Supplementary Figure Legends

Supplementary Figure 1. ERV-DC, RD-114 and endogenous FeLV are not detected in *Prionailurus bengalensis euptilura* (Tsushima leopard cat). Chromosomal DNA isolated from PBMC from *Felis silvestris catus* (*F. s. catus*) and muscle from *Prionailurus bengalensis euptilura* (*P. b. euptilura*), respectively, were used for detection of ERV-DC, RD114 and endogenous FeLV (enFeLV) by PCR with GoTaq polymerase (Promega) and specific primers indicated in Supplementary Table 4. DNA samples #3 and #5 from *P. b. euptilura* were also used for Southern blot analysis as shown in Fig. 2A.

Supplementary Figure 2. Infection of cell lines with ERV-DC10 and ERV-DC18. Several cell lines were infected with culture supernatant (300 μl) from HEK293T cells persistently infected with ERV-DC10 or ERV-DC18. After infection, cells were cultured for 2 to 7 days then lysed and cellular DNA was used for PCR with Fe-13S and Fe-18R to detect the ERV-DC *env* gene. M; Mock infection.

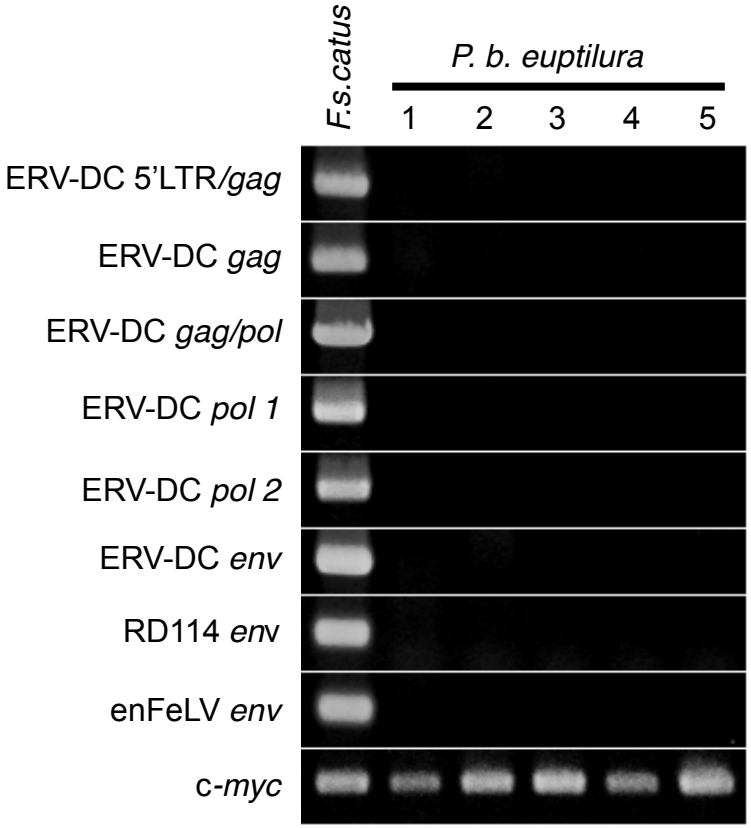
Supplementary Figure 3. Structures and sequences of the genomes of full length FeLV-D/ON-T and partial FeLV-D strains. (A) Alignment of ERV-DC Env with FeLV-D Env. (B) FeLV-D proviruses contain LTR sequences from exogenous FeLV prototype. FeLV-D/ON-C A2 and B4 clones were obtained from the same cat and FeLV-D/ON-C B4 clone has an enhancer duplication in the LTR. (C) The *gag, pol,* and *env* genes are illustrated with the 5′ and/or 3′ LTRs and positions of the *gag* and *env* translational initiation codons (ATG). Asterisks indicate conserved stop codons.

Open boxes indicate open reading frames. Open triangle indicates a deletion of nucleotides and filled triangle indicates an insertion of nucleotides. (D) Putative map of FeLV-D *env* recombination junction in comparison with FeLV-A/61E.

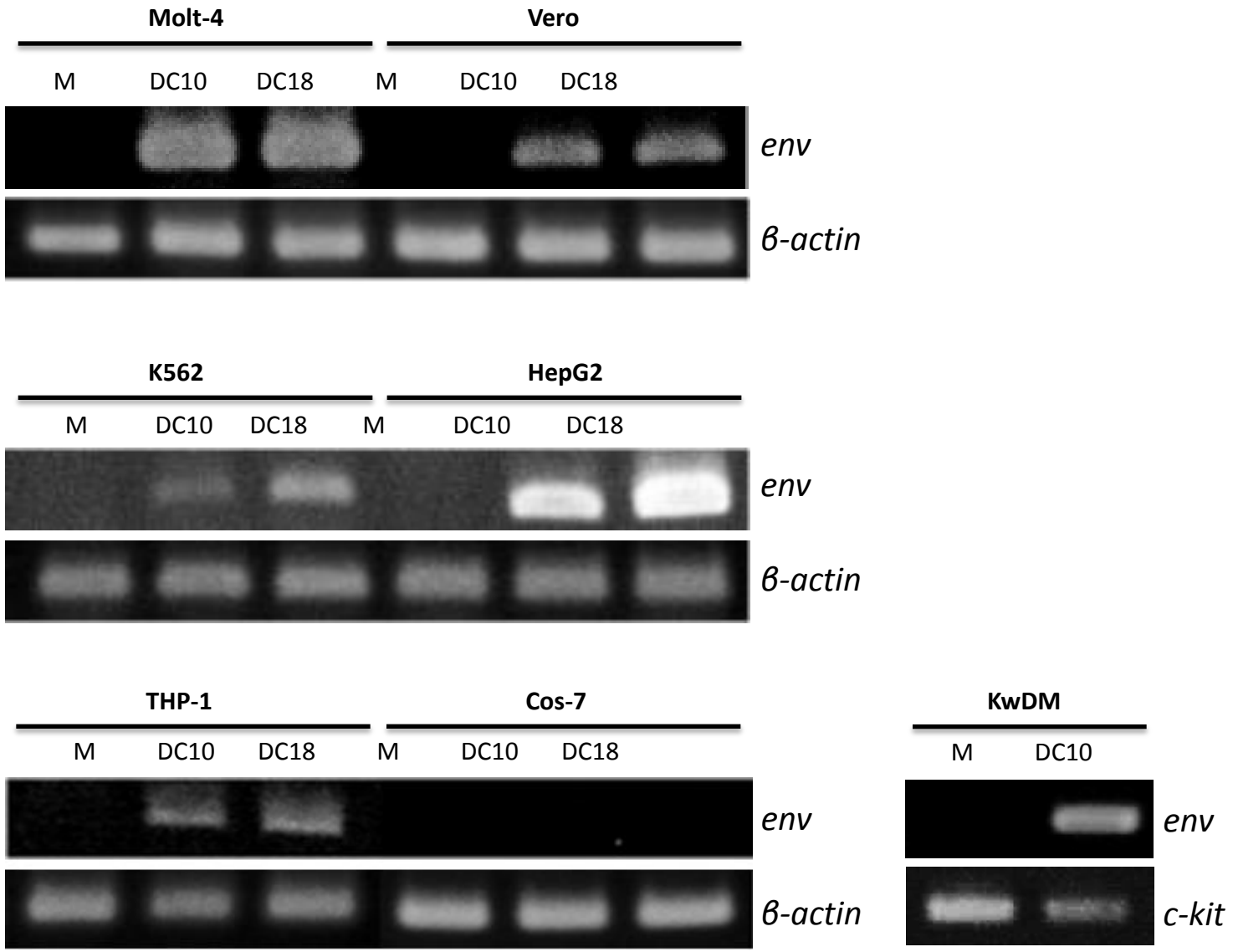
Supplementary Figure 4. Expression of FeLV-D in the spleen of cat ON-T. FeLV-D *env* (A) gene transcript and (B) spliced *env* gene transcript were detected by RT-PCR with the Fe-14S and Fe-1R primer pair and Fe-97S and Fe-21R primer pair, respectively, in the spleen from the cat with FeLV-D/ON-T. High molecular weight bands are presumably unspliced FeLV-D mRNA. SD (splice donor site) and SA (splice acceptor site) were determined by sequencing viral fragments. 1: spleen from the cat (ON-T); 2: 3201 cells (FeLV negative feline lymphoma); 3: FT-1 cells (FeLV positive feline lymphoma); 4: FL74 cells (FeLV positive feline lymphoma).

Supplementary Figure 5. Alignment of Env from FeLV-A, FeLV-B, FeLV-D and ERV-DC.

Supplementary Figure 1

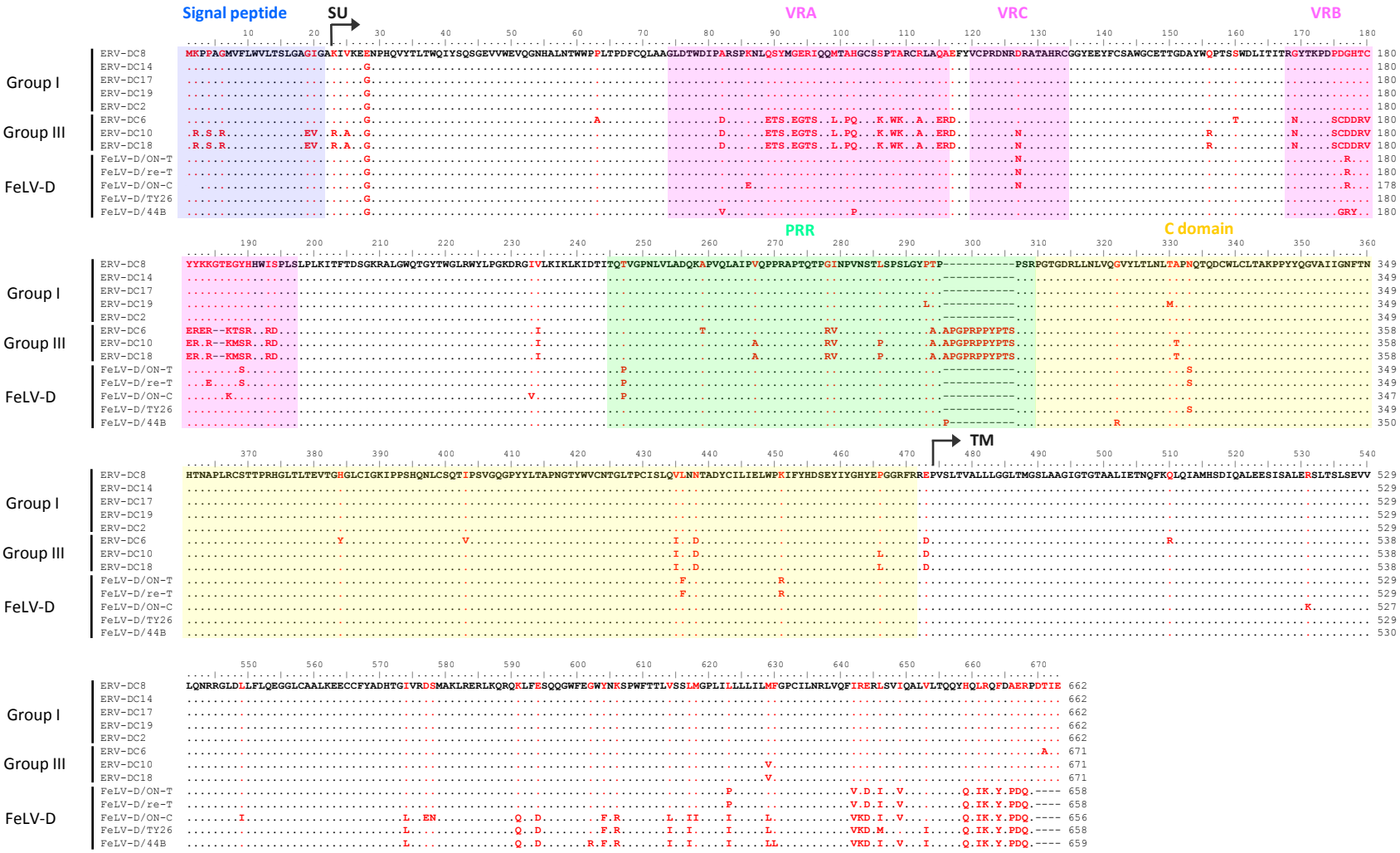


Supplementary Figure 2



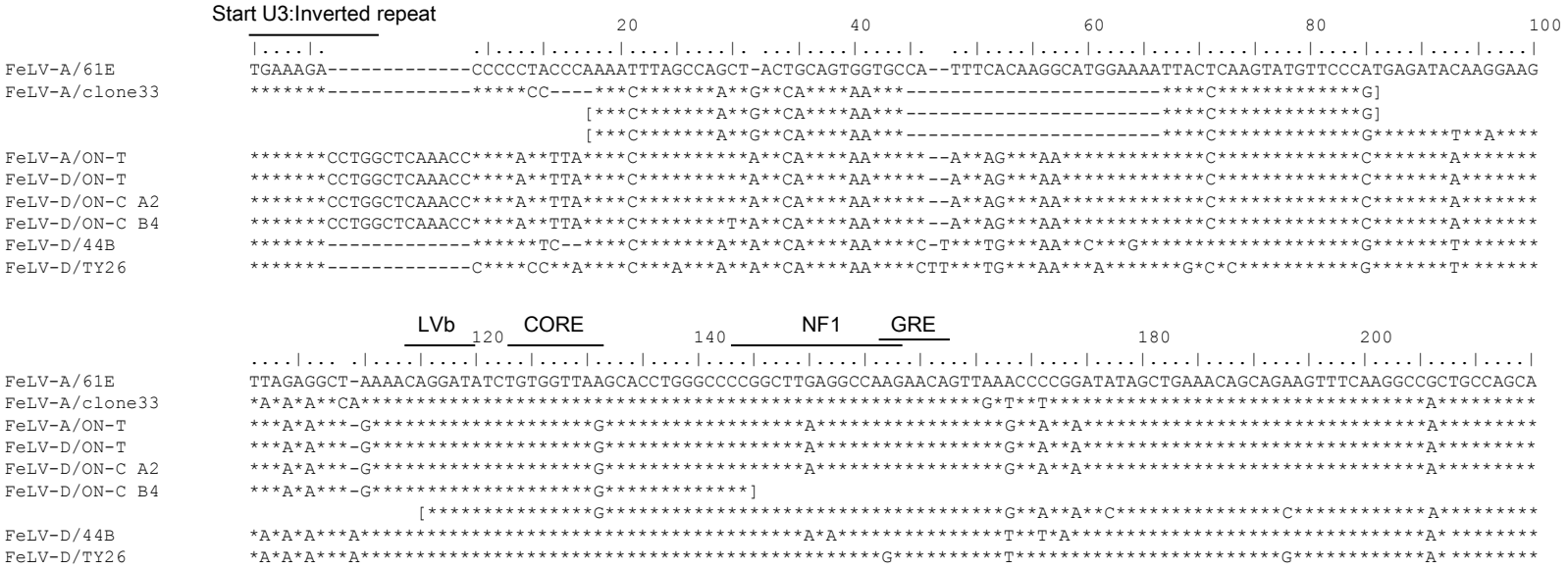
Supplementary Figure 3

A

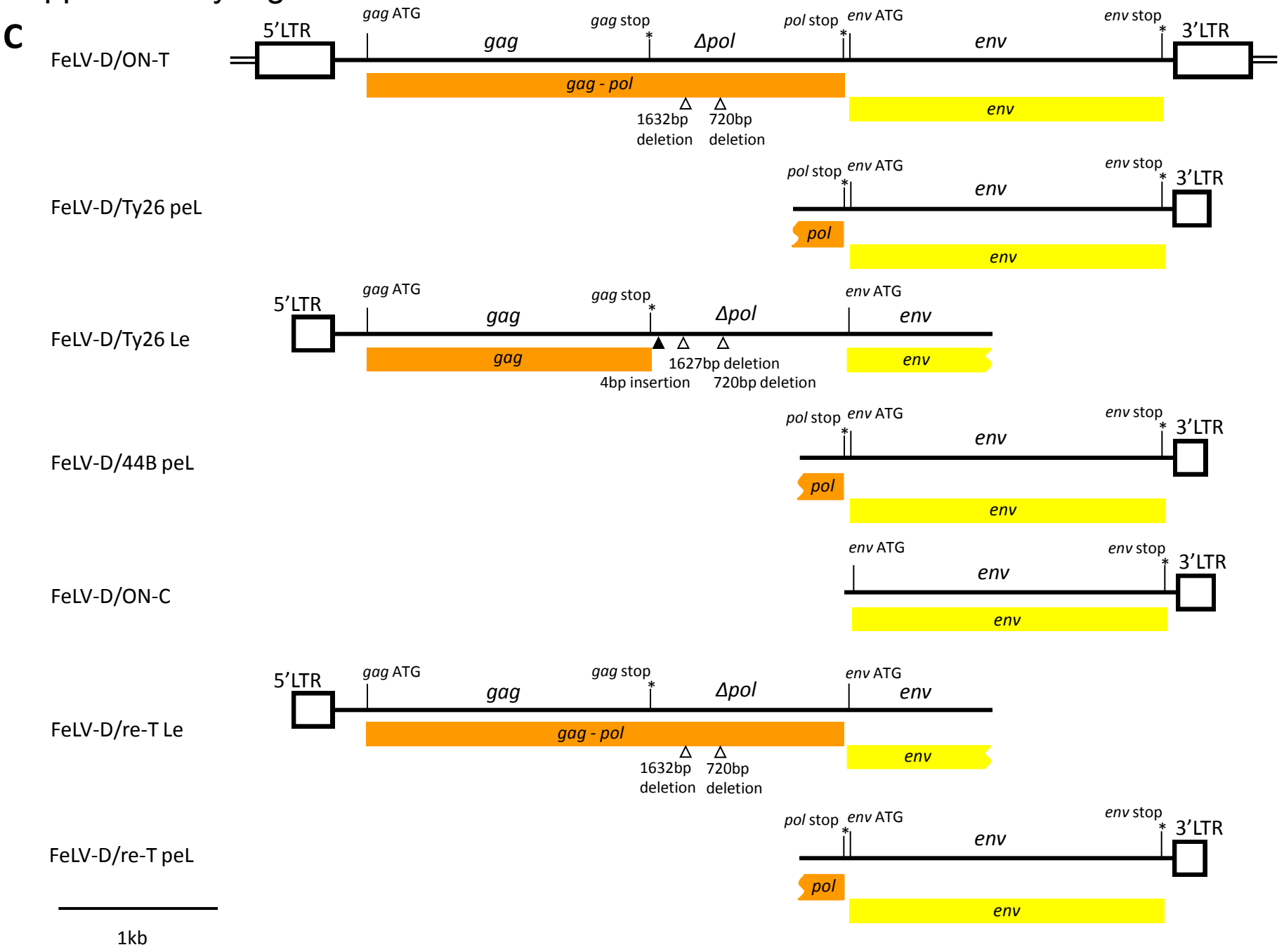


Supplementary Figure 3

B

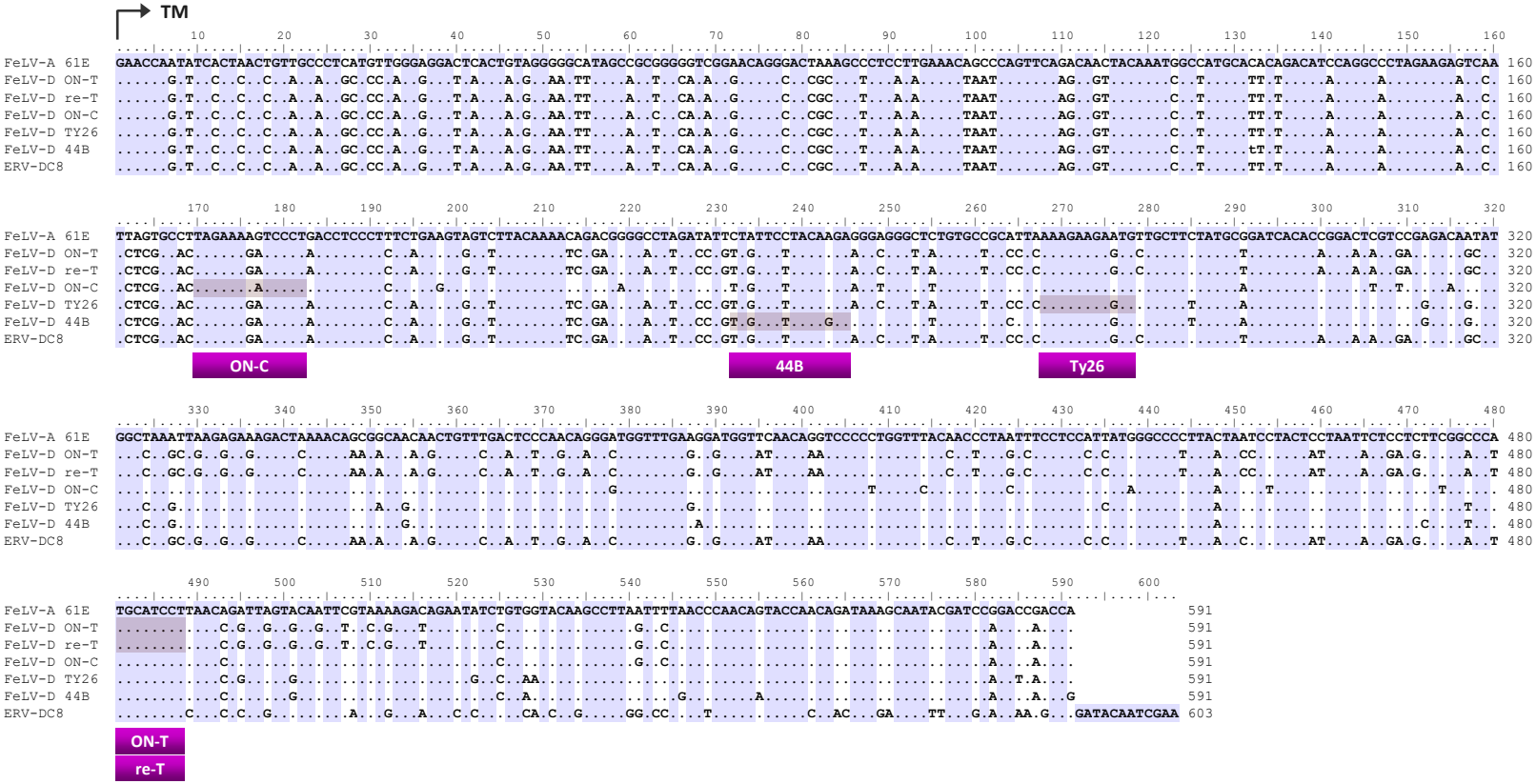


Supplementary Figure 3

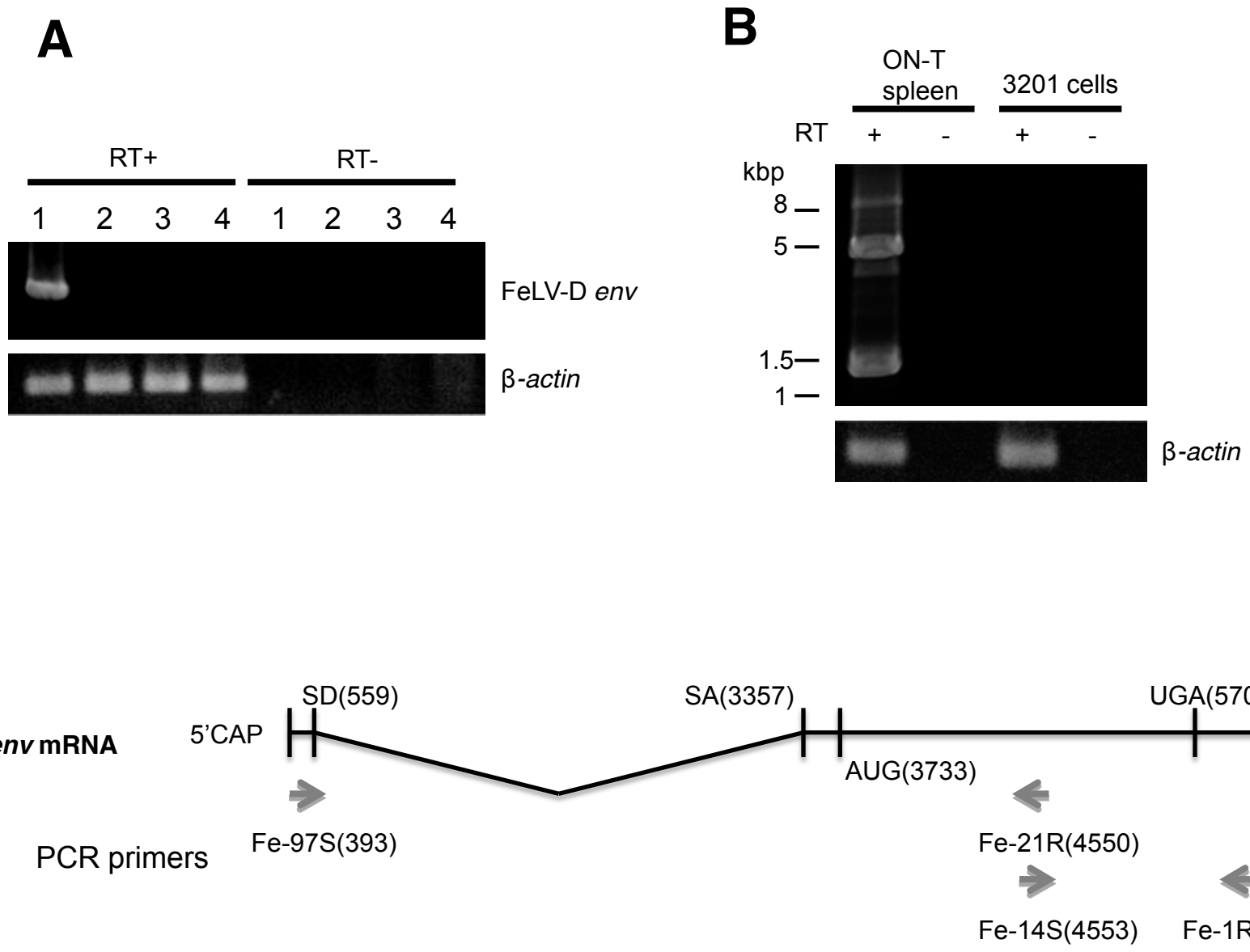


Supplementary Figure 3

D



Supplementary Figure 4



Supplementary Figure 5

Supplementary Table 1-1

Insertional polymorphisms of ERV-DC proviruses

Provirus	-/- (%)	+/- (%)	+/+ (%)	Total (%)
ERV-DC1	182 (74.6)	55 (22.5)	7 (2.9)	244 (100)
ERV-DC2	57 (23.36)	118 (48.36)	69 (28.28)	244 (100)
ERV-DC3	156 (63.9)	77 (31.6)	11 (4.5)	244 (100)
ERV-DC4	51 (20.9)	107 (43.9)	86 (35.2)	244 (100)
ERV-DC6*	3 (1.2)	-	241 (98.8)	244 (100)
ERV-DC7	0 (0)	0 (0)	244 (100)	244 (100)
ERV-DC8	76 (31.2)	113 (46.3)	55 (22.5)	244 (100)
ERV-DC10	152 (62.3)	72 (29.5)	20 (8.2)	244 (100)
ERV-DC14	238 (97.5)	6 (2.5)	0 (0)	244 (100)
ERV-DC16*	0 (0)	-	244 (100)	244 (100)
ERV-DC17	205 (84.02)	35 (14.34)	4 (1.64)	244 (100)
ERV-DC18	243 (99.6)	1 (0.4)	0 (0)	244 (100)
ERV-DC19	171 (70.1)	37 (15.2)	36 (14.7)	244 (100)

* Pre-integration site was not identified.

Supplementary Table 1-2

Insertional polymorphisms of ERV-DC proviruses in siblings from one family

Locus	sibling			
	ON-T	ON-L	ON-C	ON-H
ERV-DC1	-/-	+/-	+/-	+/-
ERV-DC2	-/-	+/+	+/-	+/-
ERV-DC3	-/-	-/-	+/-	-/-
ERV-DC4	-/-	+/+	+/+	+/-
ERV-DC6	+	+	+	+
ERV-DC7	+/+	+/+	+/+	+/+
ERV-DC8	-/-	-/-	-/-	-/-
ERV-DC10	+/-	-/-	+/-	+/-
ERV-DC14	-/-	-/-	-/-	-/-
ERV-DC16	+	+	+	+
ERV-DC17	+/-	+/-	+/-	+/-
ERV-DC18	+/-	-/-	+/-	+/-
ERV-DC19	+/+	+/+	+/+	+/+
virus	ON-T	ON-L	ON-C	ON-H
FeLV	+	-	+	+
FeLV-D	+	-	+	-

Supplementary Table 2. ERV elements found in the genomes of 12 species examined by using RetroTector©

Species	Nomenclature	Gag	Pro	Pol	Env
Human	*Homo sapiens*	2,672	2,121	3,757	1,439
Chimpanzee	*Pan troglodytes*	1,729	1,618	2,859	1,212
Orangutan	*Pongo abelii*	1,617	1,450	2,740	1,462
Macaque	*Macaca mulatta*	1,658	1,451	2,469	1,328
Mouse	*Mus musculus*	4,733	4,823	7,926	2,483
Rat	*Rattus norvegicus*	1,971	1,917	4,037	1,565
Cow	*Bos taurus*	1,336	1,489	3,248	1,539
Horse	*Equus caballus*	370	329	916	543
Dog	*Canis familiaris*	595	568	2,107	1,016
Opossum	*Monodelphis domestica*	3,857	5,264	8,236	359
Platypus	*Ornithorhynchus anatinus*	51	162	298	280
Chicken	*Gallus gallus*	95	196	335	16

Supplementary Table 3. ERVs found in several non-cat species are similar to ERV-DCs

Species	Chromosome	Gene locus of Pol[a]	Gene locus of Env[a]
Mouse	1	-	184,193,575-184,195,425
	2	57,072,703-57,069,422	57,069,479-57,067,629
	4	-	101,538,418-101,536,568
	4	-	107,821,296-107,819,446
	4	-	146,599,123-146,601,030
	5	-	145,437,032-14,5438,882
	5	-	23,208,901-23,207,039
	5	44,528,700-44,531,981	44,531,924-44,533,774
	7	30,403,326-30,406,607	-
	7	-	31,479,983-31,481,833
	8	-	122,416,121-122,414,271
	8	-	125,952,270-125,950,330
	9	-	62,293,167-62,295,017
	10	41,159,554-41,162,835	41,162,778-41,164,628
	11	-	6,652,081-6,650,231
	11	-	88,755,184-88,752,228
	11	8,823,400-8,826,681	8,826,624-8,828,474
	12	55,878,312-55,881,593	55,881,536-55,883,386
	13	-	99,758,886-99,757,036
	15	-	76,392,903-76,391,053
	16	93,703,582-93,700,301	93,700,358-93,698,508
	18	82,865,942-82,869,223	82,869,166-82,871,016
Rat	1	12,807,811-12,811,104	12,810,909-12,812,831
	1	161,820,310-161,817,017	161,817,074-161,815,251
	1	67,211,080-67,214,373	-
	2	14,875,612-14,878,905	14,878,848-14,880,671
	2	188,716,457-188,719,768	-
	3	126,586,378-126,583,085	126,583,280-126,581,358
	5	162,275,009-162,271,716	-
	5	-	51,524,508-51,522,586
	6	84,256,315-84,253,232	84,253,427-84,251,505
	8	16,479,431-16,482,724	-
	8	-	43,589,920-43,591,824
	11	-	23,031,253-23,029,430
	11	-	40,261,704-40,263,626
	12	-	27,870,829-27,869,007
	14	70,068,348-70,065,055	70,065,250-70,063,328
	15	-	55,097,060-55,098,982
	15	-	77,703,733-77,705,672
	15	92,791,054-92,794,347	-
	X	159,655,885-159,659,178	159,658,983-159,660,905
Chimpanzee	1	24,165,782-24,169,031	-
	Y	21,678,398-21,675,140	-
	Y	21,910,354-21,913,613	-
Macaque	1	91,524,508-91,521,256	-
	5	107,359,987-107,363,239	-

A dash indicates that an ORF was truncated by substitutions and/or indels. Boldface indicates that the ORF sequence was used as a representative one in Figure 5A and 5B

Supplementary Table 4-1. Primers used for PCR cloning of full-length ERV-DCs

Provirus locus	Forward	Reverse	Template DNA(cat genome)
ERV-DC1	Fe-60S	Fe-68R	IS10
ERV-DC4	Fe-56S	Fe-58R	IS10
ERV-DC8	Fe-57S	Fe-54R	IS10
ERV-DC10	Fe-90S	Fe-38R	GF33
ERV-DC14	Fe-58S	Fe-42R	SO38
ERV-DC17	Fe-75S	Fe-80R	ON-T
ERV-DC18	Fe-76S	Fe-81R	ON-T
ERV-DC19	Fe-77S	Fe-82R	ON-T

Supplementary Table 4-2. Primers used for PCR cloning of ERV-DC2, DC3, DC-6, DC7 and DC16

Provirus locus	5'LTR flanking→env (gag)		env→3'LTR flanking		Template DNA(cat genome)
	Forward	Reverse	Forward	Reverse	
ERV-DC2 *	Fe-55S	Fe-102R (gag)	Fe-19S	Fe-22R	IS10
ERV-DC3	Fe-61S	Fe-78R	Fe-19S	Fe-26R	GF33
ERV-DC6			Fe-19S	Fe-30R	IS10
ERV-DC7	Fe-66S	Fe-78R	Fe-19S	Fe-34R	IS10
ERV-DC16			Fe-19S	Fe-44R	GF33

* The fragment PCR-amplified with primers, Fe-55S and Fe-102R was directly sequenced.

Supplementary Table 4-3. Primers used for detection of each ERV-DC pre-integration site

Pre-integration locus of ERV-DC	Forward	Reverse
ERV-DC1	Fe-60S	Fe-68R
ERV-DC2	Fe-55S	Fe-22R
ERV-DC3	Fe-61S	Fe-69R
ERV-DC4	Fe-56S	Fe-58R
ERV-DC7	Fe-66S	Fe-53R
ERV-DC8	Fe-57S	Fe-54R
ERV-DC10	Fe-122S	Fe-38R
ERV-DC14	Fe-58S	Fe-56R
ERV-DC17	Fe-75S	Fe-80R
ERV-DC18	Fe-76S	Fe-81R
ERV-DC19	Fe-77S	Fe-82R

Supplementary Table 4-4. Primers used for analysis of insertional polymorphisms of ERV-DC

Provirus locus	Forward	Reverse
ERV-DC1	Fe-36S	Fe-20R
	Fe-45S	Fe-20R
ERV-DC2	Fe-36S	Fe-22R
	Fe-45S	Fe-22R
ERV-DC3	Fe-36S	Fe-26R
ERV-DC4	Fe-36S	Fe-27R
	Fe-45S	Fe-27R
ERV-DC6	Fe-36S	Fe-30R
	Fe-45S	Fe-30R
ERV-DC7	Fe-36S	Fe-34R
	Fe-45S	Fe-34R
ERV-DC8	Fe-36S	Fe-35R
	Fe-45S	Fe-35R
ERV-DC10	Fe-36S	Fe-38R
ERV-DC14	Fe-36S	Fe-42R
	Fe-45S	Fe-42R
ERV-DC16	Fe-36S	Fe-44R
ERV-DC17	Fe-36S	Fe-80R
	Fe-45S	Fe-80R
ERV-DC18	Fe-36S	Fe-81R
	Fe-46S	Fe-81R
ERV-DC19	Fe-36S	Fe-82R
	Fe-45S	Fe-82R

Supplementary Table 4-5. Primers used in supplementary Fig. 1

Gene	Forward	Reverse
ERV-DC 5'LTR/gag	Fe-103S	Fe-102R
ERV-DC gag	Fe-94S	Fe-102R
ERV-DC gag/pol	Fe-87S	Fe-71R
ERV-DC pol1	Fe-73S	Fe-96R
ERV-DC pol2	Fe-79S	Fe-95R
ERV-DC env	Fe-13S	Fe-18R
RD114 env	Fe-15S	Fe-63R
enFeLV env	PRB1	Fe-62R
c-myc	MY1F	MY2R

Supplementary Table 4-6. Primers used for detection of ERV-DC or FeLV in Fig.3,4 and Supplementary Fig. 2

Gene	Forward	Reverse
ERV-DC env	Fe-13S	Fe-18R
ERV-DC pol	Fe-73S	Fe-96R
ERV-DC LTR	Fe-147S	Fe-60R
FeLV env	Fe-2S	Fe-1R
β-actin	Hub-b-actin(DNA)s	Hub-b-actin(DNA)r
c-kit	dog-ckit-1S	dog-ckit-1R

Supplementary Table 4-7. Primers used for FeLV-D screening and cloning in Fig. 6 and Supplementary Fig. 3

Gene	Forward	Reverse
pol-LTR (peL)	Fe-9S	Fe-7R
env-LTR (eL)	Fe-130S	Fe-7R
LTR-env (Le)	Fe-37S	Fe-21R
FeLV-D/ON-T	Fe-63S	Fe-73R
FeLV-D screening	Fe-14S	Fe-3R

Supplementary Table 4-8. Primers used for RT-PCR in Supplementary Fig. 4

Gene	Forward	Reverse
5'LTR-env (for FeLV-D)	Fe-97S	Fe-21R
env-3'LTR (for FeLV-D)	Fe-14S	Fe-1R

Supplementary Table 4-9. Primers used for expression plasmid costruction in Fig. 7

Expression plasmid	Template	Forward	Reverse
pFUΔssA5	pFGA5	Fe-44S	Fe-50R
pFUΔssGB	pFGB	Fe-44S	Fe-50R
pFUΔssSC	pFSC	Fe-44S	Fe-50R
pFUΔssTY2.0	pCR4_TY26-1	Fe-44S	Fe-50R
pFUΔssON-T	pON-TpeL	Fe-130S	Fe-50R
pFUΔssDC10	ERV-DC/pDC10	Fe-130S	Fe-126R

Supplementary Table 4-10. Sequences of primers used in this study

Fe-2S	5'-CAATACGATCCRGACCRACCATG-3'
Fe-9S	5'-GAGACCTCTAGCGGCGGCCTAC-3'
Fe-13S	5'-CGGTCCAGCTAGCCATCCCAGTC-3'
Fe-14S	5'-CTCAGACACCGGGAATTAACCCTGTT-3'
Fe-15S	5'-AATACGGTCTGGGAGCCTCAACG-3'
Fe-19S	5'-ACTCTCCCGTGTCTGACTGTTAATC-3'
Fe-36S	5'-AACCGCTTGGTACARTTCATAAGAG-3'
Fe-37S	5'-GTCTCCAGGCTCCCCAGTTGAC-3'
Fe-44S	5'-CGGAATTCATCGAGATGGAAGGTCC-3'
Fe-45S	5'-ACCAGCCTGTATGCAAATGTAACTC-3'
Fe-46S	5'-ACCAGCCTGTATGCAAATAAGACTC-3'
Fe-55S	5'-CTGAGCCAAAGTGGGACACTTAAC-3'
Fe-56S	5'-GAATTGAGCCTGTCTACAGCTCTTC-3'
Fe-57S	5'-TTAGAGGAATAAGCTCGGGGTAACT-3'
Fe-58S	5'-CATTCAGACTTGCAGTTAAGGGACT-3'
Fe-60S	5'-GTACTAACGGTTTTTGGAAACATGC-3'
Fe-61S	5'-ATCTAGACACCAGACATGTGAACCA-3'
Fe-63S	5'-CGGCTACATTACAAAATGGACTAGC-3'
Fe-66S	5'-CCGAAAAMTTCCTGACTGTTTAAGA-3'
Fe-73S	5'-AATTTGGACCTCCGGTTACCTTG-3'
Fe-75S	5'-GAGTTCTAAAATTTGCCTCTGCGTG-3'
Fe-76S	5'-CAGTAGCCTAAGGAGATCAAATGGA-3'
Fe-77S	5'-CGTTAGAGCCGGCTTACTTACCGAT-3'
Fe-79S	5'-GCCTGTAAGGTCTGTCAACAGGT-3'
Fe-87S	5'-CTGTACGTCAGCCCCATCCT-3'
Fe-90S	5'-ATCCTGTGAGTTGGTGAGAGACC-3'
Fe-94S	5'-TCGTCAGACTCCCCAAATCC-3'
Fe-97S	5'-CGTGTACCGAATAAACCTCTTGC-3'
Fe-103S	5'-GAGCTTGGTTCCTAACATTTGGTG-3'
Fe-122S	5'-TGAAGGAAGGAACTTTTCATGTAGG-3'
Fe-130S	5'-CCGAATTCTRCACAAACCCAAAATGA-3'
Fe-147S	5'-TGAGAGACCCCTGGTCTAGCTT-3'
PRB1	5'-CTGTTCACTCCTCGACAACG-3'
MY1F	5'-GAGGAGGAGAACTTCTACCAGCA-3'
Hub-b-acrtin(DNA)s	5'-ATCATGTTTGAGACCTTCAA-3'
dog-ckit-1S	5'-CCCATGTATGAAGTACAGTGGAAG-3'
Fe-1R	5'-GGTACCCGGGGCGGTCAAGTCTCGGCAAAG-3'
Fe-3R	5'-CATGGTYGGTCYGGATCGTATTG-3'
Fe-7R	5'-GTCAACTGGGGAGCCTGGAGAC-3'
Fe-18R	5'-ACAGATCTGCCGCCGGGTTCGTAGTGGCC-3'
Fe-20R	5'-CTCGAAATCTCAAAAGAGCAGAATC-3'
Fe-21R	5'-AACAGGGTTAATTCCCGGTGTCTGAGTTG-3'
Fe-22R	5'-GTCTCTGCATCACCTAAAGGAATGT-3'
Fe-25R	5'-TGATCTGTTCCTCTGTTGAATGAAG-3'
Fe-26R	5'-TTATAAGGGTGGACTCCTCATGAAT-3'
Fe-27R	5'-ACATTTAGGTGCAGAGCTCAAAATC-3'
Fe-30R	5'-CGAAGGAGTTCTAGAAGGAGGAAGA-3'
Fe-34R	5'-TCGAATTCGAAACGGAAAGCGTCTATCAGTAAA-3'
Fe-35R	5'-CTGAATTCATGATCTCATGGCTTCTGGGTTC-3'
Fe-38R	5'-CACACATGCTCTAGACACAATACCC-3'
Fe-42R	5'-CCATAGCAGCTGACTAGTTTGAATG-3'
Fe-44R	5'-TGCAGACAGAACATACTGTGACAAA-3'
Fe-50R	5'-TTGAATTCTCATGGTTGGTCTGGATCGTATTG-3'
Fe-53R	5'-AGAGGAAATAAACCGGGTAGTGTGT-3'
Fe-54R	5'-GGTGCTCATTGTTAGGAGAGAAAAA-3'
Fe-55R	5'-TGTTAGGAATCCTGTAGCAAAGTGC-3'
Fe-56R	5'-CTCTGAGCACACTACTCTCAACTGC-3'
Fe-58R	5'-GAGTCTCAGGGAAGTGAAAGGACT-3'
Fe-60R	5'-GAGTCTTATTTGCATACAGGCTGGT-3'
Fe-62R	5'-GGGTTTTTGATCAGGCAGGA-3'
Fe-63R	5'-CTGACTTTGGGCAGGGCTAA-3'
Fe-68R	5'-AGCGAATGTACACATTGGTCTCTC-3'
Fe-69R	5'-TAAACAGACTAAGGTGGAGGATTGC-3'
Fe-70R	5'-CCACCCAGTCTGTTATTTTCGTTAC-3'
Fe-71R	5'-ATTTTTCTTCCTGTCGCTCCTTG-3'
Fe-73R	5'-AATCTGCACTTCATTTTCAGAGTCC-3'
Fe-78R	5'-CCGTCGACGGAGTAGATTTGCCAAGTCAAGGTA-3'
Fe-80R	5'-GAATTAACCCTGACATCTGGATGAG-3'
Fe-81R	5'-AAGAATCTCCAGTGAAGACCGTATG-3'
Fe-82R	5'-ATCTGGGCTAAGCCTAAACATTTTC-3'
Fe-95R	5'-GGGGGAGAAGGAATTGAGC-3'
Fe-96R	5'-TTCCTTTCGGGGAAGGACTA-3'
Fe-102R	5'-GGATGAGATCCTCCCAGGTG-3'
Fe-126R	5'-CAGAATTCTCTCATTCCCCCATTTTCTTT-3'
MY2R	5'-CTGCAGGTACAAGCTGGAGGT-3'
Hub-b-acrtin(DNA)r	5'-AGATGGGCACAGTGTGGGT-3'
dog-ckit-1R	5'-GTTCCCTAAAGTCATTGTTACACG-3'

Supplementary Table 5. Pol and Env genes used in the phylogenetic analysis

ID	Virus	genus	Accession # of Pol[a]	Accession # of Env[a]
ALV	Avian leukosis virus	a	ABO60875.1	AAU06813.1
MAV	Avian myeloblastosis virus	a	AAA46304.1	AAA46303.1
HERV-K[b]	Human endogenous retrovirus K	b	CAA76882.1	CAA76886.1
JSRV	Jaagsiekte sheep retrovirus	b	NP_041186.1	AAD45228.2
MMTV	Mouse mammary tumor virus	b	NP_955564.1	BAA03768.1
MPMV	Mason-Pfizer monkey virus	b	AAA47711.1	AAA47712.1
SRV-4	Simian retrovirus 4	b	ADC33201.1	ADC52789.1
BaEV_M7[b]	Baboon endogenous retrovirus	g	P10272.1	P10269.1
enFeLV_AGTT[b]	Endogenous feline leukemia virus	g	AY364318.1	AY364318.1
ERV-DC_ECE1[b]	Feline endogenous retrovirus	g	CAB38566.1	CAB38567.1
ERV-DC18[b]	Feline endogenous retrovirus	g	-	-
F-MuLV	Friend murine leukemia virus	g	CAA26560.1	CAA26561.1
FeLV-A_61E	Feline leukemia virus	g	AAA93092.1	AAA93093.1
FeLV-A_clone33	Feline leukemia virus	g	BAL04139.1	BAB63924.1
GaLV	Gibbon ape leukemia virus	g	AAA46810.1	AAA46811.1
KoRV	Koala retrovirus	g	AAF15098.1	AAF15099.1
M-MuLV	Moloney murine leukemia virus	g	AAC82568.1	AAB59943.1
PERV-C[b, c]	Porcine endogenous retrovirus	g	ABM65596.1	ABM65597.1
RD-114_SC3C[b]	Feline endogenous retrovirus-related virus	g	ABS71856.1	ABS71857.1
REV-A	Reticuloendotheliosis virus	g	ABC26818.1	AAW57301.1
XMRV	Xenotropic murine leukemia virus-related virus	g	ABD49687.1	ADU55752.1
Mouse ERVs[b, c]	ERVs found in the *M. musculus* genome	g	-	-
Rat ERVs[b, c]	ERVs found in the *R. norvegicus* genome	g	-	-
Chimpanzee ERVs[b, c]	ERVs found in the *P. troglodytes* genome	g	-	-
Macaque ERVs[b, c]	ERVs found in the *M. mulatta* genome	g	-	-

[a]A dash (-) indicates that the amino acids sequence was obtained in this study. [b]A virus is of endogenous origin. [c]An ERV was found by RetroTector©. [d]A ψ indicates that the ORF was truncated by substituions and/or indels.