

Supplementary Materials for

**Multiple infiltration and cross-species transmission of foamy viruses
across Paleozoic to Cenozoic era**

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This PDF file includes:

- **Fig. S1** Detailed descriptions of the putative genomes of consensus ERV-Spuma-Rbi, ERV-Spuma-Smu, ERV-Spuma.a-Ame and ERV-Spuma.b-Ame
- **Table S1** The endogenous foamy viruses or expressed foamy viruses identified in amphibians
- **Table S2** Information on the representative retroviruses
- **Data set S1** The nucleotide sequences of consensus genomes of 4 EFVs
- **Data set S2** The alignments used to build the phylogenetic trees for RT represented in Fig.1
- **Data set S3** The alignments used to build the phylogenetic trees for Pol represented in Fig.3
- **Data set S4** The alignments used to build the phylogenetic trees for Env represented in Fig.3
- **Data set S5** The alignments used to build the phylogenetic trees for Gag-Pol-Env represented in Fig.4

>ERV-Spuma-Rbi

5' -LTR

1	TGTCAGAAAATATCTTAATATTTTGTGCTTTATTGATAACTTATATTTAGTGAAGTC	60
61	AGTAATCAATTAGCCATAAAGAAACATGTTAGCATTTAATACCCATAAGCCTTACTTTT	120
121	AAAAGCCATGACATCGGTCATGGCCTGTGCTGAAAAAGCTCCAGCACATAGCTTTCACCT	180
181	TTCCCTACTTAAAACCTCAAGATTTACCTTTGTCCACTTTTCAGACTTTGAGAGTACA	240
241	GTTGTTTACCACTTATCTCTTATCTCAAGTAAGAAAGCACCTGCATTTTATGACATTGAG	300
301	CATCCTAAACGCAGGTGTCATGATTGACCACCTAAAAACAGATGGCCAGCCAATTAAGC	360
361	GTGAATCTTGTGACAGAAGGGAGTGAAAAAGATTTTCTCTTAGAACTACAAAAGAAGATT	420
421	TATCCAATTA AAAATCAAAAATGGGCGAAGCTATAAACAGAATAAGAATAAATCCTATAT	480
481	TTTACTGTTCTGATATGAAAAATTGATTGAACCTTAGTCAAGGTCTCTAGAAATGAAGTT	540
541	CTTCAAAGGCTAAAATATAGATGTGTTGATGGAAGTGTAACAGCGACCCTGGATCAAAGG	600
601	AATCAAAGGGTCTTAAGTGTATAAAACAGTGAGCAGTTTGAGGGAGAGGGAGAGGTGCTA	660
661	CTTAGACTTTCTTCGCACGTGATTGAGAGAGACACAGAGCGGGTGCTTCAGATTAATTG	720
721	GTAAATATAATTTTTTATTCAAGTATATGAGAACCTTTAAATTGCTATTGTTTCTACATT	780
781	GGCAGATGTATTAGAAATGTATTAATTTCTAAAAAGATGACATTAATAGACATTTATCTG	840
841	ATATTAATAATTTCAATTACTTTTTTTAATGGCTCTTGCATTGATTGTAGGATATACTC	900
901	TGGTAAAGTTAAGATTTGAACATAAAAAGTGTTCCTTAGTCATTTAGAGATATTTATTCAT	960
961	GCCTTTCTTTATCTGTGAAATAAAGAAAATATTTTTACAATAAACTGACTGGTTTATTTA	1020
1021	TGCATGATGTGCTGCAAGAATTAATGGTTAATAAAAAATTTCTGTGGTAGATTCGAACAC	1080
1081	ACCTCTGAAAGTAACTTTTTGTCTCAAGGCAGAAAGGGTAGGGAAATAGAAGTGAAGT	1140
1141	GGGAGTATTTTATCCAGGCAGGATCCCTGGTTTTAAATTCTGCTAAGGGTAGAAGCCTC	1200
1201	AATACTTCCATTCAAATTTACCACA TGGCGCCCAACGTGGTTTAAATCTCCTGTAGAAT	1260

1261 TAAATATTATTTCCAGTCTATGTAATTTTGCCTTTTGCAGCAGTTTTTATAATTGGTTG 1320
 |→ Gag ORF start

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1381 AAGCCAATCATATCAGGGAAGATCAGTCCTTTGCCTGCATTTACAAGTGGCCAGTGACT 1440
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1441 CGTCACCGTGCTTTTCATGTTGACATTTGTCGTTTAAAAGCTTTACTGCACAGGGCAGAC 1500
 S S P C F H V D I C R L K A L T A Q G R

1501 ACCAGGGGCTAAATAGAAGAGCAGAAGAGGATTTTGTTCCTTTTGCTCTCCCTGATTGTC 1560
 H Q G L N R R A E E D F V P F A L P D C

1561 AGATGTCTTTTCACTTGGTAAATGCTTATTTGTAGAGAATCCGGTAATTCCGTTTCTG 1620
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1801 CGCCTGGAGAATTCGGGGCCCGTAGTGAGATTGATCGAAAAGCAGATAGAGTAAGGCGGG 1860
 T P G E F G A R S E I D R K A D R V R R

1861 CTTTGGGGACGCTTCCAGCTGATGTTAATCTGATACCTGAACATCTGGCCACTAGACTAG 1920
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 V A L E A V T G A C N S R T R H Y I I S

1981 CTCTGATGCCACAGAATTTGGTTCCTCCCCCTCATTCTGCGATAGCTGGGGCAGTTATT 2040
 T L M P Q N L V P P P S F C D S W G S Y

2041 ACGGGTGGACTTATCGTTCGATATTTGGGAAACCGTTAATCACAAATCTCGGTGAAGTGC 2100
 Y G W T Y R S I F G K P L I T N L G E V

2101 TGCGTCATATTTTGCAAAGTTTGGTATTTAGCTGCATATTCTTTGGCATGCTGGTTA 2160
 L R H I L Q K F G I S A A Y S L G M L V

2161 CTATGAGTAATTTTGATCAAGTATGGGAGATTTTAAAAGACGTCATGCCTGATACCTCTA 2220
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2221 TTCGTATTGATCTTAGTAATCGTTTAAAGTGCATTGGCCCCGGCAGATCGACATGAGCAGT 2280
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2281 TCCATTATTATCCAGCAAGTCTTCGAGGCGGCTGGTTCGTCATTAATCCCTTCTAAGC 2340
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2341 CACTTAAACAGGCTCAGCCAGGGTCTGACAGACCCAGGGAAAGGGCAGAGAGATCCAGC 2400
 P L K Q A Q P G S D R P R E R G R E I Q

2401 GCACTCAGCCTGAGAAAACCTCAAGACGGGTGAGTTTTTCATTTAGGAATCCTTCTTCCC 2460
 R T Q P E K T S R R V S F H F R N P S S

2461 AGGATAGAAAATCAGAGGGACAATAGGGGGTTTGGGAATTCTAGACAGGATTATACACCCC 2520
 Q D R N Q R D N R G F G N S R Q D Y T P

Gag ORF end ←|

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 P P S T K S L *
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 2641 GTAACCTAAGGCAGACCGCCCTCCCCCTTCTTCTCACAAAAAGCCTGTGAAGCGAGCCACT 2700
 | → Pol ORF start
 2701 TTCCATGGCAATGCTGGCTCCACGTCTAAACCCCTGTGGATCCAGAATAAGGAGCAGGG 2760
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 M S S W Y P R H W G F
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 P V P E P R F N P Q P L L H P Q F P L M
 Po1 ORF end ←|
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 F F T Q E A N F F Q N A P V L G R S L T
 7381 CTGCCTGTATCAGGGGTTAGCTGAGGGGTTAAATGCACTGAGGTTACTTCTGTGTTAG 7440
 A A C I R G L A E G L N D T E V T S V L
 7441 ATTTAATTGTACAGACAAAATGGCTGAATGACTCATTTCCTTGGCCGCTTGGGTGATGA 7500
 D L I V Q T K W L N D S F P L P A W V M
 7501 GAACAGCCAACAGAAAGCGCAGGAATGCTTTGAAACAGGAGGTTCAAATACATTCTTA 7560

Foamy_virus_ENV super family (c104051)

R T A N R K R R N A L K Q E V Q N T F L
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 7621 GAGCAGGTATTTTTCAATTAAGGGATTACTTAGCTCAAACCTTACAGTTAGGGATTGATG 7680
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 7681 CCATATCCACA ACTGATGAGAAAATACAGGTTCTAGCAAGAATAGAACAGCTTACTCACT 7740
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 L Q H L R M I E L T A S E W E L I L D E
 8581 TACTGAAGCCAGAGGTATTTTCAAATGCCCTGGGTCGTGCTTTTTCTGGATTAGTGGGTG 8640
 L L K P E V F S N A L G R A F S G L V G
 8641 GAATAGCTAAAACAGCTGTTGGTGTAGTTAAAACATAATGGAAGGGGCAGGTGGACTCC 8700
 G I A K T A V G V V K T I M E G A G G L
 8701 TTCATGACTTAGGGATCAATTTATCCCATTAATCCTGGGAATCATAGTAATAATTGGTG 8760
 L H D L G I N L F P L I L G I I V I I G

Env ORF end ←|

|→ Acc ORF start

8761 TTCTTTTCTTCTGTCTTAAGAGAAAT**TAG**AACGAAGAGCAGCGAACCCAGAA**ATG**GCGAGGT 8820
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 8821 GTAAACTCAAAGATACATATTCCAGCTAATCCTAGGAAGAATGCGATGATTGTCTGCCTG 8880
V N S K I H I P A N P R K N A M I V C L
 8881 GGACCTGATCTCATAAATGAGTATGCTGATTATGGAAGCTGGATGTATTCAGAAAACAAT 8940
G P D L I N E Y A D Y G S W M Y S E N N
 8941 CCTGATACATGTGCACCTTATTATCTGCATAAAAACTGTGATATTTTATTTAAGTTCCCA 9000
P D T C A P Y Y L H K N C D I L F K F P
 9001 CAATATTCCTATTGCTGGACTTGGCCAAGAAGACTGGCATCTGTTCGTGAAGCACTACGA 9060
Q Y S Y C W T W P R R L A S V R E A L R
 9061 AGAACCTTGAGTGCTCACATTTGTCAGTGTGCTCCCTGGGAACCTGTGCCCTGCTACTTC 9120
R T L S A H I C Q C A P W E L V P C Y F
 9121 AATATCTACTCTTTGGCAGAATATCAATTAGGATATGGACATGGCCTATCAAATGCCAAT 9180
N I Y S L A E Y Q L G Y G H G L S N A N
 9181 CCTGTTGCTTCAGATGGAAATCAAGAGCCTCCAGCCCGGGTTAAGCTCGAATTGGTTT 9240
P V A S D G N S R A S S P G L S S N W F
 9241 CCAGTACCTAGTCCACAGTCTTTTGCACGGATGAAGAATTGGATCCAATGCACCTTGCT 9300
P V P S P Q S F A T D E E L D P M H L A
 9301 CCGGCTAATTCTCTAACAGATGAAGGACAAGACTTTGTGCTTTGGCTGAATGCAGCTCTC 9360
P A N S L T D E G Q D F V L W L N A A L
 9361 TCCTCTGAGGATGATCAATCAGTCATTCTCCAACATCAGCAACCAAATCCTACTCAAGAT 9420
S S E D D Q S V I L Q H Q Q P N P T Q D
Acc ORF end ←|
 9421 TCTGCTCCGACTAGACCAGCAGTGGAAAGCGAGCAAACAGATTCCAATATCTATAAT**TAG** 9480
S A P T R P A V E G E Q T D S N I Y N *
 9481 TCAGACTGACTTCACAGATATCTGAAACGTCTGATCCGGCTGGATCTACTGAGAACTGTG 9540
 9541 AATAACTGTCTATTATTGACTGGACTGGTATGTGTCTTATTCAAATGCACCTTGCCATT 9600
 9601 TCAGGATCGTTGCTCATCAATTGGTAAGTATAATAGGCATTTAATGCCACAGATCCCTA 9660
 9661 CACATGATGGAATCAGTGATGACACATCACAGATTTCTGACCCATAGAGATTATTTAAT 9720
 9721 TATGAACCCTCATCTTATTTGACTGGATGAGCAGCTTCAAATTTAAAATTTACATTCCCT 9780
 9781 GGGTATGAATGTTCTCTATTTCCATAAGGAAATATTGAGAACTCTTTATATCTGGTTA 9840
 9841 TTATTAGAACTAACTCAGATTTGTCAACTCATATCTCTTTATATTCAATTTGGTAATGT 9900
 9901 AACCAATTTTTATTACACTTGTATTATTACATTTGATTTTCACTTGTATCTATGCAATGT 9960
 9961 TGAGCACTGACACAACCTTATTATATGTAGTTTATTGTGTGATTATTTCCCCCAGGCTTA 10020

10021 TTAGTGCCTTACTGATTTATATGTATCTAGCTATGTCTAGTATTTGTTTTACTGACTCCA 10080
 3' -LTR
 10081 TGGGGGGG**TGTCAGAAAATATCTTAATATTTTGTGCTTTATTGATAACTTATATTTA** 10140
 10141 **GTGAAGTCAGTAATCAATTAGCCATAAAGAAACATGTTAGCATTTAATACCCATAAGCCT** 10200
 10201 **TTACTTTTTAAAAGCCATGACATTGGTCATGGCTGTGCTGAAAAAGCTCCAGCACATAGCT** 10260
 10261 **TTACCTTTCCCTACTTAAACCTCAAGATTTACCTTTGTCCACTTTCCAGACTTTGA** 10320
 10321 **GAGTACAGTTGTTTACCACCTTCTCTTATCTCAAGTAAGAAAGCACCTGCATTTTATGAC** 10380
 10381 **ATTGAGCATCCTAACGCAGGTGTCATGATTGACCACCCTAAAAACAGATGGCCAGCCAAT** 10440
 10441 **TAAGCGTGACTCTTGTGACAGAAGGGAGTGAAAAAGATTTTCTCTTAGAACTACAAAAGA** 10500
 10501 **AATCCAATTA AAAATCAAAAATGGGCGAAGCTATAAACAGAATAAAAATATAGATGTGTTG** 10560
 10561 **ATGGAAGTGTAACAGCGACCCTGGATCAAAGGGTCTTAAGTGTATAAAAACAGTGGCAGTT** 10620
 10621 **TGAGGGAGAGGGAGAGGTGCTACTTAGACTTTCTTCGCACGTGATTGAGAGAGACACAGA** 10680
 10681 **GCGGGGTGCTTCAGATAAATTGGTAAATATAATTTTTTATTCAAGTATATGAGAACCTTT** 10740
 10741 **AAATTGCTATTGTTTCTACATTGGCAGATGTATTAGAAATGTATTAATTTCTAAAAAGAT** 10800
 10801 **GACATTAATAGACATTTATCTGATATTAATAATTTCAATTACCTTTTTAATGGTCTTGC** 10860
 10861 **ATTGATTGTAGGATATACTCTGGTAAAGTTAAGATTTGAACATAAAAAGTATTCTTAGTC** 10920
 10921 **ATTTAGAGATATTTATTCATGCCTTTCTGTATCTGTGAAATAAAGAAAATATTTTTACAA** 10980
 10981 **TAAACTGACTGGTTTATTTATGCATGATGTGCTGCAAGAATTAAGGTTAATAAAAAATT** 11040
 11041 **TCTGTGGTAGATTTCGAACACACCTCTGAAAGTAACTTTTTGTCTCAAGGCAGAAAGGGT** 11100
 11101 **AGGGAAATAGAAGTGGAAGTGGGATATTTATCCAGGCAGGATTCCTGGTTTTAAATTC** 11160
 11161 **TGCTAAGGGTAGAAGCCTCAATACTTCCATTCAAATTTACCACA** 11205

>ERV-Spuma-Smu

5' -LTR

1 TGTTACAGGCCTCAGTAGAAGTTAAGGTTAATGACTATTACAAGTCTAAGTAGAAGTTAA 60

61 GGTTAAGGATTTAACTACGCAGTACTAGTAGTTTCTGTTCCATAAGATTTTTTATGTTT 120

121 TAAAGATTAGAATGTTTTGGTTATTCTGTAAAAATGATCAACAGCTTGGCCTTGGTGATT 180

181 TTCTCTCCTGATTTTCTTCTGAGTTTTTATGACCGTTAGTACTCTTTTTGAGGTAGCG 240

241 ATACGCAGGTCTAGTTACAAAATCTTATATATATGCAGACCTTTGTTTATACTCTGGGGC 300

301 AGACCGAGAGACTGAAGCTAGACTTCATATCGAGACTGACTGGTATGTTTATTTTTATT 360

361 TTTATGCATATAAGTTTTAACAGGCATTCTATGTTATACTCTGTTTTAATTTGGATTCC 420

421 TGTAATTTTTATTATTTTTCAATAAATAATTACTATGATGAATTCTCAGTCCTTCTTAT 480

481 AATTGTGCTCACGATTTTCTATTGAATGTGAGACCTATCCACATGTATAAAATTGAAA 540

541 TTTGGTAACTTATCACTTAGGGTGGAGAATAACCTTATTTTAAGACATTACATGGGAGGA 600

601 AAGGTGTGAACCCATCACAATTGGCGCCCAACGTGGGGCTCGAGAATTCTAATTTTTTTA 660

661 TATTACCCAGATATATTTTATACCGCGTCTCTTATACGTAAGGGAAGGTACTCTCAAT 720
|→ Gag ORF start

721 ATCATGGCGAATAATTTTGTGATATACAGCGATTAAATTCATTGTGCAGATTGCAACAA 780
M A N N F A D I Q R L N S L C R L Q Q

781 GGCAGAGATGTGAAAATGATGAAGTTTTAGCACTTGAAATACAGTATGGTCCCTGGGGA 840
G R D V Q N D E V L A L E I Q Y G P W G

841 TCAGGAGCTAGATACTGCTTAATCCGTGTATTGTTGTTAGGACCAAATGGAGTTGTTTTG 900
S G A R Y C L I R V L L L G P N G V V L

901 CAAACACCTATGTTTGAGTTTGAGGATATTGATTTTAAACCCTGCCAGGCATACCATTGTT 960
Q T P M F E F E D I D F N P A R H T I V

961 AATCTGATCTATGATGAAAGTCAGATCATTTTGGGAAGAGTCCCAGTAATCCCAAATAGT 1020
N L I Y D E S Q I I L G R V P V I P N S

1021 CTTCGAGACATGGACCATATGTCCAGAGTGAGAGGTGGGGTACACCCCGTTCTAAATTA 1080
L R R H G P Y V Q S E R W G T P R S K L

1081 TATTCACCAGTGAAGAGGGGAGGAATTACCTCCACTGGCGGCTACTCTTCAACTAGAGAGA 1140
Y S P V K R E E L P P L A A T L Q L E R

1141 GAACAGTTATTAAGAGAACTGAATCTAGTCACTGCCACTTTAGAGCAGATATTAATTAGA 1200
E Q L L R E L N L V T A T L E Q I L I R

1201 GGAGCTTCAAATGTTTCTCAGTTTTTATTACAGACTACAGGAGGAATTCCTATGTCTAAC 1260
G A S N V S Q F S L Q T T G G I P M S N

1261 ATTAAGCAACTGTGGGTCAGGTTCCCTCAAATACTAAGGAGATTCCCCTATGGCTTAAT 1320
Gag_spuma super family (c126624)
I K A T V G Q V P S N T K E I P L W L N

1321 GACAGAATACATGCATTAGATGGGGTATTTCTACACCTACACCTGCACAGAAAGAAGCC 1380
D R I H A L D G V F P T P T P A Q K E A

1381 TTAATTAATGCTTTGTTACCTCCTGGTTTGTCTGTTACTCCAGGAAGCTAAAGATTGG 1440
L I N A L L P P G L S V T L Q E A K D W

1441 AATTCTATAGTGAGTACTTTGTATGAAAAGACTCATGAAAAGTTACCTTGGCTTCTTTA 1500
N S I V S T L Y E K T H G K V T L A S L

1501 GCGGACACATTAACACAAGTTCACAAGTCCAGTGGCATTGTTGCAGCATATTCTTTGGGA 1560
A D T L T Q V H K S S G I V A A Y S L G

1561 TTGAGATTCACTCAAATAATCATGAGATAGTTTGGGGTTGTTTAAAGTCCCTTATAAGG 1620
L R F T Q N N H E I V W G C L K S L I R

1621 GGACAAGGACTTATATTAGATTTAGAAAAGACAAATTGAAAGACTTCCTAAAGAGGAACGT 1680
G Q G L I L D L E R Q I E R L P K E E R

1681 TGTGAAAAGTCCCAGAYGTTTTAAAAATACTTATATTCTTTTAGGTAAGGATTTAACT 1740
C E K V P D V L K N T Y I L L G K D L T

1741 GGTGAAGGGGCGAGCCAGTAATAGACAGAAGGCAGACGAAAAAAGAAAAAGTGTTCAGTTT 1800
G E G A A S N R Q K A D E K R K S V Q F

1801 CGCGCTAGACAGTCTGACTCACGCAGGCATGCAAGGTCACAGCTTCAAGCAGTACACAGG 1860
R A R Q S D S R R H A R S Q L Q A V H R

1861 GAAGTGACTGAGAATCAGCGTAGAAGGGAAGCTCCATCTAGACCAGTGACTGAGGAATTA 1920
E V T E N Q R R R E A P S R P V T E E L

1921 AGGAGGCAGGAACCCCAAAATCGATATGCCTTGCGCCCTTTCATTTCGTACCCCTGATAGA 1980
R R Q E P Q N R Y A L R P F I R T P D R

1981 TATGGGCAGCCTCGCCAAGATGCGCGACCAAGAGAGAGATCCCAAATTGCTTCGTCTAAC 2040
Y G Q P R Q D A R P R E R S Q I A S S N

2041 AGATTTTCTGAAAGGGAGGGCAGAGTAGAAGAAAGGGTTACAGCATCTGCAGCTACATCT 2100
R F S E R E G R V E E R V T A S A A T S

2101 GCAGCTACACCCGCCCACTAAAAAGGTAATAAGATAAAGAGAACCTCAGATTCTCCT 2160
A A T P A A T K K V N K I K R T S D S P

Gag ORF end ←|

|→ Pol ORF start

2161 GCACCAGAGTCTGTAGAAAAAATAATGAGCAGTAAATGGAGAGTTTAAAATTACAAAT 2220
A P E S V E K T N E Q *

M S S K M E S L K L Q I

2221 ACTGTACAAAGACAATTTTTATACTGGACTTCTTGACACACAAGCAGACATTTTCATTAGT 2280
Underline: Spuma_A9PTase super family (c108397)

L Y K D N F Y I G L L D I Q A D I S L V

2281 ACAACCAAATATTTTACAGGAAGAAATGTTACATTATGTTTCTGTACAACTTTAGAAGG 2340
Q P N I L Q E E M L H Y V S V Q I L E G

2341 AGAAGGGTCATACCCATCTTTTTATACAAATTTAAAGATAAATGGAAAATGTGTTTCTTT 2400
E G S Y P S F Y I N L K I N G K C V S L

2401 AGAATTGGTTGAACATCCTAATTTAGATACACAGTTTCTTATTGCTTTTAAAGATGTAGC 2460

2461 **E L V E H P N L D T Q F L I A F K D V A** 2520
TCATTTTATTCAGATAACTCAGAGTACAGAAACACAAATACCTGATTTAACAATTAAGT
H E I Q I I Q S I E I Q I P D L I I K V
2521 AGATGTTGGATTTCTTATAGAACAACAAATAGCTCAATCTATTGTAGAGAATAAAGATAA 2580
D V G F L I E Q Q I A Q S I V E N K D K
2581 ATTGGCTTTATGTCTTTGTGATCATTTTCAGGTATTCCAGCAATGGGAAAATCAAGCAGG 2640
L A L C L C D H F Q V F Q Q W E N Q A G
2641 ATATAGGAGAGAGATTCTCCATCATATTGCTACGGGAACTGTTACTCCAAAGCGTCAGTC 2700
Y R R E I L H H I A I G I V I P K R Q S
2701 CCAGTATAAGATTAATCATGCCGCAATACCTAGTATTCAAATAGTGATAGATGATCTTGT 2760
RT_like super family (c102808)

Q Y K I N H A A I P S I Q I V I D D L V
2761 TAAACAAGGGATCATTAAAGAACAGTATAGTCAAATGAATACTGCTGTTTATCCTGTACC 2820
K Q G I I K E Q Y S Q M N T A V Y P V P
2821 CAAACCAAATGGTAGTTGGAGATTGGTGTAGATTACAGGGAAGTAAATAAGGTAACCTCC 2880
K P N G S W R L V L D Y R E V N K V T P
2881 CGTAGTTTCTGCTCAAAACACACATTCTGTTTCAATTTTACACGGCTTAGTCCGGAAAAG 2940
V V S A Q N T H S V S I L H G L V R K R
2941 GTTTAAACAACATTGGATCTTGCTAATGGTTTTTGGAGTCACCCCATTGATACAGATAG 3000
F K T T L D L A N G F W S H P I D T D S
3001 TTATTGGATTACAGCTTTTACTTGGCAAGGGAAGCAATATGTGTGGACTCGGCTCCCACA 3060
Y W I T A F T W Q G K Q Y V W T R L P Q
3061 AGGGTTTGTTAACTCCCCAGCTTTGTTTACAGCCGATGTAGTATCATTATTATCTGCATT 3120
G F V N S P A L F T A D V V S L L S A F
3121 TTCTAATATTGAGGTGTATGTTGATGATATTACTTATCCCATGATAGTGAAGAGGAACA 3180
S N I E V Y V D D I Y L S H D S E E E H
3181 TATTGCAGTTCTTACACAAGTCCTAGATACCTTGATAAAGCAGGATACATAGTGTCTCT 3240
I A V L T Q V L D T L Y K A G Y I V S L
3241 AAAGAAATCACAGATCGCACGTAACAAGTTACTTTTCTGGGGTTTGACATTACACATAA 3300
K K S Q I A R N K V T F L G F D I T H N
3301 TGGCAGAGGATTGTCTGATAATTACAAAGAAAAAATTGCTGCAATTAAGACCATGTAG 3360
G R G L S D N Y K E K I A A I K R P C S
3361 TTTAAAACAATTACGCAGCATTATTGGACTTTTTAATTATGCAATGTTGTTTATTCCAAA 3420
L K Q L R S I I G L F N Y A M L F I P N
3421 TTTTAATATTTTAATAGCACCATTACATGCTGCTGTTTACAGAGAAATAAGATCACAACA 3480
F N I L I A P L H A A V S R E I R S Q Q
3481 AACTAAAACCCCCTTTTCAGTGAATATGAAGGAGGAAAAAGCTTTACAAGATTTGTTGAC 3540

RT_RNaseH_2 super family (c139038)

T K T P F Q W N M K E E K A L Q D L L T
3541 AGCTGTAAATAATGATTATTTAACACAAAGAGAGCCTACACAACCGCTATCTGTTTATGT 3600
A V N N D Y L T Q R E P T Q P L S V Y V
3601 TAGTATTTCTTCTGAGGCAGCATATATACGTATTTACAATTCTGCTGAAATTGTTCCGAT 3660
S I S S E A A Y I R I Y N S A E I V P I
3661 TGACTTTTATCCTATGTATTTACAATTACAGAAAGAAAATACTTGCCGTTAGAGAAGTT 3720

V L L S Y V F T I T E R K Y L P L E K L
3721 ACTTACTGCGGTGACGGTAGCTGTGTTGAAGTCTAGAGACTTAGCTCAAGGTCAGAATAT 3780
L T A V T V A V L K S R D L A Q G Q N I
3781 TTATATTTATACTTCTGTTGCTTCACTCGCAACTTTAAAAAAGAAACAATCCCTGAAAA 3840
Y I Y T S V A S L A T L K K E T I P E K
3841 AAGGGCTTTTAAATGTCGATGGTTAAAGTGGTTAACTTTATTCTGAAGACCCCGCTTAA 3900
R A F K C R W L K W L T L F E D P Q L N
3901 TTTTGTGTATGATGCTACGTTACCCATGTTGGATGATCTTCCAACATTGTATAATAGTGT 3960
F V Y D A T L P M L D D L P T L Y N S V
3961 CCAGTGGAAGCACAAAAGCATCCAAGTATTCTATACTTATCTATATTACACAGATGG 4020
Q W E A Q K H P T D F Y T Y L Y Y T D G
4021 TTCAGCAGTTAACTCTAACAAGGAAGGAGTTAATAGATCTGCGGGGGTAGGCATTGCTAA 4080

RNase_H_like super family (c114782)

S A V N S N K E G V N R S A G V G I A K
4081 ATACTCCTCGGATATGAGTTTGTAAAACTTGGCAGCTCCCGATAGGAGATCATTGCTC 4140
Y S S D M S L L K T W Q L P I G D H S S
4141 ACAATATGCTGAGATATATGCATTGGTTTTTGCATTAAAAGAAGCTTTAAGTGATAAGGG 4200
Q Y A E I Y A L V F A L K E A L S D K G
4201 TCCTGTTCTTGTGTTACTGATTCTGCTTATTTAGCACGATCTGCTAATGAAGATCTTCG 4260
P V L V V T D S A Y L A R S A N E D L R
4261 TATATGGAGATCAAATGGTTTTCTCACGGCTAAAAAGAAGCCGTTAATGCACATTGCTAA 4320
I W R S N G F L T A K K K P L M H I A K
4321 ATGGAAGCAATTTCTGCTTATCTCAATTATAAGCCTGATATTGAAATTGTACATGAACC 4380
W K A I S A Y L N Y K P D I E I V H E P
4381 GGCTCATAGGAAGCTTGGTTCGTCTGCTCACACACTGGGTAATCAGCTTGTGATTCTCT 4440
A H R K L G S S A H T L G N Q L V D S L
4441 CGCACAAGCTGTTAGTCAAAAATATGCTGTGAACCAAGTTAAAACCAGGTCACAAGCAAA 4500
A Q A V S Q K Y A V N Q V K T R S Q A K
4501 ACCAGCCAGTCTCGATGCAGAGTTGAATGCCTGTTTGGATGATTCCAGACCTAATCCACC 4560
P A S L D A E L N A C L D D S R P N P P
4561 TGGATATCCAAGAATATATGCATATAAAGTGCAAGATGAACACTGTATTGTCACTATTAA 4620
G Y P R I Y A Y K V Q D E H C I V T I K
4621 GGAAGTTGATTATATCCTTCCACCTAAAGAAGAAAGGGTCCGAATTGCCAATAAAGCACA 4680

Integrase_H2C2 (pfam17921)

E V D Y I L P P K E E R V R I A N K A H
4681 TGCAAGTATTGGTCATCCACATTTGGGACGTGACAATGTTCTTCAAGCACTTAAGAAAAA 4740
A S I G H P H L G R D N V L Q A L K K K
4741 ATATTGGTGGCCTAATATGAGAAAAACGGTGTGATATGTGGTAGGTAATTGTAAACCATG 4800
Y W W P N M R K T V S Y V V G N C K P C
4801 TTTGTTAGTTAATAATCCTAACCATCAAAAGCCACCACATATTGTTAAAGAAATTCCTAA 4860
L L V N N P N H Q K P P H I V K E I P N
4861 CAAACCTTTTGTATCTAATTTATCTTGATCATATTGGTCCACTGCCACCTTCTCATGGTTA 4920

rve (pfam00665)

K P F D L I Y L D H I G P L P P S H G Y

4921 CCTATATGTGTTAGTATGTGTTGATGCCTGTACTAGGTTTACTTGGTTGTACCCCGTACG 4980
 L Y V L V C V D A C T R F T W L Y P V R
 4981 TGCTACGAATTCTAACACCACGCTTAGTTGTCTCAATTTTTTGGTAGGTGCTGGAAAACC 5040
 A T N S N T T L S C L N F L V G A G K P
 5041 AAAGATCTTACACTCGGACGGCGGTCCGGCTTTCACGGCTGTGAAAACCCAAGAGTGGGC 5100
 K I L H S D G G P A F T A V K T Q E W A
 5101 TCATGCCCTAGGTATTAATGGGAATTCAGTCCCCTTACCATCCTCAAAGTAGTGGGGT 5160
 H A L G I K W E F S S P Y H P Q S S G V
 5161 TGTGAAAGGAAAAATGCCGAAATAAACGACTCCTAACCAAGTTGTTGTATTCTCGTCC 5220
 V E R K N A E I K R L L T K L L Y S R P
 5221 CACACAGTGGTACCCATTGTTACCTCAGGTACAAC TAGGTATTAACAATATTCTGCTTC 5280
 T Q W Y P L L P Q V Q L G I N N I P A S
 5281 AAATTCAGGTA AACACCTTTTGAATTGATGTATGGTGTCCAATGAATACTGATTTTGT 5340
 N S G K T P F E L M Y G V P M N T D F V
 5341 TGA CTCTTCTATTTCTGCACCAGGGAGACTAGAACAATTATCTTTTCTACAGGAGTTGCG 5400
 D S S I S A P G R L E Q L S F L Q E L R
 5401 AGACGCTTTGTCTCACCTGCGTACGCACCAGATACCACACATGCATGGACTCCACAGGT 5460
 D A L S H P A Y A P D T T H A W T P Q V
 5461 TGGCCATTTTGTCCAGGAGAGGGTATCTACTATAAAGCCCTTACGACCACGTTGGAAGCC 5520
SH3_11 super family (c139492)
 G H F V Q E R V S T I K P L R P R W K P
 5521 TCCAGCAGAGATTA AAACTGTTATTAATGAACGGACTTTTATTATAGTTGATAAACAAGG 5580
 P A E I K T V I N E R T F I I V D K Q G
 5581 CCGTCAAAGA ACTGTGAGTATTGACAATTTAAACCTGTTCTTTATCTGTGATATTCA 5640
 R Q R T V S I D N L K P V P L S C D I Q
 |→ Env ORF start
 5641 GCATGGAGGAGAAACCACCTCTA ACTTACTCTCAATGGCTGACCATGGCAAATGTGCAGA 5700
 H G G E T T S N L L S M A D H G K C A D
 M E E K P P L T Y S Q W L T M A N V Q
 Po1 ORF end ←|
 5701 CGCAGGAAAACCAGCAGGACATTTTGT TGAATATCAATCGTGTGCCACAGAAGATGTGC 5760
 A G K P A G H F V *
 T Q E N Q Q D I L F E Y Q S C A T E D V
 5761 AGACATCAGGTGAGAAAGAGACTTTCATTGATATACTGATTGCACTAAAATGCCTTCTT 5820
 Q T S G E K E T F I D I P D C T K M P S
 5821 TGAAGCAAAAACATGTCTGTGGATTTTGAATAAGACCCAGTAAGTTTGAGAAA ACTGG 5880
 L K Q K H V C G F C N K T P V S L R K L
 5881 GTTACTTTTTTCTTGCA TTTTTCATCCTGTTGTTGTTAATAACTACAATCGGTGTTGCAA 5940
 G Y F F L A F F I L L L L I T T I G V A
 5941 TTTTTCGCATT CAGTGGTATTTTATCACACAACGTCTCGGAATCACCTGACATGGAATC 6000
Foamy_virus_ENV super family (c104051)
 I F R I Q W Y F I T Q R P G I T L T W N
 6001 AGACCAAATTCATCCAGGTATTGGGAATGCTAAACATGTACATAAAAGAGCTTTGATGT 6060
 Q T Q I H P G I G N A K H V H K R A L M

6061 CTAATAATGTTCTGTGAGTGTACAGGTACAGGACTGGAACAAGGTCTGTACTGGAAGC 6120
S N N V P V S V Q V T G L E Q G L Y W K
6121 CATATCCAACGCCTATTGTGGAGAAGAAGAAAGTCTGGGTATATCCAAGTGGTACTTA 6180
P Y P T P I V E K K K V L G I S Q V V L
6181 TAGACTCTAATATTCTTGCAAAAACAGCTGGAATTGTTTCTGATGAAGGACGTGCTCTGG 6240
I D S N I L A K T A G I V S D E G R A L
6241 TAAAGTTATACCTAGATGACCAGATGAAAAAGGTACAAGCTGTTACCCTGCCATATAAGT 6300
V K L Y L D D Q M K K V Q A V T L P Y K
6301 TGCCTTTACAGGACCACCGGAAACAACAAACATATAGAGAAAAGATGTGTTATGTTTCTC 6360
L P L Q D H R K Q Q T Y R E K M C Y V S
6361 TTGGACATTGTTATTTTGTGGATTTTCAAGGCGTAAGAATCTGGCCAACACCGGAAATAA 6420
L G H C Y F V D F Q G V R I W P T P E I
6421 AGGCTGATCAGTGTCCYCGTCCAGGTACTACACAGGACAAGGTAACATATAAAGGTTATC 6480
K A D Q C P R P G T T Q D K V T Y K G Y
6481 CTATTTTTTATTTGAATACAGGACAAACTACTCAAAAAGGATTTGTCCCCTTCAGAAGGA 6540
P I F Y L N T G Q T T Q K G F V P F R R
6541 ATGACACACGTATTGATTTTTGGGAAGATGCAGAAGAGGAGGAATATCGATTTCTGGAG 6600
N D T R I D F W E D A E E E E Y R F P G
6601 GTGTAAGACCTTATAAAGGTGCTGTTTTTTGTTCTAATTTGCTTTACTCAGAATGGTGGGA 6660
G V R P Y K G A V F C S N L L Y S E W W
6661 AACCGGAATTTTATGATGATGATGGCTATGATGCCTTGATGAAGCAACTACATGTTGAGG 6720
K P E F Y D D D G Y D A L M K Q L H V E
6721 TACAAAATCCGGAACGGGTGAATTAAGAGACAGGCATTACCCCCTGAGTGGCAGGCAA 6780
V Q N P E T G E L K R Q A L P P E W Q A
6781 AAGGACAGAAAAAGTTATTTTCGAGTCTGACGGAATGGGATATCTGTACAATGCCAAGAT 6840
K G Q K K L F R S L T E W D I C T M P R
6841 TTCCCTCGTTTCTGAATACATCGTATTTTAGTCACTCTTGCAAAGCAAAGGTAATCCGT 6900
F P S F L N T S Y F S H S C K A K G N P
6901 GCGGTATTACTTACGAAAGTTTGATAGAACAAGGAATATGTGATCCAAACATTCCTCAC 6960
C G I T Y E S L I E Q G I C D P N I P S
6961 AGGTTTATAGATGCACTTCTTGTTCAATTTTACAATTTGACTGATAACATTTTCAAGT 7020
Q V Y R C T S C S F F Y N L T D N I F K
7021 GGCAGCCTAAACAAATCGACCAAGGATTTTACATTACAGCGGACTTCTGGTTTTTGGT 7080
W Q P K Q I D Q G F L H Y S G L P G F W
7081 GCGTGCAGAAATCTAAATTTGTTAAAACAAATTATACGGTTTACTCCCTGTTTCAGAAAT 7140
C V Q K S K F V K T N Y T V Y S L F Q K
7141 GTTTGACAGACAGCACCATATATGATGTGAAAAGTGTGATAAAAGGTATACAGGATAAAA 7200
C L T D S T I Y D V E T V I K G I Q D K
7201 TGAATGTATATATTGGTACTGATGACAAACCATGTGAGTATATACAGTGTAACAAAAA 7260
M N V Y I G T D D K P C E Y I Q C K T K
7261 ATATCGCTGATATGCCATATGCTGAAGCAGTGTGGGAACAAATAACACATTTGCAAATA 7320
N I A D M P Y A E A V W G T N N T F A N
7321 TACATTATCAAAAACATTACAAAAAAGTGATGAATGTGAAAATGTTTTGTTAACGA 7380
I H Y Q N N I T Q K S D E C E N V L L T

8641 CTAAAGGTAACAAGTTCTGAAGAAG**ATGA**ATGCTGCAGCTTTTGACAGGCTCATTAGAAA 8700
P K G K Q V R R R *
M N A A A F D R L I R N

8701 CATTTTTAATACACCTGTTTTAACTTCCAGGATACTGGTGGATGTGTGGACACACTTCT 8760
I F N T P V L T S R I L V D V W T H F L

8761 GTTGGGTGTGGAAGTTAGAAAGAATCAAGATGTAGTAACGTATGACCTGTCTTACCGTTG 8820
L G V E V R K N Q D V V T Y D L S Y R C

8821 CGAGATATGTAACACCAAATAAGTGACGTTAATAATCCTTATGTGTTTGATGATCTTGT 8880
E I C N T K I S D V N N P Y V F D D L V

8881 AGGATTAGTCGTAATCCCATGATATCACAGAGATATTGGGACATTCTTTGGAATCATT 8940
G L V V I P M I S Q R Y W D I L W N H Y
| → Acc2 ORF start

8941 TAGTCACTGCA**ATG**ATACATCCTCACAAACCGAATTGCAAAGCCTCCCACAGAGTCC 9000
S H C N D T S S Q Q T E L Q S L P Q S P
M I H P H N K R N C K A S H R V

9001 CACGGAGACAGAATCTCAAGGTTCAAGGAGACAACAGAGTACTCATATCTACAACGTCTC 9060
T E T E S Q G S G D N R V L I S T T V S
P R R Q N L K V Q E I T E Y S Y L Q L S

9061 CAGCGGTGAACAAGATACAGACGCCAGTGAATATGAAAGATTTTCTATATCACCTCCCAT 9120
S G E Q D T D A S E Y E R F S I S P P I
P A V N K I Q T P V N M K D F L Y H L P

9121 TACAATCAGTGGGTCCGTTACTGATTCTGACACCGAAGGGAACTTTACTTTGAGGAATC 9180
T I S G S V T D S D T E G N F T F E E S
L Q S V G P L L I L I P K G I L L S R N
Acc1 ORF end ← |

9181 TCAAGACCAATTACATTTTTYTGCAACTCATGGGTTTCGAGGAATTTTT**TAA**TCCATCGT 9240
Q D Q L H F L A T H G F E E F F *
L K T N Y I F W Q L M G S R N F S N P S

9241 TCTTTGAATGCGTCAATAAAGACAAACAAATTTTCCAATTGATATTACAACTAAACAAG 9300
F F E C V N K D K Q I F Q L I L Q T K Q

9301 AAGGACTTCTTAATATTGTAAGCCATGGAACTTTGGTTGCACAGTTTTGCTTGCTTGCA 9360
E G L L N I V S H G I F G C I V L L A C

9361 ATGGACCTCCTCATGAGACTTGTGTTGGTGGGATATGGAGAAATACTTTGTTGCATCTGT 9420
N G P P H E T C E G G I W R N T L L H L

9421 ATACAGAGTCTTATGCATTTTCAGTTGGGTGATTTTTATCAATTGCAGAGTTCTCATGAAA 9480
Y T E S Y A F Q L G D F Y Q L Q S S H E

9481 ATATAACTTGTGATCATGTATGGTGTTCACATTGTAATGTTTTGTGTTTCATGAAATCG 9540
N I T C D H V W C S H C K C F V F H E I
Acc2 ORF end ← |

9541 CGGAAACACCTTTCTTTTTCTTTTCCACCAATAGATTTAGAATGTGG**TGA**TTCTAATTTT 9600
A E T P F F F F I N R F R M W *

9601 GTTGATTAATTTAAGTTAATGTTATTAGCTGGACCAAGTAATCATAATTTTTTTGCCCA 9660
3' -LTR

9661 GCTAATGGAGAGGGAC**TGTTACAGGCCTCAGTAGAAGTTAAGGTTAATGACTATTACAAG** 9720

9721	TCTAAGTAGAAGTTAAGGTTAAGGATTTAACTACGCAGTACTAGTAGTTTCTGTTACATA	9780
9781	AGATTTTTTTATGTTTTAAAGATTAGAATGTTTTGGTTATTCTGTAAAAATGATCAACAG	9840
9841	CTTGGCCTTGGTGATTTTCCTCTCCTGATTTTCTTCTGAGTTTTTTTTATGACCGTTAGTA	9900
9901	CTCTTTTTGAGGTAGCGATACGCAGGTCTAGTTACAAAATCTTATATATATGCAGACCTT	9960
9961	TGTTTATACTCTGGGGCAGACCGAGAGACTGAAGCTAGACTTCATATCGAGACTGACTGG	10020
10021	TATGTTTATTTTTATTTTTATGCATATAAGTTTTAACAGGCATTCTATGTTATACTCTG	10080
10081	TTTTAATTTTGGATTCCTGTAATTTTTATTATTTTCAATAAATAATTACTATGATGAAT	10140
10141	TCTCAGTCCTTTCTTATAATTGTGCTCACGATTTTCATCTATTGAATGTGAGACCTATCCA	10200
10201	CATGTATAAAATTGAAATTTGGTAACTTATCACTTAGGGTGGAGAATAACCTCTTTTTAA	10260
10261	GACATTACATGGGAGGAAAGGTGTGAACCCATCACA	10296

>ERV-Spuma . a -Ame

5' -LTR

1	TGTCATGATTTACAAAGGTTACAAACGAGTTAAGGCAGGTGTGCCACAGACTTCCTAACC	60
61	ACAGATTAGCAGCCGTTGGTCTTCAACGRCTTAATGCCTTGAAAATACACGTGGTCTTGA	120
121	CACCATCATAGTAATAAGCTATGGATGTTCTTTGGGCAAAAAACACTCATTACACACAAA	180
181	TGCAAGTGTGGCTTTCAAGAGACAGAATCGGACACTAACTGTAAACCCACAGGCACCTTGC	240
241	CCTTAGGGTCAGCTAAAGGGGAACAGTTTCTCCTTAAGCCAGCCACAAGTATCAGCTTC	300
301	CTGTGTTAGATGGRCTCGTAGCAGAAAGCAGCCATAGACAGGAAGCAGGGTACCAGAATA	360
361	CATGTGTGGTTAAAGCGTCAAAGCAATAGTCACATTTAAACCCCTTCAGAAAACGCATT	420
421	CAATATAATGGCATTTCGAAGTAGGCCAGAAAAAATACAGCACCTTGCCTGTTCTTCGAGC	480
481	GGAAGGCCATGCATTTCAATGGAATAATCAAGAAGCAAGGACATCACCTTTCACCTGGG	540
541	TTCTCACATAGGTAAATAATGTGTGCACTGCAAACCGAAGTATAAGAGCAGATTACAGACT	600
601	CTAGACTTTCTCTCCAGATCGAGGAAGTGACGCACATAGTACATGTAGGCTAAGTCACGG	660
661	GTGTTAATATAAAAAGCACAAACAGACTAAGGCTDAGCGAGATTCCCAGCAGGCAGCAGGCA	720
721	GACCAHAAGATYGTGGGGGGTGGGAAGAGCADKYGMTAGCAGGTCGGAGCAGCAAGCCC	780
781	WGGATACCGTGAGTTTTAAGTGTGTTGGTTGAACCTCTYTTGCATATGTTAGACTGACGG	840
841	CGTGTTTTATTATGTCACTCCACTCCTGATCATACCATAGTATAGCTTAGACAAACATAA	900
901	CATGAACTCCATGATTGCTCAAGCTGGTGTTCAAAATGATGAATTGACTTTATCTTTG	960
961	TTAAATGCAAATCATGCTTATAGCTTATGCAACAATGCTTTTTCTCTATCTGACAGTATG	1020
1021	CTATGTTTTTACTGCGTTAATTATAGCAGGTGTAATGATGATCAAAGCTGGTAGAGAACA	1080
1081	GAAGTGATATTAATATATTGACTTGCTACCTTCAAGTGTGAGCTTCATATTTCTGAGTA	1140
1141	ATGCTTCATAATGAGGTCTCTYTGAGTCAAAASGAACTACACAATATTTCTGGCTGTAT	1200
1201	TTTGGTCAATTATGTCAAGGGGTGCAAACACTCAGGGAACTGTCAAAGCGCTAGGCCAA	1260

1261 ACCCCTGAGGCGCCTCTCATATAAATTAAGACTTTTGATTCTGTGCCCACTCCACACAG 1320

1321 CCCTACCTAGGGTSGAGGGRGGGGGCAGGAATCACGCCCTAAGGGGCAATCAAGTCAGA 1380

1381 TGGCACCCCAAMAGATGGGACGTCTTAGAGATGACCAGAGCATTACTAATATTTAAATA 1440
|→ Gag ORF start

1441 ACCTC**ATG**TCCCAGTCACGGGAGAAGGACAGGGCAGAAWTTTTTTTTTCTAAAAASGTTT 1500
M S Q S R E K D R A E X F F S K X V

1501 TTTTAAATAAGAGGTTAGAGTGCCTACAGAAGATGGCGCACAATGAAATCAATATTTCCA 1560
F L N K R L E C V Q K M A H N E I N I P

1561 TCCATTGCAGAATGGCTCTATATGATTGGCTGAGAGCTGCGCACTGTCATGCAGTGAACA 1620
I H C R M A L Y D W L R A A H C H A V N

1621 CAAATTTACAGTAGCAGTGGCGCAACTTGGTGGACTACCAGCAGAATCACTCTTTACTT 1680
T N F T V A V A Q L G G L P A E S L F T

1681 ACTTAAAGACCCAGCTAACAGGACAAATAATGTATATGCAACTCTCCTAGTGAGRGGAG 1740
Y L K T P A N R T N N V Y A T L L V R G

1741 ACTTAGACACCATTTCAGTATCGCCATACAGTATCCTGAATTGGCTTTAACACATACAA 1800
D L D T I Q Y R P Y Q Y P E L A L T H T

1801 ATCATGTCAACTGGTTTGGAGGTAATCTAGTTTACCCACAAACAGGTGCAAGGCATGGCC 1860
N H V N W F G G N L V Y P Q T G A R H G

1861 CATTAGCTACACCAATCTGTCACTAGAATTCTTAGCCCGTTTCATCCAAACCGTGGAG 1920
P L A T P N L S L E F L A R F H P N R G

1921 GTCCATTTTTGCAGGCTGACTACCAATTGTTAGCCACCCACTTTGACACAGTGCAGAAACA 1980
G P F L Q A D Y Q L L A T H F D T V R N

1981 TTGCGCTGCAATATGCAGCTCAGCAGGTATAGCACCTGCGCAGCAACCTCAAGGACAGA 2040
I A L Q Y A A Q Q G I A P A Q Q P Q G Q

2041 TGGATGCAGGTGGGGTACAACACTACAGACATTGAGAATAATATTGGGATCCTGTCCATCCA 2100
Gag_spuma super family (c126624)
M D A G G V Q L Q T L R I I L G S C P S

2101 AGAATGAAGACATTCCAAGTGGTATTAGAAAAATTAGGACAATTGCAAGCTGCTTATC 2160
K N E D I P K W Y S E K L G Q L Q A A Y

2161 CACAAGTAACTCCCAGCACAGACACAGGGCCCTAGCTATGTTTCTTCCATCTGGCTGCA 2220
P Q V T P Q H R H R A L A M F L P S G C

2221 CACCGCCTCTAGCGAGCTGTGACAGCTGGATCTCAATCTATAGCTGGCTTTATTTACAGC 2280
T P P L A S C D S W I S I Y S W L Y L Q

2281 TGATAGGCACGCCGTCCATCACATCACTAGCACTGATACTAGCTGACATCATGGGAACAC 2340
L I G T P S I T S L A L I L A D I M G T

2341 AAGGCGCGCCGAGCCATGAATCTAGGCCTGTCTATAGCATCTAACAATTATCAATGG 2400
Q G A A A A M N L G L S I A S N N Y Q M

2401 TTGAGAGCATAATCCTACCCTTATTAAGGAGAGCCTGCAAGGTTAGAAGTCCATAGAA 2460
V E S I I L P L L K G E P A R L E V H R

2461 AATTGTCCCAATTAATGAGCAAGAAAAAAGGGAGCAATTTGGAGACATAGTGACATCCA 2520
K L S Q L N E Q E K R E Q F G D I V T S

2521 CCTATCAATCATTGGGCAGGGATCACTTGGGCAGAAGACCAGCAGACACACAGAAAAAGG 2580

T Y Q S L G R D H L G R R P A D T Q K K
 2581 GTAACAAGGATCTTAAGCCAGATAAAGGACACACACCATGAAGGGAGATCCTCGAAAGGAC 2640
 G N K D L K P D K D T H H E G R S S K G
 2641 GGGGATCATTCCAGGGTAAAAAGGGCAATAAGCCACAGAGGGCGCAATTGTCACCCATAG 2700
 R G S F Q G K K G N K P Q R R Q L S P I
 2701 AGGAAGAAAGATATCCAGAGCATGGGCATAAAAAATGAGAAATCTGCAGGAGATAGGCAGA 2760
 E E E R Y P E H G H K N E K S A G D R Q
 2761 GCCCGCAGTGGCAAGGTAACCACAGGGGTAGACGGTCCTGGGGTAAGACCGGGGGCCAGT 2820
 S P Q W Q G N H R G R R S W G K T G G Q
 2821 CCCATTTTAGACCTACTGACTATGATTTTAGAGACAGGAAACACATGAAAAGTCCCCAGA 2880
 S H F R P T D Y D F R D R K H M K S P Q
 2881 AGTACGGCACTGATGAGACTTCATCTCCTTCCCAGCAGGCACGAACACCAGATCGTTCTA 2940
 K Y G T D E T S S P S Q Q A R T P D R S
 2941 AGGCTGAGGGGAAGGAAGTGAAGTTGAGAAAAACACACGGCAGCACTACAGTTTCAC 3000
 K A E G K E V K V E K K H T A A L Q V S

Gag ORF end ←|

|→ Pol ORF start

3001 AGA**ATG**CAGAGTCCACGCACTCATCGCATCGTTCCCAAGACT**TAAG**CGACACACTGATTGG 3060
 Q N A E S T H S S H R S Q D *
 M Q S P R T H R I V P K T K R H T D W
 3061 ATTGAGGTCTATTAGACTCTGGGTCTGACATTTCCATATTTGAATGCAGCCACAAGGCA 3120
 I E V L L D S G S D I S I F E C S H K A
 3121 CTATTGGAGCACACAAGGGCACACAGGAATGCACAGATCACTACTCCCACTGGGCAGACA 3180
 L L E H T R A H R N A Q I T T P T G Q T
 3181 TTGGCACATAATGAAGTGTATTTTGTAAACAATTCAGCTAGAAGGCGAACACCCCAAAAAG 3240
 L A H N E V Y F V T I Q L E G E H P K K
 3241 ATTGAAGCACTATTTTGGCCACAGCTACACATTCAATATAAAGGGCTGTTAGCATTTCAA 3300
 I E A L F W P Q L H I Q Y K G L L A F Q
 3301 GACTGGCCACCTTTGTATGTAAGGCAAGCACCAAGGGGTGAAGAAGTGGTAATGCCTGCC 3360
 D W P P L Y V R Q A P R G E E V V M P A
 3361 TTTTCAAAGAGGTGAGTGGGGAATAATGCAAAAATATGCAAGAAAATGGTCAGCGCTG 3420
 F S K E V S G E L M Q K Y A R K W S A L
 3421 GCAGCAGTGCAGCTGTTTAAAAATCATGTAGGGCATGATAAAGAATGTCCAGCACATGTG 3480
 A A V Q L F K N H V G H D K E C P A H V
 3481 ATTCCAGTGCTGAAACCACCCCGCCACAAAGCAGTATCCAGTTAAACCACAGGCAGTT 3540

RT_like super family (c102808)

I P V L K P P P P Q R Q Y P V K P Q A V
 3541 GCCCACATGCAAACCATAGTAGACCAGCTAATGGACCAGGGAGTAATCATAAAGCAAGCT 3600
 A H M Q T I V D Q L M D Q G V I I K Q A
 3601 AGCCACATAACAGTCCCKGTGCTCCCAAGTTTAAAAACCTGATGGTACCTACCGTTTTATT 3660
 S P H N S P V L P V L K P D G T Y R F I
 3661 GTAGATTTTGAATTTTGAATGCACATTGTAAGACAGAGGCCGTCCAGAACCAACACAGT 3720
 V D F R I L N A H C K T E A V Q N Q H S
 3721 TCTGGATTGCTAGCCAACCTTACACAGATGCAAAATATAAAAACAAACCTTGATCTAGGCAAT 3780

S G L L A N L H R C K Y K T N L D L G N
 3781 GGGTATTTACACAACCTTTAAGTGTAGAAAAGCCAGAAATACACTGCATTACKTTTAAAG 3840
 G Y F T Q P L S V E S Q K Y T A F T F K
 3841 GGAACTCATTTCAGTTCACTAGAATAATGCAGGGGTATAAAAATTCACCTAGCACATTC 3900
 G T H F Q F T R I M Q G Y K N S P S T F
 3901 TCAAGCAGAATACAGAGCTTACTTGCAGACATTCTAATTGTTGGCAGTATGTAGATGAT 3960
 S S R I Q S L L A D I P N C W Q Y V D D
 3961 ATTTACATCACCCATGAGAATCTCAGTGAACACTTGAAGAAGTAGACAGAGTCATTAC 4020
 I Y I T H E N L S E H L Q E V D R V I H
 4021 ACGTTGGCTGCAAAAGGATACCTGATTAATTTYAAAAAATCAAGAATAGCTCATCGTGAG 4080
 T L A A K G Y L I N F K K S R I A H R E
 4081 GTTACCTTTCTGGGATTCACTCTTTCAGATGAGGGCAGAGGGTTGTCAGCAGATTTTCTT 4140
 V T F L G F T L S D E G R G L S A D F L
 4141 GAGAAGTGTGCCAATATAAGACCGCCACTACGCTTAGGCAGTTACAGGCCATTCTAGGG 4200
 E K C A N I R P P T T L R Q L Q A I L G
 4201 CTGTTAAATTTTGGCAGATCGTATGTTTCTAATTTTGGCTGAGCTAGTGAAACCATTGTAT 4260
 L L N F G R S Y V S N F A E L V K P L Y
 4261 GCTTTGATAAAACCAAATTTCAAGGCAGCTCACTGGCTGCCAGAACACACTCATATTCTG 4320
 A L I K P N F K A A H W L P E H T H I L
 4321 CACCAGGTATATTCATTAATGACTCACACTGGTCCCTTTGCAGGACAGGAATACAGATAAA 4380
 H Q V Y S L M T H T G P L Q D R N T D K
 4381 GACTTAGAGATAAACCTTGTGGTGGGAGACAATGCTTTCACATACACAGTGTGCAATCTA 4440
 D L E I N L V V G D N A F T Y T V C N L
 4441 GGGGAGACTAAACCAATTGCATATAAGTCACATGTATATTCACACCTGAGTTAAATTT 4500
 G E T K P I A Y K S H V Y S T P E L K F
 4501 ACACCTGAGGAGAAAATTCTGGCTTCAGTTCAGATGATTATTCAGAAAGAGAGACCACTG 4560
 T P E E K I L A S V Q M I I Q K E R P L
 4561 GCAGCAAATAGAACCATACATAAACACACCTTTAGCTCAACTAGAAGCTGCCACAAAA 4620
 A A N R T I H I N T P L A Q L E A A T K
 4621 GCTAGCGTCCCAAATGCAAAAGCATTACACACTAGATGGATTCAATGGTCAGCATCTCAA 4680
 A S V P N A K A L H T R W I Q W S A S Q
 4681 CATGCTCCAGATGTAAAGTACCATTATAAGGCAGAATTGCAAAGACTGAGTGGATTGAGT 4740
 H A P D V K Y H Y K A E L Q R L S G L S
 4741 TGGACAATGGACACAGAGCCAGACATCTCACGGCCTGACATACCATTGTTTGTATTTTTC 4800
 W T M D T E P D I S R P D I P L F D F F
 4801 CAGGTGATTTACTCAGATGGGTCAGCTATCCCAGCAGTGGGGACACGGTCTAAGTACGCT 4860
RNase_H_like super family (c114782)
 Q V I Y S D G S A I P A V G T R S K Y A
 4861 GCCGCATGCGCAGCAGTCGTAGGATACTTCACACATGAAGAAGAATTTATACATACTGAT 4920
 A A C A A V V G Y F T H E E E F I H T D
 4921 ATTGCAACCAAGCACCTGGGAGACATGTCTGCCAGACTGCTGAATTGCATGGGTTACTA 4980
 I A T K H L G D M S A Q T A E L H G L L
 4981 CTTGCATTGCGCCAAGCAGATTCAGGGAAGCCCACTCTAGTAGTCTCAGATTAGATTAC 5040
 L A L R Q A D S G K P T L V V S D S D Y

5041 ATTGTCAGGGCTTATAACACTGACTTGCATTGGTGGATGCAAAATGACTTCAAAGACATT 5100
 I V R A Y N T D L H W W M Q N D F K D I
 5101 AGGCATAAAACTATTGCTTCCAGGCAGCTCTGGAAGCAGGTTTGGGATCTTAAACAGACT 5160
 R H K T I A S R Q L W K Q V W D L K Q T
 5161 TGCCCTTTACTATGGGTAATGCACACAAGAGCACATACCAAAGGGCACATTCATAGCACT 5220
 C P L L W V M H T R A H T K G H I H S T
 5221 GGCAATGCATTGGCAGATAAATATGCCAAAGAGCACACAGTGAGAAAAACAATAGCAGCC 5280
 G N A L A D K Y A K E H T V R K T I A A
 5281 ATAACCTGCTCAGCGACTGCAATGGATGAGGAAATAAAAGAGGCTTGTTTAGGTATTGTA 5340
 I T R S A T A M D E E I K E A C L G I V
 5341 CCTAGGCCAAAAGGTTTCCCCAGTAATTATATGTATGACATTGAAAATAATAGAGCAATA 5400
 P R P K G F P S N Y M Y D I E N N R A I
 5401 GTCACAATCCCTATGAAAAAGGGGATCCTATTCAAAGATTAATACCAAATAGAGCAGAC 5460
 V T I P M K K G D P I Q R L I P N R A D
 5461 AGGGAAAAGCTGATTGCAGCCACACACGCTGGACTTGCATCTACCCATTTTGGGGTGAGT 5520
Integrase_H2C2 (pfam17921)
 R E K L I A A T H A G L A S T H F G V S
 5521 GCAACTGCACAGCTGCTCCTTGATCGCTTCTGGTGGCCAGGGCTTCGACAGCAGGTGAAA 5580
 A T A Q L L L D R F W W P G L R Q Q V K
 5581 ATATATATTGCAAAGTGTGACACATGTTTACAGACAAGTGTGGACCACAGCAAAAAACCT 5640
 I Y I A N C D T C L Q T T V D H S K K P
 5641 AAGGAGGTTCTTTGAGAAAGGCAGCCTCGCCCTTTGAGATCCAATATATGGACCATATA 5700
rve (pfam00665)
 K E V P L R K A A S P F E I Q Y M D H I
 5701 GGCCCACTACCAGCAGTAAACAAGTACAAGTACATTCTAGTAATAGTAGATTCTTGCAGT 5760
 G P L P A V N K Y K Y I L V I V D S C T
 5761 AGGTTTACCTGGATGATTCTCTCAAAGAAAAGCAGACTGCAAATCAGTCATACAGGCACCT 5820
 R F T W M I P Q K K A D C K S V I Q A L
 5821 AGGACTGTAGTAGCCATGACAGCAACTCAAACGTTCCATGCTGACAATGGTCCAGCTTTT 5880
 R T V V A M T A T Q T F H A D N G P A F
 5881 TCGGGGCGGGCCCTGAAGAAGGCATTAGAGGCATGGGGAACAGAGATGCATTTCTCACAC 5940
 S G R A L K K A L E A W G T E M H F S H
 5941 CCATTCTCGCCGAAATCGAACGGAATTGTGGAGAGGGCAAACCAAGTCTGTAAAAATGGGC 6000
 P F S P K S N G I V E R A N Q S V K M G
 6001 TTGACTAAAAGCATTCTGTCTTGGGGGGAACTGGSTAGACCATGTGCCTTTAGTGATC 6060
 L T K S I L S L G G N W X D H V P L V I
 6061 AGGAGTGTGAATAATTTACCACGCCAGTCTCTATGCAACGGTAAGACCCCATTTGAACTC 6120
 R S V N N L P R Q S L C N G K T P F E L
 6121 TTGTTTGGGAGAAAGATGTATATGCCTGACCTGCATGCTCTTCCAGCCCCATACCCAGG 6180
 L F G R K M Y M P D L H A L P S P I P R
 6181 AACGAGCAACTGCTGGCGACAACGCTGCTGAGGGAATCCCTCCAGGTGGAAGCTGCTGAG 6240
 N E Q L L A T T L L R E S L Q V E A A E
 6241 GCCAGTCTGAGAACACTCTCAAAGCAGGAGATTGGGTCTGGAAAAGATCCATGACAAG 6300
 A S P E N T L K A G D W V L E K I H D K

6301 ACTCCATTTGGCCCGTCTTACAGACCAGCAGTGCAAGTAATCAGAGTGAAAGGTTCCAGA 6360
T P F G P S Y R P A V Q V I R V K G S R

6361 ACTGCCATCCTACCCGCAATACCACCTAAGAGAGGTAAGGCAAGTTTCTGTGGACCAC 6420
T A I L P A I P P K R G T R Q V S V D H

Po1 ORF end ←|

|→ Env ORF start

6421 CTAAAACCTGTGCCAGATGGTTTCCGCAATGTTTCCACGGAACCTCCCTCTTCCAAGTGA 6480
L K P V P D G F R N V S T E P P S S K *
M V S A M F P R N L P L P S E

6481 GGAGCCCACGGAAGATGAAGAAATGGAGATCCGGCAAATGATGATGATAGGTGTGCAAGA 6540
E P T E D E E M E I R Q M M M I G V Q D

6541 TGGGGAAGAATATGCCACTCTTGATTACACGTCCACAATTCAGGAAAGTACTGCAAGTCT 6600
G E E Y A T L D Y T S T I Q E S T A S L

6601 GCCAATTTGGAACAGAAAGCCTTCCAAGTTGCTAAAGTGATGAAAGAATTCTTTGGAC 6660
P I W K Q K A F Q V A K V M K E F F W T

6661 AGACTTCCTAAAACGGTGTATAAAATACTGGCAGTGTATTTCTCCTACTGTGGTTCAG 6720
D F L K R C Y K I L A V Y F L L L W F S

6721 CCTCATTTTATTCTTCATCTCACTGACTTCTGGGCATTTTCTGAGCAAGGTTTCCACTCC 6780
L I L F F I S L T S G H F L S K V S T P

6781 ACCTGTAAGCAAAGAAGTTGTTCTAAAGCCTTTAAGTTCTTACACATGTTAGAGAAAAG 6840
P V S K E V V L K P L S S S H M L E K R

6841 AGAGCTCCCAGAGCCAGGAECTCCAGTCTCAATACAAATGTTTCTCTAACTATGGGTCA 6900
E L P E P G T P V S I Q M F P L T M G H

6901 CGTGTGGATGCCATCATTCAAGACCTATAATGGCCAGCAACACAGCTACAAGTCCACAC 6960
V W M P S F K T Y N G P A T Q L Q V H T

6961 CTTTTCTGTGATTGATGAATCCAGACTGTTTGCACCCAGTAATCCTGTGTCTAGAACATA 7020
F S V I D E S R L F A P S N P V S R T Y

7021 CAGAGAAGTGTAAAGAACTAGGCTTCAGACATTTGCACAAAATGCATTATTTGATGTGTT 7080
R E L L R T R L Q T F A Q N A L F D V F

7081 TGATGATGTGGAGGACCTCCATGAAATGGGGCCCCATGTGTGTTATGTGCGATATTACAA 7140
D D V E D L H E M G P H V C Y V R Y Y N

7141 TGCCTTTTTACTTGTCAAACGTGAGCCAATCTGTGGCCTAAATACACATTCTGGGAACA 7200
A F L L V K R E P I L W P K Y T F W E H

7201 CTGTGCAGTGCCTTTCCAAACTGATAGTCTGAATTCAAAGCACAGTTCCCATATATTTTC 7260
C A V P F Q T D S P E F K A Q F P Y I S

7261 ACTGAGACCATATCAAGCAGGGGATTACATGTTTAAAATCAGTACAAATCCCTCCTGA 7320
L R P Y Q A G D Y M F E N Q Y K F P P E

7321 GCCACATGATGCACAACATATGTATGTTGCAGATTCAGTCATCTTTGACAGAGAATACTT 7380
P H D A Q H M Y V A D S V I F D R E Y F

7381 TGCAAACATGACTGAACAAACATGGCGGGGAACTGTCCCTCTATGGTCTACTTGGGGTCA 7440
A N M T E Q T W R G T V P L W S T W G Q

7441 ACAGATATGGCAAATTAAGGGGTTACACGTTAGATATGGCTTGTAGGTTCCACATTT 7500
Q I W Q I K G V H T L D M A C R F P H L

7501 AATGTATTTCTTAAATTATACGCAGTTCAGACCACTTGAGCAATAGGAACCTGAGTTT 7560

M Y F L N Y T Q F Q T T C S N R N L S F
 7561 CTACCCTGAATGGGAGAAAACAGAAGGTGAGTTCTGGAGTGCCTATAGAGAAGCAAA 7620
 Y P E W E K T E G E F W S A S Y R E A K
 7621 AGAACGCAATGGCACCAAGCATATTACTTATGCATCAGGGGGACCTGTGTTATGGGCGGT 7680
 E R N G T K H I T Y A S G G P V L W A V
 7681 TCAAGCAAATGAATGCAATAAAAGAAAAGCAGGACTCAGTGTGGGCCCATATAGGGCTTG 7740
 Q A N E C N K R K A G L S V G P Y R A W
 7741 GAACTCCATAACACCTCCCTGACACAAGCTATATCAATAGGTAAGCTGTGCCAAGGAAT 7800
 N S H N T S L T Q A I S I G K L C Q G M
 7801 GCTTTCACAATATCACCTGAGTGAGGTGATACAATCTCTAGATAACTTCATAAAAGAAGA 7860
 L S Q Y H L S E V I Q S L D N F I K E E
 7861 GAATTGGACAGCTATCATGCAGTCAGCTGCTGGTCTGAGGCGCACCCAAAGTGGGCGTGT 7920
 N W T A I M Q S A A G L R R T Q S G R V
 7921 CAGGAGAGCAGCTACCTGCACCACCTCTGACCCTAGYGTACCTTGTGAGGTGGGACAAGC 7980
 R R A A T C T T S D P S V P C E V G Q A
 7981 ATCCATAACAGGAAAACTTACACTTGGTCACAAGCAATAATGCAAATCCTGCAAAGTGA 8040
 S I T G K T Y T W S Q A I M Q I L Q T E
 8041 AAGTGAGGCAGTACAGCGAGGATTTTCATGTTTCAGATGCTAATGATCAAGCGCTACAACA 8100

Foamy_virus_ENV super family (c104051)

S E A V Q R G F H V S D A N D Q A L Q Q
 8101 AGGCTTCTATGCGCTAAGAGATGTCATAACAGATGTTGTGGGTTTGATTCAAATGACTT 8160
 G F Y A L R D V I T D V V G L I Q N D L
 8161 ATCTATCATTAGAAACGACCAAGAGGCCTCAGTAAGTCTTTCTGTAGTAAGTATTTTTT 8220
 S I I R N D Q E A S V S L S V V T D F L
 8221 GGACACTCTCAGCAGAGGAGTCCCAGATTGGAATGTGATTTTCATGGCCTGAACAAATACA 8280
 D T L S R G V P D W N V I S W P E Q I Q
 8281 GGCACCTAACTTGTCCAAGGTTGCAACACGCCAGGCAATGTCCGGCTCCACTTTCTTATT 8340
 A L N L S K V A T R Q A M S G S T F L L
 8341 GCTTAGTGTGTTAGCAAAGAGTGTAGTGGCAGCATCTGCTTGGGCGTCAGGCTCCACAAA 8400
 L S V L A K S V V A A S A W A S G S T N
 8401 TTGGATAGTGCACGGGGTACTAGACATTCCCATTCAAACAGCACCTCTATCATATGTCA 8460
 W I V H G V L D I P I Q T A P S I I C Q
 8461 AGAATTACACTCTTGGGGTAATGTACATTGGGTGAATGATACGTGGATCAGAGAAGATTA 8520
 E L H S W G N V H W V N D T W I R E D Y
 8521 TGTGGTACCATATTCACATGCATGTGTGTCATCAGCTAGGCCTGAACTGACACTGTACTC 8580
 V V P Y S H A C V S S A R P E L T L Y S
 8581 ATTACGTGATTGCAAAGGTTCTACTAGAATAATGTGTGAACATGCTGAGCCAGTGAATTC 8640
 L R D C K G S T R I M C E H A E P V N S
 8641 CTGTGACAGTAACTCGAAATGCACACTGCATATTGCACCAATTGACTCATTCTACTGTAA 8700
 C D S N S K C T L H I A P I D S F Y C K
 8701 AGCACATAGATTGCAAATGGTTCATATTTGGTGCATTTCAACCAATCTTGCTGTCATGT 8760
 A H R L Q N G S Y L V H F N Q S C C H V
 8761 CCCAATAGGAATACCAACTCTGATCACCGTAGGCACACAAGTTAAATGCTGTGGGTTTCAT 8820
 P I G I P T L I T V G T Q V K C C G F I

8821 TTTGGATCCACCTAGCCCATTTCAATTGAAATCATTACACTGGCCTGGCTTCAATTTACA 8880
L D P P S P F Q L K S L H W P G F N L Q

8881 AAAAATTGAGTACCCGAAATTGAGTTTATACATAGCAAAGCTGTAAAAATGCGGTTGGA 8940
K L E Y P K L S L Y I A K L L K M R L E

Env ORF end ←|

8941 AGTGTGAAGTACTGAAGATACTATCTGCAAGCACACTCCGCTGTGGTCAAACAGATTGC 9000
V *

9001 ATCTCTGCTAGGCTCCGAACATACAAGGCAGGAAGCCTTGCACTCTCTGATTGACAGCTC 9060

9061 ACAGTTTAATGGGGCCAATACTGGCCTTTCTGCAATCACTAAAGTAGCTTCGAGTCTCCT 9120

9121 ACATAAAGGGCTGATTGCCTTGACACAGTCATTAGAACATTGACTTCGTCGAGTGCTTG 9180

9181 GTACAGTTGGCTGCTGATAATACCTGGACTTTTTCTCATATTTTGCTGTAGACACTGAAA 9240
|→ Acc1 ORF start

9241 ATTATGACAAGCCACAGAATTACGGCCCTGGAAGCAACCCGTCTCCGGTACAGAACAGAG 9300
M T S H R I T A L E A T R L R Y R T E

9301 CTGTGCAGACGTATGGGATATGAGCAGTGTTCCTGTTTCAAAGCATTATTTTSTCA 9360
L C R R M G Y E Q C S L F Q K H F I X S

9361 TTRACCAGGAAGAARTCTACYGTGTCAGCCATCGCTAAGTGCYGAGTSTGTACCARGAR 9420
L T R K K S T V S A I A K C X V C H Q E

9421 TCATTGCTTGMAAGAACGTGGGAGTYRCAGCSTCRCCTTCTAGACTGCCACTGTGGCKC 9480
S L L A K N V G V X A S P S R L P L W X

9481 AATAGAATCTCCAGGACATTGGCTGTGCATAGAGACATTTGYGGMATTGAGAGTACTTC 9540
N R I S R T L A V H R D I C G I Q R Y F

|→ Acc2 ORF

start

9541 CCACAAGTATTCTATTGTGAGTTCATTGAGAGTCCCTCTGACACCRGCGCTGATAATGGG 9600
P Q V F Y C E F I E S P S D T X P D N G
M G

9601 GKCATGCCAGAGCAAGAGAACTGCKCAGAGAACGAHRWAAGCGATTATTGCCMAATGCA 9660
X M P E Q E K L X R E R X K R L L P N A
X C Q S K R N C X E N X X S D Y C X M H

9661 TCCAGCACYYCCAMSGGCATTACCAAGGAAGCACCTGGTCCCTCTGCATCACAGCCGGAC 9720
S S T X X G I T K E A P G P S A S Q P D
P A X P X A L P R K H L V P L H H S R T

9721 CCAAGTAAGCCACAGAATGATCGATGCATGCTCTCAAACCCAGACCACAAGGCAGCTGGG 9780
P S K P Q N D R C M L S N P D H K A A G
Q V S H R M I D A C S Q I Q I T R Q L G

9781 GAAGCAAACGATGCAAATGASGGATTCTCTGGTTCCAAGAATACATGKCAGAAGGRAAA 9840
E A N D A N X G F L W F Q E Y M X E G K
K Q I M Q M X D S S G S K N T X Q K X K

Acc1 ORF end ←|

9841 AATGCCATAAASAGTGCRAGYGATGACATGAGCATTCTGTTCTCTTCTCCGCAATGCTT 9900

N A *
 M P K X V X S D D M S I L F S S P Q C F
 9901 CTTAACSTACCTCAGAAAGAGACTYGCTTTTAATTCAGTGYTCAGAACACCTGACATTCT 9960
 L T Y L R K R L A F N S V X R T P D I L
 9961 ACACAGGTCATCYAAGCAAGCTGCTCAGTCAGACAGCACTGAACTGAAGAATTATCACAT 10020
 H R S S K Q A A Q S D S T E L K N Y H I
 10021 TCTACCTCAAGATGCAARTATGAATGCAAAGCAAACATATGAACTGGATGACCTCCACGT 10080
 L P Q D A X M N A K Q T Y E L D D L H V
 10081 GCTGATCGCTGTGAGTGACAAAGACACTCACATACTGGTTTATTTCCAAGGACACCGATT 10140
 L I A V S D K D T H I L V Y F Q G H R F
 10141 YAGACTATTAAGTGTATGTCATGTGASAATGTGCTCAAGATCACAAGCTCGACAGCTCA 10200
 R L L T V Y A C X N V L K I T S S T A H
 10201 TTGGKTCAAAAAACCAGGACSCAAGCTATGTTGGGTGCTAATTACTAATGGATTCTCAA 10260
 W X K K P G X K L C W V L I T N G F S K
 10261 RGATCCTGYAGCGTATTTTGAAGCCATYGCCAGTAATGATTTTGAATCAACCTAAATAC 10320
 D P X A Y F E A I A S N D F A I N L N I

Acc2 ORF end ←|

10321 CTCCTTGTGAAYACAKGCATTATTAGCTAGGTCCAGTRACAATATAATGGACTCATGCTG 10380
 S L *

10381 AATACCTCAATGTTGGATATATGTAYTCATTTCATGCTAATGTTAGCAAGTAGTGCTAACC 10440

10441 CTTTCTAAATTTGATGCAGCTGTTGATGKTTATTTTTGTGTATAGCACACATTACAGGC 10500

10501 TCATAGGCGCTTTGCAWATATATCAAGCRGCTTAGTTAATTCTTGATGCAACAGCTKT 10560

10561 GTGCTRAAATATGATGTATACATGATRRTTTCCTTKTGCCACCAATATAGGCAATCTTTAT 10620

10621 GTAAYTATAGCTCCAGTAAGCGTATTCATGACTTCACAGAGCTACAGKTCTTTGATCTA 10680

3' -LTR

10681 TGKCAAAGTGCCTTGANGGGGGTATGTCATGATTTACAAAKGYTACRAACGAGYTAAGRC 10740

10741 AGSTRTGCCACAGACTTCCTAACCACAGATTAGCAGCCGTTGGTCTTCAACGACTTAATG 10800

10801 CCTTGAAATTACACGTGGTTTTGACACCATCATAGTAATAAGCTATGGATGTTCTTTGGG 10860

10861 CAAAAACACGCATTACACACAATGCAAGCGTGGCTTTCAAAGACAAAATCAGACACT 10920

10921 AACTGTAACTCACAGGCACTTGCCGTTAGGGTCAGCTAAAGGTGAACAGTTTCTCCTT 10980

10981 CAACCACAAGTAACAGCTTCTGTTTTAGATGGGCTCGTAGCAGAAAGCAGCCATGACAG 11040

11041 GAAGCAGGGTACCAGAATACATGTGTGGTTAAAGTGTCAAAGCAATAGTCACATTTAAA 11100

11101 CCCCTTCAGAAAATGCATTTCATATAATGGCATTGAAATAGGCCAGGAAAAAACACAGC 11160

11161	ACCTTGCCTGTTTCGTCAAGCGGAAGGCCATGCATTTCAATGGAAATAATCAAGAAGCAAG	11220
11221	GACATCACCTTTCACTTGGGTTTTACATAGGTAAATAATGTGTGCAATGCAAACCTAAG	11280
11281	CACAAGAGCAGGTTGAGACTGTAGACGTTCTGTCCARGGCGAGGAAGTGACGCACATAGT	11340
11341	ACATGTAGGCTAAGTCACGGGTGTTAATATAAAAAAGCACAAACAGACTAAGGCTAAGAAAA	11400
11401	TTCCGCGCCAAGCAGACCACGATCGTGGGGGTTGGGAAGAGCAGTCGATAGCAGGTCGG	11460
11461	AACAGCAAGCCCAGGAAACCGTGAGTTTCAAGTGTGTTGGTTGAACCTCTCTTGCAATG	11520
11521	GTAGACTGACGGCGTGTTTTATTATGTCACTCCACTCCTGATCATACCATAGYATAGCTT	11580
11581	AGACAAACATAACATGAACTCCATGATTGCTCAAGCTGGTGTTTCAGAATGATGAATTGT	11640
11641	ACTTTATCTTTGTAAATGCAAATCATGCTTATAGCTTATGCAACAATGCTTTTTCTCTA	11700
11701	TCTGACAGTATGCTATGTTTTACTGCGTTAATTATAGCTGGTGTAAATGATGATCAAATC	11760
11761	TGGTAGAGAACAGAAGTGATATTAATATATTGACTTGCTACCTTTCAGTGTGAGCTTCA	11820
11821	ATTTTTTGTAGTAATGCTTCAAATGAGGTCTCTCTGAGTCAAACGAACTACACAATATT	11880
11881	TCTGGCTGAATTTTGTCAATTATGACAAGAGGTGCAAACACTCAGAGGAAGTCAAAGC	11940
11941	GCTAGGCCGGAACCCATGAGGCGCCTCTCATCATAACTTAAAGACTTTGATTCTGTGCC	12000
12001	ACACCACACAGCCCTACCTAGGGTCGAGGGGGCGGGCAGGGAATCACGCCCTAAGGGGC	12060
12061	AATCAAGTCAG	12071

>ERV-Spuma . b -Ame

5' -LTR

1	TGTCAAGTAATCTGAARCAATGTCTGAAGCAATTCAGCACTTTTAAAACAGCGTTCGCAA	60
61	TATTGCATTATGTGCAATTCTGAAGCAATATTATCAGTATTAAGTTTGTATGCTTTATC	120
121	ATGCTTTGAAACATGTATGCGACAGTAATATGAGAAATATGAGAAAAGTGCTGTCAAGAA	180
181	AGCGTATATGTATGTTTCAGCTTCGCACAGCTTGGCTTTTGTATTAAGCAGTTCCAAATA	240
241	TGGAAATCCGATTCCGGACACAAAATGTCGGATTCATGATAACTAATATGGGCAGGTATT	300
301	CCGGCGTTTAGACTGGCTACTTTAAAATGGCGTCTTAAGCATCCGGATAGCCATATATGG	360
361	TTAGAACCATATATGGACAACCGACATTTCTATACTTGGCTATACAAAGGTTACTGGTG	420
421	GGCACTGCCGTACAAAGGTAACCTAGTGCGTCTTGATATTAACACGAGGAATGAGAAGG	480
481	GGTTATTCGAGAGCATTTCAGGTGAAGCTGGTTGGATAGCGGCCAGGACAAGAGGACTTG	540
541	GCAARAAWTGGATGGCTTCCAGCCAGGACACAAAGTGTGGCTTGAACCCAGCCAGGACA	600
601	AATTGGCTGCCGCCCCAGCAAATGAGTCATCTAGCGATCTCTGCGGAGACTATAAATAAA	660
661	CCGCAAGCGCGGAGACATTRGGAGACGCAGGGCTGGAGGTGACAGGCAGCGAGCAGGTGC	720
721	TTCCCCGAGCGCAATGAACCGGGACAGAGTTCAAGCCAAAGCATAGCGCATAGCGCTTA	780
781	GATGTGAGTAGTTATGTTGGAGATATTTTACCTTATGCAACGATGCTATGCACTGTGATT	840
841	GATGGAAAAGAAATAAGATAATACCAAACGAGGCTTGTGGATTATGTGCTAGCATATCA	900
901	TTTAGAAAAGAAATAATGCAACAAGAGATATGCTGGTTCTATACGCAACTATAATCCTAA	960
961	TATTAACCATTTTTGCTTATTTCTGTAACATCGCTATTTTGATGATACTTAGCTTTATAT	1020
1021	ATAGGAAAATAAATACTTTATAAACTCAAACCTCTGAGTGRATCTATGCGTGAGAGATG	1080
1081	TAATCATAATGTATTTTGAACCTAAGTGCTCACATTTAATAAATTCATGTCTAGCTAACT	1140
1141	TATGCGGGCTCTGGGATGAACAGCGGGCGCAGTTCCAAACAGAGATTTCCAATGAGCAGG	1200
1201	CTATCCTAAAACGTGATATAGTTCTCAGCTCTCCCAGGGGTAACCAGGGGAGGGTGGG	1260

1261 GCTCTATAAACACGACCCTAGGAGTGTGAAAACGTGACAAAGTGGCGCCCAACGTGGGGCC 1320
 1321 TTAGGTCAAAGGTTAAAGGTCAAGTTAACCCCTTAGAGCTCAAGGGATAATTCATAAATAA 1380
 1381 TATACCTCCCTTTTGGAGACTGAAGAGGCTGCAAAAGGGTTGTTAAGCTTAACAGTAAAA 1440
 | → Gag ORF start
 1441 GGAAACCTTCTAAGAACCATTAGAAGGGTTAACTGCTGCAGCTATGGCTGCCTATGTAG 1500
 M A A Y V
 1501 ATGTGGACATACCTGCTGTTTGCCGAGCAGCTGTGAATCGCTGGCTTGATGATGGAGGAG 1560
 D V D I P A V C R A A V N R W L D D G G
 1561 TAAGGGCAATTAATCAAAATTTTACGGTAGTAGTAGGACAACCAGGAGGATTGCCAGGGG 1620
 V R A I N Q N F T V V V G Q P G G L P G
 1621 AAACCTTTTTTACTTACATGAAAACACCCGGTGCTAGAGCAGCAGGAGTTTTTGATAAAT 1680
 E T L F T Y M K T P G A R A A G V F D K
 1681 TAAGAATACACAAAACTGAACACAATAGAGTATAGACCTTATGTATTTTCAGAGTTAG 1740
 L R I H K N L N T I E Y R P Y V F S E L
 1741 CTCTGCAACACATAGACCATCTGAATTGGTTTGAGGCGAGATTGCAGTATCCTGACACCT 1800
 A L Q H I D H L N W F G G R L Q Y P D T
 1801 TAGCCAGACATGGTCCGTTTCATACATGCAGGATTGTCAATCCAACAACCTGGCTAAATTC 1860
 L A R H G P F I H A G L S I Q Q L A K F
 1861 ACCCAAACAGAGAGGGACCATATGACAGGGAGCAGTACAGACTGTTGGCTACACATTTTG 1920
 H P N R E G P Y D R E Q Y R L L A T H F
 1921 AAAATGCAAGAAATCGTGCTTTAGAGTATGCCATGCAAAATACCAATGGGTGCACAACCAC 1980
 E N A R N R A L E Y A M Q I P M G A Q P
 1981 CAGGGGTTCCGCCACCAGATGGGGGAGGAATACAATTTTCAGACACTGAAACCTTGCTAG 2040
 Gag_spuma super family (c126624)
 P G V P P P D G G G I Q F Q T L K P L L
 2041 GACAGATGCCTAGGGAAGTGGGGGATTACCCAAATGGTATTTCAGAAAAATAGGGCAAC 2100
 G Q M P R E V G D L P K W Y S E K I G Q
 2101 TACAAGCTGCATTTCCACAAGTCACAGCTCTGCAGAGGCAGAGAGCTCTAGCGATGGTAC 2160
 L Q A A F P Q V T A L Q R Q R A L A M V
 2161 TCCCAGCAGGATGTACTCCGCCGTTAGAAAAGTTGTGAAAGCTGGATGTCAAGTGTACAGCT 2220
 L P A G C T P P L E S C E S W M S V Y S
 2221 GGCTATACATACAACTGATAGGCACTCCGTCTATAACAGCCCTGAATACTATACTGAAGG 2280
 W L Y I Q L I G T P S I T A L N T I L K
 2281 ATATAATAAACTCACAAGGAGCAGCAGCCATGAACCTAGGACTGGCAATATCAGGAG 2340
 D I I N S Q G A A A A M N L G L A I S G
 2341 GAAATTACCCGATGGTAGAAGGAATAATAATGCCTTTACTTAGAGGAGAGTCTGCCAGGT 2400
 G N Y P M V E G I I M P L L R G E S A R
 2401 TAGAGATTAACAATAGGCTCAACCCGCTCACCTTCAGCAGAAACAGGAACAATTTGGGG 2460
 L E I N N R L N P L T L Q Q K Q E Q F G
 2461 ACATAGTAACTGCTGTATACAGATCAATAGGCAGAGACCACCTGGGAAGGAAACCAGGGG 2520
 D I V T A V Y R S I G R D H L G R K P G
 2521 AAAATGTAAGAAAGGAATCCAAGATGCGCAGCCTGAAAAAGGCAATGCTCCCAGAGGTA 2580

3781 N G F F A Q P L A P E S Y K Y T A F T H 3840
 CGTGAAAGCACTTTTCAGATGACACGGTTAATGCAAGGATACAAAAATAGTCCGGGAATA
 3841 R G K H F Q M T R L M Q G Y K N S P G I 3900
 TTCTCCAGTAGAATACAACTCTTTTAGCAGATATAGGAACTGCTGGCAATATGTTGAT
 3901 F S S R I Q T L L A D I G N C W Q Y V D 3960
 GACATATACTGTACAGATGATGATCTAGAAGAGCACCTTGAGAGAGTAGACCAGATAGTG
 3961 D I Y C T D D D L E E H L E R V D Q I V 4020
 CGTACTCTAGCTTCCAAGGGATACATATTTAATTTTAAGAAATCTTTAATAGCACATAGA
 4021 R T L A S K G Y I F N F K K S L I A H R 4080
 GAAGTTACATTTTTAGGGTTTACACTTACTGATCAAGGAAGAGGGCTTTCCACCAATTT
 4081 E V T F L G F T L T D Q G R G L S P N F 4140
 TTAGAGAAATGTGCAAATCTGCAGAGTCCTCGTAGTTTGAAGCAACTACAGGCTATGCTA
 4141 L E K C A N L Q S P R S L K Q L Q A M L 4200
 GGATTATTAATTTATGGGAGAACATATGTACCAACTATGCAGAATTGATCAAACCACTA
 4201 G L L N Y G R T Y V P N Y A E L I K P L 4260
 TATGCACTGTTGAAACCAATTTCCGTCCATCAGACTGGAAATCAGAACATGCAAATATT
 4261 Y A L L K P N F R P S D W K S E H A N I 4320
 TTGAATCATGTATATACATTAATGACTCAGACAGGTCCATTGCAGGACAGAAACCCAGAA
 4321 L N H V Y T L M T Q T G P L Q D R N P E 4380
 AAGGATTTGGAGGTTTCGCTAATGCCAGTAAAAATGCTTTTGCATACACTATGTGTAAC
 4381 K D L E V S L M P G K N A F A Y T M C N 4440
 AGAGGGGATAATAGGCCAATAGCCTACAGGTCACACATATACACTATAACCAGAGCAGAAA
 4441 R G D N R P I A Y R S H I Y T I P E Q K 4500
 TTTGCACTGGAGGAGCGGATTCTGGCAGCAGTTCAGATAATACTCCAGAAGGAACGTCT
 4501 F A L E E R I L A A V Q I I L Q K E R S 4560
 ATAGCAGCCGAAAGACCATACATATAATAACCAATCGCACAACTAGAAGCTACAAAT
 4561 I A A G K T I H I I T P I A Q L E A T N 4620
 CGTGCTAGTATACCTAATTCAAAGCACAAACATACCAGGTGGGTACAATGGATGTCCACT
 4621 R A S I P N S K A Q H T R W V Q W M S T 4680
 AGGGCAGCACCAGATGTACAGTTCATTACAAGGAAGAATTATTACCAATGTGTAATCTT
 4681 R A A P D V Q F H Y K E E L L P M C N L 4740
 GAATGGACACTACAAAATGAAGAAGATGTTAAAGAACCAGACATTCCATTATGGATGTAT
 4741 E W T L Q N E E D V K E P D I P L W M Y 4800
 GCTCATGTTTTATACACCGATGGATCGGCGATACCGGCTATAGGAACTAGGTCAAATAC

RNase_H_like super family (c114782)

4801 A H V L Y T D G S A I P A I G T R S K Y 4860
 TCAGCAGCTTGTTTCAGTAGTGAAAGGAAGATTCAATCATCACAATGAATTTGAACCCTTA
 4861 S A A C S V V K G R F N H H N E F E P L 4920
 GACACACAACTAAACATCTAGGGGACACTTCAGCACAAGTAGCAGAATTGCAAGGTTTA
 4921 D T Q T K H L G D T S A Q V A E L Q G L 4980
 CTATTGGCACTCCGACAAGTTGTACCGAACCAACCAACATTAATAGTATCTGATTCAGAC
 4981 L L A L R Q V V P N Q P T L I V S D S D 5040
 TATGTGGTCAGAGCATTCAATACTGACCTACAATGGTGGGTAAAAAATGATTTTAAAGAT
 Y V V R A F N T D L Q W W V K N D F K D

5041 TCAAAGGAAAGCCCATCTCAGCGAAGCAACTGTGGCAACAGGTGTGGAAAGTAAAAGAG 5100
 S K G K P I S A K Q L W Q Q V W K V K E
 5101 GGAAACTCTCTTTTATGGGTAACACATACTAAAGCACATAAAACTGACCATGTGCACAGT 5160
 G N S L L W V T H T K A H K T D H V H S
 5161 ACCGGCAATGCGCTGGCTGACTTATCCGCAAGGAAAAGGTCAACAAAATTAGTGGTAGCG 5220
 T G N A L A D L S A R E R S T K L V V A
 5221 GCACTAACCCGCTCAGCTACACGCATAGATGAGGATATACAGGCATGCCTAAAGGGTGGT 5280
 A L T R S A T R I D E D I Q A C L K G G
 5281 CCATACCCCTAAAGGCTATCCAAACACTTATGGTTATAGTGAAGAAGATAATGTAGTGCGA 5340
 P Y P K G Y P N T Y G Y S E E D N V V R
 5341 GTAACAATTCCAATGAAGAAAGGCGATCCCATCAAGAGGGTTCTACCGAACCAATCTGAA 5400
 V T I P M K K G D P I K R V L P N Q S E
 5401 AGAGAGAAAATGATAACAGCAGCACATGCAGGGCTGTCATCTACGCATTTTGGTATAAAT 5460
Integrase_H2C2 (pfam17921)
 R E K M I T A A H A G L S S T H F G I N
 5461 GCAACCACTCAGTTGCTACAAGCTAGATACTGGTGGCCGGAATTGAGAAAGCAAGTAAAA 5520
 A T T Q L L Q A R Y W W P E L R K Q V K
 5521 CACTACATTGCTAATTGTACCACTTGTCTACAGACAACGGTGGATCATACTAAGAAGCCT 5580
 H Y I A N C T T C L Q T T V D H T K K P
 5581 AAAGAAACCCATTACCAAGGGCACAGGTACCTTTTGGTGCATGTTTATGGACCACATT 5640
rve (pfam00665)
 K E T P L P R A Q V P F E C M F M D H I
 5641 GGTCCATTACCACAGTGAATAAATCAAATATCTACTCATCATAGTTGATTGATTGATTGACC 5700
 G P L P P V N K F K Y L L I I V D S C T
 5701 AGGTACACCTGGATATACCCTCAACGGAATGCTGATTGCAGGACAGTCATAAAGGACTTG 5760
 R Y T W I Y P Q R N A D C R T V I K D L
 5761 CGATCCTTATTTGCTATGACATCAGTACAAACCTCTATGCTGACAATGGCCCAGCCTTT 5820
 R S L F A M T S V Q T L Y A D N G P A F
 5821 ACTGGCAAAGCCGTTTCCAGGAGGCTGTGACAAGTATGGGGGCAAAACTGTCTTTCTCAACC 5880
 T G K A V Q E A V T S M G A K L S F S T
 5881 CCTTTTCAACCGGAAGGGAATGGAGTTGTGGAAAGGGCTAACGGGATTATTAACAAGCC 5940
 P F H P E G N G V V E R A N G I I K Q A
 5941 CTGACTAAATGCATTTTGGCTGGAGGAGTAACTGGCTAGAACATGTACCCTTGGTAATG 6000
 L T K C I L A G G G N W L E H V P L V M
 6001 AGAAGCATAAAACAACCTGCCTCGTCAATCACAGTGCAATGGTAAATCTCCTCATGAACTC 6060
 R S I N N L P R Q S Q C N G K S P H E L
 6061 TTGTTTGGCGTCCCAATGTATATGCCTGACTTACATAATCCCTCCAGTCCCTCAACCAGG 6120
 L F G V P M Y M P D L H N P S S P S T R
 6121 CCAGATCAGCTGCTGCTAACAACGCTGTTGAGAGATTCTCTCCAGGAGACGACTTCAGAG 6180
 P D Q L L L T T L L R D S L Q E T T S E
 6181 CCACCTGAAGAACCGACCCTGAAGAAAGGAGACTGGGTGTTGGAGAAAATCCATGACAGA 6240
 P P E E P T L K K G D W V L E K I H D R
 6241 ACGCCATTGGGTCCATACTACCGTCCGGCAGTTCAAGTGATCAGTGTCAAAGGAACAAGA 6300
 T P L G P Y Y R P A V Q V I S V K G T R

6301 ACAGTGGTAATTCCAGCTCTTCCGCCGAAGAAAGGTACACGCCAAGTGTCCATCGATCAT 6360
T V V I P A L P P K K G T R Q V S I D H
 Po1 ORF end ←|

|→ Env ORF start

6361 CTTAAACCAGCACCTG**ATGG**TACTGCAATGTTTCCAAGGGA**ACTACAGACTCTGAATGA** 6420
L K P A P D G Y C N V S K G T T D S E *
M V T A M F P R E L Q T L N E

6421 AGGTCATGAGGAATTTGCATTGGTACCTCGAGTAAGA**ACTAGTGACGTGCCAAGTGT**CAC 6480
G H E E F A L V P R V R T S D V P S V T

6481 ACGAGGACTAAATATTCGACCAAGTTAGTGACCTTTTTGCAAGAAAAAAGCAGTAAATT 6540
R G L N I R P R L V T F L Q E K S S K F

6541 TGTCCAGCAAATTCAGAGACTGTATTGGACTAGAAGATGGAAGATGATCTACATACTACT 6600
V Q Q I Q R L Y W T R R W K M I Y I L L

6601 GGCAGCATTCTACTTTTTGCTGTGGCTAAGTCTCATAGTCTTTTATGCCACACTTACCAC 6660
A A F Y F L L W L S L I V F Y A T L T T

6661 TGGACACTTTTTAAACATCTGTCAATCCACACCCAGAAAGCAGCCTGGTTAATTTAACACC 6720
G H F L T S V N P H P E S S L V N L T P

6721 ATTAGCGTCTCACATGTATTGCATAAAAGGGGAATAAAGGATAAGGATAAAACCGTAAC 6780
L A S S H V L H K R G I K D K D K T V T

6781 AATAAGCATATATCCACTCCCTTAGGCCAGTTCTGGATCCCTCARTACAGAACATTTGA 6840
I S I Y P L P L G Q F W I P Q Y R T F D

6841 TGGGCCGTCATTGCAAATACAAGTACATACTCTATCTGTAATAGATGAGTCACGCCTTTT 6900
G P S L Q I Q V H T L S V I D E S R L F

6901 TACACCTAACATTCCAGTTTCTCAAATGTACAGGGATATGCTTAGGGCTAAGCTTGTAA**C** 6960
T P N I P V S Q M Y R D M L R A K L V T

6961 ATTCACACAAGGGGCACTGYTAGATCCCGAGGATGATATTGAGGATTTACATAGCCTAGC 7020
F T Q G A L L D P E D D I E D L H S L A

7021 AGAACAYATTTGCTATGTGAGGTA**CTATGACACCTTTCTATTTTATAAACATGAACCTAT** 7080
E H I C Y V R Y Y D T F L F Y K H E P I

7081 AAGATGGATAAAAYCACACACACTGGGAACATTGTGCAGTACCCTTTGTAACCTCAAGTAA 7140
R W I N H T H W E H C A V P F V T S S N

7141 TGAGTTTAAAGCTCAATTCCCATATATAACTCCAGGAGTCTATAAACTGGGAGATTATAG 7200
E F K A Q F P Y I T P G V Y K L G D Y R

7201 ATATGAGAATCAATATGAGTTTCTCCAGAGCCAAAGGGCAAAACATTCTATTGGTCAAC 7260
Y E N Q Y E F P P E P K G K T F Y W S T

7261 CCAGTCAGTAGTGTATGACAGGGGGTTCTATAGGAACATGACAGAAGAATCCTGGAAAGA 7320
Q S V V Y D R G F Y R N M T E E S W K E

7321 AGCKGTACCGTTAAACTCCACATGGGGGGTGAACACTGGCAGATTMGGGGAGATGAATC 7380
A V P L N S T W G G E H W Q I R G D E S

7381 CCTAGATCTAGCATGTAGGTTTCCCATCTCATGTACTTTTTAAATTACACTCACTATCA 7440
L D L A C R F P H L M Y F L N Y T H Y Q

7441 AACAACTGCAGTAAGCATAATACCTCTTCTACCCTGATTGGGAGATGGTAGATGGGGA 7500
T T C S K H N T S F Y P D W E M V D G D

7501 TTTCTGGAATGCTAGCTATAGGGAYAAKATGAARCTGAATGGTTCTAAACCAATCACATA 7560

F W N A S Y R D X M K L N G S K P I T Y
 7561 TGCTTCAGGGATCCCAGTACTCTGGGCAGTACAGGCTAATGAGTGTAACAGGAGACGGTT 7620
 A S G I P V L W A V Q A N E C N R R R F
 7621 TGGTGCTAGCGTAGGTCCATACAGGGCTTGGGCAACGCACAATAACTCACAGACATATGC 7680
 G A S V G P Y R A W A T H N N S Q T Y A
 7681 AATTTCCATAGGAAAATTGTGCCAGGCTATGTCTCACACTACACATCTGAGTGAGGTATT 7740
 I S I G K L C Q A M S H T T H L S E V L
 7741 ATCAACGATAGAAGCCTGGGGAAAATCAGAAAATTGGACAGAAAATCATGAACTAGTCTC 7800
 S T I E A W G K S E N W T E I M K L V S
 7801 CCAATGGGAGGATAATAGTTCTAAGCGAACAAAAAGAGAAGTCAGCTGTAARAGTGATGC 7860
 Q W E D N S S K R T K R E V S C K S D A
 7861 TGAGACGTGTAGCAGAGATAGTAACACATACACTTGAAGGAAGTCATCCTAGCTATCCA 7920
 E T C S R D S N T Y T W K E V I L A I Q
 7921 GAAAACAGAGCAAGAAGCGGTAAGGAAGGCTTTAAAGCAGCGGATGAAAACCTTCTACCA 7980

Foamy_virus_ENV super family (c104051)

K T E Q E A V K E G F K A A D E N F Y Q
 7981 GCTACAACAGGGATTGTACATTCTGAGAGATGTAGTTACTTCTGTGATAGGAACTCTGCA 8040
 L Q Q G L Y I L R D V V T S V I G T L Q
 8041 GCATGATCTATCTGCAATCAGAAATGATCAACAGGCAGCTTCCAGCTTGACTTTAGTATC 8100
 H D L S A I R N D Q Q A A S S L T L V S
 8101 AAACCTTTCTGGATACACTGACCAGAGGTGTGCCAGACTGGACTCTAATCACATGGCCAAA 8160
 N F L D T L T R G V P D W T L I T W P N
 8161 CCAAATGAATGAGCTGAATTTAACTAAGAGAGCAAAGCGGCAAGCTATGAAAAGGACTTC 8220
 Q M N E L N L T K R A K R Q A M K R T S
 8221 CTACACGCTGTAAAGCACTCTCAGCAAAAAGTTTTATTCTTCATCAGCATGGTCAGACGA 8280
 Y T L L S T L S K K F Y S S S A W S D D
 8281 TGTACAATCATGGACGATTTCATGGCATTTTGGACATTCCAGTAGCAAGCGTTTCCACTAT 8340
 V Q S W T I H G I L D I P V A S V S T M
 8341 GTACTGTCATGCCTTAATGAACTGGGGTACTATGCATCGAGTGGAAGGACAATGGATACG 8400
 Y C H A L M N W G T M H R V E G Q W I R
 8401 CTCCAGCTACGTGGTGCCTTACACTCAGCTTGTGTCACACATGAAGATCCRACAGTGAG 8460
 S S Y V V P Y T H A C V T H E D P T V R
 8461 ACTTTATGCTTTAGTGAAGTGTGTWGGGGCAGCACGATTACAATGTCARGAAGTTACRAG 8520
 L Y A L V N C V G A A R L Q C Q E V T R
 8521 GAAAAATCCWTGTAGTCAGWCAGTCCAAGATGAATGCGTGCTGCATGCAGATAAAATGGG 8580
 K N P C S Q X V Q D E C V L H A D K M G
 8581 AACATTTTCGAGCAAAGCGCATCTACTGCCAAATGGATCMTATGTCGTCCARTTCAACAC 8640
 T F S S K A H L L P N G S Y V V Q F N T
 8641 GTCATGTTGTAATATTCCAAAAGGAGTAACAACGCTGATAACCGTCACGTCAACAGTCAA 8700
 S C C N I P K G V T T L I T V T S T V K
 8701 ATGCTGTGGATATATGTTGACGCCGCCAGTACAGGTCAGGCCGACCCAACCTAAATGGCC 8760
 C C G Y M L T P P V Q V R P T Q L K W P
 8761 AAAACTCGTACTTCAACAGATGGATTTTCTGTGCTGACGCTCAGGTTGGCTGAACTCAG 8820
 K L V L Q Q M D F P V L T L R L A E L S

8821 TAAATGAAAATAATCATTAAAAGCACTGCTCAGACATTGAAGAAGCAGCATCAAATGC 8880
 K M K I I I K S T A Q T F E E A A S N A
 8881 CATACTAACAGAGAACCTTTTGGCTGCTACGTCATCTTGGGGCGAGGCCCTGAGTGC 8940
 I H L T E N L L A A T S S W G E A L S A
 8941 ATTGCTTAAAAGCTCATCGTTTCAAGGATCACTTCAATTTTAAGCAACATCACAGACTG 9000
 L L K S S S F Q G F T S I L S N I T D W
 9001 GGCATCAAGTGAATCAGTACAGCAGGAAAAGGTGCTCCTCGGTCTGATCTCGACTCTGGC 9060
 A S S A I S T A G K G V L G L I S T L A
 9061 TTCCGGCCTTTCACCTTTGTTCTACATTGCTCTGATAGGAGGTTGTTTTTAATTCTCTT 9120
 S G L S P L F Y I A L I G G L F L I L F

Env ORF end ←|

|→ Acc1 ORF start

9121 TCTGTTGCTAAGACACTGACAAAAGCGATGCTGCTTTTCTGGAAATGCTTTGACAAGT 9180
 L L L R H *

M A A F P G N A L T S

9181 GAACAAATGCGCATGCGCAARAWAACTTGTGAAATACTTGGCTATGAAACTATCAGAGAG 9240
 E Q M R M R K X T C E I L G Y E T I R E
 9241 TATAATGACACTTTCATGTTCTCTCTAGAACGCATCCGGGAGAGACATAAGGTGGTTGCA 9300
 Y N D T F M F S L E R I R E R H K V V A
 9301 GACTGTCGCTTCTGCTACGAAAGAATTCTGCTAATACCAGAAGTGCAGACAACACTGACA 9360
 D C R F C Y E R I L L I P E V R R Q L T
 9361 TTTGACTCCAAGCTTAGACGCAGACATAGAACTTGGCTCTCTCAACATCGTGATCAGTGT 9420
 F D S K L R R R H R T W L S Q H R D Q C
 9421 GCCACACAAGTTCTATATCCTGAAATCTTCTGTTTCAGCCTCAATTGCTGAAGGCAACCCG 9480
 A T Q V L Y P E I F C S A S I A E G N P

|→ Acc2 ORF start

9481 CTATTGCCTGCACAGGAAGCTCAAGATGGTCTCAGAGTTGCAGCAAGCAGGAGAAGCGTCA 9540
 L L P A Q E A Q D G S E L Q Q A G E A S

M G Q S C S K Q E K R Q

9541 ACAGAGCAGGCGTCTCTGAGCTACCGAGACCCAACCGGCGGTGCTCACCGAGTTTCAA 9600
 T E Q A S S E L T E T Q P A V L T E F Q
 Q S R R P L S S P R P N R R C S P S E N
 9601 CCAGCGCTGCTCGCCGAGTCTCAACAGACGGTGCTCACCGAACTTCAACCAGCGGCCA 9660
 P A L L A E S Q Q T V L T E L Q P A A P
 Q R C S P S L N R R C S P N E N Q R R Q
 9661 GGAGGATACCTATGTAACCATGGAACCTCTGCTTCATCCATTGAGACCCATGGGCCAGAC 9720
 G G Y L C N H G T S A S S I E T H G P D
 E D T Y V T M E P L L H P L R P M G Q T
 9721 TCCATGTTCAACATTGATGGTGCGCCATGGAATGACATCACATCAGAAGAGATCGCAACT 9780
 S M F N I D G A P W N D I T S E E I A T
 P C S T L M V R H G M T S H Q K R S Q L

Acc1 ORF end ←|

9781 TGGCTTCTCGAGATTGCCTCTTCGTCCAAAAGTCCATGGGCCAGGAATGGTTACTA 9840
 W L L E I A S S S *

9841 G F S R L P L R P K N C P W A R N G Y Y 9900
 TGCTCCAGGAGTCAACAGAGGCCTATGGAGTCCACCAATTGTGAGAAATCCGCAAACATT
 9901 A P G V N R G L W S P P I V R N P Q T L 9960
 GGTTCATCATACTACATTGCAGATTGTTTAAGAACTTTCCGTACGCCACTCCAGAACCGAT
 9961 V I I L H C R L E K N F P Y A T P E P I 10020
 TGCGGTGGGTAACGAGAGAAAATATTGCTTTCCGACTCTGCAGCCACGTCCAGGACCGTC
 10021 A V G N E R K Y C F P T L Q P R P G P S 10080
 ATTTACTTCATATGATTATGGAAGCTGGCTGAACTTAGAGCACATGCATATTGAAGTCAC
 10081 F I S Y D Y G S W L N L E H M H I E V I 10140
 TGTAGGTGATTTAGGTACTCGTATACTGCATATGATATATCCGCTTCTGCAAGATCTCA
 10141 V G D L G T R I L T Y D I S A S A R S H 10200
 TCTTTGGGTGGTGTACTTCTGTACYAAAAGATTGATTATAGAATCAGGCCCGATGGTATG
 10201 L W V V Y F C T K R L I I E S G P M V W 10260
 GGAAGGTGACTCAAGAATCCCTTTGTATTGGAATATAATTATGTCTGGTCAGAGTGGTTT
 10261 E G D S R I P L Y W N I I M S G Q S G F 10320
 YAACGATGCACCAGATTTCCGTGCRCTTTACAAATTATGCCTTTGGCTAATGCTAACTCA
 N D A P D F R A L Y K L C L W L M L T Q
Acc2 ORF end ←|
 10321 GATTCTTGAAGCATTTTAAATTAATACTGTATGTTTTTTGACTGTGTGTTAGCCTCGCCT 10380
 I L E A F * 3' -LTR
 10381 TGTGTCTCATCTGAACATTGGGGGGTGTCAAGTAATAGCAAGTCTGAAGCATTTCAGCA 10440
 CTTTAAAACAGTGTTAGCAATATTAAGCACATGTCTTAATGCAATATTGCAGTTTACGA 10500
 10501 TATATTATCAGTATTAAGTTTGTTATGCTTTATCATGCCTTGAAAACATGTATGCGACAG 10560
 10561 AAATATGAGAAATATGAGAAAAGTGCTGTCATTAGAAAAGCGTTATGTATGTTTCAGCTTCG 10620
 10621 CACAGCTTGGCTTTTGGCTATTAAGCGGTTCCAAATATGGAATTCCGATTCCGGACACAAA 10680
 10681 ATGTCGGATTAATGTACTAATATGGGCAGAGGTTCCGGCGTTTACTGACTGGCTACCTTAAA 10740
 10741 ATGGCGTCTTAAGCATCCGGATAGACATATATGGTAGAACCATATATGGACAACCGACAT 10800
 10801 TTCCTATACTTGGCTGTACAAAGGTTACTGTGGATGGGCATGCCGTACAAAGGTAACCTCT 10860
 10861 AGTGC GTTGGTATTAACACGAGGAATGAGAAGGTTATTCGAGAGCATTTCGTGAGCTGG 10920
 10921 TTGGATAGCGGCCAGACAAGAGGTTTGGCAGAAATGGATGGCTTCCGCCAGGACACAATG 10980
 10981 TTGGCTTGAACCCAGCCAGGCACAAATTGGCTGCCGCCAGCAAATGAGTCATCTAGCG 11040
 11041 ATCTCTGCGGAGACTATAAATAAACC GCAAGCGCGGAGACATTGAGAGACGCAGAGCTGG 11100

11101 **AGGTGACAGGCAGCGAGCAGGTGCTTCCCCGCAGCGCAATGAACCGGGACAGAGTTCAAG** 11160
 11161 **CCAAAGCATAGCGCATAGCGCTTAGATGTGAGTAGTTATGTTGGAGATATTTTACCTTAT** 11220
 11221 **GCAATGATGCTATGCACTGTGATTGATGAAAAGGAAATGAATAATACAAACGAGGCTTGT** 11280
 11281 **TGGATTATGTGCTAGCATATCATTAGAAAGAGAAATAATGCAACAAAAGATATGCTGGTT** 11340
 11341 **CTATACCAACTATAATCCTAATATTAACCACTTTTGCTTATTTCTGTAACATCGCTATTT** 11400
 11401 **TGATGATACTTAGCTTTATATATAGGAAAATAAATACTTTATAAACTCAAACCTCCTGAG** 11460
 11461 **TGAATCTATGCGTGAGAGATGTAATCATAATGTATTTTGAACCTAAGTGCTCACATTTAA** 11520
 11521 **TAAATTCATGTCTAGCTAACTTATGCGGGCTCTGGGATGAACAGCGGGCGCAGTTCCAAA** 11580
 11581 **CAGAGATTTCCAATGAGCAGGCTATCCTAAAACCTGTGATATAGTTCTCAGCTCTCCCCAG** 11640
 11641 **GGGTAACCAGGGGAGGGTGGGGCTCTATAAACACGACCCTAGGAGTGTGAAAACGTGA** 11698

Fig. S1 Detailed descriptions of the putative genomes of consensus ERV-Spuma-Rbi, ERV-Spuma-Smu, ERV-Spuma.a-Ame and ERV-Spuma.b-Ame. The location of the proteins encoded by the gag, pol, env and accessory genes were determined via homology to representative foamy viruses, searching CDD, and the distribution of start and stop codons, determined by ORFfinder (<https://www.ncbi.nlm.nih.gov/orffinder/>). The conserved domains were determined by searching against the CDD and highlighted in darker colors.

Table S1 The endogenous foamy viruses or expressed foamy viruses identified in amphibians

Name	Accession	Start	End
ERV-Spuma.1-Rbi	NC_042615.1	57913154	57923911
ERV-Spuma.2-Rbi	NC_042615.1	114546185	114557134
ERV-Spuma.3-Rbi	NC_042615.1	176373255	176384027
ERV-Spuma.4-Rbi	NC_042615.1	186770869	186781941
ERV-Spuma.5-Rbi	NC_042615.1	403426764	403430415
ERV-Spuma.6-Rbi	NC_042615.1	446625627	446636700
ERV-Spuma.7-Rbi	NC_042615.1	515087848	515094280
ERV-Spuma.8-Rbi	NC_042615.1	515097901	515101715
ERV-Spuma.9-Rbi	NC_042615.1	548052230	548063158
ERV-Spuma.10-Rbi	NC_042615.1	589501560	589512639
ERV-Spuma.11-Rbi	NC_042615.1	635649370	635660442
ERV-Spuma.12-Rbi	NC_042615.1	671043665	671054909
ERV-Spuma.13-Rbi	NC_042615.1	675516579	675527635
ERV-Spuma.14-Rbi	NC_042615.1	777987655	777998718
ERV-Spuma.15-Rbi	NC_042615.1	825609939	825620627
ERV-Spuma.16-Rbi	NC_042615.1	826747553	826752189
ERV-Spuma.17-Rbi	NC_042615.1	826826061	826830692
ERV-Spuma.18-Rbi	NC_042615.1	827968128	827976005
ERV-Spuma.19-Rbi	NC_042615.1	836123690	836128117
ERV-Spuma.20-Rbi	NC_042615.1	836447044	836451469
ERV-Spuma.21-Rbi	NC_042616.1	43444302	43455378
ERV-Spuma.22-Rbi	NC_042616.1	52543808	52554540
ERV-Spuma.23-Rbi	NC_042616.1	66710433	66721175
ERV-Spuma.24-Rbi	NC_042616.1	253245806	253256618
ERV-Spuma.25-Rbi	NC_042616.1	269613232	269624173
ERV-Spuma.26-Rbi	NC_042616.1	376726602	376737688
ERV-Spuma.27-Rbi	NC_042616.1	682563473	682574561
ERV-Spuma.28-Rbi	NC_042616.1	691545221	691553333
ERV-Spuma.29-Rbi	NC_042616.1	746413620	746424607
ERV-Spuma.30-Rbi	NC_042616.1	750302072	750313335
ERV-Spuma.31-Rbi	NC_042617.1	2007834	2018809
ERV-Spuma.32-Rbi	NC_042617.1	29442792	29453871
ERV-Spuma.33-Rbi	NC_042617.1	159236272	159239483
ERV-Spuma.34-Rbi	NC_042617.1	160600721	160611797
ERV-Spuma.35-Rbi	NC_042617.1	169204364	169215436
ERV-Spuma.36-Rbi	NC_042617.1	214902017	214913071
ERV-Spuma.37-Rbi	NC_042617.1	219308229	219319305
ERV-Spuma.41-Rbi	NC_042617.1	489103847	489115246
ERV-Spuma.42-Rbi	NC_042617.1	552774854	552785928
ERV-Spuma.43-Rbi	NC_042618.1	47926199	47937269
ERV-Spuma.44-Rbi	NC_042618.1	237803481	237806878

ERV-Spuma.45-Rbi	NC_042619.1	116756494	116767721
ERV-Spuma.46-Rbi	NC_042619.1	186128395	186139463
ERV-Spuma.47-Rbi	NC_042619.1	197444532	197455605
ERV-Spuma.48-Rbi	NC_042619.1	266144830	266147964
ERV-Spuma.49-Rbi	NC_042619.1	360008464	360013251
ERV-Spuma.50-Rbi	NC_042619.1	360018300	360024753
ERV-Spuma.51-Rbi	NC_042620.1	266267256	266276476
ERV-Spuma.52-Rbi	NC_042620.1	267358459	267369541
ERV-Spuma.53-Rbi	NC_042620.1	368612820	368619308
ERV-Spuma.54-Rbi	NC_042620.1	371475210	371484296
ERV-Spuma.55-Rbi	NC_042621.1	107758018	107769092
ERV-Spuma.56-Rbi	NC_042623.1	130432355	130443436
ERV-Spuma.57-Rbi	NC_042623.1	199024438	199035509
ERV-Spuma.58-Rbi	NC_042628.1	62603328	62614595
ERV-Spuma.59-Rbi	NC_042628.1	75436985	75443604
ERV-Spuma.60-Rbi	NC_042630.1	45827674	45838744
ERV-Spuma.61-Rbi	NC_042630.1	65454091	65459864
ERV-Spuma.62-Rbi	NC_042630.1	65572022	65577794
ERV-Spuma.63-Rbi	NC_042631.1	54174916	54185932
ERV-Spuma.64-Rbi	NC_042631.1	54524554	54535631
ERV-Spuma.65-Rbi	NC_042631.1	56301530	56312580
ERV-Spuma.66-Rbi	NC_042633.1	11426635	11433226
ERV-Spuma.67-Rbi	NW_021820742.1	26371	37447
ERV-Spuma.1-Smu	VKOC01000001.1	49875522	49884790
ERV-Spuma.2-Smu	VKOC01000003.1	20706007	20713074
ERV-Spuma.3-Smu	VKOC01000006.1	40686824	40692669
ERV-Spuma.4-Smu	VKOC01000006.1	42271905	42281821
ERV-Spuma.5-Smu	VKOC01000008.1	22953512	22963804
ERV-Spuma.6-Smu	VKOC01008314.1	72	4465
ERV-Spuma.7-Smu	VKOC01015915.1	24811	29338
ERV-Spuma.8-Smu	VKOC01016144.1	1	7755
ERV-Spuma.9-Smu	VKOC01019137.1	1	5488
ERV-Spuma.10-Smu	VKOC01022720.1	9967	17303
ERV-Spuma.11-Smu	VKOC01027761.1	1232	5594
ERV-Spuma.12-Smu	VKOC01030981.1	5362	12987
ERV-Spuma.13-Smu	VKOC01047117.1	2187	9405
ERV-Spuma.14-Smu	VKOC01047174.1	12676	17559
ERV-Spuma.15-Smu	VKOC01047612.1	1	8318
ERV-Spuma.16-Smu	VKOC01047638.1	51517	57974
ERV-Spuma.17-Smu	VKOC01047639.1	1	9956
ERV-Spuma.18-Smu	VKOC01047906.1	1	8658
ERV-Spuma.a1-Ame	PGSH01000001.1	6264623	6267657
ERV-Spuma.a2-Ame	PGSH01000019.1	572302	576144
ERV-Spuma.a3-Ame	PGSH01001354.1	555509	563270

ERV-Spuma.a4-Ame	PGSH01003802.1	2637539	2640797
ERV-Spuma.a5-Ame	PGSH01003802.1	2643293	2652371
ERV-Spuma.a6-Ame	PGSH01003802.1	2795137	2799409
ERV-Spuma.a7-Ame	PGSH01003848.1	851768	862610
ERV-Spuma.a8-Ame	PGSH01005059.1	1810596	1820414
ERV-Spuma.a9-Ame	PGSH01006364.1	1286001	1298399
ERV-Spuma.a10-Ame	PGSH01006377.1	1349714	1360518
ERV-Spuma.a11-Ame	PGSH01008812.1	5983673	5988862
ERV-Spuma.a12-Ame	PGSH01008910.1	34169	44350
ERV-Spuma.a13-Ame	PGSH01015195.1	85161	93425
ERV-Spuma.a14-Ame	PGSH01017662.1	306645	310263
ERV-Spuma.a15-Ame	PGSH01019491.1	43209	47300
ERV-Spuma.a16-Ame	PGSH01022653.1	643815	648455
ERV-Spuma.a17-Ame	PGSH01022653.1	649552	655147
ERV-Spuma.a18-Ame	PGSH01022702.1	672427	681080
ERV-Spuma.a19-Ame	PGSH01023909.1	4301897	4306935
ERV-Spuma.a20-Ame	PGSH01023909.1	4308211	4316186
ERV-Spuma.a21-Ame	PGSH01023919.1	1782266	1788445
ERV-Spuma.a22-Ame	PGSH01023926.1	30405	39752
ERV-Spuma.a23-Ame	PGSH01025177.1	967861	971103
ERV-Spuma.a24-Ame	PGSH01025178.1	5518044	5521398
ERV-Spuma.a25-Ame	PGSH01026441.1	131750	142196
ERV-Spuma.a26-Ame	PGSH01029025.1	1683076	1687173
ERV-Spuma.a27-Ame	PGSH01030205.1	993950	1001601
ERV-Spuma.a28-Ame	PGSH01032736.1	1117474	1120770
ERV-Spuma.a29-Ame	PGSH01033995.1	972640	978255
ERV-Spuma.a30-Ame	PGSH01034008.1	1396115	1401348
ERV-Spuma.a31-Ame	PGSH01035224.1	4829807	4839514
ERV-Spuma.a32-Ame	PGSH01035230.1	10592945	10597437
ERV-Spuma.a33-Ame	PGSH01035230.1	10605747	10610588
ERV-Spuma.a34-Ame	PGSH01036982.1	44567	50958
ERV-Spuma.a35-Ame	PGSH01037750.1	9586908	9591575
ERV-Spuma.a36-Ame	PGSH01037750.1	9602460	9607446
ERV-Spuma.a37-Ame	PGSH01037795.1	441215	449694
ERV-Spuma.a38-Ame	PGSH01039009.1	736658	741438
ERV-Spuma.a39-Ame	PGSH01043872.1	13638	19084
ERV-Spuma.a40-Ame	PGSH01046624.1	472273	477951
ERV-Spuma.a41-Ame	PGSH01047791.1	1994291	1997564
ERV-Spuma.a42-Ame	PGSH01047807.1	665304	673128
ERV-Spuma.a43-Ame	PGSH01049050.1	16481460	16490136
ERV-Spuma.a44-Ame	PGSH01049058.1	1894964	1902054
ERV-Spuma.a45-Ame	PGSH01049058.1	1950661	1957766
ERV-Spuma.a46-Ame	PGSH01050305.1	1869649	1876045
ERV-Spuma.a47-Ame	PGSH01050305.1	1882929	1889312

ERV-Spuma.a48-Ame	PGSH01051580.1	1077128	1087744
ERV-Spuma.a49-Ame	PGSH01051633.1	2618829	2622168
ERV-Spuma.a50-Ame	PGSH01051633.1	2623526	2628865
ERV-Spuma.a51-Ame	PGSH01052865.1	992597	997697
ERV-Spuma.a52-Ame	PGSH01054917.1	12397	18661
ERV-Spuma.a53-Ame	PGSH01055349.1	9566365	9569774
ERV-Spuma.a54-Ame	PGSH01057862.1	4793216	4796588
ERV-Spuma.a55-Ame	PGSH01057870.1	4232904	4241020
ERV-Spuma.a56-Ame	PGSH01057881.1	703789	709262
ERV-Spuma.a57-Ame	PGSH01060410.1	827933	832837
ERV-Spuma.a58-Ame	PGSH01062881.1	8654193	8663329
ERV-Spuma.a59-Ame	PGSH01062896.1	3784661	3788417
ERV-Spuma.a60-Ame	PGSH01062901.1	1178310	1181523
ERV-Spuma.a61-Ame	PGSH01064163.1	1073398	1083889
ERV-Spuma.a62-Ame	PGSH01065393.1	6957205	6962511
ERV-Spuma.a63-Ame	PGSH01067909.1	1509927	1513403
ERV-Spuma.a64-Ame	PGSH01067909.1	1700246	1704153
ERV-Spuma.a65-Ame	PGSH01070491.1	99158	109904
ERV-Spuma.a66-Ame	PGSH01071679.1	6588104	6592597
ERV-Spuma.a67-Ame	PGSH01072403.1	1662	5885
ERV-Spuma.a68-Ame	PGSH01072685.1	65496	68671
ERV-Spuma.a69-Ame	PGSH01074283.1	326019	330747
ERV-Spuma.a70-Ame	PGSH01075472.1	2710195	2716979
ERV-Spuma.a71-Ame	PGSH01079228.1	746545	753238
ERV-Spuma.a72-Ame	PGSH01081731.1	4076265	4080190
ERV-Spuma.a73-Ame	PGSH01084338.1	572747	576511
ERV-Spuma.a74-Ame	PGSH01085509.1	308613	319277
ERV-Spuma.a75-Ame	PGSH01085530.1	5737018	5744714
ERV-Spuma.a76-Ame	PGSH01086819.1	1064789	1074635
ERV-Spuma.a77-Ame	PGSH01088054.1	326123	331822
ERV-Spuma.a78-Ame	PGSH01091798.1	8331330	8337974
ERV-Spuma.a79-Ame	PGSH01093946.1	7321	11182
ERV-Spuma.a80-Ame	PGSH01095646.1	1332326	1341984
ERV-Spuma.a81-Ame	PGSH01096895.1	4085	7987
ERV-Spuma.a82-Ame	PGSH01099332.1	8461150	8468446
ERV-Spuma.a83-Ame	PGSH01100611.1	2144219	2147769
ERV-Spuma.a84-Ame	PGSH01101911.1	1027820	1034529
ERV-Spuma.a85-Ame	PGSH01105615.1	111866	115558
ERV-Spuma.a86-Ame	PGSH01107798.1	139949	144829
ERV-Spuma.a87-Ame	PGSH01110649.1	5211457	5214522
ERV-Spuma.a88-Ame	PGSH01111904.1	4678043	4684351
ERV-Spuma.a89-Ame	PGSH01111946.1	3496631	3501789
ERV-Spuma.a90-Ame	PGSH01111964.1	558823	563324
ERV-Spuma.a91-Ame	PGSH01111964.1	569931	573478

ERV-Spuma.a92-Ame	PGSH01113211.1	3124537	3130660
ERV-Spuma.a93-Ame	PGSH01113211.1	3186483	3192927
ERV-Spuma.a94-Ame	PGSH01116945.1	3120342	3124437
ERV-Spuma.a95-Ame	PGSH01116968.1	4014285	4017766
ERV-Spuma.a96-Ame	PGSH01116988.1	469969	473094
ERV-Spuma.a97-Ame	PGSH01116988.1	491221	500666
ERV-Spuma.a98-Ame	PGSH01118041.1	3253	7879
ERV-Spuma.a99-Ame	PGSH01120713.1	2653730	2657003
ERV-Spuma.a100-Ame	PGSH01120737.1	1147325	1152636
ERV-Spuma.a101-Ame	PGSH01123219.1	4599142	4604089
ERV-Spuma.a102-Ame	PGSH01123259.1	768141	773390
ERV-Spuma.a103-Ame	PGSH01124477.1	2392164	2396241
ERV-Spuma.a104-Ame	PGSH01124515.1	2103928	2108029
ERV-Spuma.b1-Ame	PGSH01013857.1	3716665	3724126
ERV-Spuma.b2-Ame	PGSH01022713.1	412568	419627
ERV-Spuma.b3-Ame	PGSH01039549.1	1	4596
ERV-Spuma.b4-Ame	PGSH01049260.1	13796	25687
ERV-Spuma.b5-Ame	PGSH01052820.1	1286669	1294732
ERV-Spuma.b6-Ame	PGSH01052855.1	1819277	1830789
ERV-Spuma.b7-Ame	PGSH01052855.1	1841230	1852739
ERV-Spuma.b8-Ame	PGSH01061660.1	1251738	1258069
ERV-Spuma.b9-Ame	PGSH01064174.1	2474792	2478237
ERV-Spuma.b10-Ame	PGSH01067933.1	1036349	1043201
ERV-Spuma.b11-Ame	PGSH01079222.1	380294	392002
ERV-Spuma.b12-Ame	PGSH01088166.1	10449	20384
ERV-Spuma.b13-Ame	PGSH01095560.1	5815558	5821922
ERV-Spuma.b14-Ame	PGSH01095560.1	5823376	5826854
ERV-Spuma.b15-Ame	PGSH01099775.1	196771	204944
ERV-Spuma.b16-Ame	PGSH01104359.1	6174362	6180900
ERV-Spuma.b17-Ame	PGSH01117526.1	90425	96126
ERV-Spuma.b18-Ame	PGSH01125197.1	1	6277
ERV-Spuma.c1-Ame	PGSH01013853.1	2765005	2768130
ERV-Spuma.c2-Ame	PGSH01030304.1	176750	179767
ERV-Spuma.c3-Ame	PGSH01040306.1	769718	773099
ERV-Spuma.c4-Ame	PGSH01044064.1	1430704	1433816
ERV-Spuma.c5-Ame	PGSH01047522.1	30545	33607
ERV-Spuma.c6-Ame	PGSH01049103.1	1960557	1963689
ERV-Spuma.c7-Ame	PGSH01052863.1	3352473	3355691
ERV-Spuma.c8-Ame	PGSH01073018.1	1756240	1760655
ERV-Spuma.c9-Ame	PGSH01100626.1	1691532	1706401
exCFVrbi.1	GFOG01006311.1	-	-
exCFVrbi.2	GFOG01069762.1	-	-
exCFVrbi.3	GFOG01077101.1	-	-
exCFVrbi.4	GFOG01077102.1	-	-

exCFVrbi.5	GFOG01077103.1	-	-
exCFVrbi.6	GFOG01077104.1	-	-
exCFVrbi.7	GFOG01078659.1	-	-
exCFVrbi.8	GFOG01078660.1	-	-
exCFVrbi.9	GFOG01079534.1	-	-
exCFVrbi.10	GFOG01079535.1	-	-
exNFVtwe.1	GESS01001565.1	-	-
exNFVtwe.2	GESS01002659.1	-	-
exNFVtwe.3	GESS01003942.1	-	-
exNFVtwe.4	GESS01005316.1	-	-
exNFVtwe.5	GESS01007562.1	-	-
exNFVtwe.6	GESS01007969.1	-	-
exNFVtwe.7	GESS01009667.1	-	-
exNFVtwe.8	GESS01011049.1	-	-
exNFVtwe.9	GESS01013777.1	-	-
exNFVtwe.10	GESS01017131.1	-	-
exNFVtwe.11	GESS01017642.1	-	-
exNFVtwe.12	GESS01018187.1	-	-
exNFVtwe.13	GESS01019137.1	-	-
exNFVtwe.14	GESS01019796.1	-	-
exNFVtwe.15	GESS01020812.1	-	-
exNFVtwe.16	GESS01021729.1	-	-
exNFVtwe.17	GESS01022913.1	-	-
exNFVtwe.18	GESS01025204.1	-	-
exNFVtwe.19	GESS01026764.1	-	-
exNFVtwe.20	GESS01027683.1	-	-
exNFVtwe.21	GESS01027743.1	-	-
exNFVtwe.22	GESS01029986.1	-	-
exNFVtwe.23	GESS01032245.1	-	-
exNFVtwe.24	GESS01034318.1	-	-
exNFVtwe.25	GESS01034453.1	-	-
exNFVtwe.26	GESS01034683.1	-	-
exNFVtwe.27	GESS01035964.1	-	-
exNFVtwe.28	GESS01040058.1	-	-
exNFVtwe.29	GESS01042189.1	-	-
exNFVtwe.30	GESS01045812.1	-	-
exNFVtwe.31	GESS01047392.1	-	-
exNFVtwe.32	GESS01047931.1	-	-
exNFVtwe.33	GESS01049718.1	-	-
exNFVtwe.34	GESS01050984.1	-	-
exNFVtwe.35	GESS01052035.1	-	-
exNFVtwe.36	GESS01053545.1	-	-
exNFVtwe.37	GESS01054044.1	-	-
exNFVtwe.38	GESS01056758.1	-	-

exNFVtwe.39	GESS01057315.1	-	-
exNFVtwe.40	GESS01057826.1	-	-
exNFVtwe.41	GESS01060880.1	-	-
exNFVtwe.42	GESS01067778.1	-	-
exNFVtwe.43	GESS01069249.1	-	-
exNFVtwe.44	GESS01070572.1	-	-
exNFVtwe.45	GESS01070828.1	-	-
exNFVtwe.46	GESS01071089.1	-	-
exNFVtwe.47	GESS01071383.1	-	-
exNFVtwe.48	GESS01071839.1	-	-
exNFVtwe.49	GESS01072787.1	-	-
exNFVtwe.50	GESS01073239.1	-	-
exNFVtwe.51	GESS01075865.1	-	-
exNFVtwe.52	GESS01075905.1	-	-
exNFVtwe.53	GESS01076856.1	-	-
exNFVtwe.54	GESS01080392.1	-	-
exNFVtwe.55	GESS01080711.1	-	-
exNFVtwe.56	GESS01081005.1	-	-
exNFVtwe.57	GESS01083141.1	-	-
exNFVtwe.58	GESS01085009.1	-	-
exNFVtgr.1	GHKF01001559.1	-	-
exNFVtgr.2	GHKF01001561.1	-	-
exNFVtgr.3	GHKF01002865.1	-	-
exNFVtgr.4	GHKF01002869.1	-	-
exNFVtgr.5	GHKF01002870.1	-	-
exNFVtgr.6	GHKF01002875.1	-	-
exNFVtgr.7	GHKF01016867.1	-	-
exNFVtgr.8	GHKF01016981.1	-	-
exNFVtgr.9	GHKF01016985.1	-	-
exNFVtgr.10	GHKF01028783.1	-	-
exNFVtgr.11	GHKF01029063.1	-	-
exNFVtgr.12	GHKF01029065.1	-	-
exNFVtgr.13	GHKF01029068.1	-	-
exNFVtgr.14	GHKF01029069.1	-	-
exNFVtgr.15	GHKF01034141.1	-	-
exNFVtgr.16	GHKF01034142.1	-	-
exNFVtgr.17	GHKF01034145.1	-	-
exNFVtgr.18	GHKF01034147.1	-	-
exNFVtgr.19	GHKF01055770.1	-	-
exNFVtgr.20	GHKF01056004.1	-	-
exNFVtgr.21	GHKF01056005.1	-	-
exNFVtgr.22	GHKF01056006.1	-	-
exNFVtgr.23	GHKF01056007.1	-	-
exNFVtgr.24	GHKF01056009.1	-	-

exNFVtgr.25	GHKF01056010.1	-	-
exNFVtgr.26	GHKF01056011.1	-	-
exNFVtgr.27	GHKF01056012.1	-	-
exNFVtgr.28	GHKF01056013.1	-	-
exNFVtgr.29	GHKF01056015.1	-	-
exNFVtgr.30	GHKF01056016.1	-	-
exNFVtgr.31	GHKF01056017.1	-	-
exNFVtgr.32	GHKF01056019.1	-	-
exNFVtgr.33	GHKF01056082.1	-	-
exNFVtgr.34	GHKF01056087.1	-	-
exNFVtgr.35	GHKF01056088.1	-	-
exNFVtgr.36	GHKF01056783.1	-	-
exNFVtgr.37	GHKF01056786.1	-	-
exNFVtgr.38	GHKF01056788.1	-	-
exNFVtgr.39	GHKF01056790.1	-	-
exNFVtgr.40	GHKF01057945.1	-	-
exNFVtgr.41	GHKF01057947.1	-	-
exNFVtgr.42	GHKF01057948.1	-	-
exNFVtgr.43	GHKF01061402.1	-	-
exNFVtgr.44	GHKF01061705.1	-	-
exNFVtgr.45	GHKF01069133.1	-	-
exNFVtgr.46	GHKF01069281.1	-	-
exNFVtgr.47	GHKF01070483.1	-	-
exNFVtgr.48	GHKF01076429.1	-	-
exNFVtgr.49	GHKF01082040.1	-	-
exNFVtgr.50	GHKF01083078.1	-	-
exNFVtgr.51	GHKF01083083.1	-	-
exNFVtgr.52	GHKF01083851.1	-	-
exNFVtgr.53	GHKF01084413.1	-	-
exNFVtgr.54	GHKF01084414.1	-	-
exNFVtgr.55	GHKF01087742.1	-	-
exNFVtgr.56	GHKF01087744.1	-	-
exNFVtgr.57	GHKF01104466.1	-	-
exNFVtgr.58	GHKF01104481.1	-	-
exNFVtgr.59	GHKF01104484.1	-	-
exNFVtgr.60	GHKF01109457.1	-	-
exNFVtgr.61	GHKF01112814.1	-	-
exNFVtgr.62	GHKF01112817.1	-	-
exNFVtgr.63	GHKF01115947.1	-	-
exNFVtgr.64	GHKF01115948.1	-	-
exNFVtgr.65	GHKF01115949.1	-	-
exNFVtgr.66	GHKF01115950.1	-	-
exNFVtgr.67	GHKF01115951.1	-	-
exNFVtgr.68	GHKF01115952.1	-	-

exNFVtgr.69	GHKF01115953.1	-	-
exNFVtgr.70	GHKF01115954.1	-	-
exNFVtgr.71	GHKF01115956.1	-	-
exNFVtgr.72	GHKF01115957.1	-	-
exNFVtgr.73	GHKF01115958.1	-	-
exNFVtgr.74	GHKF01121458.1	-	-
exNFVtgr.75	GHKF01121464.1	-	-
exNFVtgr.76	GHKF01121480.1	-	-
exNFVtgr.77	GHKF01121679.1	-	-
exNFVtgr.78	GHKF01121680.1	-	-
exNFVtgr.79	GHKF01121682.1	-	-
exNFVtgr.80	GHKF01121683.1	-	-
exNFVtgr.81	GHKF01121684.1	-	-
exNFVtgr.82	GHKF01121686.1	-	-
exNFVtgr.83	GHKF01139758.1	-	-
exNFVtgr.84	GHKF01139759.1	-	-
exNFVtgr.85	GHKF01139761.1	-	-
exNFVtgr.86	GHKF01139762.1	-	-
exNFVtgr.87	GHKF01139766.1	-	-
exNFVtgr.88	GHKF01139771.1	-	-
exNFVtgr.89	GHKF01139774.1	-	-
exNFVtgr.90	GHKF01142573.1	-	-
exNFVtgr.91	GHKF01145954.1	-	-
exNFVtgr.92	GHKF01145986.1	-	-
exNFVtgr.93	GHKF01145989.1	-	-
exNFVtgr.94	GHKF01145993.1	-	-
exNFVtgr.95	GHKF01146165.1	-	-
exNFVtgr.96	GHKF01146166.1	-	-
exNFVtgr.97	GHKF01146167.1	-	-
exNFVtgr.98	GHKF01148202.1	-	-
exNFVtgr.99	GHKF01152802.1	-	-
exNFVtgr.100	GHKF01152803.1	-	-
exNFVtgr.101	GHKF01153066.1	-	-
exNFVtgr.102	GHKF01154047.1	-	-
exNFVtgr.103	GHKF01154049.1	-	-
exNFVtgr.104	GHKF01156341.1	-	-
exNFVtgr.105	GHKF01156345.1	-	-
exNFVtgr.106	GHKF01164620.1	-	-
exNFVtgr.107	GHKF01164621.1	-	-
exNFVtgr.108	GHKF01164625.1	-	-
exNFVtgr.109	GHKF01164628.1	-	-
exNFVtgr.110	GHKF01164632.1	-	-
exNFVtgr.111	GHKF01164633.1	-	-
exNFVtgr.112	GHKF01164638.1	-	-

exNFVtgr.113	GHKF01164639.1	-	-
exNFVtgr.114	GHKF01165992.1	-	-
exNFVtgr.115	GHKF01165993.1	-	-
exNFVtgr.116	GHKF01165994.1	-	-
exNFVtgr.117	GHKF01179326.1	-	-
exNFVtgr.118	GHKF01179328.1	-	-
exNFVtgr.119	GHKF01179330.1	-	-
exNFVtgr.120	GHKF01179339.1	-	-
exNFVtgr.121	GHKF01179340.1	-	-
exNFVtgr.122	GHKF01179346.1	-	-
exNFVtgr.123	GHKF01179348.1	-	-
exNFVtgr.124	GHKF01179349.1	-	-
exNFVtgr.125	GHKF01179350.1	-	-
exNFVtgr.126	GHKF01179352.1	-	-
exNFVtgr.127	GHKF01179353.1	-	-
exNFVtgr.128	GHKF01179354.1	-	-
exNFVtgr.129	GHKF01179355.1	-	-
exNFVtgr.130	GHKF01179357.1	-	-
exNFVtgr.131	GHKF01179362.1	-	-

Table S2 Information on the representative retroviruses

No.	Virus name	Genus	Abbreviation	Natural host	Accession no.
1	Avian leukemia virus	Alpharetrovirus	ALV	Chicken	NC_015116
2	Lymphoproliferative disease virus	Alpharetrovirus	LDV	Turkey	U09568
3	Mouse mammary tumor virus	Betaretrovirus	MMTV	Mouse	NC_001503
4	Mason-Pfizer monkey virus	Betaretrovirus	MPMV	Primate	NC_001550
5	Simian retrovirus 1	Betaretrovirus	SRV1	Primate	M11841
6	Bovine leukemia virus	Deltaretrovirus	BLV	Cattle	NC_001414
7	Human T-lymphotropic virus 1	Deltaretrovirus	HTLV1	Human	NC_001436
8	Simian T-lymphotropic virus 2	Deltaretrovirus	STLV2	Non-human primate	NC_001815
9	Walleye dermal sarcoma virus	Epsilonretrovirus	WDSV	Fish	NC_001867
10	Walleye epidermal hyperplasia virus type 1	Epsilonretrovirus	WEHV1	Fish	AF133051
11	Walleye epidermal hyperplasia virus type 2	Epsilonretrovirus	WEHV2	Fish	AF133052
12	Atlantic salmon swim bladder sarcoma virus	Gamma-epsilon	SSSV	Atlantic salmon	NC_007654
13	Feline leukemia virus	Gammaretrovirus	FeLV	Cat	NC_001940
14	Friend murine leukemia virus	Gammaretrovirus	F-MuLV	Mouse	NC_001362
15	Mus dunni endogenous retrovirus	Gammaretrovirus	MDEV	Mouse	AF053745
16	Porcine endogenous retrovirus A	Gammaretrovirus	PERV-A	Pig	AJ293656
17	Rhinolophus ferrumequinum retrovirus	Gammaretrovirus	RfRV	Greater horseshoe bat	JQ303225
18	Equine infectious anemia virus	Lentivirus	EIAV	Horse	NC_001450
19	Feline immunodeficiency virus	Lentivirus	FIV	Cat	NC_001482
20	Human immunodeficiency virus 1	Lentivirus	HIV1	Human	NC_001802
21	Visna/Maedi virus	Lentivirus	VMV	Sheep	NC_001452
22	Bovine foamy virus	Spumavirus	BFVbta	Cattle	NC_001831
23	Equine foamy virus	Spumavirus	EFVeca	Horse	NC_002201
24	Feline foamy virus	Spumavirus	FFVfca	Cat	NC_001871

25	Brown greater galago prosimian foamy virus	Spumavirus	SFVocr	Greater galago	KM233624
26	White-tufted-ear marmoset simian foamy virus	Spumavirus	SFVcja	Common marmoset	GU356395
27	Squirrel monkey simian foamy virus	Spumavirus	SFVssc	Squirrel monkey	GU356394
28	Orangutan Simian foamy virus	Spumavirus	SFVppy	Pongo pygmaeus pygmaeus	AJ544579
29	Macaque simian foamy virus	Spumavirus	SFVmcy	Macaque	NC_010819
30	African green monkey simian foamy virus	Spumavirus	SFVcae	African green monkey	NC_010820
31	Western chimpanzee simian foamy virus	Spumavirus	SFVpve	Western chimpanzee	NC_001364
32	Western lowland gorilla simian foamy virus	Spumavirus	SFVggo	Western lowland gorilla	NC_039029
33	Spider monkey simian foamy virus	Spumavirus	SFVaxx	Spider monkey	NC_039027
34	Sloth endogenous foamy virus	Spumavirus	SloEFV	Sloth	ABVD02350954
35	Sphenodon punctatus endogenous foamy virus	Spumavirus	ERV-Spuma-Spu	Tuatara	Ref. 1
36	Coelacanth endogenous foamy-like virus	Spumavirus	CoeEFV	Coelacanth	Ref. 2
37	Amphilophus citrinellus fomy-like virus	Spumavirus	AciFLERV_1	Midas cichlid	CCOE01002251
38	Amphilophus citrinellus fomy-like virus	Spumavirus	AciFLERV_2	Midas cichlid	CCOE01002087
39	Austrofundulus limnaeus fomy-like virus	Spumavirus	AliFLERV	Annual killifish	Ref. 3
40	Notophthalmus viridescens	Spumavirus	NviFLERV	Eastern newt	Ref. 3
41	latyfish endogenous retrovirus	Spumavirus	PlatyfishEFV	Platyfish	Ref. 4
42	Danio rerio foamy virus	Spumavirus	DrFV-1	Zebrafish	CABZ01054182
43	Cynops pyrrhogaster fomy-like virus	Spumavirus	CpyFLERV_1	Japanese fire belly newt	FS313726
44	Cynops pyrrhogaster fomy-like virus	Spumavirus	CpyFLERV_2	Japanese fire belly newt	FS296312
45	Pleurodeles waltl fomy-like virus	Spumavirus	PwaFLERV	Iberian ribbed newt	JG015238
46	Poecilia reticulata fomy-like virus	Spumavirus	PreFLERV	Guppy	AZHG01028727
47	Poecilia formosa fomy-like virus	Spumavirus	PfoFLERV_1	Amazon molly	AYCK01023761
48	Poecilia formosa fomy-like virus	Spumavirus	PfoFLERV_2	Amazon molly	AYCK01027102
49	Larimichthys crocea fomy-like virus	Spumavirus	LcrFLERV	Large yellow croaker	JRPU01021077

50	<i>Stegastes partitus</i> fomy-like virus	Spumavirus	SpaFLERV	Bicolor damselfish	JMKM01038484
51	<i>Fundulus heteroclitus</i> fomy-like virus	Spumavirus	FheFLERV	Mummichog	JXMV01100753
52	<i>Lates calcarifer</i> fomy-like virus	Spumavirus	LcaFLERV	Barramundi	LBLR01010097
53	<i>Gadus morhua</i> fomy-like virus	Spumavirus	GmoFLERV_1	Atlantic cod	CAEA01131311
54	<i>Gadus morhua</i> fomy-like virus	Spumavirus	GmoFLERV_2	Atlantic cod	CAEA01539013
55	<i>Dicentrarchus labrax</i> fomy-like virus	Spumavirus	DlaFLERV	European bass	CBXY010016181
56	<i>Oreochromis niloticus</i> fomy-like virus	Spumavirus	OniFLERV	Nile tilapia	AERX01018483
57	<i>Cynoglossus semilaevis</i> fomy-like virus	Spumavirus	CseFLERV	Tongue sole	AGRG01002780
58	<i>Sebastes rubrivinctus</i> fomy-like virus	Spumavirus	SruFLERV	Flag rockfish	AUPQ01030678
59	<i>Sebastes nigrocinctus</i> fomy-like virus	Spumavirus	SniFLERV	Tiger rockfish	AUPR01019601
60	<i>Pimephales promelas</i> fomy-like virus	Spumavirus	PprFLERV_1	Fathead minnow	JNCD01073002
61	<i>Pimephales promelas</i> fomy-like virus	Spumavirus	PprFLERV_2	Fathead minnow	JNCD01029789
62	<i>Thunnus orientalis</i> fomy-like virus	Spumavirus	TorFLERV	Pacific bluefin tuna	BADN01112239
63	<i>Periophthalmus magnuspinnatus</i> fomy-like virus	Spumavirus	PmaFLERV	Mudskipper	JACL01052273
64	<i>Periophthalmodon schlosseri</i> fomy-like virus	Spumavirus	PscFLERV	Mudskipper	JACM01000693
65	<i>Anoplopoma fimbria</i> fomy-like virus	Spumavirus	AfiFLERV	Sablefish	AWGY01041462
66	<i>Cyprinus carpio</i> fomy-like virus	Spumavirus	CcaFLERV	Common carp	LN590673
67	<i>Nothobranchius furzeri</i> fomy-like virus	Spumavirus	NfuFLERV	Turquoise killifish	JNBZ01063262
68	<i>Esox lucius</i> fomy-like virus	Spumavirus	EluFLERV	Common pike	AZJR02000232
69	<i>Callorhynchusmilii</i> fomy-like virus	Spumavirus	CmiFLERV_1	Australian ghostshark	XM_007890932
70	<i>Callorhynchusmilii</i> fomy-like virus	Spumavirus	CmiFLERV_2	Australian ghostshark	AAVX02030290
71	<i>Hynobius retardatus</i> fomy-like virus	Spumavirus	HreFLERV	Hokkaido salamander	LE148029
72	Snakehead retrovirus	Unclassified	SnRV	Fish (snakehead fish)	NC_001724

1. Wei X, Chen Y, Duan G, Holmes EC, Cui J. 2019. A reptilian endogenous foamy virus sheds light on the early evolution of retroviruses. *Virus Evol* 5:vez001.
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3. Aiewsakun P, Katzourakis A. 2017. Marine origin of retroviruses in the early Palaeozoic Era. *Nat Commun* 8:13954.
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Data set S1. The nucleotide sequences of consensus genomes of 4 EFVs

>ERV-Spuma.a-Ame Consensus Sequence

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>ERV-Spuma.b-Ame Consensus Sequence

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>ERV-Spuma-Rbi Consensus Sequence

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>ERV-Spuma-Smu Consensus Sequence

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GCATTCTATGTTATAcTCTGTTTTAATTTTGGATTCCGTGAaTTTTTATtATTTTT
cAATAAATAATtACTATgaTGAATTCTCAGTCCTTTCTTATAaTTGTGCTCACgA
TTTCATCTATTGAATGTGAGACCTATCCACAgtATAAAATTGAAATTTGGTA
ACTTATCACTTAGGGTgGAGAATAACCTctTTTTAAGACATTACATGGGAGGA
AAGGTgTGAACCcATCACA

Data set S2. The alignments used to build the phylogenetic trees for RT re presented in Fig.1

>ERV-Spuma.a57-Ame

QYPVKPQAVAHMQTNSRPAMDQGVIIQSCAPSFKPDCTYRFVVDLFRILNAHCK
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>ERV-Spuma.a65-Ame

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MQGYKNAPSIFSSRIQSLADINC-QYVDDI-ITHENISEHV-EVDRTVIHTKGYPI--

>ERV-Spuma.a9-Ame

-HPVKPQAVAHMQTTVDQLMDQGVITSPVLPVLKPDGTYRFIVDFLILKAHCK
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RIMQGYKNSPSTFSSRIQSLADINCWQYVDDIYITHENLSEHLQEVDRTVIHTK
EYLIKKSRIHEVTFLGFTL

>ERV-Spuma.a80-Ame

-----AVPHMQTIVDQLMDQGVITSPVLPVLKPDGIYRFIVDFRILNAHCKTEAV
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>ERV-Spuma.a20-Ame

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>ERV-Spuma.a102-Ame

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TNSPSTFSSIIQSLADINCWQYVDDIYITHENLSKHLQEVDRTVIHTKGYLIKKS
RIAHEVTFLGFTL

>ERV-Spuma.a52-Ame

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YLIKKSRIAHEVTFLGFTL

>ERV-Spuma.a101-Ame

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GYLVKKSRIAHEVTFLGFTL

>ERV-Spuma.a49-Ame

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>ERV-Spuma.a10-Ame

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VTFLGFTL

>ERV-Spuma.a42-Ame

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YLIKKSRTAHEVTFLGFTL

>ERV-Spuma.a21-Ame

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GYLIKKSRIAH-VTFLGFTL

>ERV-Spuma.a54-Ame

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>ERV-Spuma.a97-Ame

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>ERV-Spuma.a74-Ame

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VMQGYKNPSTFSSRIQSLLADINCCQYV-DIYITHENLSEHLQEVERTVIHTKGY
LIKKSRIAHEVTFLGFTL

>ERV-Spuma.a96-Ame

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>ERV-Spuma.a63-Ame

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>ERV-Spuma.a79-Ame

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>ERV-Spuma.a73-Ame

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YLIRKSGIANEDVFLGFTL

>ERV-Spuma.a13-Ame

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I-----

>ERV-Spuma.a26-Ame

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>ERV-Spuma.a62-Ame

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>ERV-Spuma.a85-Ame

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-IMQWYKSSPSTFSSRIQSLLADINCWQNVDDI-ITHENLGEHLQEVDKSFTSKD
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>ERV-Spuma.a22-Ame

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AHEVTFLGFSL

>ERV-Spuma.a83-Ame

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QSLLADINLGQYVDDIYITHENHIEHLQEVNRVIHTKGYPIKKSRIAHEVTFLG
FTL

>ERV-Spuma.a84-Ame

QYPVTPQAVVHVQTISSRLAHITLMVPTVL-----LILEF----MHTKTEAVQNNQ
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GIAHEVTLVGFSL

>ERV-Spuma.a69-Ame

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LGYLSHSF

>ERV-Spuma.b11-Ame

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>ERV-Spuma.b10-Ame

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>ERV-Spuma.b6-Ame

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>ERV-Spuma.b1-Ame

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>ERV-Spuma.b16-Ame

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>ERV-Spuma.b17-Ame

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>ERV-Spuma.b5-Ame

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K--IFKKSIAHEVTFLGFTL

>ERV-Spuma.b12-Ame

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>ERV-Spuma.a58-Ame

SRPANGPG-----INHSVLPVLKPDGTPF----YCRFNFECTLDRGRPEPTF
WIASQL--TQMINKPSRQWYFTQPLSVETAFTFKGTHFQFTRIMRGYKNSPST
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>ERV-Spuma.a7-Ame

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>exNFVtwe.17

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>exNFVtwe.30

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>exNFVtwe.16

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>exNFVtgr.88

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>exNFVtgr.86

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>exNFVtgr.85

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>exNFVtgr.84

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>exNFVtgr.83

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>CpyFLERV-1

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F-----

>exNFVtgr.20

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>exNFVtgr.23

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>exNFVtgr.25

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>CpyFLERV-2

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>NviFLERV

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>PwaFLERV

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DF-VLFLGHKL

>ERV-Spuma.a24-Ame

QYPVKPHAVGHMQTIVDQLMDQGVII SPVLPVLKPHGTYHFIVDFRILNAHCK
SRPEPTQF-----WMDCKKQTNLSLGN-----SFPFTRIMQGIKHSQAEY
RAYLQTFLI-----VAVHHPNLSEHLQEVDRIHTKGYLIKTKIKNSSGYLSH
TF

>ERV-Spuma.12-Smu

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>ERV-Spuma.4-Smu

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VKKSQIARKVTFLGFDI

>ERV-Spuma.2-Smu

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VKKSQIARKVTFLGFDI

>ERV-Spuma.5-Smu

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>ERV-Spuma.17-Smu

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VKKSQIARKVTFLGFDI

>ERV-Spuma.16-Smu

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VKKSQIARKVTFLGFDI

>ERV-Spuma.9-Smu

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VKKSQIARKVTFLGFDI

>ERV-Spuma.1-Smu

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V-----

>ERV-Spuma.15-Smu

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V-----

>ERV-Spuma.3-Smu

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>BFVbta

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>EFVeca

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>FFVfca

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>SFVcae

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>SFVmcy

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>SFVggo

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>SFVpve

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>SFVppy

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>SFVaxx

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>SFVssc

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>SFVocr

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>CoeEFV

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>LmeFLERV

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>ERV-Spuma-Cma

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>ERV-Spuma-Cbo

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>SloEFV

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>ERV-Spuma-Spu

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>ERV-Spuma.41-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLPVPKPNGSTRMVIDYRVLNASSET
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>ERV-Spuma.10-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.45-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.60-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.46-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLPVPKPNGSTRMVIDYRVLNASSET
VAAQTLNPASTIDNLPRPRWKATLDLANGFWSIPISTSTAFTFRGKQYQYTRLP
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VAKARIGFEVKFLGFLI

>ERV-Spuma.35-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.34-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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QGFKNSPVLFSAAVEELLQNINAVPYVDDIYLASDKLDVLWDSVVQLIQVEGF
VVAKARIGFEVKFLGFLI

>ERV-Spuma.4-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.6-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.14-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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QGFKNSPVLFSAAVEELLQNINAVPYVDDIYLASDKLDVLWDSVVQLIQVEGF
VVAKARIGFEVKFLGFLI

>ERV-Spuma.23-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.11-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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QGFKNSPVLFSAAVEELLQNINAVPYVDDIYLASDKLDVLWDSVVQLIQVEGF
VVAKARIGFEVKFLGFLI

>ERV-Spuma.26-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLSPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.42-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.37-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.21-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.36-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.3-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.65-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.43-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.15-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.1-Rbi

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VVAKARIGFEVKFLGFLI

>ERV-Spuma.31-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.24-Rbi

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VVAKARIGFEVKFLGFLI

>ERV-Spuma.13-Rbi

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VVAKARIGFEVKFLGFLI

>ERV-Spuma.58-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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>ERV-Spuma.56-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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>ERV-Spuma.32-Rbi

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>ERV-Spuma.22-Rbi

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>ERV-Spuma.9-Rbi

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>ERV-Spuma.67-Rbi

QYPVHKKFYNDLNIIISQKLTRGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.52-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VVAKARIGFEVKFLGFLI

>ERV-Spuma.63-Rbi

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>ERV-Spuma.50-Rbi

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KARIGFEVKFLGFLI

>ERV-Spuma.8-Rbi

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VVAKARIGFEVKFLGFLI

>ERV-Spuma.47-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.57-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.55-Rbi

QYPVHKKFYHDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VVATARIGFEVKFLGFLI

>ERV-Spuma.29-Rbi

QYPVHKKFYNDLNIIISQKLTQGVLISPLLVPKPNGSTRMVIDYRVLNASSET
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VAKARIGFEVKFLGFLI

>ERV-Spuma.30-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.2-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.12-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.25-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.27-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.66-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.54-Rbi

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VAKARIGFEVKFLGFLI

>ERV-Spuma.61-Rbi

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IAKARIGFGVKFLGFLI

>ERV-Spuma.62-Rbi

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IAKARIGFGVKFLGFLI

>ERV-Spuma.51-Rbi

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VIAKARIGFEVVFLGFLI

>exCFVrbi.6

-----ITAIPYVDVIYLASDKLDVLWNSVVKLIQVEGFVAKARIG
FEVKFLGFLI

>ERV-Spuma.33-Rbi

QYLVH-TFWNDLNIIIFQKLTQGV LISPLLPV PKPNGSTRMVIDYRVLNASSETV
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GFKNSPVLFSAAVEELLQNITAIPYVDVIYL ASDKLDVLWNSVVKLIHVEGFVI
AKARISFEVKFLGFLI

>ERV-Spuma.18-Rbi

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QG---SPVLFSAAVEELLQNINAIPYVDDIYL ASDKLDVLWNSVVKLIQVEGFVI
AKARIGFEVKFLGFLI

>ERV-Spuma.28-Rbi

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VIAKARIGFEVS--GIFN

>AciFLERV-1

QYPLNPGAVKEMDLIVRELLTLGVIRSPIQAVKKPEGGWRPVINFKALNRRTV
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>LcaFLERV

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>JSpaFLERV

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>OniFLERV

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>JXFheFLERV

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>SruFLERV

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>SniFLERV

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>DrFV-1

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>PprFLERV-1

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>PprFLERV-2

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>CcaFLERV

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>AfiFLERV

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>NfuFLERV

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>PmaFLERV

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>AciFLERV-2

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>EluFLERV

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>TorFLERV

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>CmiFLERV-1

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>HreFLERV

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VFL---L

>SnRV

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>MDEV

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>PERV-A

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>RfRV

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>WDSV

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>WEHV-2

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>ALV

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>LDV

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>SRV-1

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>BLV

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>STLV-2

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>EIAV

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>FIV

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>HIV-1

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>XtrFLERV

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ACTPVLEF-L

**Data set S3. The alignments used to build the phylogenetic trees for Pol r
represented in Fig.3**

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>FFVfca

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>SFVcae

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>SFVpve

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>SFVggo

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>SFVppy

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>SFVaxx

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>SFVssc

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>SFVocr

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>ERV-Spuma-Cma

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>ERV-Spuma_Cbo

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>ERV-Spuma-Spu

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>CoeEFV

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>SloEFV

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>ERV-Spuma-Smu

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>AciFLERV-1

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>AliFLERV

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>PlatyfishEFV

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>exCFVrbi.6

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>ERV-Spuma-Rbi

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>ERV-Spuma.b-Ame

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>ERV-Spuma.a-Ame

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>PfoFLERV-2

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>PfoFLERV-1

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>PreFLERV

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>LcrFLERV

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>JSpaFLERV

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>LcaFLERV

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PQANGVVER

>JXfheFLERV

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>CseFLERV

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>DrFV-1

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>PprFLERV-1

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>PprFLERV-2

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LTC DSEYVADGLNKHKEQWEKIAETVHCYHQVHPSYNIQME LRLRNL
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>CcaFLERV

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>PmaFLERV

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>AciFLERV-2

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>NfuFLERV

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>NviFLERV

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>exNFVtgr.84

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>exNFVtwe.30

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HTAHAGVQATITLLQQR CRRTKQYVLCDDICQQIKGSNIKRRPL-----

**Data set S4. The alignments used to build the phylogenetic trees for Env r
e presented in Fig.3**

>exNFVtwe.26

SQQDAAARLRQIDQKNLQKALAVVDNGMNILSDRIYTLNNIVSSAIDIIQSDVS
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YKGVPPVIRPVFQVLSNGSYVLLNSEDCCGM RAGIVYIVSVSMIVTCCGNV
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>NviFLERV

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>exNFVtgr.91

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>exNFVtgr.9

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>ERV-Spuma.b-Ame

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>ERV-Spuma.a-Ame

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>SloEFV

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>SFVppy

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>SFVcae

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>SFVaxx

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>SFVcja

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>SFVocr

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>BFVbta

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>FFVfca

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>ERV-Spuma-Cma

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>ERV-Spuma-Cbo

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>ERV-Spuma-Hha

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>ERV-Spuma-Ppi

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>ERV-Spuma-Gja

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>ERV-Spuma-Spu

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>ERV-Spuma-Smu

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>CoeEFV

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>exCFVrbi.5

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>ERV-Spuma-Rbi

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>AciFLERV

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>AliFLERV

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LEEEGF EWVGP

Data set S5. The alignments used to build the phylogenetic trees for Gag-Pol-Env represented in Fig.4

>ERV-Spuma.a-Ame

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>ERV-Spuma.b-Ame

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>exNFVtwe

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>exNFVtgr

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IENGFESARGKTVAHKELWEKIAELRTQL-DLDVEHQKAHTK--EGSYWEGND
EVDRFVQQRKIVLIGAEK-----VTPKGKEVPEYVAEVVVTMHGHLGAGL
LPTRRGLVKQNLWIPM-KQIQVLRCTVCGKYNAGRRGKRTEGLTIKSTIPW
GSICMDVAGPMTGKGEKYLIVLVDSMSGFVVVRPVRKANGNSVVSMLDYT
CALGIPRELRTDNGTHFKNVQVNRWCEQHGMVRYSPPYTPQANGVAECTIG
LVKNWLAKN--ANSKEWSLKSVDIGRALNDRDRAG-RSPSPDEL----NQRPFV---
TEETGRSQEADPAPLEACPFVAVGQK VWL KARSTGAVKPKYEEVDTVTKVLDQ
NTVLLKKK----GIQGVQLK PALMTGKPTSQKNPLPKHSCGKYGNLTCWNTS
ARNLFMPWDANQTS ENQTDSWNRKRMGTDELAR-QNFSTDHRWTISNLLAT
EDHETKTTKCNWIQPEGEPPEHQGYWQYEAVFPAPHKHIFEFWGHYDLKCDK
IP---EKYN--TVDECLADITRLDSCIMPLGPLWFQTYYYTWRSIFSPTRAMHEE
WLNYTFVHYEGDFPEG-----STRNRG-----VQKLPTVQELKSVPKGD FDKI
DKCVARRIFLSLNDSEWEGHGASPRCKLWQVDISFVSTWRYDCTGINSTKELL
QGWVEGHSRDKTRTWGWFQR----EEMEHVVIPCLSQSDNY-WVKYQYIATVY
SKEHIWSSAIYRPRDRYVRPRPWK-----TCIKSGH-ACTVSLARRPCSELATVWT
KTRPTTYTKLISNATNTWRRAMACDHCVIPSPDTMITIAESHACLGLEEEFE
WVG--PNLLYSNLTCKYPEEVPDSDKH---TCAWYETLQTMAREVKTLAKGAIE
IVAEGAGAVEEG----MVELLEKIWPYCLTLGILVLAACLALRELC