

Introduction/background

Morbillivirus is highly infectious, spreading via respiratory pathways and causing severe illness and high mortality. The genus includes Measles virus (MV), Rinderpest virus (RPV), peste des petits ruminants virus (PPRV), and the focus of this study, canine distemper virus (CDV). Canine distemper virus (CDV) infects carnivores and is known for its severe immunosuppressive effects. An infection with CDV can lead to the destruction of nearly all lymphocytes in the host (de Vries et al. 2015). CDV is capable of causing outbreaks in various species, including phocids, felids, and primates (Belser, Katz and Tumpey; 2011, Qiu, W. 2011). It exhibits interspecies transmission, with a broad host range and adaptability. This paper investigates the transmission dynamics of canine distemper virus (CDV) from *Vulpes vulpes* (red fox) to CDV-susceptible mammals. Studies such as Kumar et al. (2021), Di Sabatino et al. (2014), and Beineke et al. (2015) have explored zoonotic pathways involving red foxes. By integrating phylogenetic, ecological, and spatial analyses, this study assesses zoonotic risks, impacts on vulnerable species, and human health threats. These insights support targeted conservation, vaccination, habitat management, and public health measures to prevent outbreaks and protect ecosystems.

Methods

The canine distemper virus (CDV), identified by the NCBI accession number NC_001921.1, was analyzed using the BLASTn tool against the Core Nucleotide BLAST database. From the results, RNA polymerase (L) gene sequences from various host species were selected, and the outputs were saved in FASTA format. 23 sequences were collected, including outgroup sequences from other Morbillivirus species. The selected sequences were aligned using Clustal Omega for multiple sequence alignment, as detailed in the appendix. The alignment data was then used to construct a phylogenetic tree, which was visualized using iTOL (Interactive Tree of Life). A rectangular, midpoint-rooted phylogenetic tree was generated to represent evolutionary relationships. The focal host species selected is *Vulpes vulpes* (red fox), chosen for its extensive geographic distribution and adaptability to diverse habitats, including areas shared with human populations. The study evaluates the risk of CDV spillover into other wildlife species and assess potential threats to human populations due to the overlapping habitats of red foxes. The list of susceptible species includes terrestrial and aquatic species that are ecologically and geographically linked to *Vulpes vulpes*. Many of these species, such as *Pusa caspica* and *Mustela lutreola*, are of high conservation concern due to their endangered status (Table 1 in Appendix). The inclusion of species

like *Panthera pardus* and *Lupulella mesomelas* emphasizes the potential for cross-species transmission in diverse habitats. This selection aims to evaluate the broader risks of CDV spillover and its impact on wildlife conservation. Uniform susceptibility across species was assumed for this analysis. Distribution data for *Vulpes vulpes* and the selected CDV-susceptible species were sourced from the IUCN Red List database. The map was generated in R using tools such as sf, ggplot2, and rnaturalearth for geographic visualization. The range of *Vulpes vulpes* was depicted with a striped pattern, overlaid with filled polygons representing the distributions of CDV-susceptible species, each assigned a unique color (Fig. 2). Spatial overlap between the ranges of *Vulpes vulpes* and susceptible species was quantified using geographic information system (GIS) tools, calculating both the absolute area of overlap and the percentage overlap relative to each susceptible species' total range. The geographic ranges of *Vulpes vulpes* (red fox) and selected CDV-susceptible species were analyzed alongside human population density data to identify overlapping regions. Species distribution data were sourced from the IUCN Red List, and human population density information was obtained from global datasets like GPWv4. High-risk areas were determined by isolating the top 5% of human population density values within each species' range and mapping these regions (Fig.3). This method allowed for a comprehensive evaluation of potential hotspots where human-wildlife interactions may heighten the risk of *Canine distemper virus* (CDV) transmission.

Results

The phylogenetic tree (Fig. 1) depicts the evolutionary relationships among various morbilliviruses, including *Canine distemper virus* (CDV) isolates from diverse hosts and geographic regions. Outgroup species are included to provide rooting and context. The phylogenetic tree reveals distinct clustering of CDV isolates based on host species, such as dogs, raccoons, seals, and lions, as well as geographic regions like China and Japan. This highlights the virus's adaptability and its potential for cross-species transmission among diverse terrestrial and diverse terrestrial and aquatic mammals. Fig.2 highlights the spatial overlap between the focal species, *Vulpes vulpes* (red fox), and selected CDV-susceptible species. Key species showing extensive overlap include *Panthera leo* (lion), *Panthera pardus* (leopard), and *Mustela lutreola* (European mink), emphasizing the potential for CDV spillover. Quantitative analysis of the overlaps revealed that the highest percentage of range overlap occurred with *Procyon lotor* (raccoon). This further depicts the risk of CDV spillover to domestic animals, increasing concern for human healthcare. Table 1 depicts the quantitative analysis of spatial overlap. From this table we see species such as *Pusa sibirica* (Baikal seal) exhibiting minimal distribution overlap with red foxes. Although they may not live in the same habitat, these two species may

transmit CDV directly on coastal areas, and indirectly due to environmental contamination and scavenging behaviours. It is therefore essential to monitor CDV in both aquatic and terrestrial wildlife. This further underscores the diverse ecosystems and host species at risk, reinforcing the importance of understanding spatial dynamics to predict and mitigate spillover risks.

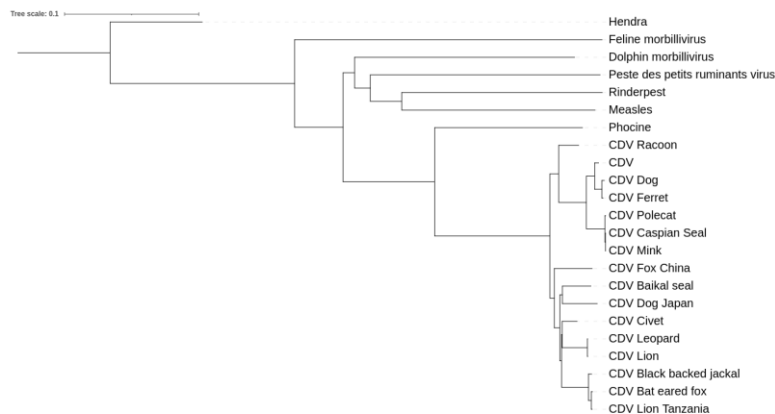


Figure 1. A midpoint-rooted phylogenetic tree of the Morbillivirus genus constructed using partial RNA polymerase (L) protein sequences.

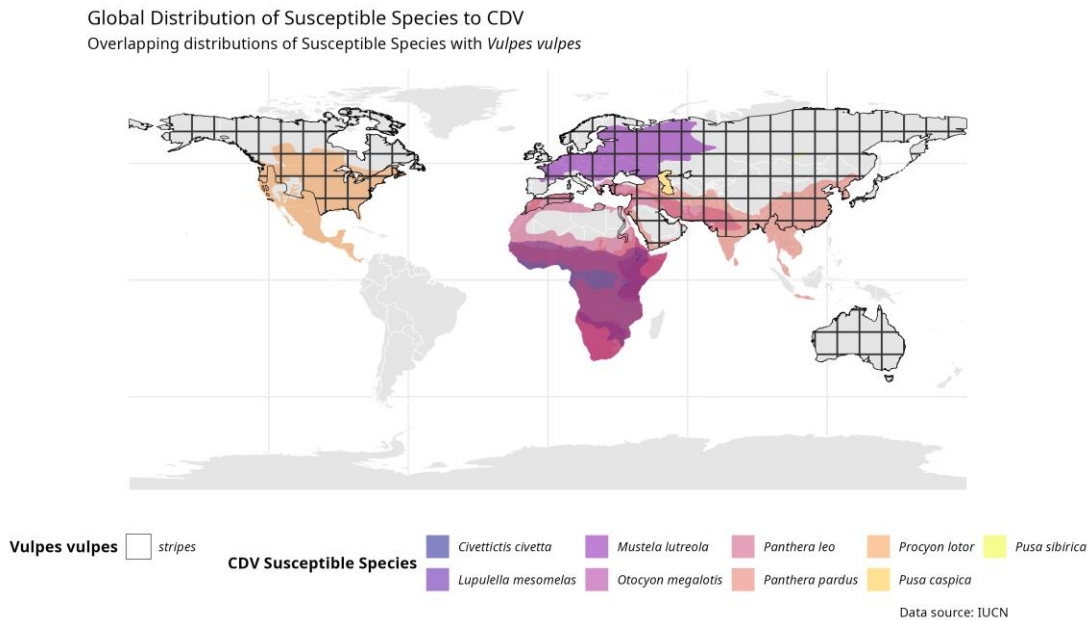


Figure 2. Global distribution of *Vulpes vulpes* and CDV-susceptible species. Overlapping areas highlight the geographic ranges of the red fox (striped) and other species at risk of CDV spillover. Data source: IUCN.

Table 1. Quantitative analysis of the spatial overlap between *Vulpes vulpes* (red fox) and CDV-susceptible species. Including the total range area of each susceptible species, the area of overlap with *Vulpes vulpes*, and the percentage of the susceptible species' range that overlaps with the red fox. **delimitate a limitation in the distribution due to both species being aquatic, do not directly overlap with foxes, but may be in contact with them.

CDV Susceptible Species	Area range of Species (km ²)	Area of Overlap with <i>Vulpes vulpes</i> (km ²)	% Area Overlap with <i>Vulpes vulpes</i>
<i>Mustela lutreola</i>	11167190000000	6775602000000	60.67
<i>Panthera leo</i>	16734800000000	4021887000000	24.03
<i>Panthera pardus</i>	5429129000000	3719261000000	68.51
<i>Procyon lotor</i>	20595150000000	15260190000000	74.1
<i>Pusa caspica</i>	699167300000	11391170000000	**
<i>Pusa sibirica</i>	90125990000	90125990000	**

The analysis of spatial overlap between *Vulpes vulpes* (red fox) and CDV-susceptible species with areas of high human population density reveals distinct trends. Species such as *Civettictis civetta* and *Panthera pardus*, whose ranges intersect densely populated regions, demonstrate elevated median population densities, suggesting a heightened likelihood of human-wildlife interactions. This overlap is particularly significant in zones experiencing urban expansion or agricultural development, where habitat encroachment facilitates increased contact between species and humans. This overlap does not directly signify an interaction between humans and species, as leopards avoid humans due to their elusive and nocturnal nature. However, their behavior can vary depending on the region, availability of prey, and level of habitat encroachment. It is therefore also important to consider animal behaviour in future research. Although racoons have less overlap with high human density locations, but suburban ecosystems and therefore increase risk of spillover in peri-urban landscapes where human-wildlife interfaces are frequent. Overall, species residing in mixed or fragmented habitats are at greater risk due to their proximity to human settlements. These findings emphasize the necessity of implementing focused surveillance and mitigation strategies in regions with significant spatial overlap to mitigate spillover risks and protect both biodiversity and public health.

Table 2. Summary of human population density metrics within the geographic ranges of CDV-susceptible species. The table includes the scientific names of the species, their mean, median, minimum, and maximum population density values (people per km²) within their ranges.

Scientific name	Mean density	Median density	Min density	Max density
<i>Otocyon megalotis</i>	37.32	9.90	0	6646.63
<i>Lupulella mesomelas</i>	49.45	12.27	0	6646.63
<i>Pusa caspica</i>	136.91	7.22	0	5209.26
<i>Panthera pardus</i>	458.61	35.58	0	29819.70
<i>Civettictis civetta</i>	408.61	183.54	0	17154.54
<i>Mustela lutreola</i>	63.34	16.27	0	11588.53
<i>Pusa sibirica</i>	3.52	0.98	0	676.92

<i>Procyon lotor</i>	17.41	1.64	0	11672.90
<i>Panthera leo</i>	28.77	11.17	0	29819.70
<i>Mustela putorius</i>	89.97	26.77	0	11588.53

Global Distribution of CDV Species and Human Population Density Hotspots
Overlapping distributions of CDV species with human population hotspots

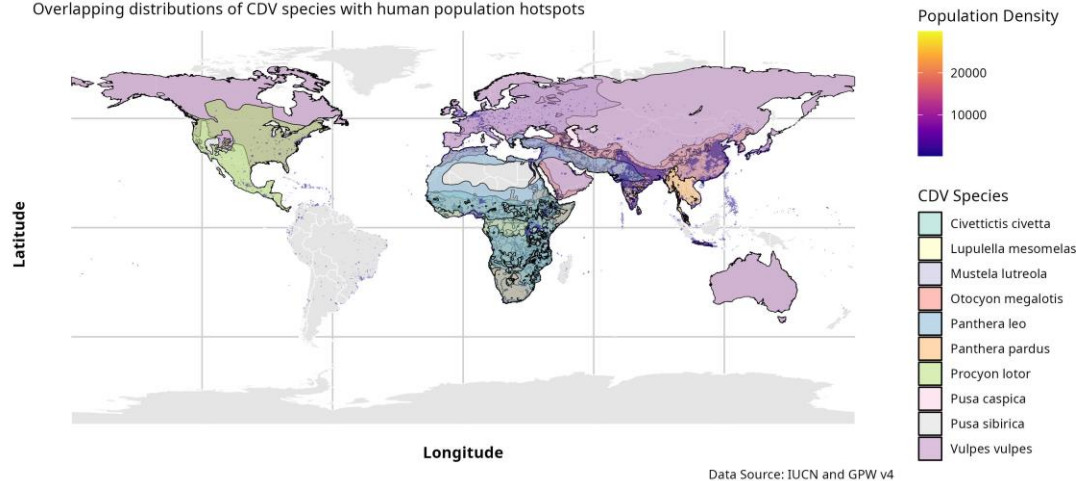


Fig 3 Spatial overlap between red fox, selected CDV susceptible species and humans.

Discussion & Mitigation

CDV poses a significant threat to vulnerable species, such as leopards and lions, and is a potential risk to humans in densely populated areas. This paper does not consider domestic animals, but spillover of CDV resulting from interactions of dogs and various wild species has led to mass mortalities in several wildlife species (Beineke, Baumgärtner and Wohlsein, 2015). Evidence from the Serengeti shows CDV transmission from domestic dogs to lions, as peaks in dog infections preceded those in lions (Viana et al. 2015), though later outbreaks suggested other wildlife sources. It is therefore important for further control of CDV outbreaks in both domestic and wildlife animals, as they pose a threat to human healthcare. Mass vaccination of domestic dogs would reduce CDV transmission to wildlife and humans. Human-wildlife interactions, driven by habitat encroachment and urbanization, exacerbate these risks, particularly for species whose ranges overlap or interact indirectly, such as aquatic and terrestrial animals in coastal areas. This study was limited by incomplete data on species distributions and population density at finer scales, and assumptions of uniform susceptibility across species. Future research should integrate ecological data, animal behaviour, real-time monitoring of human-wildlife interactions, and explore other paramyxoviruses to improve spillover models. Effective mitigation strategies include mass vaccination campaigns, surveillance in high-risk regions, responsible dog ownership, and community education.

References

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- Viana, M. et al. (2015)** 'Dynamics of a morbillivirus at the domestic-wildlife interface: Canine distemper virus in domestic dogs and lions', *Proceedings of the National Academy of Sciences of the United States of America*, 112(5), pp. 1464–1469. Available at: <https://doi.org/10.1073/pnas.1411623112>.

Appendix

Table 1. Summary of species of concern for potential *Canine distemper virus* (CDV) spillover. The table includes species names, their IUCN conservation status, and the rationale for their selection, highlighting factors such as habitat overlap with *Vulpes vulpes* (red fox), susceptibility to CDV, and conservation significance. The species listed represent both terrestrial and aquatic mammals, with varying levels of conservation concern.

Species Name	IUCN Status	Selection Rationale
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<i>Procyon lotor</i> (Raccoon)	Least Concern (LC)	Frequently overlaps with fox habitats; known to carry and transmit CDV.
<i>Mustela putorius</i> (Polecat)	Least Concern (LC)	Phylogenetically related carnivore; susceptible to CDV.
<i>Pusa caspica</i> (Caspian seal)	Endangered (EN)	Aquatic mammal with significant conservation concern; susceptible to CDV.
<i>Mustela lutreola</i> (European mink)	Critically Endangered (CR)	Highly threatened species with potential overlap in habitats; at risk from CDV.
<i>Civettictis civetta</i> (Civet)	Least Concern (LC)	Shares overlapping habitats with <i>Vulpes vulpes</i> ; potential spillover host.
<i>Panthera pardus</i> (Leopard)	Vulnerable (VU)	Habitat overlap with foxes; endangered carnivore susceptible to CDV.
<i>Panthera leo</i> (Lion)	Vulnerable (VU)	Endangered apex predator known to be affected by CDV outbreaks.
<i>Lupulella mesomelas</i> (Black-backed jackal)	Least Concern (LC)	Shares ecological niches with foxes; known CDV host.
<i>Otocyon megalotis</i> (Bat-eared fox)	Least Concern (LC)	Overlapping habitats with foxes; potential spillover host.
<i>Pusa sibirica</i> (Baikal seal)	Endangered (EN)	Aquatic mammal at risk of CDV spillover; significant conservation concern.

Clustalo Omega Multiple Alignment Sequences (representative selection)

Hendra	CAGGGAAATTGATTTAGCTATAGAATATGCGCAGTTGAGACATAACCAACCGAATGGGG	280
Feline_morbillivirus	TTTCCAAATTAGTAGGATTTTAGAATACGCCCAAATTGCTCATAATCAACAATTATCAG	146
Phocine	CCAACAAGTTAGTTGCTATTTCTGAGTATGCGCGGATTAAGCACAACTACCAACTCAGT	146
CDV_Raccoon	CCAATAAACTAGTATCTATTTTAGAGTATGCACGGATTAGACATAACTATCAGCTCCTTG	9153
CDV_Polecat	CCAATAAGCTAGTAGCTATTTTAGAATACGCACGAATTAGACATAGCTACCAACTCCTTG	9153
CDV_Mink	CCAATAAGCTAGTAGCTATTTTAGAATACGCACGAATTAGACATAGCTATCAACTCCTTG	9153
CDV_Caspian_Seal	CCAATAAGCTAGTAGCTATTTTAGAATACGCACGAATTAGACATAGCTATCAACTCCTTG	9153
CDV,	CCAATAAGCTAGTATCTATTTTAGAATACGCACGAATTAGACATAACTATCAGCTCCTTG	124
CDV_Ferret	CCAATAAGCTAGTATCTATTTTAGAATACGCACGAATTAGACATAACTATCAGCTCCTTG	9153
CDV_Dog	CCAATAAGCTAGTATCTATTTTAGAATACGCACGAATTAGACATAACTATCAGCTCCTTG	9153
CDV_Fox_China	CCAATAAGCTAGTGGCTATTTTAGAGTATGCACGAATTAGACATAACTATCGACTCCTTG	9046
CDV_Dog_Japan	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGGCATAGCTATCAGCTCCTTG	9153
CDV_Baikal_seal	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGACATAGCTATCAACTCCTCG	9153
CDV_Lion_Tanzania	CCAATAAGCTAGTTGCCATCCTTAGAGTATGCACGAATTAGACACAACATATGTTCTTG	9077
CDV_Bat_eared_fox	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGACACAACATATCAACTTCTTG	9077
CDV_Black_backed_jackal	CCAATAAGCTAGTAGCTATTTTAGAATATGCACGAATTAGACACAACATATCAACTTCTTG	9077
CDV_Civet	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGACATAACTATCAACTCCTTG	9153
CDV_Lion	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGACATAATTATCAACTCCTTG	9077
CDV_Leopard	CCAATAAGCTAGTAGCTATTTTAGAGTATGCACGAATTAGACATAATTATCAACTCCTTG	9077
Dolphin_morbillivirus,	CTAATAAGTTAGTAGCTATACTGGAGTACTCTCGGGTAACCCATGGGTACATTCTGGAGG	124
Peste_des_petits_ruminants_virus,	CAACAAAGCTAGTTGCCATCCTTAGAGTACTCGGGTATCGACCATAACTATGTTCTTG	124
Measles	CCAATAAGTAGTAGCTATCCTGGAGTATGCTCGAGTCCCTCACGCTTACAGCCTGGAGG	146
Rinderpest	-----AGCTGGTTGCCATATTAGAGTATGCCCGGATCCACATAAGTACGCTCTCGAGG	54
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Hendra	ACAAGAGATTAAGTGAATATCAAAATTAACCTTACAGGGCAAAAAGAAGTGTGTATA	340
Feline_morbillivirus	ACCGTACAATTATCAAGAATATTCAATTTAGATTAAAGGAA-----CGGATTTAA	195
Phocine	ATACCACATTAGTGACAATATAAGAGAAAGGATTACAGA-----AGGGTTATC	195
CDV_Raccoon	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----GGGGTTCTC	9202
CDV_Polecat	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	9202
CDV_Mink	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	9202
CDV_Caspian_Seal	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	9202
CDV,	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	173
CDV_Ferret	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	9202
CDV_Dog	ATACAACATTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTCTC	9202
CDV_Fox_China	ACACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9095
CDV_Dog_Japan	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9202
CDV_Baikal_seal	ATACAACGTTAGTGCGTAATATCAAAGAGAGGATTTCAGA-----AGGGTTATC	9202
CDV_Lion_Tanzania	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9126
CDV_Bat_eared_fox	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9126
CDV_Black_backed_jackal	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9126
CDV_Civet	ATACAACGTTAGTGCGTAATATCAAAGAGAGAATTTCAGA-----AGGGTTATC	9202
CDV_Lion	ATACAACGTTAATGCGTAATATCAAAGAGAGAATTTCAGA-----GGGGTTATC	9126
CDV_Leopard	ATACAACGTTAATGCGTAATATCAAAGAGAGAATTTCAGA-----GGGGTTATC	9126
Dolphin_morbillivirus,	ATCAGACATTGACAAAGAATATTGCTATAGGGTCGAGAA-----TGTTACTC	173
Peste_des_petits_ruminants_virus,	ACCAGACCTTGTCAAGAATATTAGGTATAGACTGGGGTG-----CGGTTTTTC	173
Measles	ACCCTACACTGTGTGAGAACATCAAGCACCCTCAAAAA-----CGGATTCTC	195
Rinderpest	ATCCAACCTCTGCAAAAAATATAAAGCATCGCTAGATAG-----CGGTTTTTC	103
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Hendra	TATCCAGA-----CAATCTAGAC-TTGGAAATTACATTAGAGACAATATAAAGA	388
Feline_morbillivirus	TAGTTCAAGGGTACAGGTACTATC-AGCTATGGGTGAAATTATCAACAAAATTAGAAATA	254
Phocine	AAATCAGATGA-TAATTCATTGCATAGAAATTGGAGTATTATCAACCAACACTTACTGT	254
CDV_Raccoon	AAACCAGATGA-TCATTAACGTGATCGAAATTGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV_Polecat	AAACCAGATGA-TCATTAACGTGATCGAAATCGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV_Mink	AAACCAGATGA-TCATTAACGTGATCGAAATCGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV_Caspian_Seal	AAACCAGATGA-TCATTAACGTGATCGAAATCGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV,	AAACCAGATGA-TCATTAACGTGATCGAAATTTGGGAGCATTATTAATCAGACCTTGTAT	232
CDV_Ferret	AAACCAGATGA-TCATTAACGTGATCGAAATTTGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV_Dog	AAACCAGATGA-TCATTAACGTGATCGAAATTTGGGAGCATTATTAATCAGACCTTGTAT	9261
CDV_Fox_China	AAACCAGATGA-TCATTAACGTACCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9154
CDV_Dog_Japan	AAACCAGATGA-TCATCAACTGTATCGAAATTTGGGAGCATTGTCAATCAGACCTTGTAT	9261
CDV_Baikal_seal	GAACCAGATGA-TCATTAATTGTATCGAAATTTGGGAGCATTGTAATCAGACCTTGTAT	9261
CDV_Lion_Tanzania	AAACCAGCTGA-TTATTAACGTGATCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9185
CDV_Bat_eared_fox	AAACCAGATGA-TTATTAACGTGATCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9185
CDV_Black_backed_jackal	AAACCAGATGA-TTATTAACGTGATCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9185
CDV_Civet	AAACCAGATGA-TCATTAACGTGATCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9261
CDV_Lion	AAACCAGATGA-TCATTAACGTCTCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9185
CDV_Leopard	AAACCAGATGA-TCATTAACGTCTCGAAATTTGGGAGCATTGTTAATCAGACCTTGTAT	9185
Dolphin_morbillivirus,	CAATCAAATGA-TTATAAATAACCTCGAAATTTGGGAATGTGGTAAATCTAAGACTCATGA	232
Peste_des_petits_ruminants_virus,	AAATCAAATGA-TCATCAATAACAGGGGGTGGGTGAAACAGTCAATTTCAAACCAAAA	232
Measles	CAACCAAATGA-TTATAACAATGTGGAAGTTGGGAATGTCATCAAGTCCAAGCTTAGGA	254
Rinderpest	AAATCAGATGA-TCATCAACAATGTTGAGATAGGGAATGTTGTCCAATCCAACCTCAAAG	162
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Hendra	ATTTGAAGGAATTTCTACATGTATCATATCCCGAGTGCATAAATCTTTATTCTCTCTCA	448
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Phocine	CCTACCCTCAATACAAACATGTGATATACCCGAATTGTAACAAGTCATTGTTTCACGCAC	314
CDV_Raccoon	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9321
CDV_Polecat	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	9321
CDV_Mink	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	9321
CDV_Caspian_Seal	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	9321
CDV,	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	292
CDV_Ferret	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	9321
CDV_Dog	CTTATCCCAAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTATTTTCATGCAC	9321
CDV_Fox_China	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9214
CDV_Dog_Japan	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9321
CDV_Baikal_seal	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTGCTGTTTCATGCAC	9321
CDV_Lion_Tanzania	CTTATCCTAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTGTTCCATGCAC	9245
CDV_Bat_eared_fox	CTTATCCTAAACACAACCATGTGATATACCCAAATTGCAACAAAACCTTCTGTTCCATGCAC	9245
CDV_Black_backed_jackal	CTTATCCTAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTCCATGCAC	9245
CDV_Civet	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9321
CDV_Lion	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9245
CDV_Leopard	CTTATCCCAAAACACAACCATGTGATATATCCAAATTGCAACAAAACCTTCTGTTTCATGCAC	9245
Dolphin_morbillivirus,	GTTACCCCTACCACAGGCACAAGATCTACCCGACTGTAATTATGACCTATTTCCATATTT	292
Peste_des_petits_ruminants_virus,	GTTACCCCATAAATCGTCATATCATATACCCGGATTGCAATAAGGAGTTGTTTTGTATCA	292
Measles	GTTATCCGGCCCACTCTCATATTCATATCCAAATTGTAATCAGGATTTATTTAACATAG	314
Rinderpest	GTTATCCGAACCATGAGCAGATCCCATATCCAGAATGCAACCAAGAGTTGTTCAATGCTC	222
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Hendra	ATATCGTGAGCAGAAAAATCATAGAGAT -GTTACAAAACATCACCAGGAATCTCATAACT	567
Feline_morbillivirus	ACACACTGTATCTCAAGATTCGATCAGATATCATAAAATGTTTGATAGATT--GAAAA	419
Phocine	ATAGTATCTATAGCAAAATTAACAGATGGGATCAAAAGATGCTCTAGTTAATAT--TAACT	419
CDV_Racoon	ATAGCATCTATAGTAAAAAACAGATGGGGTCAAAAGATGCTTAAACGATAT--TAATC	9426
CDV_Polecat	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9426
CDV_Mink	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9426
CDV_Caspian_Seal	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9426
CDV,	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	397
CDV_Ferret	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9426
CDV_Dog	ATAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9426
CDV_Fox_China	ATAGCATCTATAGTAAAAATTAACAGACGGGGTCAAAAAATGCTTAAACGATAT--TAATC	9319
CDV_Dog_Japan	ACAGCATCTATAGTAAAAATTAACAGACGGGGTCAAAAGATGCTTAAACGATAT--TAACC	9426
CDV_Baikal_seal	ACAGCATCTATAGTAAAAATTAACAGACGGGGTCAAAAGATGCTTAAACGATAT--TAATC	9426
CDV_Lion_Tanzania	ACAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAGATGCTTAAATGATAT--TAATC	9350
CDV_Bat_eared_fox	ACAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAGATGCTTAAATGATAT--TAATC	9350
CDV_Black_backed_jackal	ACAGCATCTATAGCAAAATTAACAGACGGGGTCAAAAGATGCTTAAATGATAT--TAATC	9350
CDV_Civet	ACAGCATCTATAGTAAAAATTAACAGACGGGGTCAAAAGATGCTTAAACGATAT--TAGTC	9426
CDV_Lion	ACAGCATCTATAGTAAAAATTAACAGATGGGGTCAAAAGATGCTTAAACGATAT--TAACC	9350
CDV_Leopard	ACAGCATCTATAGTAAAAATTAACAGATGGGGTCAAAAGATGCTTAAACGATAT--TAACC	9350
Dolphin_morbillivirus,	ATACAATATATACTAAGATCAGCGGAAAAAATTATTGAATGTATGAAGGGAGT--GAATT	397
Peste_des_petits_ruminants_virus,	ATTCCCTGTACTCTAAGATAAGTCACCAAGTACTGGATTGCTTAAGAGAGT--CAATG	397
Measles	ATTCTGCTACTCTCAAGTCAGTGATAAGGTTTTCCAATGCCTGAGGGACAC--TAATC	419
Rinderpest	CCACCTGTACACCAAAATCAGTGATAAAGGTGTGTACATGCTTAGAGACTGC--TAACT	327

Hendra	CA----GGACCAAAAGGATGAAGTTT	AGGTATTTATGAGCAGGACAGACTCAGTAACA	622
Feline_morbillivirus	TGAAAATGAATATAAA---	GAATGATCTTCTTAATGACAATAGTCAATTGATTCAGATC	476
Phocine	TAAATATTGGCTGGG---	TGAGACATTGGATAAAACAGTGAGAACAAACATAGATGAAG	476
CDV_Raccoon	TTAATATTGGTTTAGG---	GGATGCACTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9483
CDV_Polecat	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	9483
CDV_Mink	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	9483
CDV_Caspian_Seal	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	9483
CDV,	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	454
CDV_Ferret	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	9483
CDV_Dog	TTAATATTGGTTTAGG---	GGGTGCACTGGACAAGACTATTGGGACCAAAATTGATGAAG	9483
CDV_Fox_China	TTAGTATTGGTTTAGG---	AGGTGCATTGGATAAGACTATTGGGGCCAAAAGTTGATGAAG	9376
CDV_Dog_Japan	TTAGTATTGGTTTAGG---	TGATGCACTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9483
CDV_Baikal_seal	TTAGTATTGGTTTAGG---	AGATGCACTGGACAAGACTATCGGGGCCAAAATTGATGAAG	9483
CDV_Lion_Tanzania	TCAGTATTGGTTTAGG---	AGATGCATTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9407
CDV_Bat_eared_fox	TCAGTATTGGTTTAGG---	AGATGCATTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9407
CDV_Black_backed_jackal	TTAGTCTTGGTTTAGG---	AGATGCATTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9407
CDV_Civet	TTAGTATTGGTTTAGG---	AGATGCACTGGACAAGACTATTGGGGCCAAAATTGATGAAG	9483
CDV_Lion	TTAGTATTGGTTTAGG---	AGATGCACTGGACAAGACCATTGGGGCCAAAATTGATGAAG	9407
CDV_Leopard	TTAGTATTGGTTTAGG---	AGATGCACTGGACAAGACCATTGGGGCCAAAATTGATGAAG	9407
Dolphin_morbillivirus,	CAAGGCTAGGGATAAG---	CAGTGATTTAAGTAAAGAAGTTACGACAGGGATCACAGATT	454
Peste_des_petits_ruminants_virus,	GGAAATTAGGCCTGGG---	CACAGATCTTACCTATGGTCTGAAGGAGGGTATCCTTGACC	454
Measles	CACGGCTTGGCTAGG---	CTCCGAATTGAGGGAGGACATCAAGGAGAAAATTATTAAC	476
Rinderpest	CAAGACTAGGATTGGG---	TGCGCACTTAGGAATTGGGATCAAGGAGAAAGATCTGAGTC	384