

**Table S1. The representative retrovirus genomes used for data screening and phylogenetic reconstruction**

Name	Full name	Accession No.	Type
RELIK	Rabbit endogenous lentivirus type K	1	Lentivirus
RELIK_Lepus	Rabbit endogenous lentivirus type K	2	Lentivirus
EIAV	Equine infectious anemia virus	NC_001450	Lentivirus
EIAVliaoning	Equine infectious anemia virus	AF327877	Lentivirus
FIVsubC	Feline immunodeficiency virus	AF474246	Lentivirus
FIVoma	Feline immunodeficiency virus	U56928	Lentivirus
FIVpuma	Feline immunodeficiency virus	EF455614	Lentivirus
FIVPPR	Feline immunodeficiency virus	M36968	Lentivirus
Visna	Ovine maedivisna virus	NC_001511	Lentivirus
CAEV	Caprine arthritisencephalitis virus	NC_001463	Lentivirus
BIV	Bovine immunodeficiency virus	NC_001413	Lentivirus
Jembrana	Jembrana disease virus	NC_001654	Lentivirus
pSIVgml	Gray mouse lemur prosimian immunodeficiency virus	3	Lentivirus
pSIV_Cheirogaleus	Fat-tailed dwarf lemur prosimian immunodeficiency virus	4	Lentivirus
HIV1	Human immunodeficiency virus	EF029066	Lentivirus
HIV2	Human immunodeficiency virus	NC_001722	Lentivirus
SIVhoest	Simian immunodeficiency virus	AF188116	Lentivirus
SIVsyk	Simian immunodeficiency virus	L06042	Lentivirus
SIVcol	Simian immunodeficiency virus	AF301156	Lentivirus
SIVmnd	Simian immunodeficiency virus	NC_004455	Lentivirus
SIVtal	Simian immunodeficiency virus	AY655744	Lentivirus
LDV	Lymphoproliferate Disease Virus	X64337	Alpharetrovirus
HTLV1	Human T-cell leukemia virus type 1	NC_001436	Deltaretrovirus
BLV	Bovine leukemia virus	D00647.1	Deltaretrovirus
RSV	Rous sarcoma virus	NC_001407	Alpharetrovirus
SRV1	Simian SRV-1 type D retrovirus	M11841	Betaretrovirus
HTLV2	Human T-cell leukemia virus type 2	NC_001488	Deltaretrovirus
Jaagsiekte	Jaagsiekte sheep retrovirus	NC_001494	Betaretrovirus
MMTV	Exogenous mouse mammary tumor virus	AF228552	Betaretrovirus

**Note**

- 1 Katzourakis A, Tristem M, Pybus OG, Gifford RJ (2007) Discovery and analysis of the first endogenous lentivirus. *Proc Natl Acad Sci USA* 104: 6261-6265.
- 2 Keckesova Z, Ylinen LM, Towers GJ, Gifford RJ, Katzourakis A (2009) Identification of a RELIK orthologue in the European hare (*Lepus europaeus*) reveals a minimum age of 12 million years for the lagomorph lentiviruses. *Virology* 384:7-11.
- 3 Gifford RJ, et al. (2008) A transitional endogenous lentivirus from the genome of a basal primate and implications for lentivirus evolution. *Proc Natl Acad Sci USA* 105:20362-20367.
- 4 Gilbert C, Maxfield DG, Goodman SM, Feschotte C (2009) Parallel germline infiltration of a lentivirus in two Malagasy lemurs. *PLoS Genet* 5:e1000425.

**Table 2. The *M. Putorius* matching contigs identified during genome screening**

Contig Number	Genomic Regions Represent
contig006467	5'LTR-gag-pol
contig111284	5'LTR-gag-pol
contig098598	5'LTR-gag-pol-env-3'LTR
contig023783	5'LTR-gag-pol-env-3'LTR
contig113944	gag
contig068467	pol-env-3'LTR
contig040515	solo-LTR
contig027041	solo-LTR
contig076031	solo-LTR
contig037068	solo-LTR
contig005647	solo-LTR
contig022531	solo-LTR
contig079075	solo-LTR
contig023782	solo-LTR
contig023486	solo-LTR
contig001647	solo-LTR
contig023754	solo-LTR
contig034784	solo-LTR
contig040860	solo-LTR

**Fig S1 MELVmpf consensus sequence. Two putative accessory genes, *vif*, and *tat*, were identified by sequence similarity and conserved domain searches (Marchler-Bauer and Bryant 2004). Although no significant matches to lentiviral *rev* genes were found using similarity searches, a putative *rev* gene was identified by both its genomic location (overlapping the 3' end of the *env* gene in an alternative reading frame) and its arginine-rich nuclear localization signal (NLS) motif**

5' -LTR  
 GAGGGAGGCCTGTGAGCATGAGCCCCACTGTTGCAGAGCTTCCCAGCAGACAAAGGGCTTCCAAGAAGCTTATGAAGT  
 AGGAGGTGTTATGCAGGATGTTATAGCCGACCGCAGATAGACCACCGGGACATGGGGTACGTGCTACAAGCAACATCAA  
 CAGCAGCAGACGAGCAGCCTCGCACGTACAGCAGACCGCAGATTAACCGCAAGCGCCTTTGACGCAGTGAAGTGG  
 CATATAAGCAGCACTGGCCCTCTGCTTGTGTCAGAGTGTGCTCTTGGGACACTCTCGCTCAGATCATCTCCCGGTCGATG  
 CACCCAAAAGGTGTGCTCCAGGGAGGGGATCGGTACCTTCTCGGTGATGCACCCAAACGGTGTGCTCCAGAGAAGGG  
 GATCGGGCGGGAGTACCCTGGGCCCTCTCCCTAGCCCACGCGGTAGAGTTGTCTGCTTTGTATTAGCTATTGTGTGGT  
TAR  
 ACGCGTAATAAACAGCTTTTCGTTTTCAGTTATTGTGTGTGACCCGTTTGGCTTCCACCATCGGACCGGCTCACTCCCT  
GGGAGCTCCGTGAGCGGCAGAGAGCTCCAGTTGGCGAGCCAGCCAGGAGGACACAGACGAAGTAGAGTGAGCCATCCT  
TCGAGCCTCTAAAGCCTCAGTGGTGAGTACTCCCCGAGATCTTGAAACAGAGATCTGAGACTGTCCAAGAGGGGATAG  
 -> *gag*  
 GAAAAACAGCC ATGGGGGCTGGATTAAGTAAGAGTGATGAGAAGCGGTTGCAACCGGTCTTCAAGGCGATGTCGAGAG  
M G A G L S K S D E K R L Q P V F K A M S R V  
R K C L G S K E T V T S G N C I W A L K T A I E A T  
CGGGACGCCGGTTAAGGAGGTGACAGAGGAATCACTAGAGGACCTAATTCAGAGATGGGTGGAAGCAAAGGAAACAAA  
G T P V K E V T E E S L E D L I Q R W V E A K G N K  
CCAGACGGGTTATACAAGGTCTGCTTGGAACTTTATGTTGCATATGGTGTCTTCTAAAAAATTTAAGATAAGAGAGT  
P D G L Y K V C L E T L C C I W C L L K K F K I R E L  
TGTCAGAGGGACTTGTNCAATACAAGGTTTGTCTATCCAGGCTTTGGAGATGAGGATGTCAAAAAATCCCCAAAGCAGGA  
S E G L ? Q Y K V C H P T G F G D E D V K N P P K Q D  
TGATCAAAAGGTCAGGCTGCATATCCAGTAGTTGTAGGCATGGCCAACAAGAATATGAACAATTTAATCCAGATTC  
D Q K V Q A A Y P V V V R H G Q Q E Y E Q F N P R F  
TATAGCAGTTGGATAGGCAAGGTACAGGAGTCAGGACTTCTTGCTCAGGCAACTCTCCAATATTTGGGATCATCACGG  
Y S S W I G K V Q E S G L L A Q A T L Q Y F G I I T A  
CAAGTAGTACTTCGCGGAGATGAATGGGCTTTTGTAGCATAGTCCAGGGGCTCGGGGCAAAGGAACCTTTTGTTCGC  
S S T S P E M N G L L D I V P G A S G Q K E L L L A  
CAAATGAATGAGAGGCTAGAAGAATATGAGAGGATGCATCCACCAGGCCCTGGTGCAGCAGGACCTCGCCACCTG  
K L N E R L E E Y E R M H P P P G P G A A G P R H L  
ACGGTGGCAGAAATAGAGGTCTAAACATGACAAATGAAGAAGTGCCAGACCAGAATGGAATGTGGCTAGAAACCTAT  
T V A E I R G L N M T N E E A A R P E W N V A R N L  
Y  
ATAGAAACATGATTCTTGAAGCCTTCCAGGATGCCATCAGAGTCTATAAGGGGGCTCCTAAGGCCACATCCATCAGACA  
R N M I L E A F Q D A I R V Y K G A P K A T S I R Q  
GGGCCAAAAGAACCTTATCCAGATTCATAGATAGATTATTCGGCCAAATAGATCAAGAAATAACAGATCAGGAATC  
G P K E P Y P D F I D R L F G Q I D Q E I T D Q E I  
AAGGCATACCTAAAACAGCAGCTAAGTATAAATAATGCAAATGAGGACTGCAAGGCAGCCATGAGAAATCTAAGACCAG  
K A Y L K Q Q L S I N N A N E D C K A A M R N L R P E  
AAGATCCTCTAGAGGACAAAATGTATGCCTGTAGGGAGATAGGGTCAAATAAACCAAATGGCTCTCCTAGCCGAAGC  
D P L E D K M Y A C R E I G S N K H K M A L L A E A  
CCTGCAGGCAGGGCTGCAACAAGGAAGGAGGGGAAATGGAGAAAAATGTTTAAATGTGGCAAACCTGGTCACGTAGCA  
L Q A G L Q Q G R R G N G E K C F N C G K P G H V A  
Ribosomal frameshift site  
 -> *pol*  
 AGGCAATGTCGGGCGCCAAGCAACAACAAAAATGACTTGCTTTAAATGTGGAAAACCAGGCCACATGCAGAAGGAGT  
R Q C R A P K Q Q Q K M T C F K C G K P G H M Q K E C  
M W K T R P H A E G V  
GCAACAGGGAAACGGGACGCGCCCCAGGGGATGTCCCCTGGGAAGGTAATGCAGGCGAGCCATCTGCCATCAGGA  
K Q G N G Q R P Q G M S P G K V M Q A S E S A H Q E  
Q T G K R A A P P G D V P W E G N A G E R I C P S G  
 -> *gag* <-  
 GGGGGGACCAACAACTATATCCCTCCCTGTCTTAGCCTAAATAGTAGGCCTATAGCCCCAGTGTATATTAATGAAA  
G G T N K L Y P S L S L A \*

G G D Q Q T I S L P V L S L N S R P I A P V Y I N E K  
AAGAGATTCATATGCTGATAGACTGGGGCCGATACATCAATTATCAGCAACAAGGAAGCAAGAAAATTGGATCTAGG  
E I H M L I D T G A D T S I I S N K E A R K L D L G  
ACCATGCTTAGAGTAGTCAACATAATTGGAGTAGGGGCTCCAAAGATTTCAAATAATGGTCCCTTAAATATTCAA  
P C L E V V N I I G V G G L O R F O K Y G P L N I C  
GTAGGAGAAAAAAGGATTTCTTCAAATACTTGGTAGGAGAAGTCCCCTTAAATCTCTTGGGAAGAGATATTTTAAAGA  
V G E K R I S S K I L V G E V P L N L L G R D I L K K  
AACTAAGGGTAAAATAATATGTGCTAATCTATCAGATAAGATTAGGCCCTACAAGGTACAACCTTAAAGACCCTACTAA  
L R V K L I C A N L S D K I R P Y K V Q L K D P T K  
GGGACCCCAATAAAAACAATGGCCCTTAGCAAGGATAAATTAGAGGAATTACAGAAATCATAGAGAAGTTATTAAG  
G P L G K I Q W P L S K D K L E G I T E I E K L L W  
GAAGGAAAAATAGAAGAAGCAGCATGGGATAACCCCTGGAATACCCCATATTTTGCATAAAAAAGAAGTCAGGAAAA  
E G K I E E A A W D N P W N T P I F C I K K K S G K Y  
ACAGACTGTTAATAGATTTTCAAGGAGCTTAATAAGATGACTTTAAAGGGAGAAGAAATACAATTGGGAATTCCTTCCC  
R L L I D F R E L N K M T L K G E E I Q L G I P F H  
TGCAGGGTTGCCAGAAAAGAAATATATAACTGTTTGTAGATATAGCAGATGCCTACTTTACTATCCCATTGGATCTGAT  
A G L F E K K Y I T V L D I A D A Y E T I P L D P E  
TTTAGCCCTTACAGGCATTTACCCTACCCTTAAACAATCAAGGACCAGCCAGAAGGTTCCCAATGGTGTCTGTCC  
F R P Y T A F T L P S L N N Q G P A R R F Q W C C L P  
CACAAGGCTGGAGTCACAGCCCTGCTATATATCAAGGCACCCTTAGAGATATTCTCTTGCCTGGAGAGAACAACATCC  
Q G W S H S P A I Y Q G T L R D I L L P W R E Q H E  
TGAGATATTATTATACCAATACATGGATGATTTACTAATAGGATCATATTTAAGCAAAAAGGAGCATCAAAAGGTAGTG  
E I L L Y Q Y M D D L L I G S Y L S K K E H Q K V V  
CAAAATCTTAGACATGCTACTTCAATGGGGTTGAGACCCAGAGGAGAACTACAGGAACTCCCCATATAAAT  
Q N L R D M L L O W G F E T P E E K L O E T P P Y N W  
GGATGGGGTATGAATTAGAACCTAAAACCTGGAATTTGCAAAAAAGGAACTGGAAATCCCAGAAAAACCAACTTAAA  
M G Y E L E P K T W K L Q K W E L E I P E K P T L N  
CCAAGTGCAGAAGATATTAGGGAAGATCAATTGGGCTAGCTCCATGATACCAGGATTAAGATAAAAAACTTATGTAAG  
Q L Q K I L G K I N W A S S M I P G L K I K N L C K  
TTAATGAGAGGCAATATGCAATTAGACTCCCATAGGGAATGGACAACAGAAGCTTTAGAGGAAGTAAAATATGCCAAC  
L M R N M Q L D S H R E W T T E A L E E V K Y A Q C  
AAAAATAACAGAAAATCAAGGATATCATTACTACATATCAGAAAAGGAGGTTTATTGCAAGATTGTAAGGATTCTCA  
K I T E N Q G Y H Y Y I S E K E V Y C K I V K D S Q  
GGAAATAAATTATGGAATATATCAGGAAGAGCAAGGAAAAACAATGCTATGGGTTGGAAGACAATCATTAAAGAGG  
E I N Y G I Y O E E O G K K O M L W V G R O S L K H  
GATATTGGGAAATCTATCCTAGATAAATGGCCATAGCTATTCAGAATATTTGCACAGAATGCAAAATCAGATTAGGGG  
D I G K S I L D K L A I A I Q N I C T E C K I R L G V  
TAGAACCATTTACTTCCCATGGAAAAAGACCTTAGAAAATTGGTACAGCCAACAAAATATCTTCGCTGGTT  
E P I I L L P M E K R T L E N W Y S Q Q N Y L R W F  
TCCCATGTCAAACATAAATGCAGATTTAATGTTTAAAGGAAGTCTAGCAAACCAAAGTGATGATCCTTTAGAGGAT  
P H V K L I N A D L M F K E V L A N O S D D P L E D  
GTGGAAGTCTTCTATACAGATGGAGGGAGAAAGGAACAACAACAAGGCAGGGTATGTTACATCCACAGGAAAAATA  
V E V F A Y T D G G R K E Q Q T R A G Y V T T S T G K N R  
GAATAGAATATAGTAGGATCAATCAGCAAGCAGAAAAATATGCAATAAAAATGGCCTTCAAGATTCAAGTCCGCA  
I E H I V G S N O Q A E K Y A I K M A F O D S G P C  
AGTTAACATCATCACAGATAGCAAGTACTGCTTCTCCATTTTAAAGAGCTAGACCAGACCAGAAACCATAGAAGATAGT  
V N I I T D S K Y C F S I L R A R P D P E T I E D S  
TTATGGAAGGAGATAATTTTATTAGCTATGAAAAAGGACAATTGGTATATAGGATGGGTACCAGGACATAAGGGGTAC  
L W K E I I S L A M K K D N W Y I G W V P G H K G V P  
CTGGAAACACAGAAGCAGACCAATTAGTATCTATTGTTGTGGAGGGAGAAAATATTAAGGACAAAAGACCAGAAGATGT  
G N T E A D Q L V S I V V E G E N I K D K R P E D V  
AGGCTATGATCTATGTACCCCAAAAGATTTATTTCTATTACCTAGGAAATTATAAAACTAAACATAGAAAACAAAATA  
G Y D L C T P K D L F L L P R E I I K L N I E T K I  
GAGATCCCAAGAGGACTGGGGTTGGATAACCCAAAAATCATCCCTAGGCTTAAAGGCCTACAATCCAGGGAGGAA  
E I P R G H W G W I T O K S S L G L K G L O I O G G T  
CTATAGATCAAGGGTTAGAGGTAATATTCAAGTCTGTTATTAATGGAGGAAGGAGGAAAATTTTATTACAATCAGG  
I D O G F R G N I O V L L L L N G G R R K I L L Q S G  
ACAAAAATAGCACAATTAATCATCTTACCCTTATTACCTAGGCTTAAACAAGGCACAGTAGATAAAATATACAGAA  
Q K I A Q L I I L P L F H E P L K Q G T V D K Y T E  
AGGGGGCAAAATGGGTTTGGCAGCACAGGTGTCTTTTCAACTGGGTAGACAACCTGAGTCAAATAAAGGAAGAATG  
E G O N G F G S T G V F F N W V D N L S O I K E E H E  
AAAAATGGCATAAATTTGGAGGGATTTAAATTTGAAATATGGTCTCCCTACCACAGTGGCAAAAGAAAATAATTAACA  
K W H N N W R D L K L K Y G L P T T V A K E I I R Q

ATGTCCAAACTGCATTAAGGGGCAAACCCAGTAAGAGGCATCAACCTGTAGACTCCCAACTATGGCAGTTANCGGCC  
C P N C I K G A N P V R G I N P V D S Q L W Q L ? A  
TGTCACAGTCTCCTCAGGATACTTGTCATGCAGTTATCTCTGCCTCAGAATCAGGAAAGGCCACTGCTGTGGCCATATTA  
C H S S S G Y L H A V I L P S E S G K A T A V A I L N  
ATTTATACAAACTATGGAATGTAACTGGATCCACTCAGATAATGGGCCAAATTCCTTCCAGACAGGTGGAAGGAAT  
L Y K L W N V N W I H S D N G P N F T S R Q V E G I  
ATGTCAATACTTAAATATAAAACACACATACGGCATTCCATGGAATCCTCAAAGTCAGGCCATAATAGAAAATAAGCAC  
C Q Y L N I K H T Y G I F W N P O S O A I I E N K H  
AAGGAGTTAAAAAGACTGACTAATCAGTTCAAAGAGCAAACAGAGACCTTACAGGCTGCATTGGACTTAGCATTGATAG  
K E L K R L T N Q F K E Q T E T L Q A A L D L A L I V  
TGCTTAATAAAAAACAAAGGGGTGAATAGGGGATGTCACACCTTGGAACTAATGATATACCAGATGAATACAGATA  
L N K K O R G G I G D V T P W E L M I Y O M N T D N  
CCAAGAACAATAAATTTCTACAAAACCTCAAATAACAAAAAATTTCTGTTATTACAGACTTCAGCAAGGAAAGCAAAAG  
Q E Q I N F Y K T Q N N K K F C Y Y R L Q Q G K Q M  
GGGAATTGGCAAGGTCTGCCTGTATCCTTTGGAAAGGGGAAGGTCTATAGTAATACAAACACCTGATGGGCCAGTCC  
S N W Q G P A C I L W K G E G A I V I Q T P D G P V L

*pol* <-

TCATCCCTAATAAGAACTTTAAGGAGGTACCTAACCCGGAGGATTAGGCCACATAACCCATGGCGAACAACTTTTAGTA  
I P N K N F K E V P N P E D \*  
GCACCTGAAAAACCAATGTCATTAGAATTACAAGCTGTAAAAGAGGAACCCAAGAATTTACGTTAGGCAGGGATTAGG

-> *vif*

CTTCTTCGAAAGAAGAAGTCAAGAAGACATGAGGAGGCTGTTTCAGGTTAAATTTAGACATGCAAAATTTAGAAGATGAA  
M R R L F R L N L D M Q N L E D E  
GATATCTGGTACAACAGGTATAAGGTAGTAATAGGAACAGGGTTGATTGGGAAAATGGGAAGGAAATGGGATAAGC  
D I W Y N R Y K V V I G T R V D W E N W E G K W D K P  
CAGGAGTGTTTGGTCTGTTGTGCAGATTAGCATCATGTGGGGAGCACACCTCAGACTGGTGGAACTCCTCTTACAGG  
G V F G L L C R L A S C G E H T S D W W K L L L T G  
ACAAGAACCCCAAGATGCTTTGAATGCGCTCTGTAGCAATTATTTGGAAACCCCGCCAAATAGCCTGCAAAGAAGA  
Q E P P R C F E C A L L A I I L E T P P N S L Q R R  
GCTGCACTTGCATATGTAGAGGGAAAAGGGGCACCTCCTTTGCCAAACATCATAAAATATGACAAATTTATATACAGGC  
A A L A Y V E G K G A P P L N I I K Y D K F I Y R P  
CCCATATGACAAATATGGATCGAACCTACTCCTAAGACCCCATACCCAGCTAAAGTTTCTCCTTGACCTAGAATGGTG  
H M T N M D R T L L L R P H T Q L K F L L D L E W C

<- *vif*

TTAGATGGAGAATGAGACTTGCAACTGCTATGCCAAGCTATAGAGCATAAGCTCTCAAAGGATCAACTCCAGAGAGTA  
\*

-> *tat*

AAAGTCATTATAATGTTTCAGACCCCAAGGCGCAGAAAGATACCTGCAATGGCTAGCATGGAGATTGAGTATCAAAG  
M A S M E I E Y Q R

*env*->

AGCTAAAGTAGGATGTAACCTCATGCGCTTTCCACTGCCAGCTTTGCTTTCTTCAGAAATATTTAGGAATAGCTTATAAA  
A K V G C N S C A F H C Q L C F L Q K Y L G I A Y K

TGCAAAACCAGGAGGACACGAAAAAGAAGCCATGGACCCAGGAAGAAGCAGAGGTCATGTGGGACTGGCATCAACTCAC  
C K T R R T R K R S H G P R K K Q R S C G T G I N S P  
Q N Q E D T K K K P W T Q E E A E V M W D W H Q L T  
CTTTGGAGGAGGAGTCTCAACCCCTCCGAGAAGGAGAACCCTGACATGGAGCAGTGGCAGCCTATCCTGGAAAGG  
L E E E V S T P S E K E N T L T W S S G S L S W K G  
F G G G G L N P F R E G E H P D M E Q W Q P I L E R

<- *tat*

TTGAATGCTGAACGGGTGACATATGGTAATGTGACCATGATAAGATTAGAAGCACTATGGGAAAGGGATCAAAAACATA  
\*

L N A E R V T Y G N V T M I R L E A L W E R D Q K L R  
GAAGGAAGGAAAGGATAGAAAAATGCTGGACACTAATCTTAGCCTGTATAGGTGGGCTAATTTTAAATACACACCTGCCT  
R K E R I E K C W T L I L A C I G G L I L I H T C I  
GATATTAGCCATGTTTGGCGGGAATAGCCAAACCAAGGCGGAAAGGGTTATTCTGCTAGCCACTCCCCGGGAGTGATC  
I L A M F G G N S Q T K A E R V I L L A T P P G V I  
CCAGCGGAGGAATGCCACCATGGTGGTGCCTCCGACAACCCTGGATGCTTAGGTCAGGCACTAATGGCCGG  
P A E E L P P W W C A S D N H P G C S R S E A L M P E  
AGGGAAGGTTACTTTTAAATGAAACATTCCAAGGAATGAATGCCTCCCTCCTGGCTGCAGATGTGTTAAAATCCTTCAT  
G K V T F N E T F Q G M N A S L L A A D V L K S F I  
CAAATTTGGCCATAAAGGTTGCAAGGAGAGGGGGAGTTCCAGCCAAGGTTTATTTGGGGAAGTGACAATTATAACAGCT  
K L A I K G C K E R G S S S Q G L F G E V T I I T A

AATAGTACATGGGTCTCACTTGAGAATATCTCAATAGAGACTAGCTATTACACCTGTAACCTGGAAAGGCTACACAATT  
N S T W V S L E N I S I E T S Y Y T C N L E R L H N W  
GGGCTGCAGGAGGCAGAAAATTATCTTTGTGTCTAACAGAGGGTTACTTCTTTCTAAGAGAACGAACTTTGCAGTATTG  
A A G G R K L S L C L T E G Y F F L R E R T L Q Y C  
CATTACTAACCTTTCTAGTACTCTTATCAATCAAACCATGATCTCAGAACCGATCTTTGGACCTAATGGAACACTTTAT  
I T N L S S T L I N Q T M I S E P I F G P N G T L Y  
GGGAGCATGTCTGGCGTTGACAAATGTAACCTACACATATCATTTGGGTACCAAGAAATATGTCTGTCAACTGCTCCAGAA  
G S M S G V D K C N Y T Y H W V P R N M S V N C S R T  
CCATCTGGAAACAAAGATATCAACACAAGGCAAATTTTGGGGTTTCCCCTATCATATTTGAGCTATAAGGAAAAAAG  
I W K Q R V S T Q G K F W G F P L S Y L S Y K E K R  
GTATAGCAATTGAAATGCAATTACTGGTGACCTTTGGAGGCCAGATGGAGCAGTATTAATCTATGGAAGGCAAT  
Y R Q L K C N Y T G D P W R P D G A V L N L W K V N  
ACCAGCCGCCCTCAAGAAAACCTGCCAGGTGGTTCCTATTTCCCTGGCACTCAAAGAACTTTAGCGTCATCATACAAT  
T S R P Q E N P A R W F L F P C H S K N F S V I I Q C  
GTCCTTGCATAGATGGCAAAAACGAAAGTTCTCCCTGCGGTAACACAAATGACACCTCAGTAGATTGGAATAACTGTAC  
P C I D G K N E S S P C G N T N D T S V D W N N C T  
AATAGCAAAGAATATCTCTTCTGGGATGGAGGAGCCGGAGGTTAATAGCTAATTTGGAGCAGAACATCCCTCAAAGC  
I A K N I L F W D G G A G G L I A N W S R T S L K S  
ATGACAGGGAAGTGGACATGCTATAATGCCTGGAAAGGGTTCTATAACAGCAGCTGTAATAATTTACTGAAGGAGATG  
M T G N W T C Y N A W K G F Y N S S C N N S T E G D E  
AATGCTCATGCCAAAATAATACCATTATAAATTTTATAGATCCATACTCTAACCTTATGCATCAGTAAAAGACTACTC  
C S C Q N N T I I N F I D P Y S N L M H Q L K D Y S  
CATAGTCAAACAACCTTCAATAGGAGTGTTCAGGGAAAGTGAATTTCCCAATGTGGGGACCAAAAAGGTCGATTGGCAGG  
I V K Q P S I G V F R E S E F P M W G T K R S I G R  
AGGAAAAGAGCTGTACAGGTACCATTGCTTCTGTTCTCCTGTGATGAGTGGAATCGGAGCCGATCAGGGATAACTG  
R K R A V Q V P L L L F S L L M S G I G A A S G I T G  
GAGTGTCCAATCTTACGGGCTGGTAGGAGTCTTGAAGGAGCAACAGAACTCCTGAGAGGCATCCTTGAACCCAGGG  
V L Q S S G L V G V L K E Q Q K L L R G I L E T Q G  
ATTGTTGTTGCACAGACAGGAGGCCCTGGAGGCAGGCCTGATGGAATCGGAGGCAAGAGTAGACAGAATCGATTGGATC  
L L L L H R Q E A L E A G L M E L E A R V D R I D W I  
CTGGGAACAGCCCAATTAATGAATTTGGCCGGATGTGGGAGTTTTACCCAGTATGTCTGACCCACCTTGTGTTGGAATT  
L G T A Q L M N L A G C G S F T P V C L T H L V W N S

RRE

CCACATATAACATTACCATGAAGAATAGGACCATGAGCAACTGGTTAAATCAAAGCAGGACATATAAGGAGTTAATACT  
T Y N I T M K N R T M S N W L N Q S R T Y K E L I I  
GCAGCAACTGGCTGAGAGTGGCGCCTCGTTCCAATCATTAGAGGTACAACCTCAAAAATTTGGGGGAGTCAAATTTGGCTA  
Q Q L A E S G A S F Q S L E V Q L K N L G E S N W L  
ACTACCATATGGAATAAGTTCAAGGATCTGTGGAGATCATGGGGTCTTAGCACTTATAGTACTGCTTACTTCTTT  
T T I W N K F K D L W R S W G V L A L I V L L L L L F

-> rev

TCGGGCCATGCCTCTTTCAATGCGTTCAAAAATATGCTTTATAAGTTTGTAGGTTATCTCTTATATCTGAACAGGACCA  
G P C L F Q C V Q N M L Y K F V G Y S L I S E Q D Q

T G P

AATCCTTCTGCCATGTCTGTGGCGGACCAGATAATGACGGCAGACATCCTTGGGGAGGCAGACGTAGAGGTCGGCGAC  
I L P A M S V A D Q I M T A D I L G E A D V E V G D

-----NLS motif-----

N P S C H V C G G P D N D G R H P W G G R R R G R R R  
GATTCCTCGCTCAGCAAGGCGTCAAGCCAGGGAAGGACTGGAAGCCCAATTTGCGCAGCTCCACTTGGTGGCTGAATG  
D S S L E Q G V K P G K D W K P N L R S S T W W L N V  
F L A R A R R Q A R E G L E A Q F A Q L H L V A E C

rev <-

TTCGAGATAAGGTACAGAACATCAGGAACAAACTGCCCAAAAACAGATATCCTCGACTTCCCACAGAGAGGAAGGAGC  
R D K V Q N I R N K L P Q N K I S S T S H R E E G A  
S R \*

env <-

3' -LTR

ACCATCATAAGAATTAACCCACCATCTTGCCACAATAGAAAAGAAAAGGGTGGACTGAGGGAGTCTGTGAGCATGAA  
P S \*  
CCCCACTGTTGCAGAACTTCCCAGCAGACAAAGGGCTTCAAGAACTGTTATGAACTAGAAGGTGTTATGCAGGATGTT  
ATAGCTGACCGCAGATAGACCACCGGACATGGTGTACGTGCTACAAGCAACATTAGCAGCAGCAGACGAGCAGCCTCG  
CACGTACAGCAGACCGCAGATTAACCGCAAGCGCCCTTGACGCAGTGAAGTGGCATATAAGCAGCACTGGCCCTC  
TGCTTGTGAGAGTGTCTCTTGGGACTCTCGCTCAGATCATCTCCGCACCCAAATGGTGTGCTCCAGAGAAGGGGA  
TCGAGGGGGAGTACCCTGGGCCCTTCCCTAGCCACGCGGCTAGAGTTGTCTGTCTTGTATTAGCTACTGTGTGGTAC

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A

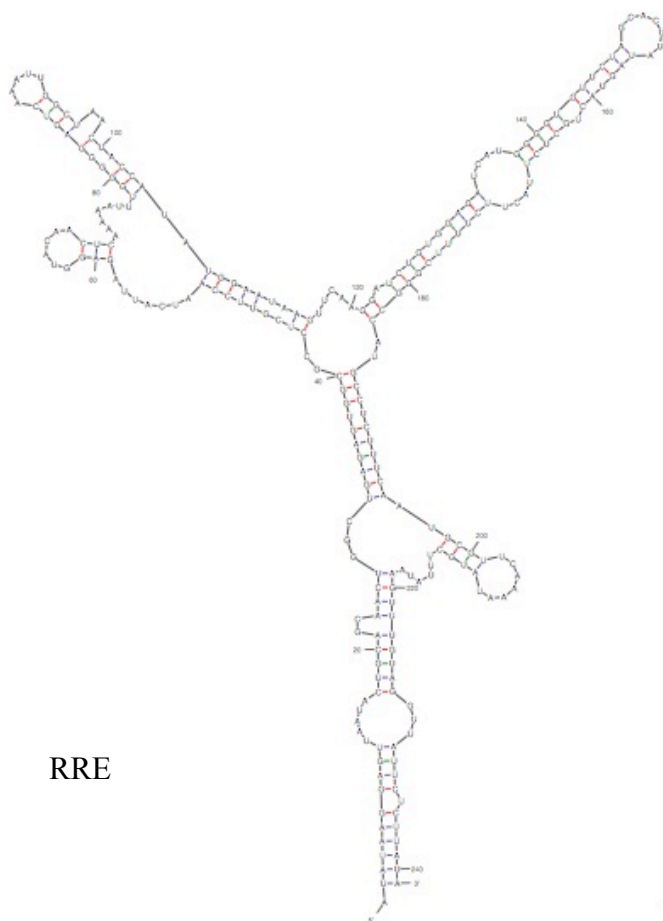
```
MELVmpf      41 WdkPGVFGLLCRLASCGEHTSDWWKLLLTGQE--PPR-CF
pfam05851   146 WG-PGMVGVVIKAFSCGERKYDWTTPMMVIRGEidPQKwCG
          ECALLAIILETPPNSLQRRALA 100
E-value=8.92e-04 DCWNLICLRNSPPGSLQRLA 207
```

B

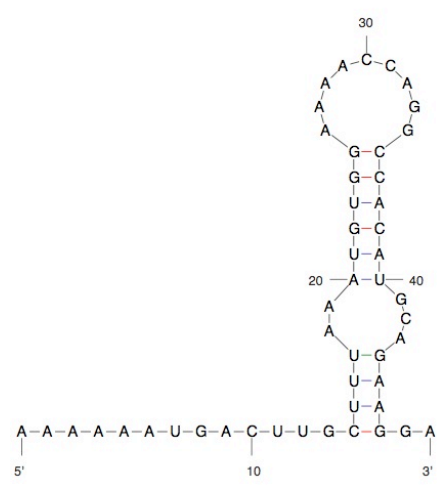
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RELIK       44 RPLAEQRWVPGMYGLASRATSCWFCKKSKNWKKVIRIGKL
pfam05851   139 GGEPSPGWGPGMVGVVIKAFSCGERKYDWTTPMMVIRGEID
          EEGVIRRVFLVCCL--TPQGTLQRLAALA 110
E-value=4.05e-04 PQKWCGDCWNLICLRnSPPGSLQRLA 207
```

Fig S2. Conserved domain alignment of the deduced amino acid sequences from the MELVmpf (A) and RELIK (B) *vif* genes and the lentiviral Vif superfamily (pfam05851). Pfam is a large collection and classification of protein domains and families. Numbers refer to the position in the original protein or domain. Identical amino acid residues are highlighted in red, and blue and gray indicate different amino acid residues or a gap, respectively. The representative RELIK *vif* gene used here is encoded by *O. cuniculus* genome cont2.81652 (version 2). The expectation values (e-value) were generated by a conserved domain search. Black rectangles represent the SLQXLA conserved sequence motif of Vif protein. RELIK has an SLQXLA conserved sequence motif with only one S->T substitution. This substitution is also present in feline immunodeficiency virus (FIV) (Oberste and Gonda 1992). It is worth noting that the RELIK *vif* element described here is derived from the second assembly of the European rabbit, released in 2009; the initial analysis of RELIK was published with the preliminary assembly that was available in 2005.

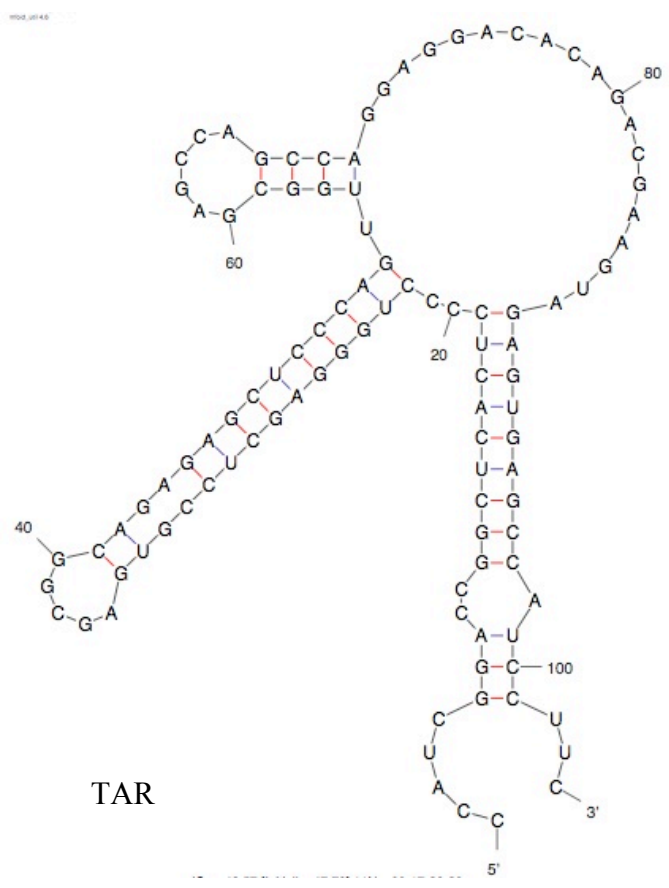




RRE



Ribosomal frameshift site



TAR

Fig S3. RNA secondary structure of RRE, Ribosomal frameshift site, and TAR. The structure was predicted using the mfold Web Server.

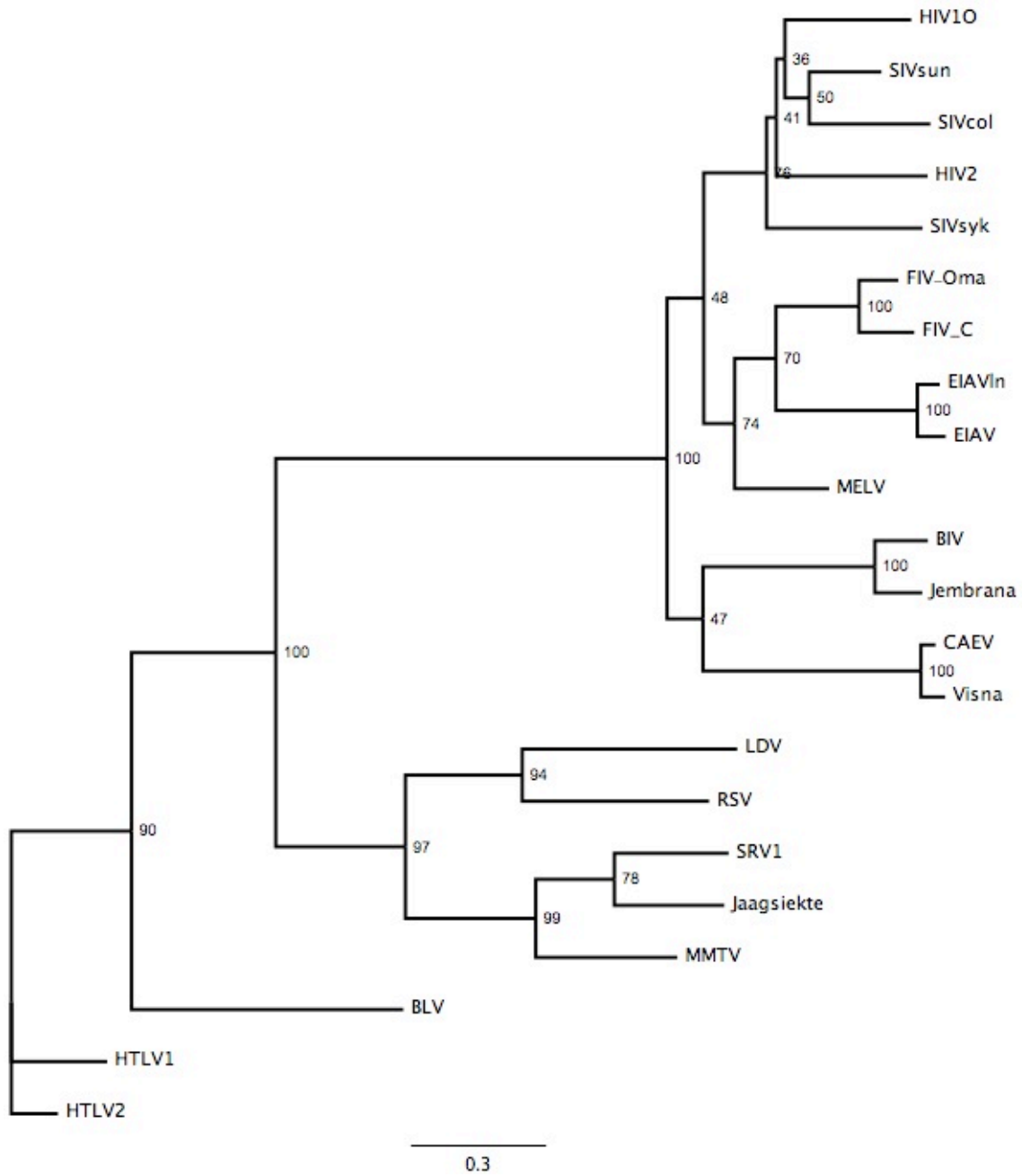


Fig S4. Phylogenetic relationships of MELVmpf and other retroviruses. Tree was reconstructed using ML method with 500 nonparametric bootstrap replicates. Support indices are indicated as percent.