbors a catalytic DEDD tetrad. (A) Multiple sequence alignment of KmAgo with several other biochemically or structurally characterized Ago proteins. The catalytically dead variant of the KmAgo protein (KmAgo_DM) with amino acid substitutions within the catalytic tetrad is shown. The protein sequence identity of those Ago proteins between KmAgo are also shown. (B) Size exclusion diagram showing the elution peak of KmAgo (Upper panel). The purity of the purified KmAgo was determined using SDS-PAGE (Lower panel). M, marker; In, Heparin purified KmAgo; 5-22, chromatography fractions containing KmAgo. (C) Repeating experiment in Figure 1C with non-labeled tDNA. DNA marker

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(33, 34, 35 nt) were partially hydrolyzed tDNA. (D) Repeating experiment in Figure 1D with nonlabeled tRNA. RNA marker (33, 34, 35 nt) were partially hydrolyzed tRNA. The experiments in (C) and (D) were performed at the 4:2:1 KmAgo:guide:target molar ratio in reaction buffer containing Mn²⁺ ions for 30 min at 37 °C.



Supplementary Figure S2. Effects of different cations on KmAgo. (A) Effects of different cations on DNA cleavage activity mediated by 5'P-gDNA. (B) Effects of different cations on RNA cleavage activity mediated by 5'P-gRNA. (C) Effects of different cations on DNA cleavage activity mediated by 5'P-gRNA. (D) Effects of different cations on RNA cleavage activity mediated by 5'P-gRNA. (E) Effects of Mn2+ concentration (Upper panel) and Mg2+ concentration (Lower panel) on DNA cleavage activity mediated by 5'P-gDNA. (F) Effects of Mn2+ concentration (Upper panel) on RNA cleavage activity mediated by 5'P-gDNA. (G) Effects of Mn2+ concentration on DNA cleavage activity (Upper panel) and Mg2+ concentration on DNA cleavage activity (Upper panel) and RNA cleavage activity (Lower panel) mediated by 5'P-gRNA. (H) Effects of different cations on DNA cleavage activity mediated by 5'P-gRNA. (J) Effects of Mn2+ concentration on DNA cleavage activity (Lower panel) mediated by 5'P-gRNA. (H) Effects of different cations on DNA cleavage activity mediated by 5'OH-gDNA. (J) Effects of Mn²⁺ concentration on DNA cleavage activity mediated by 5'OH-gDNA. (J) Effects of Mn²⁺ concentration on DNA cleavage activity mediated by 5'OH-gDNA. (J) Effects of Mn²⁺ concentration on DNA cleavage activity mediated by 5'OH-gDNA. (J) Effects of Mn²⁺ concentration on DNA cleavage activity mediated by 5'OH-gDNA. (J) Effects of Mn²⁺ concentration on DNA cleavage activity mediated by 5'OH-gDNA. All reactions were carried out for 15 min at 37 °C, at the 4:2:1 KmAgo:guide:target molar ratio (800 nM KmAgo preloaded with 400 nM guide, plus 200 nM target).



Supplementary Figure S3. Electrophoresis mobility shift assay (EMSA) of the binding of the KmAgo to 5'P-gRNA and 5'P-gRNA/tRNA duplex. (A) Effects of different cations on the loading of RNA guides to KmAgo. (Upper panel) 5 mM Mn²⁺, (Middle panel) 5 mM Mg²⁺, (Lower panel) 5 mM EDTA. (B) Effects of different cations on the loading of 5'P-gRNA/tRNA duplex to KmAgo_DM. (Upper panel) 5 mM Mn²⁺, (Middle panel) 5 mM Mg²⁺, (Lower panel) 5 mM EDTA. The 5'P-gRNA and tRNA are 3' end FAM-labeled and 5' end FAM-labeled, respectively.



Supplementary Figure S4. Representative denaturing PAGE (one of three independent experiments) showing KmAgo activity with different temperatures. Cleavage efficiencies from three independent experiments were quantified and plotted against temperature (Figure 3). (A) Representative denaturing PAGEs (one of three independent experiments) showing effects of temperature on DNA cleavage activity (left panel) and RNA cleavage activity (right panel) using 5'P-gDNA. The no Ago reaction was carried out for 15 min at 80 °C. (B) Representative denaturing PAGEs (one of three independent experiments) showing effects of temperature on DNA cleavage activity (left panel) and RNA cleavage activity (right panel) using 5'P-gDNA. The no Ago reaction was carried out for 15 min at 37 °C. (C) Representative denaturing PAGEs (one of three independent experiments) showing effects of temperature on DNA cleavage activity (left panel) and RNA cleavage activity (right panel) using 5'P-gRNA. The no Ago reaction was carried out for 15 min at 37 °C. (C) Representative denaturing PAGEs (one of three independent experiments) showing effects of temperature on DNA cleavage activity (left panel) and RNA cleavage activity (right panel) using 5'P-gRNA. The no Ago reaction was carried out for 15 min at 37 °C. (C) Representative denaturing PAGEs (one of three independent experiments) showing effects of temperature on DNA cleavage activity (left panel) and RNA cleavage activity (right panel) using 5'OH-gDNA. The no Ago reaction was carried out for 15 min at 37 °C.



Supplementary Figure S5. Representative denaturing PAGE showing the results of DNA and RNA cleavage kinetics in the presence of 5 mM MnCl₂. Assays were performed in three independent replicates, and time points were taken at 0, 1, 5, 15, 30, 60, and 120 min. Cleavage efficiencies from three independent experiments were quantified and plotted against time (Figure 3D). (A) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gDNA. (B) Representative denaturing PAGE (one of three independent experiments) showing RNA cleavage kinetics using 5'P-gDNA. (C) Representative denaturing PAGE (one of three independent experiments) showing RNA cleavage kinetics using 5'P-gRNA. (D) Representative denaturing PAGEs (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA. (E) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage kinetics using 5'P-gRNA.



Supplementary Figure S6. Representative denaturing PAGEs (one of three independent experiments) showing KmAgo cleavage efficiencies with different nucleotides at the 5' end of the guide and their respective targets. Cleavage efficiencies from three independent experiments were quantified and plotted against 5' end nucleotide of the guide. (A) Representative denaturing PAGEs (one of three independent experiments) showing RNA cleavage efficiencies (left panel) and DNA cleavage efficiencies (middle panel) with different nucleotides at the 5' end of the 5'P-gRNA. Cleavage efficiencies from three independent experiments were quantified and plotted against 5' end nucleotide of the 5'P-gRNA (right panel). (B) Representative denaturing PAGE (one of three independent experiments) showing DNA cleavage efficiencies (left panel) with different nucleotides at the 5'OH-gRNA. Cleavage efficiencies at the 5'OH-gDNA. Cleavage efficiencies from three independent experiments) showing DNA cleavage efficiencies from three independent experiments were quantified against 5' end nucleotides at the 5'OH-gDNA. Cleavage efficiencies from three independent experiments were quantified against 5' end nucleotide of the 5'OH-gDNA.



Supplementary Figure S7. Representative denaturing PAGE (one of three independent experiments) showing effects of mismatches in the guide-target duplex on the slicing activity of KmAgo. Quantification of the data (means and standard deviations from three independent experiments) is shown on the Figure 6. Representative denaturing PAGE (one of three independent experiments) showing effects of mismatches in the gDNA-tDNA (Figure S6A), gDNA-tRNA (Figure S6B), gRNA-tDNA (Figure S6C), and gRNA-tRNA (Figure S6D) duplex on the slicing activity of KmAgo. C, control reactions with guide variants containing no substitutions; MM, mismatch position.



Supplementary Figure S8. (A) The effects of KmAgo-gDNA duplex preloaded temperature on plasmid cleavage activity. Plasmid cleavage assay performed by preloading KmAgo with the indicated 5'P-gDNAs at different temperatures for 30 min, followed by incubation with the target plasmid at 37 °C for 2 h, and analysis of the target plasmid by electrophoresis. gDNA preloaded temperature, the temperature of KmAgo-gDNA duplex formation stage; NC guide, C-gDNA; FW guide, 29GC-F; RV guide, 29GC-R; M, molecular weight marker; Lin, linearized plasmid; SC, supercoiled plasmid; OC, open circular plasmid. (B) KmAgo is unable to cleave linear plasmids. Plasmids were digested with *Nde*I or *Sca*I before cleavage by two KmAgo-gDNA complexes. M, molecular weight marker; Lin, linearized plasmid. (C) Sanger sequencing analysis of pUC19 cleavage products by KmAgo-gDNA complexes. The position of cleavage site is indicated by the termination of primer extension in the sequencing reaction. Sequencing artifacts are shown with an asterisk above the corresponding peaks. (D) Secondary structure of HIV-1 Δ DIS 5'UTR predicted by SHAPE, which is copied from Figure 3C of Dayeh et al (1).

Supplementary tables

Oligonucleotide	Sequence (5'-3')	Description
FAM-IDNA		5 FAM labeled 1-tDNA
	AAACGACGGCCAGTGCCAAGCTT	
M1	FAM-	5' FAM labeled 34 nt DNA
	AAACGACGGCCAGTGCCAAGCTT	
	ACTATACAACC	
FAM-tRNA	FAM-	5' FAM labeled U-tRNA
	AAACGACGGCCAGUGCCAAGCUU	
	ACUAUACAACCUACUACCUCAU	
M2	FAM-	5' FAM labeled 34 nt RNA
	AAACGACGGCCAGUGCCAAGCUU	
	ACUAUACAACC	
FAM-gRNA	UGAGGUAGUAGGUUGUAU-FAM	3' FAM labeled U-gRNA
C-gDNA	CGAGGTAGTAGGTTGTAT	guide forms 5'-C pair with
		C-tDNA/C-tRNA
T-gDNA	TGAGGTAGTAGGTTGTAT	guide forms 5'-T pair with
		T-tDNA/T-tRNA
A-gDNA	AGAGGTAGTAGGTTGTAT	guide forms 5'-A pair with
		A-tDNA/A-tRNA
G-gDNA	GGAGGTAGTAGGTTGTAT	guide forms 5'-G pair with
		G-tDNA/G-tRNA
33nt	AAACGACGGCCAGTGCCAAGCTT	33 nt DNA marker
DNA product	ACTATACAAC	
34nt	AAACGACGGCCAGTGCCAAGCTT	5' DNA product for 45 nt DNA
DNA product	ACTATACAACC	target
35nt	AAACGACGGCCAGTGCCAAGCTT	35 nt DNA marker
DNA product	ACTATACAACCT	
A-tDNA	AAACGACGGCCAGTGCCAAGCTT	let-7 based 45 nt DNA target for
	ACTATACAACCTACTACCTCTT	A-gDNA/A-gRNA
G-tDNA	AAACGACGGCCAGTGCCAAGCTT	let-7 based 45 nt DNA target for
	ACTATACAACCTACTACCTCCT	G-gDNA/G-gRNA
C-tDNA	AAACGACGGCCAGTGCCAAGCTT	let-7 based 45 nt DNA target for
	ACTATACAACCTACTACCTCGT	C-gDNA/C-gRNA
T-tDNA	AAACGACGGCCAGTGCCAAGCTT	let-7 based 45 nt DNA target for
	ACTATACAACCTACTACCTCAT	T-gDNA/U-gRNA
C-gRNA	CGAGGUAGUAGGUUGUAU	guide forms 5'-C pair with
		C-tDNA/C-tRNA
U-gRNA	UGAGGUAGUAGGUUGUAU	guide forms 5'-U pair with
		T-tDNA/T-tRNA

 Table S1. List of let-7-derived sequences used in this study.

A-gRNA	AGAGGUAGUAGGUUGUAU	guide forms 5'-A pair with
		A-tDNA/A-tRNA
G-gRNA	GGAGGUAGUAGGUUGUAU	guide forms 5'-G pair with
		G-tDNA/G-tRNA
C-tRNA	AAACGACGGCCAGUGCCAAGCUU	let-7 based 45 nt RNA target for
	ACUAUACAACCUACUACCUCGU	C-gRNA/C-gDNA
U-tRNA	AAACGACGGCCAGUGCCAAGCUU	let-7 based 45 nt RNA target for
	ACUAUACAACCUACUACCUCAU	U-gDNA/U-gRNA
A-tRNA	AAACGACGGCCAGUGCCAAGCUU	let-7 based 45 nt RNA target for
	ACUAUACAACCUACUACCUCUU	A-gDNA/A-gRNA
G-tRNA	AAACGACGGCCAGUGCCAAGCUU	let-7 based 45 nt RNA target for
	ACUAUACAACCUACUACCUCCU	G-gDNA/G-gRNA
33nt	AAACGACGGCCAGUGCCAAGCUU	33 nt RNA marker
RNA product	ACUAUACAAC	
34nt	AAACGACGGCCAGUGCCAAGCUU	5' RNA product for 45 nt RNA
RNA product	ACUAUACAACC	target
35nt	AAACGACGGCCAGUGCCAAGCUU	34 nt RNA marker
RNA product	ACUAUACAACCU	
gDNA mm1	GGAGGTAGTAGGTTGTAT	guide forms mismatched pair in
		position 1 with C-tDNA/C-tRNA
gDNA mm2	CCAGGTAGTAGGTTGTAT	guide forms mismatched pair in
		position 2 with C-tDNA/C-tRNA
gDNA mm3	CGTGGTAGTAGGTTGTAT	guide forms mismatched pair in
		position 3 with C-tDNA/C-tRNA
gDNA_mm4	CGACGTAGTAGGTTGTAT	guide forms mismatched pair in
		position 4 with C-tDNA/C-tRNA
gDNA_mm5	CGAGCTAGTAGGTTGTAT	guide forms mismatched pair in
		position 5 with C-tDNA/C-tRNA
gDNA_mm6	CGAGGAAGTAGGTTGTAT	guide forms mismatched pair in
		position 6 with C-tDNA/C-tRNA
gDNA_mm7	CGAGGTTGTAGGTTGTAT	guide forms mismatched pair in
		position 7 with C-tDNA/C-tRNA
gDNA_mm8	CGAGGTACTAGGTTGTAT	guide forms mismatched pair in
		position 8 with C-tDNA/C-tRNA
gDNA_mm9	CGAGGTAGAAGGTTGTAT	guide forms mismatched pair in
		position 9 with C-tDNA/C-tRNA
gDNA_mm10	CGAGGTAGTTGGTTGTAT	guide forms mismatched pair in
		position 10 with C-tDNA/C-
		tRNA
gDNA mm11	CGAGGTAGTACGTTGTAT	guide forms mismatched pair in
		position 11 with C-tDNA/C-
		tRNA
gDNA_mm12	CGAGGTAGTAGCTTGTAT	guide forms mismatched pair in
		position 12 with C-tDNA/C-

		tRNA
gDNA_mm13	CGAGGTAGTAGGATGTAT	guide forms mismatched pair in
		position 13 with C-tDNA/C-
		tRNA
gDNA_mm14	CGAGGTAGTAGGTAGTAT	guide forms mismatched pair in
		position 14 with C-tDNA/C-
		tRNA
gDNA_mm15	CGAGGTAGTAGGTTCTAT	guide forms mismatched pair in
		position 15 with C-tDNA/C-
		tRNA
gDNA_mm16	CGAGGTAGTAGGTTGAAT	guide forms mismatched pair in
		position 16 with C-tDNA/C-
		tRNA
gDNA_mm17	CGAGGTAGTAGGTTGTTT	guide forms mismatched pair in
		position 17 with C-tDNA/C-
		tRNA
gDNA_mm18	CGAGGTAGTAGGTTGTAA	guide forms mismatched pair in
		position 18 with C-tDNA/C-
		tRNA
gDNA_m7m8	CGAGGTTCTAGGTTGTAT	guide forms mismatched pair in
		position 7 and 8 with C-tDNA/C-
		tRNA
gDNA_m8m9	CGAGGTACAAGGTTGTAT	guide forms mismatched pair in
		position 8 and 9 with C-tDNA/C-
		tRNA
gDNA_m9m10	CGAGGTAGATGGTTGTAT	guide forms mismatched pair in
		position 9 and 10 with C-
		tDNA/C-tRNA
gDNA_m10m11	CGAGGTAGTACGTTGTAT	guide forms mismatched pair in
		position 10 and 11 with C-
		tDNA/C-tRNA
gDNA_m11m12	CGAGGTAGTTCCTTGTAT	guide forms mismatched pair in
		position 11 and 12 with C-
		tDNA/C-tRNA
gDNA_m12m13	CGAGGTAGTTGCATGTAT	guide forms mismatched pair in
		position 12 and 13 with C-
		tDNA/C-tRNA
gDNA_m13m14	CGAGGTAGTTGGAAGTAT	guide forms mismatched pair in
		position 13 and 14 with C-
		tDNA/C-tRNA
gRNA_mm1	GGAGGUAGUAGGUUGUAU	guide forms mismatched pair in
		position 1 with C-tDNA/C-tRNA
gRNA_mm2	CCAGGUAGUAGGUUGUAU	guide forms mismatched pair in
		position 2 with C-tDNA/C-tRNA

gRNA_mm3	CGUGGUAGUAGGUUGUAU	guide forms mismatched pair in
		position 3 with C-tDNA/C-tRNA
gRNA_mm4	CGACGUAGUAGGUUGUAU	guide forms mismatched pair in
		position 4 with C-tDNA/C-tRNA
gRNA_mm5	CGAGCUAGUAGGUUGUAU	guide forms mismatched pair in
		position 5 with C-tDNA/C-tRNA
gRNA_mm6	CGAGGAAGUAGGUUGUAU	guide forms mismatched pair in
		position 6 with C-tDNA/C-tRNA
gRNA_mm7	CGAGGUUGUAGGUUGUAU	guide forms mismatched pair in
		position 7 with C-tDNA/C-tRNA
gRNA_mm8	CGAGGUACUAGGUUGUAU	guide forms mismatched pair in
		position 8 with C-tDNA/C-tRNA
gRNA_mm9	CGAGGUAGAAGGUUGUAU	guide forms mismatched pair in
		position 9 with C-tDNA/C-tRNA
gRNA_mm10	CGAGGUAGUUGGUUGUAU	guide forms mismatched pair in
		position 10 with C-tDNA/C-
		tRNA
gRNA_mm11	CGAGGUAGUACGUUGUAU	guide forms mismatched pair in
		position 11 with C-tDNA/C-
		tRNA
gRNA mm12	CGAGGUAGUAGCUUGUAU	guide forms mismatched pair in
		position 12 with C-tDNA/C-
		tRNA
gRNA mm13	CGAGGUAGUAGGAUGUAU	guide forms mismatched pair in
		position 13 with C-tDNA/C-
		tRNA
gRNA mm14	CGAGGUAGUAGGUAGUAU	guide forms mismatched pair in
		position 14 with C-tDNA/C-
		tRNA
gRNA mm15	CGAGGUAGUAGGUUCUAU	guide forms mismatched pair in
		position 15 with C-tDNA/C-
		tRNA
aRNA mm16	CGAGGUAGUAGGUUGAAU	guide forms mismatched pair in
5		position 16 with C-tDNA/C-
		tRNA
aRNA_mm17	CGAGGUAGUAGGUUGUUU	guide forms mismatched pair in
9		position 17 with C-tDNA/C-
		tRNA
aRNA mm18	CGAGGUAGUAGGUUGUAA	guide forms mismatched pair in
g		position 18 with C-tDNA/C-
		tRNA
8nt C-gDNA	CGAGGTAG	8 nt quide pair with C-tDNA/C-
		tRNA
9nt C-gDNA	CGAGGTAGT	9 nt guide pair with C-tDNA/C-

		tRNA
10nt C-gDNA	CGAGGTAGTA	10 nt guide pair with C-tDNA/C-
		tRNA
11nt C-gDNA	CGAGGTAGTAG	11 nt guide pair with C-tDNA/C-
		tRNA
12nt C-gDNA	CGAGGTAGTAGG	12 nt guide pair with C-tDNA/C-
		tRNA
13nt C-gDNA	CGAGGTAGTAGGT	13 nt guide pair with C-tDNA/C- tRNA
14nt C-gDNA	CGAGGTAGTAGGTT	14 nt guide pair with C-tDNA/C-
		tRNA
15nt C-gDNA	CGAGGTAGTAGGTTG	15 nt guide pair with C-tDNA/C-
		tRNA
16nt C-gDNA	CGAGGTAGTAGGTTGT	16 nt guide pair with C-tDNA/C-
		tRNA
17nt C-gDNA	CGAGGTAGTAGGTTGTA	17 nt guide pair with C-tDNA/C-
		tRNA
19nt C-gDNA	CGAGGTAGTAGGTTGTATA	19 nt guide pair with C-tDNA/C-
		tRNA
20nt C-gDNA	CGAGGTAGTAGGTTGTATAG	20 nt guide pair with C-tDNA/C-
		tRNA
21nt C-gDNA	CGAGGTAGTAGGTTGTATAGT	21 nt guide pair with C-tDNA/C-
		tRNA
25nt C-gDNA	CGAGGTAGTAGGTTGTATAGTAAG	25 nt guide pair with C-tDNA/C-
	С	tRNA
30nt C-gDNA	CGAGGTAGTAGGTTGTATAGTAAG	30 nt guide pair with C-tDNA/C-
	CTTGGC	tRNA
40nt C-gDNA	CGAGGTAGTAGGTTGTATAGTAAG	40 nt guide pair with C-tDNA/C-
	CTTGGCACTGGCCGTC	tRNA
12nt C-gRNA	CGAGGUAGUAGG	12 nt guide pair with C-tDNA/C-
		tRNA
13nt C-gRNA	CGAGGUAGUAGGU	13 nt guide pair with C-tDNA/C-
		tRNA
14nt C-gRNA	CGAGGUAGUAGGUU	14 nt guide pair with C-tDNA/C-
		tRNA
15nt C-gRNA	CGAGGUAGUAGGUUG	15 nt guide pair with C-tDNA/C-
		tRNA
16nt C-gRNA	CGAGGUAGUAGGUUGU	16 nt guide pair with C-tDNA/C-
		tRNA
17nt C-gRNA	CGAGGUAGUAGGUGUA	17 nt guide pair with C-tDNA/C-
		tRNA
19nt C-gRNA	CGAGGUAGUAGGUUGUAUA	19 nt guide pair with C-tDNA/C-
		tRNA

20nt C-gRNA	CGAGGUAGUAGGUUGUAUAG	20 nt guide pair with C-tDNA/C- tRNA
21nt C-gRNA	CGAGGUAGUAGGUUGUAUAGU	21 nt guide pair with C-tDNA/C- tRNA
25nt C-gRNA	CGAGGUAGUAGGUUGUAUAGUA	25 nt guide pair with C-tDNA/C-
	AGC	tRNA
30nt C-gRNA	CGAGGUAGUAGGUUGUAUAGUA	30 nt guide pair with C-tDNA/C-
	AGCUUGGC	tRNA
40nt C-gRNA	CGAGGUAGUAGGUUGUAUAGUA	40 nt guide pair with C-tDNA/C-
	AGCUUGGCACUGGCCGUC	tRNA

Table S2. Sequences of HIV-1 Δ DIS 5'UTR (1).

gDNA#	Sequence (5'-3')	Target region	5' product length (nt)
gDNA_1	ACTCAAGGCAAGCTTTAT	70-87	82
gDNA_2	GACGGGCACACACTACTT	93-110	105
gDNA_3	CTAGTTACCAGAGTCACA	116-133	128
gDNA_4	GACTAAAAGGGTCTGAGG	139-156	151
gDNA_5	CACTGCTAGAGATTTTCC	162-179	174
gDNA_6	CTTTCAAGTCCCTGTTCG	185-202	197
gDNA_7	GATCTCCTCTGGCTTTAC	208-225	220
gDNA_8	GCAAGCCGAGTCCTGCGT	231-248	243
gDNA_9	CCCCTCGCCTCTTGCCGT	254-271	266
gDNA_10	TTTGGCGTACTCACCAGT	277-294	289
gDNA_11	TCTAGCCTCCGCTAGTCA	300-317	312

Table S3. List of gDNAs targeting HIV □ △DIS 5'UTR.

Table S4. List of gDNAs targeting plasmid pUC19.

gDNA	Sequence (5'-3')	GC content of target region (%)
29GC-F	TCAAAAAGGATCTTCACC	29
29GC-R	TAGGTGAAGATCCTTTTT	29
39GC-F	AAGAAACCATTATTATCA	39
39GC-R	CATGATAATAATGGTTTC	39
45GC-F	AAAAGTGCTCATCATTGG	45
45GC-R	TTCCAATGATGAGCACTT	45
46GC-F	CAACATACGAGCCGGAAG	46

46GC-R	TGCTTCCGGCTCGTATGT	46
53GC-F	CAGGGTTTTCCCAGTCAC	53
53GC-R	TCGTGACTGGGAAAACCC	53
64GC-F	CGCTCGGTCGTTCGGCTG	64
64GC-R	CGCAGCCGAACGACCGAG	64
65GC-F	TCGTGCGCTCTCCTGTTC	65
65GC-R	CGGAACAGGAGAGCGCAC	65

REFERENCES

 Dayeh,D.M., Cantara,W.A., Kitzrow,J.P., Musier-Forsyth,K. and Nakanishi,K. (2018) Argonaute-based programmable RNase as a tool for cleavage of highly-structured RNA. Nucleic Acids Res, 46, e98.