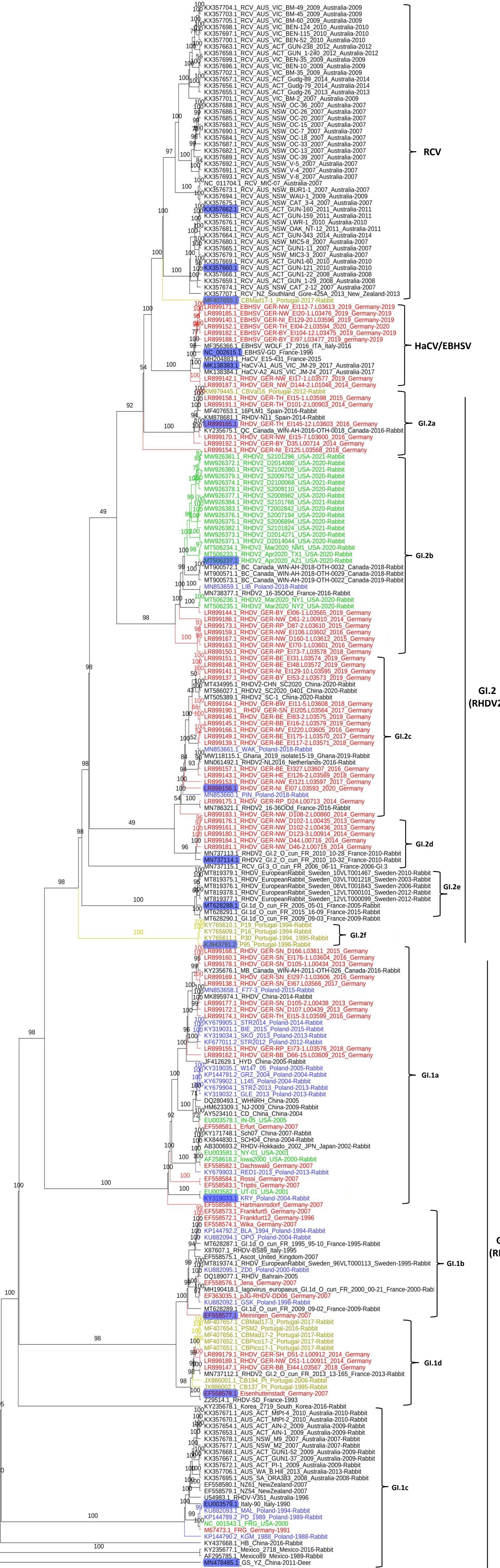


Genetic characteristics and phylogeographic dynamics of Lagoviruses, 1988-2021

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Supplementary Figure 1. The phylogenetic tree based on the full-length genome sequences of lagoviruses, 1988-2021. The unrooted ML phylogenetic tree of 240 full-length Lagovirus genomes classifying all the strains into four major clades (RCV, HaCV/EBHSV, GI.1/RHDV and GI.2/RHDV2). GI.1 can be further classified into four sub-clades (1a-1d) and GI.2 into six sub-clades (2a-2f). The major clades and sub-clades of the RHDV are indicated. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are indicated at each node. The evolutionary distances were computed using the best-fit substitution model (SYM+I+G4). The red color clades represent Germany (n=69), green USA (n=24), blue Poland (n=22) and yellow color represents Portugal (n=13). The tree was visualized and modified proportionally using FigTree v1.4. The viruses used in genomic similarity analysis (Figure 2) are highlighted using blue boxes.

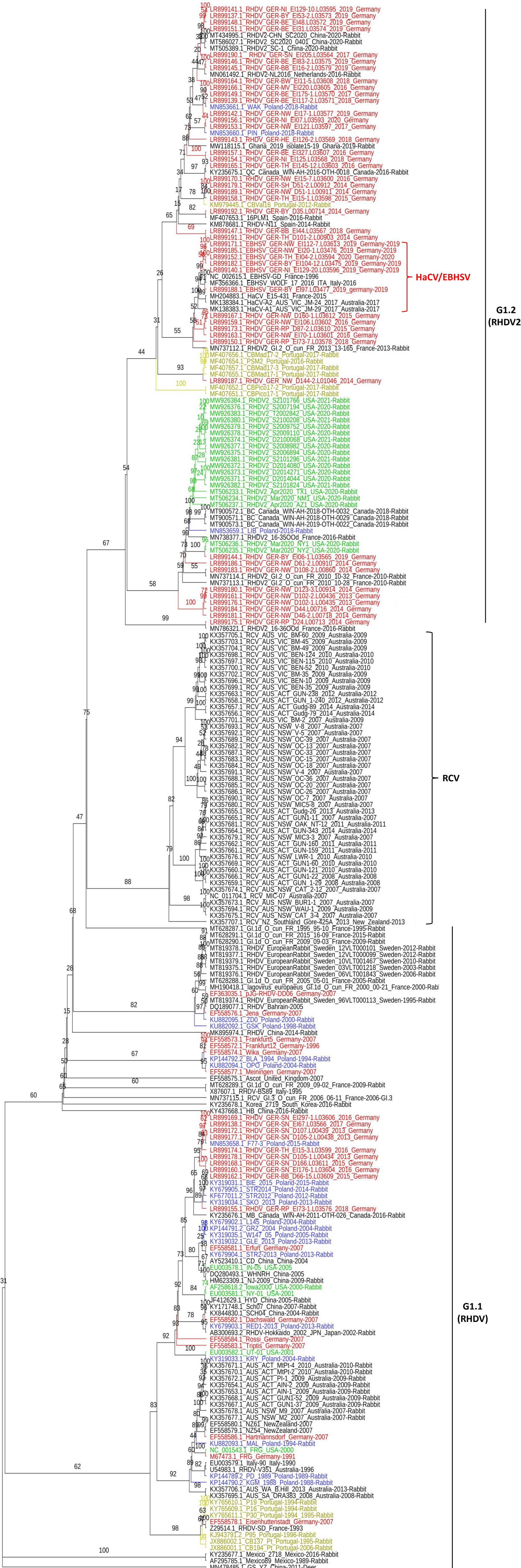


Phylogenetic tree showing the relationships between various RHDV and EBHSV strains. The tree is rooted on the left and branches out to the right. Strains are labeled with accession numbers, host names, and locations. The tree is color-coded by clade: G1.2c (red), G1.2a (yellow), G1.2b (green), G1.2d (blue), RCV (purple), HaCV/EBHSV (orange), G1.1a (pink), G1.1d (brown), G1.1b (grey), and G1.1c (black). Bootstrap values are shown at the nodes. The tree shows a clear separation between the G1.2 clades and the other clades, with G1.2c and G1.2a being the most closely related.

G1.2c

LR899151.1 RHDV GER-BE E131.L03574_2019 Germany
 LR899148.1 RHDV GER-BE E148.L03572_2019 Germany
 LR899141.1 RHDV GER-NI E129-10.L03595_2019 Germany
 LR899137.1 RHDV GER-BY E153-2.L03573_2019 Germany
 LR899164.1 RHDV GER-BW E111-5.L03608_2018 Germany
 LR899190.1 RHDV GER-SN E1205.L03564_2017 Germany
 LR899166.1 RHDV GER-MV E1220.L03605_2016 Germany
 LR899149.1 RHDV GER-BE E1175-1.L03570_2017 Germany
 LR899139.1 RHDV GER-BE E1117-2.L03571_2018 Germany
 MN853661.1 WAK Poland-2018-Rabbit
 MT505389.1 RHDV2 SC-1 China-2020-Rabbit
 MT434995.1 RHDV2 CHN SC2020 China-2020-Rabbit
 MT586027.1 RHDV2 SC2020_0401 China-2020-Rabbit
 LR899146.1 RHDV GER-BE E183-2.L03575_2019 Germany
 LR899145.1 RHDV GER-BB E116-2.L03579_2019 Germany
 LR899142.1 RHDV GER-NW E117-1.L03577_2019 Germany
 MW118115.1 Ghana 2019 isolate15-19 Ghana-2019-Rabbit
 MN061492.1 RHDV2-NL2016 Netherlands-2016-Rabbit
 LR899156.1 RHDV GER-NI E107.L03593_2020 Germany
 LR899143.1 RHDV GER-HE E1126-2.L03569_2018 Germany
 MN853660.1 PIN Poland-2018-Rabbit
 LR899153.1 RHDV GER-NW E1121.L03597_2017 Germany
 LR899157.1 RHDV GER-BE E1327.L03607_2016 Germany
 LR899154.1 RHDV GER-NI E1125.L03568_2018 Germany
 MF407653.1 16PLM1 Spain-2016-Rabbit
 LR899191.1 RHDV GER-TH D101-2.L00903_2014 Germany
 LR899187.1 RHDV GER NW D144-2.L01046_2014 Germany
 LR899173.1 RHDV GER-RP D87-2.L03610_2015 Germany
 LR899163.1 RHDV GER-NW E170-1.L03601_2016 Germany
 LR899159.1 RHDV GER-NW E1106.L03602_2016 Germany
 LR899167.1 RHDV GER-NW D160-1.L03612_2015 Germany
 LR899150.1 RHDV GER-RP E173-7.L03578_2018 Germany
 LR899147.1 RHDV GER-BB E144.L03567_2018 Germany
 MN737112.1 RHDV2 Gl.2 O cun FR 2013 13-165 France-2013-Rabbit
 LR899158.1 RHDV GER-TH E115-1.L03598_2015 Germany
 KM979445.1 CBVal16 Portugal-2012-Rabbit
 MF407657.1 CBMad17-3 Portugal-2017-Rabbit
 MF407654.1 PSM2 Portugal-2016-Rabbit
 MF407656.1 CBMad17-2 Portugal-2017-Rabbit
 MF407652.1 CBPico17-2 Portugal-2017-Rabbit
 MF407651.1 CBPico17-1 Portugal-2017-Rabbit
 LR899179.1 RHDV GER-SH D51-2.L00912_2014 Germany
 LR899189.1 RHDV GER-NW D51-1.L00911_2014 Germany
 MF407655.1 CBMad17-1 Portugal-2017-Rabbit
 KM878681.1 RHDV-N11 Spain-2014-Rabbit
 LR899165.1 RHDV GER-TH E1145-12.L03603_2016 Germany
 KY235675.1 QC Canada WIN-AH-2016-OTH-0018 Canada-2016-Rabbit
 LR899170.1 RHDV GER-NW E115-7.L03600_2016 Germany
 LR899192.1 RHDV GER-BY D35.L00714_2014 Germany
 MW926373.1 RHDV2 D2014271 USA-2020-Rabbit
 MW926371.1 RHDV2 D2014044 USA-2020-Rabbit
 MW926372.1 RHDV2 D2014080 USA-2020-Rabbit
 MW926380.1 RHDV2 S2100208 USA-2021-Rabbit
 MW926381.1 RHDV2 S2101296 USA-2021-Rabbit
 MW926379.1 RHDV2 S2009752 USA-2020-Rabbit
 MW926378.1 RHDV2 S2009110 USA-2020-Rabbit
 MW926374.1 RHDV2 D2100068 USA-2021-Rabbit
 MW926377.1 RHDV2 S2008982 USA-2020-Rabbit
 MW926384.1 RHDV2 S2101766 USA-2021-Rabbit
 MW926383.1 RHDV2 T2002842 USA-2020-Rabbit
 MW926376.1 RHDV2 S2007194 USA-2020-Rabbit
 MW926375.1 RHDV2 S2006894 USA-2020-Rabbit
 MW926382.1 RHDV2 S2101824 USA-2021-Rabbit
 MT506237.1 RHDV2 Apr2020 AZ1 USA-2020-Rabbit
 MT506233.1 RHDV2 Apr2020 TX1 USA-2020-Rabbit
 MT506234.1 RHDV2 Mar2020 NMI USA-2020-Rabbit
 MT900572.1 BC Canada WIN-AH-2018-OTH-0032 Canada-2018-Rabbit
 MT900571.1 BC Canada WIN-AH-2018-OTH-0029 Canada-2018-Rabbit
 MT900573.1 BC Canada WIN-AH-2019-OTH-0022 Canada-2019-Rabbit
 MN853659.1 LIB Poland-2018-Rabbit
 MN738377.1 RHDV2 16-350Od France-2016-Rabbit
 MT506236.1 RHDV2 Mar2020 NY1 USA-2020-Rabbit
 MT506235.1 RHDV2 Mar2020 NY2 USA-2020-Rabbit
 LR899144.1 RHDV GER-BY E106-1.L03565_2019 Germany
 LR899180.1 RHDV GER-NW D123-3.L00914_2014 Germany
 LR899176.1 RHDV GER-NW D102-1.L00435_2013 Germany
 LR899161.1 RHDV GER-NW D102-2.L00436_2013 Germany
 LR899184.1 RHDV GER-NW D44.L00716_2014 Germany
 LR899181.1 RHDV GER-NW D46-2.L00718_2014 Germany
 MN737113.1 RHDV2 Gl.2 O cun FR 2010 10-28 France-2010-Rabbit
 LR899186.1 RHDV GER-NW D61-2.L00910_2014 Germany
 MN737114.1 RHDV2 Gl.2 O cun FR 2010 10-32 France-2010-Rabbit
 LR899183.1 RHDV GER-NW D108-2.L00860_2014 Germany
 LR899175.1 RHDV GER-RP D24.L00713_2014 Germany
 MN786321.1 RHDV2 16-360Od France-2016-Rabbit
 KX357704.1 RCV AUS VIC BM-49 2009 Australia-2009
 KX357703.1 RCV AUS VIC BM-45 2009 Australia-2009
 KX357705.1 RCV AUS VIC BM-60 2009 Australia-2009
 KX357698.1 RCV AUS VIC BEN-124 2010 Australia-2010
 KX357697.1 RCV AUS VIC BEN-115 2010 Australia-2010
 KX357700.1 RCV AUS VIC BEN-52 2010 Australia-2010
 KX357663.1 RCV AUS ACT GUN-238 2012 Australia-2012
 KX357658.1 RCV AUS ACT GUN 1-240 2012 Australia-2012
 KX357702.1 RCV AUS VIC BM-35 2009 Australia-2009
 KX357696.1 RCV AUS VIC BEN-10 2009 Australia-2009
 KX357699.1 RCV AUS VIC BEN-35 2009 Australia-2009
 KX357701.1 RCV AUS VIC BM-2 2007 Australia-2009
 KX357657.1 RCV AUS ACT Guld-89 2014 Australia-2014
 KX357656.1 RCV AUS ACT Guld-79 2014 Australia-2014
 KX357693.1 RCV AUS NSW V-8 2007 Australia-2007
 KX357692.1 RCV AUS NSW V-5 2007 Australia-2007
 KX357691.1 RCV AUS NSW V-4 2007 Australia-2007
 KX357682.1 RCV AUS NSW OC-13 2007 Australia-2007
 KX357690.1 RCV AUS NSW OC-7 2007 Australia-2007
 KX357684.1 RCV AUS NSW OC-18 2007 Australia-2007
 KX357687.1 RCV AUS NSW OC-33 2007 Australia-2007
 KX357688.1 RCV AUS NSW OC-36 2007 Australia-2007
 KX357686.1 RCV AUS NSW OC-26 2007 Australia-2007
 KX357685.1 RCV AUS NSW OC-20 2007 Australia-2007
 KX357689.1 RCV AUS NSW OC-39 20

Supplementary Figure 3. The phylogenetic tree based on VP10 coding sequences of Lagoviruses, 1988-2021. An unrooted ML phylogenetic tree of 240 VP10 coding sequences of Lagoviruses classifying all the strains into three major clades (GI.1/RHDV, RCV and GI.2/RHDV2). All the HaCV/EBHSV strains appeared within the GI.2/RHDV2 clade. The major clades and sub-clades of the RHDV are indicated. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are indicated at each node. The evolutionary distances were computed using the best-fit substitution model (TIM+*F*+*I*+*G*+4). The red color clades represent Germany (n=69), green USA (n=24), blue Poland (n=22) and yellow color represents Portugal (n=13). The trees were constructed with IQ-TREE v1.6.12, visualized and modified proportionally using FigTree v1.4.



Supplementary Figure 4. The phylogenetic analysis based on the indicated fragments of lagovirus genomes involved in recombination events. Phylogenetic tree based on the region nt 1 to 3,500 (**A**), nt 3501 to 5200 (**B**), and nt 5201 to 7437 (**C**) of lagovirus genome. The viruses involved in recombination events are labelled with different symbols in the phylogenetic trees constructed using the neighbour-joining method. The recombinant, major parent and minor parent are indicated with red, orange, and blue colors respectively. The nucleotide sequence is relative to virus FRG (Germany-1991)(GenBank: M67473.1).

