# Supplementary Information

# Bats as reservoirs of mammalian paramyxoviruses

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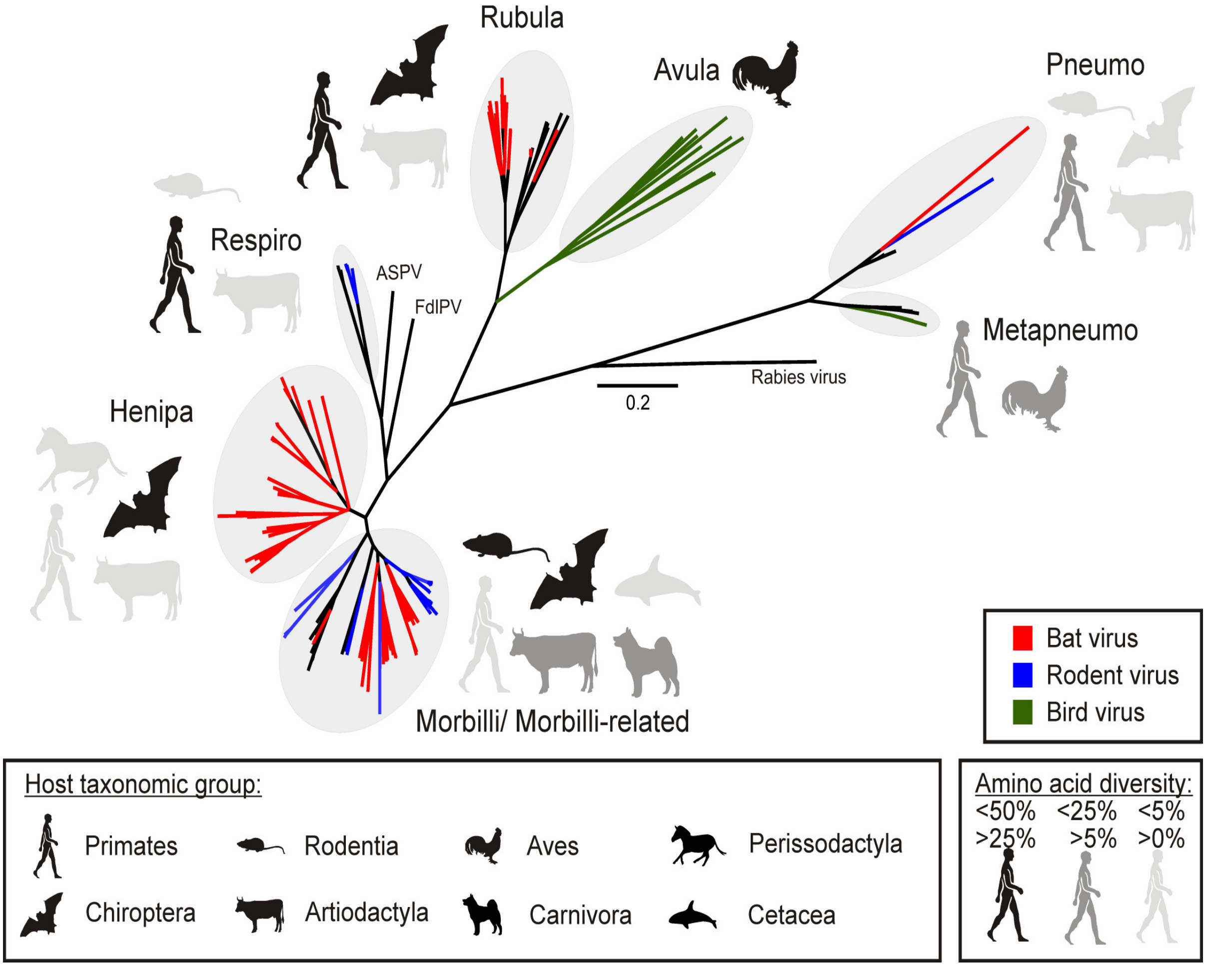
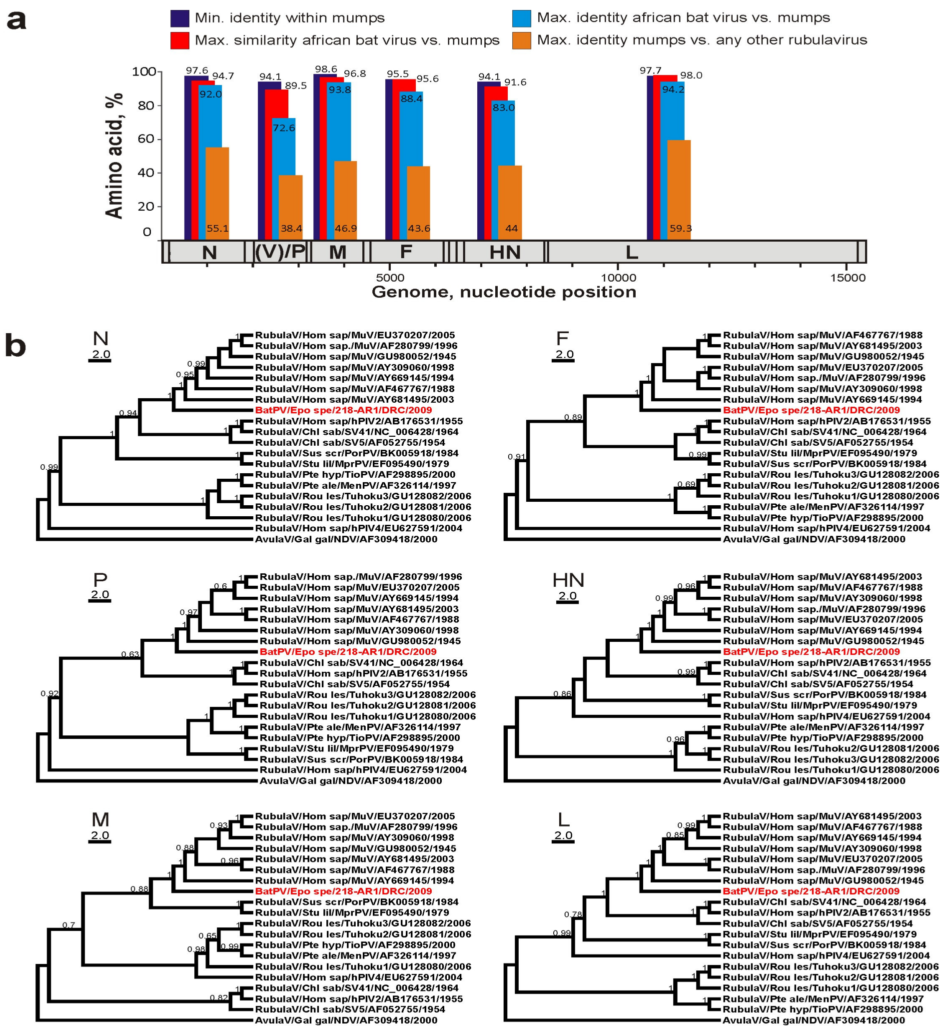


**Supplementary Figure S1 Phylogenetic relationships within the family *Paramyxoviridae* including novel viruses from small mammals**

The figure shows a Maximum Likelihood phylogeny reconstructed from 186 amino acids of the L-gene corresponding to positions 367-552 in Nipah virus strain UM-0128 RNA-dependent RNA polymerase (GenBank, AJ564623). Individual paramyxovirus clades contained in this tree are shown in detail in the main text (**Figure 2**). Branches leading to bat viruses are represented in red color, rodent viruses in blue color, and bird viruses in green color. Branches leading to viruses from other hosts are shown in black. Known hosts of major phylogenetic clades are symbolized by pictograms. The shading of pictograms represents the genetic distance of paramyxoviruses encountered in each host. Rabies virus (NC_001542) was used as an outgroup. The scale bar represents genetic distance in substitutions per site.

Overall maximum amino acid (aa) distance among all African bat henipaviruses shown was 40.3%, as opposed to 7.5% among all sequences of HeV and NiV reported from Australia and Asia[61-62] (hosted by members of the genus *Pteropus*).

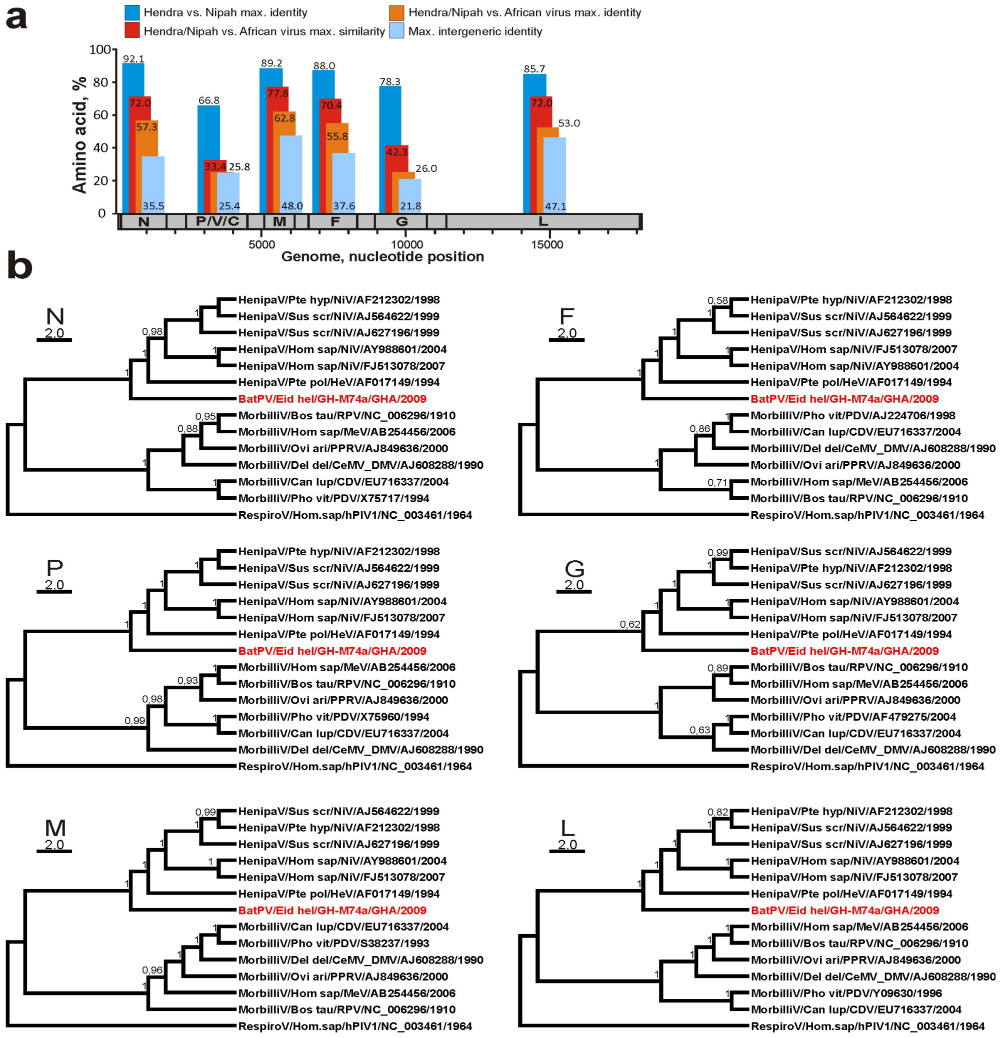


**c**

```
  Mumps 5' ACCAAGGGGAAAATGAAGAT
218-AR1 5' ....................
  Mumps 3' ..........G..A.T.A.A
218-AR1 3' ..........G..A.....A
```

**Supplementary Figure S2 Genome organization and phylogenetic analyses of individual genes of an African bat mumps virus**

**a,** Genome organization of bat mumps virus (MuV) BatPV/Epo spe/218-AR1/DRC/2009 (218-AR1, GenBank accession number HQ660095) from an Epauletted fruit bat (Epomophorus species) sampled 2009 in the Democratic Republic of Congo (genome drawn to scale; tick marks spaced at 1000 nt). The full genome comprised 15,378 nucleotides, compatible with the “rule of six”. Overall genome organization identical to that of human mumps virus, including the edited phosphoprotein ORF (insertion of 2 G residues by RNA editing). Length of all protein coding domains was identical to a reference strain (MuV strain Enders, GenBank GU980052) without any deletions or insertions. Numbers in coloured bars above the six gene symbols show amino acid sequence identities and similarities (BLOSUM62 distance matrix) within known MuV strains, between 218-AR1 and MuV strain Enders, and between MuV and the most similar rubulavirus known previously (Mapuera virus in most genes). Previously known bat rubulaviruses shared 38.4-59.3% amino acid identity with human mumps virus, while bat-MuV 218-AR1 was up to 94.2% identical (minimal identity in any gene, 72.6%). The small hydrophobic protein (SH, not shown due to space reasons) was present with 38.6% aa identity and 54.4% aa similarity (Blosum62 matrix). A putative furine-dependent cleavage site was present in the F protein at amino acids 102 and 103 within the motif RRRKR, compared to RRHKR in human mumps virus at identical amino acid positions. Amino acid exchanges in the fusion (F, A91T), haemagglutinin-neuraminidase (HN, S466N and K335E), and polymerase (L, I736V) proteins putatively associated with attenuation of the neurovirulence of human mumps virus wild type and vaccine strains[63-65] belonged to the putative neurovirulent phenotype in the bat mumps virus. **b,** Bayesian phylogenetic relations within genus Rubulavirus members including 218-AR1 (shown in red color) in six genome regions. Values to the left of tree nodes indicate posterior probabilities of the respective groups; only values above 0.6 are shown. The scale bar indicates substitutions per site. **c,** Alignment of highly conserved genome terminal sequences of MuV and 218-AR1.

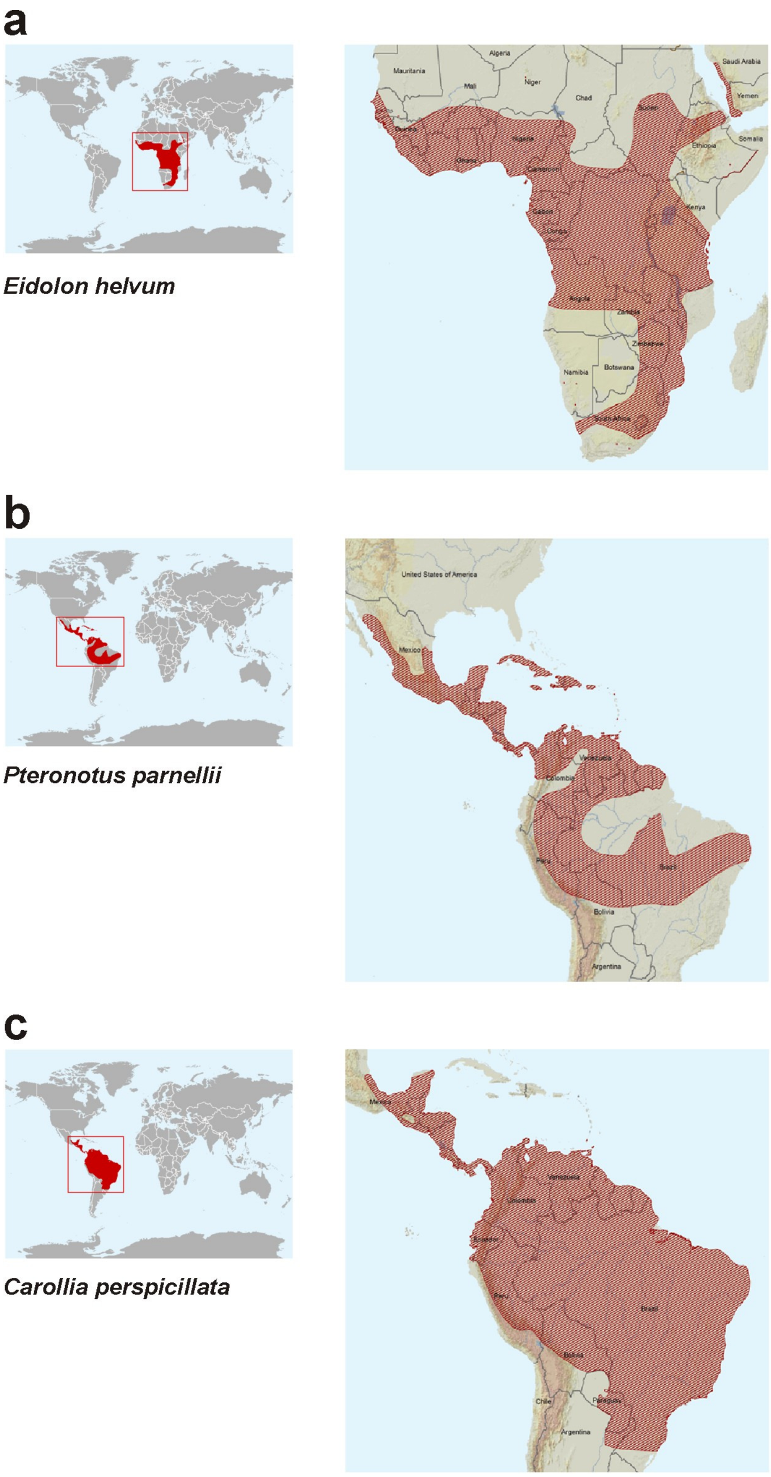


**c**

```
     NiV 5' ACCAAACAAGGGAGAATATG
     NiV 3' ...G........TA..G.A.
     HeV 5' ...G........GA......
     HeV 3' ...G........TA..G.GA
 GH-M74A 5' .AG.TTA.TA..TACTA..T
 GH-M74A 3' ....G....A..TCTGG..T
```

**Supplementary Figure S3 Genome organization and phylogenetic analyses of individual genes of an African bat henipavirus**

**a,** Genome structure of bat henipavirus BatPV/Eid hel/GH-M74a/GHA/2009 (GH-M74a, 18,530 nucleotides, GenBank accession number, HQ660129) from a Straw-colored fruit bat (*Eidolon helvum*) sampled in 2009 in Ghana (genome drawn to scale; tick marks spaced at 1000 nt). Numbers below the six gene symbols (top to bottom line) show amino acid sequence identities and similarities (BLOSUM62 distance matrix) between Hendra- (HeV) and Nipah virus (NiV) isolates, between bat henipavirus GH-M74a and NiV (AJ564623), and between GH-M74a and the next most similar known paramyxovirus outside the genus *Henipavirus*. The full phosphoprotein (P) gene reading frame was used for the P/V/C genome region. Typical long intergenic untranslated regions are indicated between genes. The Fusion protein included a tyrosine-based endocytosis signal (YTPL) and a monobasic cleavage site (PGNARFAG). M74a further contained a conserved domain at the amino-terminus of its phosphoprotein (P) which has been hypothetically associated with prevention of self-assembly of the soluble form of the nucleoprotein N0 and is structurally conserved among several *Paramyxoviridae* genera, including HeV and NiV[66]. Another structurally conserved feature of the M74a P gene was a disordered region displaying considerable structural similarity to positions 114 to 140 of the HeV and NiV P protein, in which it is associated with STAT1-binding and inactivation[67-68]. **b,** Phylogenetic relations of bat henipavirus GH-M74a (shown in red color) and members of the genera *Henipa-*, and *Morbillivirus* in six genome regions. Values to the left of tree nodes indicate posterior probabilities of the respective groups; only values above 0.6 are shown. The scale bar indicates substitutions per site. **c,** Alignment of genome terminal sequences of NiV (AJ564623), HeV (AF017149) and GH-M74a.



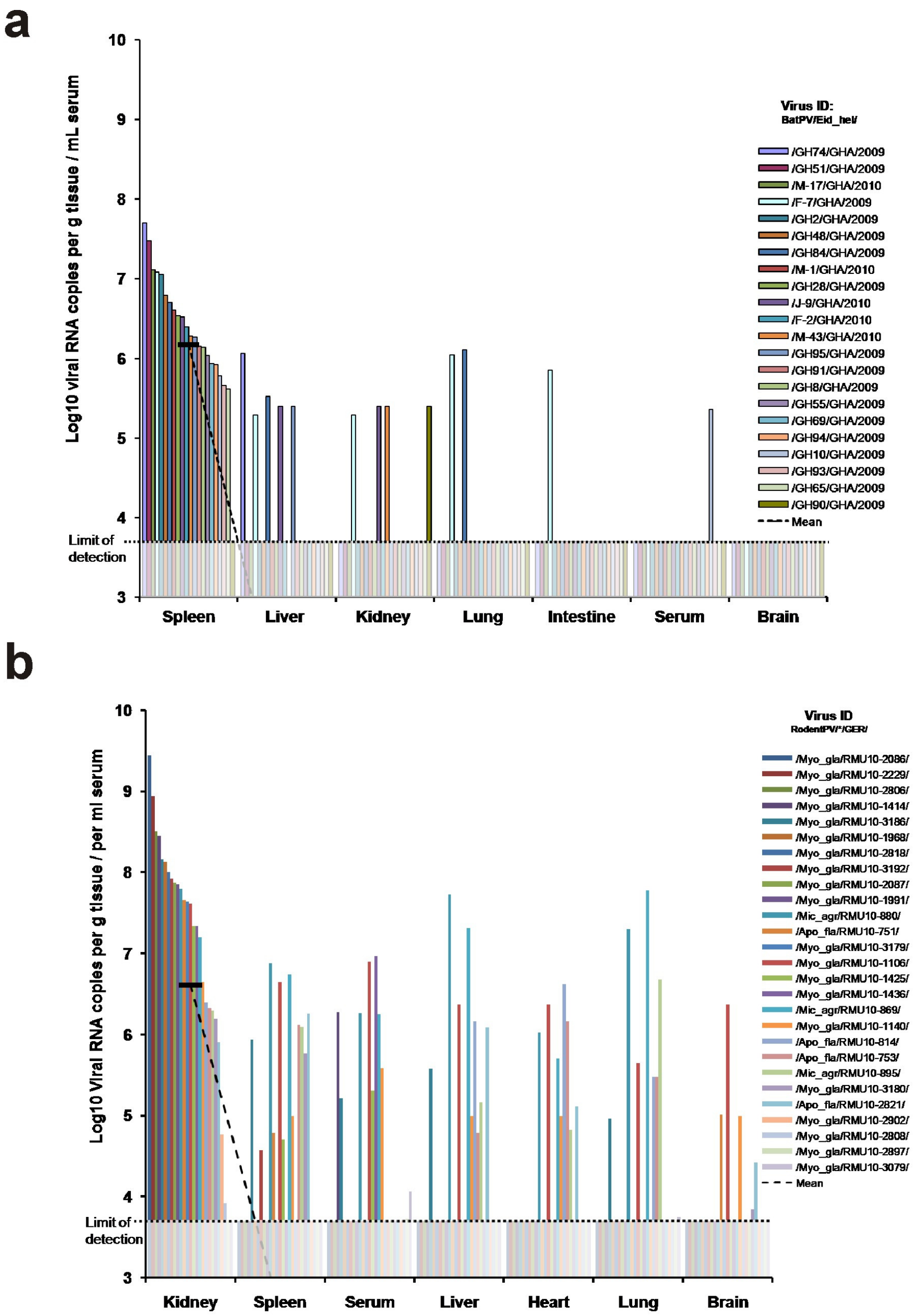
*Eidolon helvum*

*Pteronotus parnellii*

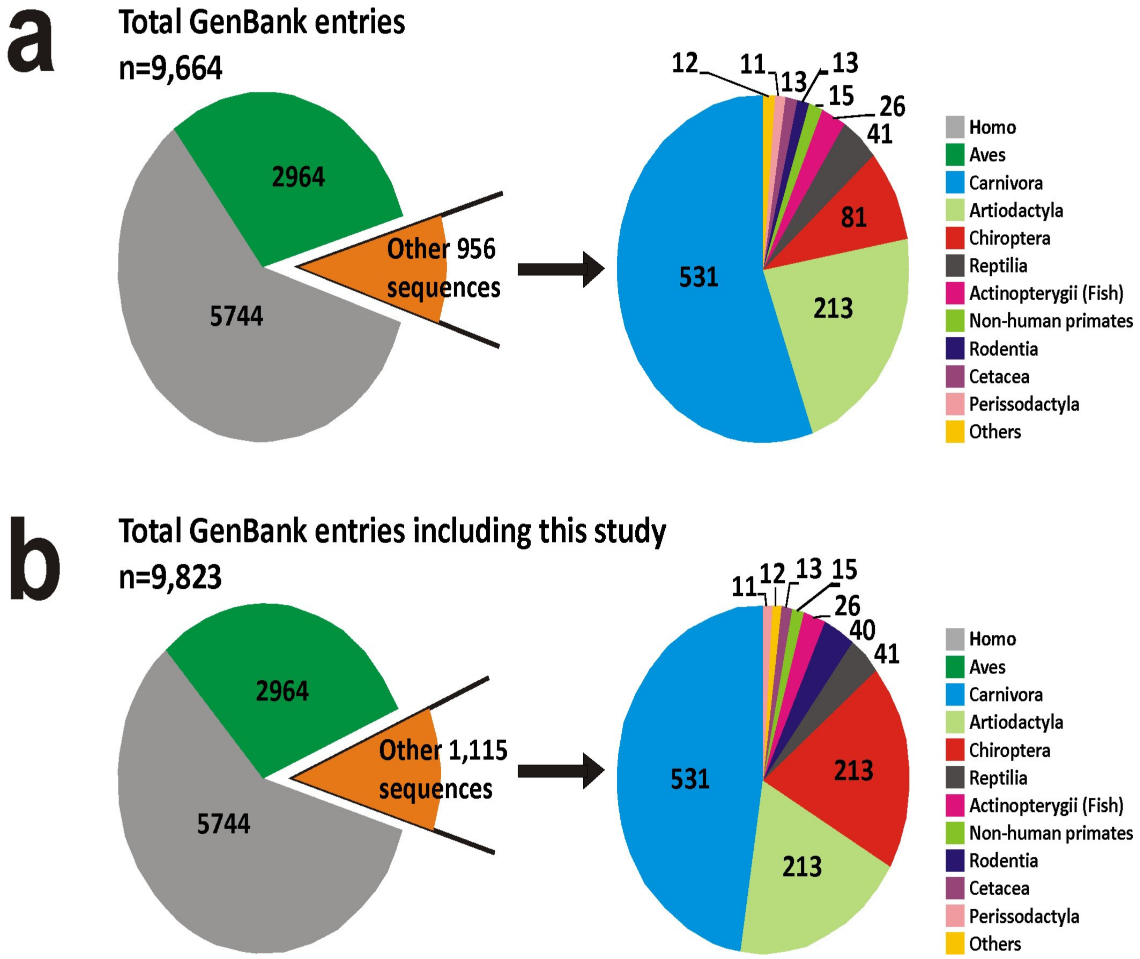
*Carollia perspicillata*

**Supplementary Figure S4 Occurrence of African and American henipavirus bat hosts**

Distribution of African *Eidolon helvum* flying foxes (a, Pteropodidae), distribution of *Pteronotus parnellii* (b, Mormoopidae) and *Carollia perspicillata* (c, Phyllostomidae) in which African and American henipaviruses were detected. Individual maps were downloaded from the IUCN redlist[69-71].



**Supplementary Figure S5 Paramyxovirus RNA concentrations in solid organs and serum of *E. helvum* flying foxes and rodents**
a, Bats sampled 2009-2010 in Kumasi, Ghana which were positive for henipaviruses by RT-PCR. b, *Myodes glareolus*, *Microtus agrestris*, and *Apodemus flavicollis* rodents sampled throughout 2010 in different states of Germany and positive for *Morbillivirus*-related viruses by RT-PCR. Virus concentrations are given in Log10 RNA copies per milliliter of serum or per gram of tissue on the y-axis for each bat organ tested (x-axis). Horizontal bars represent mean virus concentrations per organ category. Bars below the limit of detection of the real time RT-PCR assay (shaded grey) represent negative test results. Colors represent viruses from individual bats as identified in the legend.



**Supplementary Figure S6 GenBank representation of *Paramyxoviridae* hosts**
GenBank data was retrieved from a search using the terms “Paramyxoviridae [ORGANISM] AND Host [All Fields]” in the “Nucleotide” database, on November 16th, 2011. The resulting 9,664 sequences with labelled host in the “Features” part of the GenBank file are shown in (a). The same dataset expanded by novel viruses from this study is shown in (b). Hosts were sorted according to their taxonomic groups. Groups with less than 10 entries were summarised as “Others”.

# SupplementaryTable S1. Sample characteristics

| Order-Family | Species | No. of samples | Total positive (%) | RT-PCR positive per *Paramyxoviridae* genus/genetic lineage (%) | | | | | Sampling site (year) *positive location/year |
|---|---|---|---|---|---|---|---|---|---|
| | | | | ***Respirovirus*** | ***Henipavirus*** | ***Morbillivirus/* unclassified** | ***Rubulavirus*** | ***Pneumovirus*** | |
| **Chiroptera-Pteropodidae** | *Casinycteris argynnis* | 21 | | | | | | | GAB(2005,2006) |
| | *Eidolon helvum* | 722 | 84 (11.6) | | 42 (5.8) | | 29 (4.0) | 13 (1.8) | GHA(2009,2008,2010)*,RCA(2008)*, GAB(2005,2006)*DRC(2009)* |
| | *Epomophorus gambianus* | 54 | 3 (5.6) | | 3 (5.6) | | | | DRC(2009)*,GHA(2009) |
| | *Epomophorus labiatus* | 1 | | | | | | | DRC(2009) |
| | *Epomophorus minimus* | 6 | 3 (50.0) | | | | 3 (50.0) | | DRC(2009) |
| | *Epomophorus spec.* | 17 | 4 (23.5) | | 1 (5.9) | | 3 (17.7) | | DRC(2009*) |
| | *Epomophorus wahlbergi* | 4 | | | | | | | DRC(2009) |
| | *Epomops buettikoferi* | 1 | | | | | | | GHA(2009) |
| | *Epomops franqueti* | 100 | | | | | | | GAB(2005,2006),CON(2005),GHA(2009),RCA(2008) |
| | *Hypsignathus monstrosus* | 54 | 4 (7.4) | | 2 (3.7) | | 2 (3.7) | | GAB(2005,2006), CON(2005,2006), RCA(2008)*, GHA(2009) |
| | *Lissonycteris angolensis* | 3 | | | | | | | DRC(2009) |
| | *Megaloglossus woermanni* | 34 | 1 (2.9) | | | | 1 (2.9) | | GAB(2005,2006), CON(2005*,2006) |
| | *Micropteropus pusillus* | 152 | | | | | | | DRC(2009),RCA(2008),GAB(2005,2006),CON(2005, 2006),GHA(2009) |
| | *Micropteropus/Nanonycteris* | 2 | | | | | | | GHA(2009) |
| | *Myonycteris torquata* | 111 | 3 (2.7) | | 3 (2.7) | | | | GAB(2005,2006),CON(2005,2006), DRC(2009)* |
| | *Plerotes anchietae* | 1 | | | | | | | DRC(2009) |
| | *Rousettus aegyptiacus* | 213 | 18 (8.5) | | 3 (1.4) | | 15 (7.0) | | GAB(2005,2006,2009*),CON(2005,2006)* |
| **Chiroptera-Rhinolophidae** | *Rhinolophus alcyone* | 15 | | | | | | | GAB(2009) |
| | *Rhinolophus blasii* | 82 | | | | | | | BGR(2008) |
| | *Rhinolophus euryale* | 245 | | | | | | | BGR(2008) |
| | *Rhinolophus ferrum-equinum* | 46 | | | | | | | BGR(2008),ROU(2008) |
| | *Rhinolophus hipposideros* | 6 | | | | | | | BGR(2008) |
| | *Rhinolophus landeri* | 1 | | | | | | | GHA(2009) |
| | *Rhinolphus mehelyi* | 13 | | | | | | | BGR(2008) |
| **Chiroptera-Hipposideridae** | *Hipposideros abae* | 80 | 1 (1.3) | | | 1 (1.3) | | | GHA(2008,2009*) |
| | *Hipposideros cf caffer* | 20 | 1 (5.0) | | | 1(5.0) | | | GHA(2009)* |
| | *Hipposideros cf caffer/ruber* | 337 | 3 (0.9) | | | 2 (0.6) | 1 (0.3) | | GAB(2009)* |
| | *Hipposideros gigas* | 196 | 3 (1.5) | | | 2 (1.0) | 1 (0.5) | | GAB(2006,2009*) |
| | *Hipposideros cf ruber* | 117 | 2 (1.7) | | | 2 (1.7) | | | GHA(2009)* |
| | *Hipposideros sp.* | 80 | 1 (1.3) | | | 1 (1.3) | | | GHA(2008,2009*) |
| **Chiroptera-Nycteridae** | *Nycteris hispida* | 1 | | | | | | | GHA(2008) |
| | *Nycteris spec.* | 3 | | | | | | | GHA(2009),GHA(2009) |
| **Chiroptera-Emballonuridae** | *Coleura afra* | 96 | 1 (1.0) | | | 1 (1.0) | | | GHA(2008,2009) GAB(2009)* |
| | *Peropteryx kappleri* | 5 | | | | | | | CRC(2010) |
| | *Saccopteryx bilineata* | 85 | | | | | | | PAN(2008,2010), CRC(2009) |
| **Chiroptera-Phyllostomidae** | *Anoura geoffroyi* | 100 | | | | | | | CRC(2010) |
| | *Artibeus jamaicensis* | 50 | | | | | | | PAN(2008,2010) |
| | *Artibeus lituratus* | 3 | | | | | | | PAN(2010) |
| | *Carollia brevicauda* | 50 | 4 (8.0) | | | 4 (8.0) | | | BRA(2009)* |
| | *Carollia castanea* | 12 | | | | | | | PAN(2008,2010), CRC(2010) |
| | *Carollia perspicillata* | 297 | 2(0.7) | | 1(0.3) | 1(0.3) | | | BRA(2009)*, PAN(2008),CRC(2010)* |
| | *Carollia spec.* | 1 | | | | | | | BRA(2008) |
| | *Chiroderma villosum* | 2 | | | | | | | PAN(2008) |
| | *Desmodus rotundus* | 29 | 4 (13.8) | | | 4 (13.8) | | | BRA(2008*,2009) |
| | *Enchisthenes hartii* | 3 | | | | | | | CRC(2010) |
| | *Glossophaga commissarisi* | 3 | | | | | | | CRC(2010) |
| | *Glossophaga soricina* | 29 | 1 (3.4) | | | 1 (3.4) | | | BRA(2009)*,CRC(2010) |
| | *Lonchorhina aurita* | 1 | | | | | | | BRA(2009) |
| | *Lophostoma silvicolum* | 4 | | | | | | | PAN(2010) |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | *Micronycteris hirsuta* | 1 | | | | | | | PAN(2010) |
| | *Micronycteris microtis* | 4 | | | | | | | PAN(2008) |
| | *Mimon crenulatum* | 1 | | | | | | | PAN(2010) |
| | *Phyllostomus hastatus* | 3 | | | | | | | PAN(2010) |
| | *Platyrrhinus helleri* | 1 | | | | | | | PAN(2010) |
| | *Tonatia saurophila* | 5 | | | | | | | PAN(2008,2010) |
| | *Trachops cirrhosus* | 5 | | | | | | | BRA(2008), PAN(2010) |
| | *Uroderma bilobatum* | 3 | | | | | | | PAN(2010) |
| **Chiroptera-Mormoopidae** | *Pteronotus parnellii* | 40 | 5 (12.5) | | 3 (7.5) | 2 (5.0) | | | PAN(2008,2010), CRC(2010)* |
| **Chiroptera-Vespertilionidae** | *Barbastella barbastellus* | 14 | | | | | | | BGR(2008), ROU(2008) |
| | *Eptesicus serotinus* | 1 | | | | | | | GER(2009) |
| | *Glauconycteris beatrix* | 1 | | | | | | | GHA(2008) |
| | *Miniopterus inflatus* | 125 | 2 (1.6) | | | | 2 (1.6) | | GAB(2009)* |
| | *Miniopterus schreibersii* | 87 | | | | | | | BGR(2008), ROU(2008) |
| | *Myotis brandtii* | 18 | | | | | | | GER(2008,2009) |
| | *Myotis alcathoe* | 4 | 1 (25.0) | | | 1 (25.0) | | | BGR(2008,2009*) |
| | *Myotis bechsteinii* | 93 | 1 (1.1) | | | 1 (1.1) | | | GER(2008*,2009), BGR(2008,2009) |
| | *Myotis capaccini* | 9 | 1 (11.1) | | | 1 (11.1) | | | BGR(2008,2009*) |
| | *Myotis dasycneme* | 101 | | | | | | | GER(2007,2008) |
| | *Myotis daubentonii* | 276 | 1 (0.4) | | | 1 (0.4) | | | GER(2007,2008,2009*), BGR(2008,2009) |
| | *Myotis emarginatus* | 6 | | | | | | | BGR(2008) |
| | *Myotis myotis* | 258 | 5 (1.9) | | | 5 (1.9) | | | ROU(2008), GER(2008)*, BGR(2008) |
| | *Myotis mystacinus* | 56 | 3 (5.4) | | | 3 (5.4) | | | GER(2008)*, BGR(2008) |
| | *Myotis nattereri* | 70 | | | | | | | GER(2007,2008), BGR(2008) |
| | *Myotis nigricans* | 3 | | | | | | | PAN(2010) |
| | *Myotis oxygnathus* | 22 | | | | | | | ROU(2008), BGR(2008) |
| | *Nanonycteris veldkampi* | 23 | | | | | | | GHA(2009) |
| | *Nyctalus leisleri* | 13 | | | | | | | GER(2009),BGR(2008) |
| | *Nyctalus noctula* | 16 | | | | | | | ROU(2008),GER(2007,2008,2009) |
| | *Phylloderma stenops* | 1 | | | | | | | PAN(2008) |
| | *Pipistrellus deserti* | 1 | | | | | | | GHA(2008) |
| | *Pipistrellus cf nanus/nanulus* | 9 | 1(11.1) | | | 1(11.1) | | | GHA(2008*,2009) |
| | *Pipistrellus nathusii* | 19 | | | | | | | GER(2007,2008) |
| | *Pipistrellus pipistrellus* | 43 | | | | | | | GER(2008,2009) |
| | *Pipistrellus pygmaeus* | 57 | | | | | | | GER(2007,2008), BGR(2008) |
| | *Pipistrellus spec.* | 7 | | | | | | | GHA(2009) |
| | *Plecotus auritus* | 10 | | | | | | | BGR(2008), GER(2008,2009) |
| | *Plecotus austriacus* | 5 | | | | | | | GER(2008), BGR(2009) |
| | *Rhogeessa tumida* | 1 | | | | | | | PAN(2010) |
| **Chiroptera-Molossidae** | *Molossus currentium* | 5 | | | | | | | BRA(2008,2009) |
| | *Molossus rufus* | 17 | | | | | | | BRA(2008,2009) |
| | *Molossus molossus* | 1 | | | | | | | PAN(2010) |
| | *Mops spec.* | 1 | | | | | | | RCA(2008) |
| | *Tadarida spec.* | 7 | | | | | | | GHA(2008,2009) |
| **Chiroptera-Natalidae** | *Natalus lanatus* | 3 | | | | | | | CRC(2010) |
| **Bats** | **Total (86 species)** | **4954** | **163 (3.3)** | **0** | **58 (1.2)** | **35 (0.7)** | **57 (1.2)** | **13 (0.3)** | |
| **Rodentia-Muridae** | *Aethomys namaquensis* | 6 | | | | | | | RSA(2008) |
| | *Apodemus agrarius* | 92 | | | | | | | GER(2007-2010)[a] |
| | *Apodemus flavicollis* | 667 | 8 (1.2) | | | 8 (1.2) | | | GER(2007-2010) [a*] |
| | *Apodemus sp.* | 51 | | | | | | | GER(2007-2010)[a] |
| | *Apodemus sylvaticus* | 264 | | | | | | | NED(2007,2008),GER(2007-2010)[a] |
| | *Bandicota indica* | 151 | | | | | | | THA(1995,1996,2005,2006,2007) |
| | *Bandicota savilei* | 9 | | | | | | | THA(1995,1996,2005) |
| | *Bandicota sp.* | 1 | | | | | | | THA(2005) |
| | *Desmodillus sp.* | 1 | | | | | | | RSA(2008) |

| | | | | | | |
|---|---|---|---|---|---|---|
| | *Heimyscus fumosus* | 1 | | | | GAB(2011) |
| | *Hybomys univittatus* | 1 | | | | GAB(2011) |
| | *Lemniscomys striatus* | 18 | | | | GAB(2011) |
| | *Lophuromys sp.* | 1 | | | | GAB(2011) |
| | *Malacomys longipes* | 1 | | | | GAB(2011) |
| | *Mastomys spec.* | 1 | | | | RSA(2008) |
| | *Micromys minutus* | 3 | | | | GER(2007-2010)[a] |
| | *Mus musculus* | 16 | | | | GER(2007-2010)[a], GAB(2011) |
| | *Nannomys setulosus* | 7 | | | | GAB(2011) |
| | *Otomys sp.* | 21 | | | | RSA(2008) |
| | *Parotomys littledaly* | 1 | | | | RSA(2008) |
| | *Parotomys sp.* | 28 | | | | RSA(2008) |
| | *Praomys misonnei* | 25 | | | | GAB(2011) |
| | *Rattus argentiventer* | 28 | | | | THA(1995,1996,2005) |
| | *Rattus exulans* | 2 | | | | THA(2005) |
| | *Rattus losea* | 7 | | | | THA(1995) |
| | *Rattus norvegicus* | 141 | | | | THA(1995,1996),GER(2007-2010)[a] |
| | *Rattus rattus* | 163 | 1 (1.2) | 1 (1.2) | | THA(1995,1996,2005,2006,2007*),RSA(2008), GAB(2011) |
| | *Rattus tiomanicus* | 27 | | | | THA(1996,2005,2007) |
| | *Rhabdomys pumilio* | 518 | 88 (17.0) | | 88 (17.0) | RSA(2008)*,NAM(2008)* |
| **Rodentia-Cricetidae** | *Arvicola amphibius* | 3 | | | | GER(2007-2010)[a] |
| | *Microtus agrestis* | 114 | 3 (2.6) | | 3 (2.6) | GER(2007-2010)[a]* |
| | *Microtus arvalis* | 545 | 3 (0.6) | | 3 (0.6) | GER(2007-2010)[a]*,NED(2007) |
| | *Microtus sp.* | 37 | | | | GER(2007-2010)[a] |
| | *Myodes glareolus* | 1358 | 32 (2.4) | | 32 (2.4) | NED(2007,2008),GER(2007-2010)[a]* |
| **Rodentia-Nesomyidae** | *Petromyscus sp.* | 2 | | | | RSA(2008) |
| | *Cricetomys gambianus* | 1 | | | | GAB(2011) |
| **Rodentia-Sciuridae** | *Sciurus vulgaris* | 12 | | | | GER(2007-2010)[a] |
| **Rodents** | **Total (33 species)** | **4324** | **135 (3.1)** | **1 (0.0)** | **134 (3.1)** | |

[a] Rodent specimens from Germany were sampled through 2007 to 2010; individual sampling dates could not be retrieved for all specimens

## Supplementary Table S2. Results from next generation sequencing of *Eidolon helvum* sera*

| Closest hits in GenBank virus database | Representative accession no. | No. reads | No. unique sequences | % amino acid pairwise identity |
|---|---|---|---|---|
| *Retroviridae* | HV456021.1 | 144 | 8 | 24.2-76.9 |
| *Flaviviridae* | AY196904.1 | 2 | 1 | 68.1 |
| *Caliciviridae* | AY030098.1 | 1 | 1 | 46.4 |
| *Togaviridae* | U90536.1 | 2 | 1 | 28.8 |
| *Adenoviridae* | EU938324.1 | 2 | 1 | 26.8 |
| *Papillomaviridae* | S80200.1 | 2 | 2 | 48.8-72.2 |
| *Parvoviridae* | JF926696.1 | 1 | 1 | 74.7 |
| *Herpesviridae* | AF015298.1 | 6 | 5 | 29.9-70.0 |
| **Total** | | **160** | **20** | **24.2-76.9** |

*Sequencing as described in the Materials and Methods section resulted in 36,120 single reads. In total, 3,007 reads with similarities to viruses in the database were found. 234 reads remained for further analysis. 160 reads matched eukaryotic viruses and 68 reads showed similarity to a Mycobacterium phage. Absence of detectable paramyxovirus sequences may be explained by their lower abundance compared to (presumably endogenic) retroviruses; lower virus concentrations compared to vector-borne viruses (flavi- and togaviruses) and to fecal-orally transmitted viruses (calici- and adenoviruses), all of which are known to be capable of achieving high titers; genome particularities such as facilitated amplification of DNA viruses due to, e.g., the absence of a preceding reverse transcription step or circular genomes (papillomaviruses); high genomic copy numbers of viruses that are known to persist and frequently re-activate (e.g., herpesviruses).

## Supplementary Table S3. Paraymxovirus RNA concentrations in *Eidolon helvum* bat solid organs and blood

| **Animal (Virus ID)** BatPV/Eid_hel | /GH74/GHA/2009 | /GH51/GHA/2009 | /M-17/GHA/2010 | /F-7/GHA/2009 | /GH2/GHA/2009 | /GH48/GHA/2009 | /GH84/GHA/2009 | /M-1/GHA/2010 | /GH28/GHA/2009 | /J-9/GHA/2010 | /F-2/GHA/2010 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Tissue** | **LOG10 viral RNA copies per g tissue / mL serum** | | | | | | | | | | |
| Spleen | 7.70 | 7.48 | 7.11 | 7.09 | 7.06 | 6.79 | 6.71 | 6.61 | 6.53 | 6.53 | 6.39 |
| Liver | 6.06 | - | - | 5.29 | - | - | 5.52 | - | - | 5.40 | - |
| Kidney | - | - | - | 5.29 | - | - | - | - | - | 5.40 | - |
| Lung | - | - | - | 6.04 | - | - | 6.11 | - | - | - | - |
| Intestine | - | - | - | 5.86 | - | - | - | - | - | - | - |
| Serum | - | - | - | - | - | - | - | - | - | - | - |
| Brain | - | - | - | - | - | - | - | - | - | - | - |

| **Animal (Virus ID)** BatPV/Eid_hel | /M-43/GHA/2010 | /GH95/GHA/2009 | /GH91/GHA/2009 | /GH8/GHA/2009 | /GH55/GHA/2009 | /GH69/GHA/2009 | /GH94/GHA/2009 | /GH10/GHA/2009 | /GH93/GHA/2009 | /GH65/GHA/2009 | /GH90/GHA/2009 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Tissue** | **LOG10 viral RNA copies per g tissue / mL serum** | | | | | | | | | | |
| Spleen | 6.28 | 6.27 | 6.16 | 6.14 | 6.03 | 5.94 | 5.92 | 5.78 | 5.66 | 5.61 | - |
| Liver | - | 5.40 | - | - | - | - | - | - | - | - | - |
| Kidney | 5.40 | - | - | - | - | - | - | - | - | - | 5.40 |
| Lung | - | - | - | n.a. | - | - | - | - | - | - | - |
| Intestine | - | - | - | n.a. | - | - | - | n.a. | - | - | - |
| Serum | - | - | - | - | - | - | - | 5.36 | - | - | - |
| Brain | - | - | - | n.a. | - | - | - | - | - | - | - |

n.a.=not available, -=below assay detection limit

## Supplementary Table S4. Paraymxovirus RNA concentrations in rodent solid organs and blood

| **Animal (Virus ID)** RodentPV/*/GER | Myo_gla RMU10-2086 | Myo_gla RMU10-2229 | Myo_gla RMU10-2806 | Myo_gla RMU10-1414 | Myo_gla RMU10-3186 | Myo_gla RMU10-1968 | Myo_gla RMU10-2818 | Myo_gla RMU10-3192 | Myo_gla RMU10-2087 | Myo_gla RMU10-1991 | Mic_agr RMU10-880 | Apo_fla RMU10-751 | Myo_gla RMU10-3179 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Tissue** | **LOG10 viral RNA copies per g tissue / mL serum** | | | | | | | | | | | | |
| Kidney | 9.44 | 8.94 | 8.51 | 8.45 | 8.17 | 8.13 | 8.00 | 7.92 | 7.88 | 7.85 | 7.80 | 7.66 | 7.64 |
| Spleen | - | - | - | - | 5.94 | - | - | 4.57 | - | - | 6.88 | 4.78 | - |
| Serum | - | - | - | 6.27 | 5.22 | - | - | - | - | - | 6.26 | - | - |
| Liver | - | - | - | - | 5.58 | - | - | - | - | - | 7.73 | - | - |
| Heart | - | - | - | - | - | - | - | - | - | - | 6.03 | - | - |
| Lung | - | - | - | - | 4.96 | - | - | - | - | - | 7.30 | - | - |
| Brain | - | - | - | - | - | - | - | - | - | - | - | 5.01 | - |

| **Animal (Virus ID)** RodentPV/*/GER | Myo_gla RMU10-1106 | Myo_gla RMU10-1425 | Myo_gla RMU10-1436 | Mic_agr RMU10-869 | Myo_gla RMU10-1140 | Apo_fla RMU10-814 | Apo_fla RMU10-753 | Mic_agr RMU10-895 | Myo_gla RMU10-3180 | Apo_fla RMU10-2821 | Myo_gla RMU10-2902 | Myo_gla RMU10-2808 | Myo_gla RMU10-2897 | Myo_gla RMU10-3079 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Tissue** | **LOG10 viral RNA copies per g tissue / mL serum** | | | | | | | | | | | | | |
| Kidney | 7.62 | 7.34 | 7.34 | 7.20 | 6.65 | 6.39 | 6.33 | 6.30 | 6.20 | 5.91 | 4.77 | 3.92 | - | - |
| Spleen | 6.65 | 4.71 | - | 6.74 | 4.99 | - | 6.12 | 6.10 | 5.77 | 6.25 | - | - | - | - |
| Serum | 6.90 | 5.31 | 6.97 | 6.25 | 5.58 | - | - | - | - | - | - | - | 3.73 | 4.07 |
| Liver | 6.38 | - | - | 7.32 | 4.99 | 6.16 | 4.78 | 5.17 | - | 6.09 | - | - | - | - |
| Heart | 6.38 | - | - | 5.70 | 4.99 | 6.63 | 6.16 | 4.83 | - | 5.12 | - | - | - | - |
| Lung | 5.65 | - | - | 7.78 | - | 5.47 | 5.47 | 6.68 | - | - | - | - | - | 3.75 |
| Brain | 6.38 | - | - | - | 4.99 | - | - | - | 3.85 | 4.43 | - | - | - | - |

-=below assay detection limit

## Supplementary Table S5. Serological parameters tentatively associated with systemic infection in n=119 *E. helvum* bats

| | Paramyxovirus-status[a] | N[b] | Minimum | Maximum | Mean | Standard deviation | p |
|---|---|---|---|---|---|---|---|
| **LDH [U/L][e]** | - | 76 | 234 | 28537 | 2770.91 | 3939.69 | 0.525[c] |
| | + | 13 | 501 | 11779 | 3516.15 | 3600.89 | |
| **Gamma-GT[f] [U/L]** | - | 85 | 5 | 70 | 11.76 | 12.49 | 0.558[d] |
| | + | 16 | 7 | 75 | 23.75 | 27.85 | |
| **Bilirubin [mg/dl]** | - | 80 | 0.11 | 3.35 | 0.42 | 0.42 | 0.744[c] |
| | + | 12 | 0.15 | 1.38 | 0.38 | 0.35 | |
| **AST [U/L][g]** | - | 84 | 46 | 15176 | 1257.68 | 2182.92 | 0.815[c] |
| | + | 14 | 194 | 7290 | 1403.14 | 1888.11 | |
| **ALT [U/L][h]** | - | 87 | 24 | 3532 | 344.26 | 527.58 | 0.745[c] |
| | + | 14 | 71 | 901 | 297.00 | 285.84 | |
| **Albumin [g/L]** | - | 76 | 3.3 | 5.6 | 4.4 | 0.47 | 0.507[c] |
| | + | 15 | 3.4 | 5.3 | 4.4 | 0.46 | |

[a] determined by Paramyxovirus RT-PCR testing

[b] only values within technical test acceptance parameters were included, i.e., some sera per test had to be eliminated because they were scored invalid

[c] T-Test

[d] Mann-Whitney-Test due to inhomogeneity of variances

[e] LDH, lactate dehydrogenase

[f] Gamma-GT, gamma glutamyltransferase

[g] AST, aspartate aminotransferase

[h] ALT, alanine transferase

## Supplementary Table S6. Viruses used for phylogenetic analyses

| Virus ID[a,b] | Host | Collection year | Literature reference |
|---|---|---|---|
| HenipaV/Pte pol/HeV/AF017149/1994 | Grey-headed flying-foxes (*Pteropus poliocephalus*) | 1994 | 72 |
| HenipaV/Hom sap/NiV/AY988601/2004 | Human (*Homo sapiens*) | 2004 | 73 |
| HenipaV/Pte hyp/NiV/AF212302/1998 | Small flying-fox (*Pteropus hypomelanus*) | 1998 | 74 |
| HenipaV/Hom sap/NiV/FJ513078/2007 | Human (*Homo sapiens*) | 2007 | 75 |
| HenipaV/Sus scr/NiV/AJ627196/1999 | Pig (*Sus scrofa*) | 1999 | 76 |
| HenipaV/Sus scr/NiV/AJ564623/1999 | Pig (*Sus scrofa*) | 1999 | 76 |
| HenipaV/Sus scr/NiV/AJ564622/1999 | Pig (*Sus scrofa*) | 1999 | 76 |
| HenipaV/Sus scr/NiV/AJ564621/1999 | Pig (*Sus scrofa*) | 1999 | 76 |
| MorbilliV/Ovi ari/PPRV/AJ849636/2000 | Domestic sheep (*Ovis aries*) | 2000 | 77 |
| MorbilliV/Del del/CeMV_DMV/AJ608288/1990 | Dolphin (*Delphinus delphis*) | 1990 | 78-79 |
| MorbilliV/Hom sap/MeV/AF128244/1991 | Human (*Homo sapiens*) | 1991 | 80 |
| MorbilliV/Hom sap/MeV/EF565859/1993 | Human (*Homo sapiens*) | 1993 | 81 |
| MorbilliV/Hom sap/MeV/AB254456/2006 | Human (*Homo sapiens*) | 2006 | 82 |
| MorbilliV/Bos tau/RPV/NC_006296/1910 | Cow (*Bos □auben*) | 1910 | 83 |
| MorbilliV/Pho vit/PDV/Y09630/1988 | Harbor seal *(Phoca vitulina)* | 1988 | 84 |
| MorbilliV/Pro lot/CDV/AY443350/2000 | Raccoon (*Procyon lotor*) | 2000 | 85 |
| MorbilliV/Can lup/CDV/EU716337/2004 | Dog (*Canis lupus familiaris*) | 2004 | 86 |
| RespiroV/Mus mus/SeV/AB039658/1976 | House mouse (*Mus musculus*) | 1976 | 87 |
| RespiroV/Cal jac/SeV Tianj/EF679198/1999 | Cotton-eared marmoset Callithrix (*Callithrix jacchus*) | 1999 | 88 |
| RespiroV/Bos tau/bPIV3/AF178654/1984 | Cow (*Bos □auben*) | 1984 | 89 |
| RespiroV/Hom.sap/hPIV1/NC_003461/1964 | Human (*Homo sapiens*) | 1964 | 90 |
| RespiroV/Hom sap/hPIV3/Z11575/1957 | Human (*Homo sapiens*) | 1957 | 91 |
| RespiroV/Sus scr/swPIV3/EU439428/1992 | Pig (*Sus scrofa*) | 1992 | 92 |
| RespiroV/Sus scr/swPIV3/EU439429/1981 | Pig (*Sus scrofa*) | 1981 | 92 |
| RubulaV/Hom sap/hPIV4/EU627591/2004 | Human (*Homo sapiens*) | 2004 | 93 |
| RubulaV/Chl sab/SV5/AF052755/1954 | Green monkey (*Chlorocebus sabaeus*) | 1954 | 94 |
| RubulaV/Chl sab/SV41/NC_006428/1964 | Green monkey (*Chlorocebus sabaeus*) | 1964 | 95 |
| RubulaV/Pte ale/MenPV/AF326114/1997 | Black flying fox (*Pteropus alecto*) | 1997 | 96 |
| RubulaV/Stu lil/MprPV/EF095490/1979 | Little yellow-shouldered bat (*Sturnira lilium*) | 1979 | 97-98 |
| RubulaV/Hom sap./MuV/AF280799/1996 | Human (*Homo sapiens*) | 1996 | 99 |
| RubulaV/Hom sap/MuV/EU370207/2005 | Human (*Homo sapiens*) | 2005 | 100 |
| RubulaV/Hom sap/MuV/GU980052/1945 | Human (*Homo sapiens*) | 1945 | 101 |
| RubulaV/Hom sap/MuV/AY681495/2003 | Human (*Homo sapiens*) | 2003 | 102 |
| RubulaV/Hom sap/MuV/AY669145/1994 | Human (*Homo sapiens*) | 1994 | 102 |
| RubulaV/Hom sap/MuV/AY309060/1998 | Human (*Homo sapiens*) | 1998 | 103 |
| RubulaV/Hom sap/MuV/AF467767/1988 | Human (*Homo sapiens*) | 1988 | 104 |
| RubulaV/Sus scr/PorPV/BK005918/1984 | Pig (*Sus scrofa*) | 1984 | 97,105 |
| RubulaV/Pte hyp/TioPV/AF298895/2000 | Small flying-fox (*Pteropus hypomelanus*) | 2000 | 14 |
| RubulaV/Hom sap/hPIV2/AF533012/1955 | Human (*Homo sapiens*) | 1955 | 106 |
| RubulaV/Rou les/Tuhoku1/GU128080/2006 | Leschenault's rousette (*Rousettus □aubentonii□s*) | 2006 | 16 |
| RubulaV/Rou les/Tuhoku2/GU128081/2006 | Leschenault's rousette (*Rousettus □aubentonii□s*) | 2006 | 16 |
| RubulaV/Rou les/Tuhoku3/GU128082/2006 | Leschenault's rousette (*Rousettus □aubentonii□s*) | 2006 | 16 |
| AvulaV/Gal gal/NDV/AY935496/1999 | Chicken (*Gallus gallus*) | 1999 | 107 |
| AvulaV/Gal gal/APMV2/EU338414/1956 | Chicken (*Gallus gallus*) | 1956 | 108 |
| AvulaV/Mel gal/APMV3/EU403085/1975 | Turkey (*Meleagris gallopavo*) | 1975 | 109 |
| AvulaV/Ana pla/APMV4/FJ177514/1975 | Mallard duck (*Anas platyrhynchos*) | 1975 | 110 |
| AvulaV/Mel und/APMV5/GU206351/1974 | Budgerigar (*Melopsittacus □aubenton*) | 1974 | 111 |
| AvulaV/Ana dom/APMV6/AY029299/1998 | Domestic duck (*Anas domesticus*) | 1998 | 112 |
| AvulaV/Col spe/APMV7/FJ231524/1975 | Dove (Columbidae *species)* | 1975 | 113 |
| AvulaV/Bra can/APMV8/FJ215863/1976 | Canada goose (*Branta □aubentoni*) | 1976 | 114 |
| AvulaV/Ana dom/APMV9/EU910942/1978 | Domestic duck (*Anas domesticus*) | 1978 | 115 |
| AvulaV/Eud chr/APMV10/HM147142/2007 | Rockhopper penguin (*Eudyptes chrysocome*) | 2007 | 116 |
| MetapneumoV/Hom sap/hMPV/AY525843/1999 | Human (*Homo sapiens*) | 1999 | 117 |
| MetapneumoV/Hom sap/hMPV/AF371337/2000 | Human (*Homo sapiens*) | 2000 | 118 |
| MetapneumoV/Bra can/aMPV-C/DQ009484/2001 | Canada goose (*Branta □aubentoni*) | 2001 | 119 |
| MetapneumoV/Aves/aMPV-C/AY394492/1997 | Aves | 1997 | 120 |
| MetapneumoV/Mel gal/aMPV-B/AB548428/1986 | Turkey (*Meleagris gallopavo*) | 1986 | 121-122 |
| MetapneumoV/Mel gal/aMPV-A/DQ666911/1985 | Turkey (*Meleagris gallopavo*) | 1985 | 123 |
| PneumoV/Mus mus/MPV/AY743910/1939 | House mouse (*Mus musculus*) | 1939 | 124-125 |
| PneumoV/Bos tau/bRSV/AF092942/1975 | Cow (*Bos □auben*) | 1975 | 126 |
| PneumoV/Hom sap/hRSV-A2/M74568/1961 | Human (*Homo sapiens*) | 1961 | 127 |
| PneumoV/Hom sap/hRSV-B/AY353550/1977 | Human (*Homo sapiens*) | 1977 | 128 |

| | | | |
|---|---|---|---|
| PneumoV/Hom sap/hRSV-S2/U39662/1976 | Human (*Homo sapiens*) | 1976 | 129 |
| UPV/Zyg bre/NarPV/FJ362497/1962 | Short-tailed cane mouse (*Zygodontomys b. brevicauda*) | 1962 | 130 |
| UPV/Sal sal/ASPV/EU156171/1995 | Atlantic salmon (*Salmo salar*) | 1995 | 131 |
| UPV/Tup bel/TuPV/AF079780/1978 | Northern treeshrew (*Tupaia belangeri*) | 1978 | 132 |
| UPV/Rat leu/MosPV/AY286409/1970 | Cape York rat (*Rattus leucopus*) | 1970 | 133 |
| UPV/Rat nor/BeiPV/DQ100461/1998 | Norway rat (*Rattus norvegicus*) | 1998 | 134 |
| UPV/Mus mus/JPV/NC_007454/1972 | House mouse (*Mus musculus*) | 1972 | 135 |
| UPV/Bot atr/FdlPV/NC_005084/1979 | Fer-de-Lance viper (*Bothrops atrox*) | 1979 | 136 |
| BatPV/Eid hel/GH48/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | 12 |
| BatPV/Eid hel/GH10/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | 12 |

[a] Genus/typical host/abbreviation/accession number/collection year

[b] HenipaV = *Henipavirus*, MorbilliV = *Morbillivirus*, RespiroV = *Respirovirus*, RubulaV = *Rubulavirus*, AvulaV = *Avulavirus*, MetapneumoV = *Metapneumovirus*, PneumoV = *Pneumovirus*, UPV = unclassified paramyxovirus; NiV = Nipah virus, HeV = Hendra virus, PPRV = *peste des petits ruminants* virus, CeMV DMV = cetacean □aubentonii□s strain dolphin □aubentonii□s, MeV = measles virus, RPV = □aubentoni virus, PDV = phocine distemper virus, CDV = canine distemper virus, SeV = Sendai virus, bPIV3 = bovine parainfluenza virus 3, hPIV1 = human parainfluenza virus 1, hPIV3 = human parainfluenza virus 3, swPIV3 = swine parainfluenza virus 3, SV5 = simian parainfluenza virus 5, SV41 = simian virus 41, MenPV = menangle virus, MprPV = mapuera virus, MuV = mumps virus, PorPV = porcine rubulavirus, TioPV = Tioman virus, hPIV2 = human parainfluenza virus 2, APMV4 = avian paramyxovirus type 4, APMV5 = avian paramyxovirus type 5, APMV6 = avian paramyxovirus type 6, APMV9 = avian paramyxovirus type 9, APMV2 = avian paramyxovirus type 2, APMV3= avian paramyxovirus type 3, APMV7 = avian paramyxovirus type 7, APMV8 = avian paramyxovirus type 8, NDV = Newcastle disease virus, hMPV = human metapneumovirus, aMPV = avian metapneumovirus, MPV = murine pneumonia virus, bRSV = bovine respiratory syncytial virus, hRSV = human respiratory syncytial virus, NarPV = Nariva virus, ASPV = Atlantic salmon paramyxovirus, TuPV = Tupaia paramyxovirus, MosPV = Mossman virus, BeiPV = Beilong virus, JPV = J virus, FdlPV = Fer-de-lance virus.

# Supplementary Table S7. Paramyxoviruses not included into phylogenetic analyses due to partial or complete unavailability of the L-gene sequence fragment used in this study

| Paramyxovirus Genus/Virus | Exemplary GenBank Accession numbers of non-L or partial L-gene sequences | Exemplary Host | Literature reference |
|---|---|---|---|
| *Morbillivirus*/Porpoise morbillivirus | X84739, AY949833 | Porpoise (*Phocoena phocoena*) | [137-138] |
| *Morbillivirus*/Pilot whale morbillivirus | AF200818, AF200817, FJ842380, GQ149614, FJ842381, FJ842382 | Long-finned pilot whale (*Globicephala melas*), Short-finned pilot whale (*Globicephala macrorhynchus*) | [139-140] |
| *Respirovirus*/Bottlenose dolphin parainfluenzavirus 1 | EF990554, EF990553 | Bottlenose dolphin (*Tursiops □aubenton*) | [141] |
| *Respirovirus*/Guinea pig parainfluenzavirus 3 | AF394241 | Guinea pig (*Cavia porcellus*) | [142] |
| *Respirovirus*/Ovine parainfluenzavirus 3 | AF035681 | Sheep (*Ovis aries*) | [143] |
| *Rubulavirus*/Swine parainfluenzavirus (SV 5-like) | AJ278916, AJ278915, AJ749981, AJ278914 | Pig (*Sus scrofa*) | [144-145] |
| *Rubulavirus*/Canine parainfluenzavirus (SV 5-like) | AY491509, EF546392 | Dog (*Canis familiaris*) | [145-147] |
| *Rubulavirus*/Human parainfluenzavirus (SV 5-like) | AJ749986 | Human (*Homo sapiens*) | [145,148] |
| *Metapneumovirus*/aMPV-D | AJ400728, AJ400729, AJ251085, AJ400730, AJ400731, AJ288946 | Turkey (*Meleagris gallopavo*) | [149] |
| *Pneumovirus*/Dog pneumovirus (MPV-related) | HQ734815, GU247050 | Dog (*Canis familiaris*) | [150] |
| UPV[a]/Pacific salmon paramyxovirus | AY536862 | Chinook salmon (*Oncorhynchus tshawytscha*) | [151] |
| UPV/Salem virus (*Morbillivirus*-related) | AF237881 | Horse (*Equus ferus caballus*) | [152] |
| UPV/Murayama virus (*Avulavirus*-related) | D13990 | Cynomolgus monkey(*Macaca fascicularis*) | [153] |
| UPV[b]/Tortoise paramyxovirus (FdlV-related) | GQ277615 | Hermanns tortoise (*Testudo hermanni*) | [154] |
| UPV[b]/Lizard paramyxovirus FdlV-related) | GQ277626 | Flathead knob-scaled lizard (*Xenosaurus platyceps*) | [154] |

[a]UPV = unclassified paramyxovirus, Tentative genus *Aquaparamyxovirus* [155]

[b]UPV = unclassified paramyxovirus, Tentative genus *Ferlavirus* [156]

## Supplementary Table S8. Paraymxovirus RNA concentrations in bat fecal specimens

| **Animal (Virus ID: BatPV/)** | **LOG10 viral RNA copies / g feces** | | | | | | |
|---|---|---|---|---|---|---|---|
| **Pneumoviruses** | /Eid_hel/GH24P/GHA/2009 | /Eid_hel/GH25P/GHA/2009 | /Eid_hel/GH11P/GHA/2009 | /Eid_hel/GH28P/GHA/2009 | /Eid_hel/GH12P/GHA/2009 | /Eid_hel/GH30P/GHA/2009 | /Eid_hel/GH17P/GHA/2009 |
| | 6.86 | 7.14 | 6.03 | 6.98 | 5.79 | 5.79 | 5.79 |
| | /Eid_hel/GH31P/GHA/2009 | /Eid_hel/GH18P/GHA/2009 | /Eid_hel/GH22P/GHA/2009 | | | | |
| | 7.21 | 6.78 | 5.79 | | | | |
| **Henipaviruses** | /Eid_hel/GH21a/GHA/2009 | /Eid_hel/GH27a/GHA/2009 | /Eid_hel/GH15/GHA/2009 | /Pte_par/K207/CRC/2010 | /Pte_par/K209/CRC/2010 | /Pte_par/K245H/CRC/2010 | /Car_per/K396/CRC/2010 |
| | 7.85 | 6.73 | 6.49 | 5.70 | 6.26 | 6.60 | 6.43 |
| **Rubulaviruses** | /Eid_hel/GH31/GHA/2009 | /Eid_hel/GH2/GHA/2009 | /Eid_hel/GH4/GHA/2009 | /Eid_hel/GH24a/GHA/2009 | /Eid_hel/GH1a/GHA/2009 | | |
| | 6.98 | 6.72 | 6.96 | 6.74 | 6.96 | | |
| ***Morbillivirus*-related viruses** | /Pte_par/K370/CRC/2010 | /Pte_par/K245M/CRC/2010 | /Myo_myo/N78-14/GER/2008 | /Myo_myo/N78-16/GER/2008 | | | |
| | 5.70 | 5.44 | 3.85 | 5.32 | | | |

## Supplementary Table S9. Oligonucleotides used for reverse transcription (RT)-PCR screening and amplification of paramyxovirus genomes

| No. | Primer ID | Sequence (5'- 3') | Polarity | Use |
|---|---|---|---|---|
| 1 | RMH-F1 | TCITTCTTTAGAACITTYGGNCAYCC | + | Hemi-nested screening RT-PCR[31] |
| 2 | RMH-F2 | GCCATATTTTGTGGAATAATHATHAAYGG | + | |
| 3 | RMH-R | CTCATTTTGTAIGTCATYTTNGCRAA | - | |
| 4 | AR-F1 | GGTTATCCTCATTTITTYGARTGGATHCA | + | Hemi-nested screening RT-PCR[31] |
| 5 | AR-F2 | ACACTCTATGTIGGIGAICCNTTYAAYCC | + | |
| 6 | AR-R | GCAATTGCTTGATTITCICCYTGNAC | - | |
| 7 | PNE-F1 | GTGTAGGTAGIATGTTYGCNATGCARCC | + | Hemi-nested screening RT-PCR[31] |
| 8 | PNE-F2 | ACTGATCTIAGYAARTTYAAYCARGC | + | |
| 9 | PNE-R | GTCCCACAAITTTTGRCACCANCCYTC | - | |
| 10 | PmV10986F-a | GTAGAAGGGTATTGTCAGAAGCTGTGGAC | + | Hemi-nested screening RT-PCR |
| 11 | PmV10986F-b | GTTGAGGGCTTATGCCAGAAGCTGTGGAC | + | |
| 12 | PmV10986F-c | GTTGAGGGGTACTGCCAGAAGGCTTGGAC | + | |
| 13 | PmV11065F-a | GGATTGCTGCGATGGTGCAAGGAGACAA | + | |
| 14 | PmV11065F-b | GAGTTGTGAGCATGGTTCAAGGTGATAA | + | |
| 15 | PmV11065F-c | AGATGACCGCTCTATTAAACGGTGACAA | + | |
| 16 | PmV11650-Ra | GATGATGTGACTGGATCACCGATGTT | - | |
| 17 | PmV11650-Rb | GAGGTTGTGAGTGGGTCTCCGATGTT | - | |
| 18 | PmV11650-Rc | GTGGAGACTAGAGGGTCACCGATGTT | - | |
| 19 | PmV11650-Rd | GCTTCAGTGAGGAAATCAGGAGTTCT | - | |
| 20 | NowakPV-F | ATTACAATGATGAAAGGGCATGC | + | Hemi-nested screening RT-PCR |
| 21 | NowakPV-R | TAATCTTCCAACTTGCTTAATCTCC | - | |
| 22 | NowakPV-Rnest | CCAACTTGCTTAATCTCCTTCTC | - | |
| 23 | Respiro-F1 | TTTTCTTTTTTTMGGASGTTTGGKCATCC | + | Hemi-nested screening RT-PCR |
| 24 | Respiro-F2 | CATGCTGTGTTTTGTGGGATTATTATTAATGG | + | |
| 25 | Respiro-R | GCTCKCATTTTGTATGTCATTTTKGCGAA | - | |
| 26 | PV-Rub-F1087 | TGYITIATGMGIHTITGGGGICAYCC | + | 5'-extension of *Rubulavirus* screening PCR fragments |
| 27 | PV-Rub-F1207 | TTYTTYMAIGGIATITTIATIAAYGG | + | |
| 28 | PV-Rub-F1642 | GCITCWTAYTCIHTIAARGARAARGA | + | |
| 29 | PV-Pne-F1072 | TAYTTTHTITTYAGIATHTTYGGICACCC | + | 5'-extension of *Pneumovirus* screening PCR fragments |
| 30 | PV-Pne-F1190 | GAGGIGCITTYATTTATAGRATIATMAARGG | + | |
| 31 | HeNiV-F13806 | GARGGWTATAGYCARAAGTTGTGGAC | + | Amplification of *Henipavirus* GDN(Q/E)-motif coding sequence |
| 32 | HeNiV-R14122 | TGKGAYAGYATTACTCCRTCRTART | - | |
| 33 | HeNiV-R14200 | ATRTTRCTRCAAGCTGATCTWGTYTCRTC | - | |
| 34 | NiV-F262 | ATYAGRAGYCTCCTYAAYGACCCAGA | + | Amplification of *Henipavirus* genome islet |
| 35 | NiV-F334 | CCAGTRATGGAGAGGAGRGG | + | |
| 36 | NiV-F500 | CCATCGAGGCCCAGATYTGGA | + | |
| 37 | NiV-R542 | GTAACTGCTTTRGCGATCAGKATCCA | - | |
| 38 | NiV-R557 | GCWGTGTCKGGAGCTGTVACTGC | - | |
| 39 | NiV-F612 | CCATCGAGGCCCAGATYTGGAT | + | Amplification of *Henipavirus* genome islet |
| 40 | NiV-F647a | GCAGTTACAGCTCCMGACACTGC | + | |
| 41 | NiV-F647b | GCAGTGACTGCTCCAGATACAGC | + | |
| 42 | NiV-R1122 | ACWCCCATGGCAAAGCTCCA | - | |
| 43 | NiV-R1070 | TCTGAATAGATTCYTCAAGGAGCACCAT | - | |
| 44 | NiV-R1368 | CCYCCWGCWGCAAATTTDGCYTCTCT | - | |
| 45 | NiV-R1293 | GCAGCAGCSAGKTCTGCAASTTGAT | - | |
| 46 | NiV-F3609a | ATGCCYATTAAAAAGGGCACAG | + | Amplification of *Henipavirus* genome islet |
| 47 | NiV-F3609b | ATGCCYATTAAAAAGGGCA | + | |
| 48 | NiV-F3672 | TYGAAGAGTGGTGYAAYCC | + | |
| 49 | NiV-R3699 | GAACATGCCGGGTTGCACCA | - | |
| 50 | NiV-R3759 | CATTCAGTTGGRCATTCTCCGCA | - | |
| 51 | NiV-R4150 | CCTTTCCCTGGTATCATGATCAT | - | |
| 52 | NiV-R4201 | CCTATTACTGGTTTAAGCTCMGGRTT | - | |
| 53 | NiV-F5378 | GCRTACCCTTTKGGTGTTGG | + | Amplification of *Henipavirus* genome islet |
| 54 | NiV-F5159a | GATTTTAGTCCCACCTCATGGGA | + | |
| 55 | NiV-F5159b | GATTTTAGCCCTAGTTCTTGGGA | + | |
| 56 | NiV-F5273 | GAGAGGAAATACAAYAACTACATGTA | + | |
| 57 | NiV-R5415a | GGATGAGAGGCACTCTTRCCAACACC | - | |
| 58 | NiV-R5415b | GGGTGAGAAGTGCTCTTGCCAACACC | - | |
| 59 | NiV-R5550a | CCGCCAGTCAGAATCTTCTTCCATGG | - | |
| 60 | NiV-R5550b | CCACTRGTCAGTACTTTCTTCCAYGG | - | |
| 61 | NiV-F5808a | CCTTCATGCTGCACTTGGGRAACTT | + | Amplification of *Henipavirus* genome islet |
| 62 | NiV-F5808b | CTTTCATGCTCCATCTCGGGAATTT | + | |
| 63 | NiV-F5870 | TGTAGGAGGAAGATTGATAGGATG | + | |
| 64 | NiV-R6037 | GTTGAGCCAAGGATTGATGTCCAT | - | |
| 65 | NiV-R6129 | ACATCGTCATAGATCATGAAYTC | - | |
| 66 | NiV-F6738 | CATTATGAGAAAYTKAGTAARATWGG | + | Amplification of |

| | | | | |
|---|---|---|---|---|
| 67 | NiV-F6825 | GTKATWAAAATGATTCCKAATRT | + | *Henipavirus* genome islet |
| 68 | NiV-R7051 | GCWACACCTGCWGTGATTTG | - | |
| 69 | NiV-F6984a | GCCGGAGTTATAATGGCAGG | + | Amplification of *Henipavirus* genome islet |
| 70 | NiV-F6984b | GCAGGTGTGGTGATGGCAGG | + | |
| 71 | NiV-R7207a | GGAACAAGGTTAGTGTTGATGTAATCYTG | - | |
| 72 | NiV-R7207b | GGTACYAAGTTAGTATTAATGTAATCYTG | - | |
| 73 | NiV-R7315 | GGRTCYTGTARGTTRGGWCCRAA | - | |
| 74 | NiV-F7020 | GCWACTGCWGCWCAAATYACAGCAGG | + | Amplification of *Henipavirus* genome islet |
| 75 | NiV-F7179 | CAGGATTACATTAATACTAAYTTGGTWCC | + | |
| 76 | NiV-R7450 | ATTTGRCCYGTTATGCTGTCACTTTC | - | |
| 77 | NiV-R7598 | GAAATTTGGGACAATGCTGATCCATTC | - | |
| 78 | NiV-F11445 | TAYCCTGAATGTCATTTGGATAGYCC | + | Amplification of *Henipavirus* genome islet |
| 79 | NiV-F11449 | CTGAATGTCATTTGGATAGYCCTATWGT | + | |
| 80 | NiV-R11697 | ATAGARTGTTATTGCATTCRGGRTA | - | |
| 81 | NiV-R11935 | GTRAACCAGAAGAGAAAACAYTCATACCA | - | |
| 82 | NiV-F11907a | TGGTATGAGTGTTTTTTGTTTTGGTT | + | Amplification of *Henipavirus* genome islet |
| 83 | NiV-F11907b | TGGTATGAGTGTTTTCTCTTCTGGTT | + | |
| 84 | NiV-F11928 | TGGTTTACTATCAARACAGAGATG | + | |
| 85 | NiV-R12133 | ACATCACAATACATTAGAACMATTTC | - | |
| 86 | NiV-R12152a | CATCATCCTCCCTTCTAGGACATCACA | - | |
| 87 | NiV-R12152b | CATCATCCGGCCTTCCAAGACATCACA | - | |
| 88 | NiV-F16854 | AATTCGTCWTCWTGYTAYAAGGC | + | Amplification of *Henipavirus* genome islet |
| 89 | NiV-F16936 | TAGGWGAAGGKTCWGGGAGYATG | + | |
| 90 | NiV-R17161 | CCGATCCATGTKGTTTCKGGTCTTCCRTT | - | |
| 91 | NiV-R17155 | CATGTKGTTTCKGGTCTTCCRTTRAA | - | |
| 92 | NiV-F17720 | GAAGTGGGATATGATATAGGATCAG | + | Amplification of *Henipavirus* genome islet |
| 93 | NiV-F17824 | CTTCACATCATTTGGAACCGTATCCAGT | + | |
| 94 | NiV-R18122 | GATCTTCCACCAGATTTTGACTTC | - | |
| 95 | NiV-R18136 | GAGAGGTAACCTATGATCTTCCACCA | - | |
| 96 | NiV-F18099 | GAAGTTAAAATCTGGTGGAAGATMATMGGWTA | + | |
| 97 | PmV-F17361 | GATGATGATATYAATAGTTTTATMAC | + | Amplification of *Henipavirus* genome islet |
| 98 | PmV-F17367 | GATATYAATAGTTTTATMACWGA | + | |
| 99 | PmV-R18593 | CCATGTGGTTTCKGGTTTKCCGTT | - | |
| 100 | PmV-R18596 | CCKATCCATGTGGTTTCKGGTTTKCC | - | |
| 101 | PmV-F12770a | TACCCTGAATGTCATTTGGATAG | + | Amplification of *Henipavirus* genome islet |
| 102 | PmV-F12770b | TACCCTGAGGTCCATTTGGATAG | + | |
| 103 | PmV-F12773a | CCTGAATGTCATTTGGATAGTCC | + | |
| 104 | PmV-F12773b | CCTGAGGTCCATTTGGATAGTCC | + | |
| 105 | PmV-R13442 | ACATCACAGTACATTAGGACCAGTTC | - | |
| 106 | Henipa-N-F1 | TGGATACTGATCGCTAAAGCAGT | + | Amplification of *Henipavirus* genome islet |
| 107 | Henipa-N-F1nest | GATACTGATCGCTAAAGCAGTTAC | + | |
| 108 | Bei-Tup-N-F1 | CAAATTTGGATCCTGCTGGCTAAGGC | + | |
| 109 | Henipa-N-R1 | GCAACACCCATGGCAAAGCTCCA | - | |
| 110 | Henipa-N-R1nest | AACACCCATGGCAAAGCTCCACA | - | |
| 111 | Bei-Tup-N-R1 | CCAACNCCCATGGCGTAGCTC | - | |
| 112 | Bei-Tup-N-R1nest | CAACNCCCATGGCGTAGCTCCA | - | |
| 113 | Nipah-F-F1 | GCAACCGCAGCTCAAATTACTGCAG | + | Amplification of *Henipavirus* genome islet |
| 114 | Nipah-F-F2 | ACCGCAGCTCAAATTACTGCAGGTGT | + | |
| 115 | Hendra-F-F1 | GCTACTGCTGCACAGATTACAGCAG | + | |
| 116 | Hendra-F-F2 | ACTGCTGCACAGATTACAGCAGGTGT | + | |
| 117 | Beilong-F-F1 | GCGACTTCAGCGCAGATTACAGCAG | + | |
| 118 | Beilong-F-F2 | ACTTCAGCGCAGATTACAGCAGGTGT | + | |
| 119 | Tupaia-F-F1 | GCAACAGCGGCAGCAATAACGGCAG | + | |
| 120 | Tupaia-F-F2 | ACAGCGGCAGCAATAACGGCAGGTGT | + | |
| 121 | Henipa-F-R | CACTGGCATGTGACGCTTATGCAATT | - | |
| 122 | Tupaia-F-R | CAGCGGCATGCAGCTTTTGCACAGTT | - | |
| 123 | Rest-F-R | CATTTGCAGAGTACTGATGCGCAGTT | - | |
| 124 | MuV-F648 | ACAGTGTACTAATCCAGGCTTGG | + | Amplification of mumps virus genome islet |
| 125 | MuV-F669 | GGGTGATGGTCTGTAAATGTATGACAGC | + | |
| 126 | MuV-R924 | TACTTTCCGATGTCACCTACCATTGCATA | - | |
| 127 | MuV-R1156 | CATGGCATAGCTGAATATCAATGGGTA | - | |
| 128 | MuV-F2486 | CATAGACGGGAATGGAGCCTTAGCTGGGT | + | Amplification of mumps virus genome islet |
| 129 | MuV-F2525 | GTCCGGGTCTTTGAGTGGTGCAATCC | + | |
| 130 | MuV-R2827 | ACCCCTGTCGGGTTTCCAGGGTCCAT | - | |
| 131 | MuV-F3963 | GCATCCGTGTGGTTCCACCTGTGTAA | + | Amplification of mumps virus genome islet |
| 132 | MuV-R4111 | GCATGGACTAGGATGGTTGGTCCCCA | - | |
| 133 | MuV-R4240 | GCAGCTTTGATTTCGCACCCGGATGACCA | - | |
| 134 | MuV-F4876 | GCTGCGCTCGGTGTTGCGACCGCGGCACA | + | Amplification of mumps virus genome islet |
| 135 | MuV-F4923 | ATTGGTTCAAGCACAGACGAATGC | + | |
| 136 | MuV-R5175 | TTGGGGCTGAAACACTGTTGTTAATTCTGT | - | |
| 137 | MuV-F7137 | CCAATGGTTGCACGAGGATTCCATC | + | Amplification of mumps virus genome islet |
| 138 | MuV-F7166 | TCTTTAGGTAAGACACACTGGTG | + | |
| 139 | MuV-R7362 | GGGACTGTTGCAATTGAGCAGCT | - | |
| 140 | MuV-F7871 | TATCAGAGGAGTACTAGCTGGTGG | + | Amplification of mumps virus genome islet |
| 141 | MuV-R8265 | TCGCCGGTGTCTTGAAAGCAGGT | - | |
| 142 | MuV-R8340 | AGCACAGGTAGAATTTGGAATTCTCC | - | |

| | | | | |
|---|---|---|---|---|
| 143 | MuV-F9675 | GGAGGAGCCATAATGGAATCTGGCC | + | Amplification of mumps virus genome islet |
| 144 | MuV-F10172 | GAGTCATTRTTGGCTAATCATGCAGG | + | |
| 145 | MuV-F10268 | CAGATTGGTATTATATCAGAGCA | + | |
| 146 | MuV-R11118 | CACAAATCTTTTTCRACTCCATTCTC | - | |
| 147 | MuV-R11334 | GCKGATACYAATGGGTCYCCKATGTT | - | |
| 148 | MuV-F13159 | GAGCATAGATGCAGTGATGTGG | + | Amplification of mumps virus genome islet |
| 149 | MuV-F13865 | CATCTATATTTGGCAGAGGGAAG | + | |
| 150 | MuV-F13686 | CCAGTCTTGAGAAATACTCTCTCCC | + | |
| 151 | MuV-R13980 | CGTTGGGGAGGGTTCTCACCACT | - | |
| 152 | MuV-R14027 | TGTAGGGGACACTTTCAATAAACTG | - | |
| 153 | MuV-F14802 | CTTCATACAATGTAGGTCCTCTCGG | + | Amplification of mumps virus genome islet |
| 154 | MuV-F14867 | CTTATGTATACTGTGAGGAACTGG | + | |
| 155 | MuV-R15129 | CAATAGATTACACATCCGATGGCTTTCCA | - | |

ID, identification; R=G/A, Y=C/T, S=G/C, W=A/T, M=A/C, K=G/T, H=A/C/T, B=C/G/T, N=A/T/C/G, I=inosine

## Supplementary Table S10. Real time reverse transcription-PCR oligonucleotides used for virus quantification

| No. | Virus targeted | Oligonucleotide ID | Sequence (5'→3') | Orientation |
|---|---|---|---|---|
| 1 | *E. helvum* | Spl6RMH-F | CGGGATAGACATGGAGGTGTGT | + |
| | *Henipavirus* | Spl3+6RMH-P | FAM[a]-CCITCTTGTTTCCTTCCTGATCATGCATC-BHQ1[b] | Probe |
| | quantification | Spl6RMH-R | CCGTTCATCTTTTTGGATTTGAT | - |
| 2 | *E. helvum* | Spl3RMH-F | CGAGATAGACATGGAGGTGTATG | + |
| | *Henipavirus* | Spl3+6RMH-P | FAM-CCITCTTGTTTCCTTCCTGATCATGCATC-BHQ1 | Probe |
| | quantification | Spl3RMH-R | TTCTGCGCAATCCTCTATTGTCA | - |
| 3 | *E. helvum* | Spl2RMH-F | TTTACCCTTCCATCAACCTACGTT | + |
| | *Henipavirus* | Spl2RMH-P | FAM-CAACCCTCCTCAATCGTCCACTTCCA-BHQ1 | Probe |
| | quantification | Spl2RMH-R | TCTGTGTCCTTTAGATATTCTCCTGATATT | - |
| 4 | *E. helvum* | Spl33nRMH1-F | TGGTGTCTGGCCTCCTATGAA | + |
| | *Henipavirus* | Spl33nRMH1-P | FAM-TTCCCCAGGCATGTTTCAAATACCATCA-BBQ | Probe |
| | quantification | Spl33nRMH1-R | CATATGTAAGTCTGTCTCCAGATGATTG | - |
| 5 | *E. helvum* | Spl28nRMH2-F | AGATAGACACGGAGGGATTTGG | + |
| | *Henipavirus* | Spl28nRMH2-P | FAM-TGCAAACTTCCAGATCATTGTTCACCTCA-BBQ | Probe |
| | quantification | Spl28nRMH2-R | TCTCCGTTCATTTTTTTGCTTTT | - |
| 6 | *E. helvum* | PVSpl43RMH-F | TTGTGGCACCATAATAAATGGATT | + |
| | *Henipavirus* | PVSpl43RMH-P | FAM-ACTTGGCCTCCTTGCGAACTTCCTG-BHQ1 | Probe |
| | quantification | PVSpl43RMH-R | CTCTTAACCAGAGCAGAAGCATGA | - |
| 7 | *E. helvum* | PV-Spl90-69RMH-F | GTTCAGAGACAGACATGGAGGTATGT | + |
| | *Henipavirus* | PV-Spl90-69RMH-P | FAM-TGTGACCTCCCTCCACATTCTTCACCTC-BHQ1 | Probe |
| | quantification | PV-Spl90-69RMH-R | TGGATAAGGACTCAGCATTAAGTTGT | - |
| 8 | *E. helvum* | PV-Spl67-51RMH-F | TTTGTGGGACAATTATCAATGGAT | + |
| | *Henipavirus* | PV-Spl67-51RMH-P | FAM-TGGCACCTGGCCACCATGTTCTCT-BHQ1 | Probe |
| | quantification | PV-Spl67-51RMH-R | TTTTTATAAGAGGTGAAGCATGATGTG | - |
| 9 | *E. helvum* | PV-Spl48-55-91-27a-F | AAGCTTTGTCTCCCATTAAATCACA | + |
| | *Henipavirus* | PV-Spl48-55-91-27a-P | FAM-AATGCCAACATGAAATACACACCAAAGCCT-BHQ1 | Probe |
| | quantification | PV-Spl48-55-91-27a-R | GGTTCAAACTCAGCATCATTGATAA | - |
| 10 | *E. helvum* | PV-Spl63-65-F | CAGTCCTTAATTGGCGTTCGTT | + |
| | *Henipavirus* | PV-Spl 63-65-P | FAM-ATTGGGTTCAAATTTGGTGTAT-MGBNFQ[d] | Probe |
| | quantification | PV-Spl 63-65-R | TCACTATCGAGGTCTAAGGGCATA | - |
| 11 | *E. helvum* | PV-F7-F | AAAGCTCTTGCTGCGATAAGGA | + |
| | *Henipavirus* | PV-F7-P | FAM-TGAGTGGGACAGTGTTT-MGBNFQ | Probe |
| | quantification | PV-F7-R | GTTGGCTGGTAAGAGAGATTTTCC | - |
| 12 | *E. helvum* | Lunge3AR-F | CGTCAAACTCTGATGAGGTCTCT | + |
| | *Rubulavirus* | Lunge3AR-P | FAM-TGAGGGCTTGTGTCAAAAGATGTGGA-BHQ1 | Probe |
| | quantification | Lunge3AR-R | CATGCTCATCACCCTCACATC | - |
| 13 | *E. helvum* | NewSplRub-F | CGTGGGGGATCCCTTCA | + |
| | *Rubulavirus* | NewSplRub-P | FAM-CCCACCAGCAGATACCAGTCAATTTGATC-BBQ[c] | Probe |
| | quantification | NewSplRub-R | CCACCTCTGGGTGATACAATGA | - |
| 14 | *E. spec* | MuV-AR1-RT-F | CCGAGTAGAGCTCATTTCAAGGA | + |
| | mumps virus | MuV-AR1-RT-P | FAM-TCCTAGCTTAAGATGGACCCGCTCCCA-BHQ1 | Probe |
| | quantification | MuV-AR1-RT-R | GCAACATCGGAAGAATCTTTGG | - |
| 15 | Broad-range Sendai | SeV-10791-rtF | CTGTGGACCTTAATCTCAATCAGT | + |
| | virus detection and | SeV-10828-rtP | FAM-CAGCTGTGAGAGTGGGTGTCAGGGTCT-BHQ1 | Probe |
| | quantification | SeV-10894-rtR | GTCACSGCTATAGCTTGATTGTC | - |
| 16 | *D. rotundus* | BR22-27-222-rtF | GCCTGGCCACCGATTACC | + |
| | *Morbillivirus* | BR22-27-222-rtP | FAM-TCCCAGCGCATGCTTCTGCAGTC-BHQ1 | Probe |
| | detection | BR22-27-222-rtR | CACCTGATGATTGCGCATTC | - |
| 17 | *D. rotundus* | BR21-rtF | GTCATGCTCTTTTTTGTGGTATGATAA | + |
| | *Morbillivirus*-related | BR21-rtP | FAM-AAATGGTTACCGAGAAAA-MGBNFQ | Probe |
| | detection | BR21-rtR | AGGGAGGCCAAACACCACTA | - |
| 18 | *G. soricina* | BR190-rtF | AACGGATTTAGAGACAGGCATAGC | + |
| | *Morbillivirus*-related | BR190-rtP | FAM-TGGCCTCCATGTACATTCCCTAATCATGC-BHQ1 | Probe |
| | detection | BR190-rtR | CTCTCATTGTTTGATTGGAGCAAT | - |
| 19 | *C. brevicauda* | BR-96-rtF | GAAGCAACAAATGCGGCTAAT | + |
| | *Morbillivirus*-related | BR-96-rtP | FAM-AAGTCCGTGAGCACATGAACAAACCAAAA-BHQ1 | Probe |
| | detection | BR-96-rtR | TGACCTTGCATCATTGTCTCAAA | - |
| 20 | *P. parnellii* | PV-KCR-G245H-rtF | TGTCTGGCCTCCAGCCTTT | + |
| | *Henipavirus*-related | PV-KCR-G245H-rtP | FAM-TCCCATCACACGCAGATATTGCGG-BHQ1 | Probe |
| | quantification | PV-KCR-G245H-rtR | GCTTCACCATTTACTTGTGCTCTTT | - |
| 21 | *P. parnellii* | PV-KCR- G245M-rtF | GTTTGGCCACCTTGTAGATTACCT | + |
| | *Morbillivirus*-related | PV-KCR- G245M-rtP | FAM-CTCATGCCTCAGACAAAATCAAACTTGCAA-BHQ1 | Probe |
| | quantification | PV-KCR- G245M-rtR | GCACATTTCATCTGTTAGTCCTTCA | - |
| 22 | *P. parnellii* | PV-KCR-W370-rtF | AGCCCTATCATCCATAAAATCAGAA | + |
| | *Morbillivirus*-related | PV-KCR-W370-rtP | FAM-TTCCCCATACCCAGCTTATACAATGCCA-BHQ1 | Probe |
| | quantification | PV-KCR-W370-rtR | GTGAAGTACTCTGTGGTGGAGGTTT | - |
| 23 | *C. afra* | GB09-478-F | GGCGGCTCTTAAAAGTGAATG | + |
| | *Morbillivirus*-related | GB09-478-P | FAM-TCCAGCACAAACATATCCGAGAAGGCTAG-BHQ1 | Probe |

| | | | | |
|---|---|---|---|---|
| | quantification | GB09-478-R | GCGGGGTCAAATTGGTCAT | - |
| 24 | *M. myotis* maternity colony M*orbillivirus*-related quantification | NowakPVrt-F | GCCATCGAGATCGACATGGT | + |
| | | NowakPVrt-P | FAM- CATGGCCTCCTTTAACATTTCCACACCA-BBQ1 | Probe |
| | | NowakPVrt-R | GGCCTGCTTAATTCGATCACTAG | - |
| 25 | *A. sylvaticus* *Morbillivirus*-related quantification | RMU10-HY-rtF | ACTGGAAGAGCTTTGCAGGTTT | + |
| | | RMU10-HY-rtP | FAM-CACTTCAAATGTTTCATGCCGCTTGAGTT-DDQ1[e] | Probe |
| | | RMU10-HY-rtR | GCTGCAAGAGCTTTATCCTTGAG | - |
| 26 | *M. glareolus* *Morbillivirus*-related quantification | RMU10-JE-rtF | GTGGGATTCAGTCTATCCKAGA | + |
| | | RMU10-JE-rtP | FAM-CATGACTTATGCRCCTCCAAAACAAACAAC-DDQ1 | Probe |
| | | RMU10-JE-rtR | GAAAYACTTCAACCAATCTCCTTG | - |
| 27 | *A. flavicollis* *Morbillivirus*-related quantification | RMU10-751-rtF | AAGCCCTAACACATGAATCGTGTA | + |
| | | RMU10-751-rtP | FAM-TTCATGCCGCTAACACTTGACGAAGATCT-DDQ1 | Probe |
| | | RMU10-751-rtR | CAWATAGCTGCTAGTGCCTTGTC | - |
| 28 | *M. glareolus* *Morbillivirus*-related quantification | RMU10-1414-rtF | CAGTCTACCCGAGAGAATTCATGA | + |
| | | RMU10-1414-rtP | FAM-ATGTGCCTCCAAAACAAACAACATCAAGGA-DDQ1 | Probe |
| | | RMU10-1414-rtR | TCCGTGTCGTTAAGAAACACTTCA | - |
| 29 | *M. agrestis* *Morbillivirus*-related quantification | RMU10-869-rtF | GGTCATGCATTGTTCTGTGGAA | + |
| | | RMU10-869-rtP | FAM-TGGTGCATGGCCTCCTCATGAATTTC-DDQ1 | Probe |
| | | RMU10-869-rtR | CATTCTTGATTGACTGGGAAACAT | - |
| 30 | *M. glareolus* *Morbillivirus*-related quantification | RMU10-1968-rtF | GCATGCTTTGTTCTGTGGCATA | + |
| | | RMU10-1968-rtP | FAM-CTTGGCCYCCTCATGAATTTCCAGAAC-DDQ1 | Probe |
| | | RMU10-1968-rtR | GTGTAAGTGCTTCACTGTTTGTCTG | - |
| 31 | *M. glareolus* *Morbillivirus*-related quantification | RMU10-JS-rtF | TCTAYCCGAAAGAATTCATGACT | + |
| | | RMU10-JS-rtP | FAM-CCYCCAAAACAAACAACATCAAGGAGA-DDQ1 | Probe |
| | | RMU10-JS-rtR | CGGGTCAAATTCTGTATCGTTAAGA | - |

*ID, identification; [a]FAM, 6-carboxyfluorescein; [b]BHQ1, Black Hole Quencher1, [c]BBQ, Black Berry Quencher, [d]MGB, Minor Groove Binder; NFQ, Non-fluorescent Quencher, [e]DDQ, Deep Dark quencher, R=G/A, Y=C/T, S=G/C, W=A/T, I=inosine

# Supplementary Table S11. Origin and accession numbers of viruses detected in this study

| No. | Paramyxovirus Genetic lineage | Virus ID[a] | Host | Collection year | Country | Specimen | GenBank accession number |
|---|---|---|---|---|---|---|---|
| 1 | *Rubulavirus* | BatPV/Eid_hel/GH13a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971946 |
| 2 | *Rubulavirus* | BatPV/Eid_hel/GH16/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609196 |
| 3 | *Rubulavirus* | BatPV/Eid_hel/GH18/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609197 |
| 4 | *Rubulavirus* | BatPV/Eid_hel/GH1a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971943 |
| 5 | *Rubulavirus* | BatPV/Eid_hel/GH2/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971944 |
| 6 | *Rubulavirus* | BatPV/Eid_hel/GH24a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971942 |
| 7 | *Rubulavirus* | BatPV/Eid_hel/GH31/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971947 |
| 8 | *Rubulavirus* | BatPV/Eid_hel/GH4/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971941 |
| 9 | *Rubulavirus* | BatPV/Eid_hel/GH47/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609195 |
| 10 | *Rubulavirus* | BatPV/Eid_hel/GH6/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971945 |
| 11 | *Rubulavirus* | BatPV/Eid_hel/GH-L3/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Ghana | Lung | FJ971948 |
| 12 | *Rubulavirus* | BatPV/Eid_hel/GH72/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | HQ660085 |
| 13 | *Rubulavirus* | BatPV/Rou_aeg/Bel125/GAB/2009 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2009 | Gabon | Spleen | HQ660086 |
| 14 | *Rubulavirus* | BatPV/Meg_woe/CO2139/CON/2005 | Woermann's fruit bat (*Megaloglossus woermanni*) | 2005 | Republic of the Congo | Spleen | HQ660087 |
| 15 | *Rubulavirus* | BatPV/Rou_aeg/CO2784/CON/2006 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2006 | Republic of the Congo | Spleen | HQ660088 |
| 16 | *Rubulavirus* | BatPV/Eid_hel/GH9-02/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Blood | HQ660089 |
| 17 | *Rubulavirus* | BatPV/Rou_aeg/GB1415/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660090 |
| 18 | *Rubulavirus* | BatPV/Rou_aeg/GB1493/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660091 |
| 19 | *Rubulavirus* | BatPV/Eid_hel/GB3378/GAB/2006 | Straw-coloured fruit bat (*Eidolon helvum*) | 2006 | Gabon | Spleen | HQ660092 |
| 20 | *Rubulavirus* | BatPV/Rou_aeg/CO2009/CON/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Republic of the Congo | Spleen | HQ660093 |
| 21 | *Rubulavirus* | BatPV/Rou_aeg/CO2569/CON/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Republic of the Congo | Spleen | HQ660094 |
| 22 | *Rubulavirus* | BatPV/Epo_spe/AR1/DRC/2009 | Epauletted fruit bat (*Epomophorus species*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660095 (full genome |
| 23 | *Rubulavirus* | BatPV/Rou_aeg/GB1456/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660096 |
| 24 | *Rubulavirus* | BatPV/Rou_aeg/GB1494/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660097 |
| 25 | *Rubulavirus* | BatPV/Rou_aeg/GB1704/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660098 |
| 26 | *Rubulavirus* | BatPV/Hip_caf/GB091001/GAB/2009 | Sundevall's roundleaf bat (*Hipposideros caffer*) | 2009 | Gabon | Spleen | HQ660099 |
| 27 | *Rubulavirus* | BatPV/Rou_aeg/GB09156/GAB/2009 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2009 | Gabon | Spleen | HQ660100 |
| 28 | *Rubulavirus* | BatPV/Rou_aeg/GB09164/GAB/2009 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2009 | Gabon | Spleen | HQ660101 |
| 29 | *Rubulavirus* | BatPV/Rou_aeg/GB09172/GAB/2009 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2009 | Gabon | spleen | HQ660102 |
| 30 | *Rubulavirus* | BatPV/Rou_aeg/GB09182/GAB/2009 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2009 | Gabon | Spleen | HQ660103 |
| 31 | *Rubulavirus* | BatPV/Min_inf/GB09512/GAB/2009 | Greater Long-fingered bat (*Miniopterus inflatus*) | 2009 | Gabon | Spleen | HQ660104 |
| 32 | *Rubulavirus* | BatPV/Hip_gig/GB09685/GAB/2009 | Giant leaf-nosed bat (*Hipposideros gigas*) | 2009 | Gabon | Spleen | HQ660105 |
| 33 | *Rubulavirus* | BatPV/Rou_aeg/GB1400/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660106 |
| 34 | *Rubulavirus* | BatPV/Rou_aeg/GB1404/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660107 |
| 35 | *Rubulavirus* | BatPV/Rou_aeg/GB1418/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660108 |
| 36 | *Rubulavirus* | BatPV/Eid_hel/GB1661-AR/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660109 |
| 37 | *Rubulavirus* | BatPV/Eid_hel/GB1663/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660110 |
| 38 | *Rubulavirus* | BatPV/Hyp_mon/RCA-P15/RCA/2008 | Hammer-headed fruit bat (*Hypsignathus monstrosus*) | 2008 | Central African Republic | Spleen | HQ660111 |
| 39 | *Rubulavirus* | BatPV/Hyp_mon/RCA-P17/RCA/2008 | Hammer-headed fruit bat (*Hypsignathus monstrosus*) | 2008 | Central African Republic | Spleen | HQ660112 |
| 40 | *Rubulavirus* | BatPV/Pteropodidae/RCA- | Megabat (*Pteropodidae*) | 2008 | Central African | Spleen | HQ660113 |

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|---|---|---|---|---|---|---|---|
| | | P19/RCA/2008 | | | Republic | | |
| 41 | *Rubulavirus* | BatPV/Eid_hel/RCA-P4/RCA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Central African Republic | Spleen | HQ660114 |
| 42 | *Rubulavirus* | BatPV/Eid_hel/GH-M5/GHA/2010 | Straw-coloured fruit bat (*Eidolon helvum*) | 2010 | Ghana | Spleen | HQ660115 |
| 43 | *Rubulavirus* | BatPV/Eid_hel/GH85/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660116 |
| 44 | *Rubulavirus* | BatPV/Eid_hel/GH93/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660117 |
| 45 | *Henipavirus* | BatPV/Eid_hel/GH10/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609191 |
| 46 | *Henipavirus* | BatPV/Eid_hel/GH15/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971935 |
| 47 | *Henipavirus* | BatPV/Eid_hel/GH-M2/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | FJ971936 |
| 48 | *Henipavirus* | BatPV/Eid_hel//GH-M3/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | FJ971937 |
| 49 | *Henipavirus* | BatPV/Eid_hel/GH-M6/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | FJ971938 |
| 50 | *Henipavirus* | BatPV/Eid_hel/GH21a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971939 |
| 51 | *Henipavirus* | BatPV/Eid_hel/GH27a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971940 |
| 52 | *Henipavirus* | BatPV/Eid_hel/GH48/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609194 |
| 53 | *Henipavirus* | BatPV/Myo_tor/CO2225/CON/2005 | Little Collared fruit bat (*Myonycteris torquata*) | 2005 | Republic of the Congo | Spleen | HQ660118 |
| 54 | *Henipavirus* | BatPV/Hyp_mon/CO2569/CON/2006 | Hammer-headed fruit bat (*Hypsignathus monstrosus*) | 2006 | Republic of the Congo | Spleen | HQ660119 |
| 55 | *Henipavirus* | BatPV/Epo_gam/CD255/DRC/2009 | Gambian Epauletted fruit bat (*Epomophorus gambianus*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660120 |
| 56 | *Henipavirus* | BatPV/Epo_spe/CD256/DRC/2009 | Epauletted fruit bat (*Epomophorus species*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660121 |
| 57 | *Henipavirus* | BatPV/Epo_gam/CD273/DRC/2009 | Gambian Epauletted fruit bat (*Epomophorus gambianus*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660122 |
| 58 | *Henipavirus* | BatPV/Eid_hel/CD287/DRC/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660123 |
| 59 | *Henipavirus* | BatPV/Eid_hel/CD291/DRC/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660124 |
| 60 | *Henipavirus* | BatPV/Eid_hel/CD297/DRC/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660125 |
| 61 | *Henipavirus* | BatPV/Myo_tor/CD356/DRC/2009 | Little Collared fruit bat (*Myonycteris torquata*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660126 |
| 62 | *Henipavirus* | BatPV/Eid_hel/GH-M43/GHA/2010 | Straw-coloured fruit bat (*Eidolon helvum*) | 2010 | Ghana | Spleen | HQ660127 |
| 63 | *Henipavirus* | BatPV/Epo_gam/CD078/DRC/2009 | Gambian Epauletted fruit bat (*Epomophorus gambianus*) | 2009 | Democratic Republic of the Congo | Spleen | HQ660128 |
| 64 | *Henipavirus* | BatPV/Eid_hel/GH-M74a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660129 (full genome |
| 65 | *Henipavirus* | BatPV/Eid_hel/GH-M77/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660130 |
| 66 | *Henipavirus* | BatPV/Eid_hel/GH-M67a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660131 |
| 67 | *Henipavirus* | BatPV/Eid_hel/GH-M51a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660132 |
| 68 | *Henipavirus* | BatPV/Eid_hel/GH-M61a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660133 |
| 69 | *Henipavirus* | BatPV/Eid_hel/GH-M90a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660134 |
| 70 | *Henipavirus* | BatPV/Eid_hel/GH-M69a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660135 |
| 71 | *Henipavirus* | BatPV/Eid_hel/GH-M63a/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660136 |
| 72 | *Henipavirus* | BatPV/Myo_tor/GB1386/GAB/2005 | Little Collared fruit bat (*Myonycteris torquata*) | 2005 | Gabon | Spleen | HQ660137 |
| 73 | *Henipavirus* | BatPV/Rou_aeg/GB1583/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660138 |
| 74 | *Henipavirus* | BatPV/Rou_aeg/GB1590/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660139 |
| 75 | *Henipavirus* | BatPV/Eid_hel/GB1237/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660140 |
| 76 | *Henipavirus* | BatPV/Eid_hel/GB1535/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660141 |
| 77 | *Henipavirus* | BatPV/Eid_hel/GB1659/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660142 |
| 78 | *Henipavirus* | BatPV/Eid_hel/GB1661-RMH/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660143 |
| 79 | *Henipavirus* | BatPV/Eid_hel/GB1678/GAB/2005 | Straw-coloured fruit bat (*Eidolon helvum*) | 2005 | Gabon | Spleen | HQ660144 |

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|---|---|---|---|---|---|---|---|
| 80 | *Henipavirus* | BatPV/Rou_aeg/GB2009/GAB/2005 | Egyptian fruit bat (*Rousettus aegyptiacus*) | 2005 | Gabon | Spleen | HQ660145 |
| 81 | *Henipavirus* | BatPV/Eid_hel/GB3384/GAB/2006 | Straw-coloured fruit bat (*Eidolon helvum*) | 2006 | Gabon | Spleen | HQ660146 |
| 82 | *Henipavirus* | BatPV/Eid_hel/GH-M28/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660147 |
| 83 | *Henipavirus* | BatPV/Eid_hel/GH-M33/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Spleen | HQ660148 |
| 84 | *Henipavirus* | BatPV/Eid-hel/RCA-P10/RCA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Central African Republic | Spleen | HQ660149 |
| 85 | *Henipavirus* | BatPV/Eid_hel/RCA-P05/RCA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Central African Republic | Spleen | HQ660150 |
| 86 | *Henipavirus* | BatPV/Eid_hel/RCA-P09/RCA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Central African Republic | Spleen | HQ660151 |
| 87 | *Henipavirus* | BatPV/Hyp_mon/RCA-P18/RCA/2008 | Hammer-headed fruit bat (*Hypsignathus monstrosus*) | 2008 | Central African Republic | Spleen | HQ660152 |
| 88 | *Henipavirus* | BatPV/Pte_par/KCR245H/CRC/2010 | Parnell's Mustached bat (*Pteronotus parnellii*) | 2010 | Costa Rica | Feces | JF828297 |
| 89 | *Morbillivirus/ unclassified* | BatPV/Pip_nan/GH36/GHA/2008 | Banana Pipistrelle (*Pipistrellus nanus*) | 2008 | Ghana | Feces | FJ609192 |
| 90 | *Morbillivirus/ Unclassified* | BatPV/Hip_rub/GH19-140/GHA/2009 | Noack's roundleaf bat (*Hipposideros □auben*) | 2009 | Ghana | Feces | HQ660153 |
| 91 | *Morbillivirus/ unclassified* | BatPV/Hip_spec/GH19-T/GHA/2009 | Roundleaf bat (*Hipposideros sp.*) | 2009 | Ghana | Feces | HQ660154 |
| 92 | *Morbillivirus/ unclassified* | BatPV/Col_afr/GB09478/GAB/2009 | African Sheath-Tailed bat (*Coleura afra*) | 2009 | Gabon | Spleen | HQ660155 |
| 93 | *Morbillivirus/ Unclassified* | BatPV/Hip_caf/GB09670/GAB/2009 | Sundevall's roundleaf bat (*Hipposideros caffer*) | 2009 | Gabon | Spleen | HQ660156 |
| 94 | *Morbillivirus/ Unclassified* | BatPV/Hip_gig/GB09682/GAB/2009 | Giant leaf-nosed bat (*Hipposideros gigas*) | 2009 | Gabon | Spleen | HQ660157 |
| 95 | *Morbillivirus/ unclassified* | BatPV/Hip_caf/GB09790/GAB/2009 | Sundevall's roundleaf bat (*Hipposideros caffer*) | 2009 | Gabon | Spleen | HQ660158 |
| 96 | *Morbillivirus/ unclassified* | BatPV/Hip_gig/GB09898/GAB/2009 | Giant leaf-nosed bat (*Hipposideros gigas*) | 2009 | Gabon | Spleen | HQ660159 |
| 97 | *Morbillivirus/ Unclassified* | BatPV/Hip_rub/GB19-S/GHA/2009 | Noack's roundleaf bat (*Hipposideros □auben*) | 2009 | Ghana | Feces | HQ660160 |
| 98 | *Morbillivirus/ unclassified* | BatPV/Hip_caf/GB59-30/GHA/2009 | Sundevall's roundleaf bat (*Hipposideros caffer*) | 2009 | Ghana | Feces | HQ660161 |
| 99 | *Morbillivirus/ unclassified* | BatPV/Hip_aba/GB59-59/GHA/2009 | Aba roundleaf bat (*Hipposideros abae*) | 2009 | Ghana | Feces | HQ660162 |
| 100 | *Morbillivirus/ Unclassified* | BatPV/Myo_alc/3-320/BGR/2009 | Alcathoe bat (*Myotis alcathoe*) | 2009 | Bulgaria | Feces | HQ660163 |
| 101 | *Morbillivirus/ unclassified* | BatPV/Myo_cap/6-43/BGR/2009 | Long-fingered bat (*Myotis capaccinii*) | 2009 | Bulgaria | Feces | HQ660164 |
| 102 | *Morbillivirus/ unclassified* | BatPV/Myo_dau/NMS09-48/GER/2009 | Daubenton's bat (*Myotis □aubentonii*) | 2009 | Germany | Feces | HQ660165 |
| 103 | *Morbillivirus/ Unclassified* | BatPV/Myo_myo/N78-14/GER/2008 | Greater mouse-eared bat (*Myotis myotis*) | 2008 | Germany | Feces | HQ660166 |
| 104 | *Morbillivirus/ unclassified* | BatPV/Myo_myo/N78-16/GER/2008 | Greater mouse-eared bat (*Myotis myotis*) | 2008 | Germany | Feces | HQ660167 |
| 105 | *Morbillivirus/ unclassified* | BatPV/Myo_mys/NM98-140/GER/2008 | Whiskered bat (*Myotis mystacinus*) | 2008 | Germany | Feces | HQ660168 |
| 106 | *Morbillivirus/ Unclassified* | BatPV/Myo_mys/NM98-44/GER/2008 | Whiskered bat (*Myotis mystacinus*) | 2008 | Germany | Feces | HQ660169 |
| 107 | *Morbillivirus/ unclassified* | BatPV/Myo_bec/NM98-46/GER/2008 | Bechstein's bat (*Myotis bechsteinii*) | 2008 | Germany | Feces | HQ660170 |
| 108 | *Morbillivirus/ unclassified* | BatPV/Myo_mys/NM98-47/GER/2008 | Whiskered bat (*Myotis mystacinus*) | 2008 | Germany | Feces | HQ660171 |
| 109 | *Morbillivirus/ Unclassified* | RodentPV/Rha_pum/NS3-9/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660172 |
| 110 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS62/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660173 |
| 111 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS25/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660174 |
| 112 | *Morbillivirus/ Unclassified* | RodentPV/Rha_pum/NS44/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660175 |
| 113 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS13/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660176 |
| 114 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS66/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660177 |
| 115 | *Morbillivirus/ Unclassified* | RodentPV/Rha_pum/NS22/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660178 |
| 116 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS72/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660179 |
| 117 | *Morbillivirus/ unclassified* | RodentPV/Rha_pum/NS16/RSA/2009 | Four-striped grass mouse (*Rhabdomys pumilio*) | 2009 | Republic of South Africa | Serum | HQ660180 |
| 118 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-712/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | HQ660181 |
| 119 | *Morbillivirus/ unclassified* | RodentPV/Myo_gla/RMU10-1414/GER/2009 | Bank vole (*Myodes glareolus*) | 2009 | Germany | Serum | HQ660182 |
| 120 | *Morbillivirus/ Unclassified* | RodentPV/Apo_fla/RMU10-751/GER/2009 | Yellow-necked mouse (*Apodemus flavicollis*) | 2009 | Germany | Serum | HQ660183 |
| 121 | *Morbillivirus/ unclassified* | RodentPV/Mic_agr/RMU10-869/GER/2009 | Field vole (*Microtus agrestis*) | 2009 | Germany | Serum | HQ660184 |
| 122 | *Morbillivirus/ unclassified* | RodentPV/Mic_arv/RMU10-883/GER/2009 | Common vole (*Microtus arvalis*) | 2009 | Germany | Serum | HQ660185 |
| 123 | *Morbillivirus/* | RodentPV/Myo_gla/RMU10- | Bank vole (*Myodes* | 2010 | Germany | Serum | HQ660186 |

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|---|---|---|---|---|---|---|---|
| | *Unclassified* | CY/GER/2010 | *glareolus*) | | | | |
| 124 | *Morbillivirus/ unclassified* | BatPV/Des_rot/BR21/BRA/2008 | Common Vampire bat (*Desmodus rotundus*) | 2008 | Brazil | Spleen | HQ660187 |
| 125 | *Morbillivirus/ unclassified* | BatPV/Des_rot/BR22/BRA/2008 | Common Vampire bat (*Desmodus rotundus*) | 2008 | Brazil | Spleen | HQ660188 |
| 126 | *Morbillivirus/ Unclassified* | BatPV/Des_rot/BR222/BRA/2009 | Common Vampire bat (*Desmodus rotundus*) | 2009 | Brazil | Spleen | HQ660189 |
| 127 | *Morbillivirus/ unclassified* | BatPV/Glo_sor/BR190/BRA/2009 | Pallas's Long-tongued bat (*Glossophaga soricina*) | 2009 | Brazil | Spleen | HQ660190 |
| 128 | *Morbillivirus/ unclassified* | BatPV/Car_bre//BR96/BRA/2009 | Silky Short-tailed bat (*Carollia brevicauda*) | 2009 | Brazil | Spleen | HQ660191 |
| 129 | *Morbillivirus/ Unclassified* | BatPV/Car_bre/BR100/BRA/2009 | Silky Short-tailed bat (*Carollia brevicauda*) | 2009 | Brazil | Spleen | HQ660192 |
| 130 | *Morbillivirus/ unclassified* | BatPV/Car_bre/BR102/BRA/2009 | Silky Short-tailed bat (*Carollia brevicauda*) | 2009 | Brazil | Spleen | HQ660193 |
| 131 | *Morbillivirus/ unclassified* | BatPV/Car_per/BR310/BRA/2009 | Seba's Short-tailed bat (*Carollia perspicillata*) | 2009 | Brazil | Spleen | HQ660194 |
| 132 | *Morbillivirus/ unclassified* | BatPV/Pte_par/KCR245M/CRC/2010 | Parnell's Mustached bat (*Pteronotus parnellii*) | 2010 | Costa Rica | Feces | JF828295 |
| 133 | *Morbillivirus/ unclassified* | BatPV/Pte_par/KCR370/CRC/2010 | Parnell's Mustached bat (*Pteronotus parnellii*) | 2010 | Costa Rica | Feces | JF828296 |
| 134 | *Morbillivirus/ Unclassified* | RodentPV/Apo_fla/RMU10-1842/GER/2010 | Yellow-necked mouse (*Apodemus flavicollis*) | 2010 | Germany | Serum | JF828298 |
| 135 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-1968/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828299 |
| 136 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-1991/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828300 |
| 137 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-2235/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828301 |
| 138 | *Morbillivirus/ Unclassified* | RodentPV/Apo_fla/RMU10-2821/GER/2010 | Yellow-necked mouse (*Apodemus flavicollis*) | 2010 | Germany | Serum | JF828302 |
| 139 | *Morbillivirus/ Unclassified* | RodentPV/Apo_fla/RMU10-3244/GER/2010 | Yellow-necked mouse (*Apodemus flavicollis*) | 2010 | Germany | Serum | JF828303 |
| 140 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-2818/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828304 |
| 141 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-2897/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828305 |
| 142 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-2806/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828306 |
| 143 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-3079/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828307 |
| 144 | *Morbillivirus/ Unclassified* | RodentPV/Apo_fla/RMU10-3476/GER/2010 | Yellow-necked mouse (*Apodemus flavicollis*) | 2010 | Germany | Serum | JF828308 |
| 145 | *Morbillivirus/ Unclassified* | RodentPV/Myo_gla/RMU10-3179/GER/2010 | Bank vole (*Myodes glareolus*) | 2010 | Germany | Serum | JF828309 |
| 146 | *Respirovirus* | RodentPV/Rat_rat/TP180/THA/2007 | Black rat (*Rattus rattus*) | 2007 | Thailand | Serum | HQ660195 |
| 147 | *Pneumovirus* | BatPV/Eid_hel/GH33P/GHA/2008 | Straw-coloured fruit bat (*Eidolon helvum*) | 2008 | Ghana | Feces | FJ609198 |
| 148 | *Pneumovirus* | BatPV/Eid_hel/GH24P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971949 |
| 149 | *Pneumovirus* | BatPV/Eid_hel/GH11P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971950 |
| 150 | *Pneumovirus* | BatPV/Eid_hel/GH12P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971951 |
| 151 | *Pneumovirus* | BatPV/Eid_hel/GH17P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971952 |
| 152 | *Pneumovirus* | BatPV/Eid_hel/GH18P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971953 |
| 153 | *Pneumovirus* | BatPV/Eid_hel/GH19P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971954 |
| 154 | *Pneumovirus* | BatPV/Eid_hel/GH20P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971955 |
| 155 | *Pneumovirus* | BatPV/Eid_hel/GH22P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971956 |
| 156 | *Pneumovirus* | BatPV/Eid_hel/GH25P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971957 |
| 157 | *Pneumovirus* | BatPV/Eid_hel/GH28P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971958 |
| 158 | *Pneumovirus* | BatPV/Eid_hel/GH30P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971959 |
| 159 | *Pneumovirus* | BatPV/Eid_hel/GH31P/GHA/2009 | Straw-coloured fruit bat (*Eidolon helvum*) | 2009 | Ghana | Feces | FJ971960 |

## Supplementary References

61. Yob, J.M., *et al.* Nipah virus infection in bats (order Chiroptera) in peninsular Malaysia. *Emerg Infect Dis* **7**, 439-441 (2001).
62. Halpin, K., Young, P.L., Field, H.E. & Mackenzie, J.S. Isolation of Hendra virus from pteropid bats: a natural reservoir of Hendra virus. *J Gen Virol* **81**, 1927-1932 (2000).
63. Shah, D., Vidal, S., Link, M.A., Rubin, S.A. & Wright, K.E. Identification of genetic mutations associated with attenuation and changes in tropism of Urabe mumps virus. *J Med Virol* **81**, 130-138 (2009).
64. Malik, T.H., Wolbert, C., Nerret, L., Sauder, C. & Rubin, S. Single amino acid changes in the mumps virus haemagglutinin-neuraminidase and polymerase proteins are associated with neuroattenuation. *J Gen Virol* **90**, 1741-1747 (2009).
65. Sauder, C.J., *et al.* Presence of lysine at aa 335 of the hemagglutinin-neuraminidase protein of mumps virus vaccine strain Urabe AM9 is not a requirement for neurovirulence. *Vaccine* **27**, 5822-5829 (2009).
66. Karlin, D., Ferron, F., Canard, B. & Longhi, S. Structural disorder and modular organization in Paramyxovirinae N and P. *J Gen Virol* **84**, 3239-3252 (2003).
67. Ciancanelli, M.J., Volchkova, V.A., Shaw, M.L., Volchkov, V.E. & Basler, C.F. Nipah virus sequesters inactive STAT1 in the nucleus via a P gene-encoded mechanism. *J Virol* **83**, 7828-7841 (2009).
68. Rodriguez, J.J., Cruz, C.D. & Horvath, C.M. Identification of the nuclear export signal and STAT-binding domains of the Nipah virus V protein reveals mechanisms underlying interferon evasion. *J Virol* **78**, 5358-5367 (2004).
69. Miller, B., Reid, F., Arroyo-Cabrales, J., Cuarón, A.D. & de Grammont, P.C. *Pteronotus parnellii*. in *IUCN Red List of Threatened Species. Version 2010.4. Downloaded on 06 May 2011. www.iucnredlist.org* (2008).
70. Mickleburgh, S., Hutson, A.M., Bergmans, W., Fahr, J. & Racey, P.A. *Eidolon helvum*. in *IUCN Red List of Threatened Species. Version 2010.4. Downloaded on 06 May 2011. www.iucnredlist.org* (2008).
71. Barquez, R., Perez, S., Miller, B. & Diaz, M. *Carollia perspicillata*. in *IUCN 2010. IUCN Red List of Threatened Species. Version 2010.4. www.iucnredlist.org. Downloaded on 06 May 2011* (2008).
72. Murray, K., *et al.* A morbillivirus that caused fatal disease in horses and humans. *Science* **268**, 94-97 (1995).
73. Harcourt, B.H., *et al.* Genetic characterization of Nipah virus, Bangladesh, 2004. *Emerg Infect Dis* **11**, 1594-1597 (2005).
74. Chua, K.B., *et al.* Nipah virus: a recently emergent deadly paramyxovirus. *Science* **288**, 1432-1435 (2000).
75. Arankalle, V.A., *et al.* Genomic characterization of nipah virus, west bengal, India. *Emerg Infect Dis* **17**, 907-909 (2011).
76. AbuBakar, S., *et al.* Isolation and molecular identification of Nipah virus from pigs. *Emerg Infect Dis* **10**, 2228-2230 (2004).
77. Bailey, D., Banyard, A., Dash, P., Ozkul, A. & Barrett, T. Full genome sequence of peste des petits ruminants virus, a member of the Morbillivirus genus. *Virus Res* **110**, 119-124 (2005).
78. Blixenkrone-Moller, M., Bolt, G., Gottschalck, E. & Kenter, M. Comparative analysis of the gene encoding the nucleocapsid protein of dolphin morbillivirus reveals its distant evolutionary relationship to measles virus and ruminant morbilliviruses. *J Gen Virol* **75 ( Pt 10)**, 2829-2834 (1994).
79. Domingo, M., *et al.* Morbillivirus in dolphins. *Nature* **348**, 21 (1990).
80. Bankamp, B., Bellini, W.J. & Rota, P.A. Comparison of L proteins of vaccine and wild-type measles viruses. *J Gen Virol* **80 ( Pt 7)**, 1617-1625 (1999).
81. Druelle, J., Sellin, C.I., Waku-Kouomou, D., Horvat, B. & Wild, F.T. Wild type measles virus attenuation independent of type I IFN. *Virol J* **5**, 22 (2008).

82. Hotta, H., *et al.* Full-length sequence analysis of subacute sclerosing panencephalitis (SSPE) virus, a mutant of measles virus, isolated from brain tissues of a patient shortly after onset of SSPE. *Microbiol Immunol* **50**, 525-534 (2006).
83. Baron, M.D., Kamata, Y., Barras, V., Goatley, L. & Barrett, T. The genome sequence of the virulent Kabete 'O' strain of rinderpest virus: comparison with the derived vaccine. *J Gen Virol* **77 ( Pt 12)**, 3041-3046 (1996).
84. McIlhatton, M.A., Curran, M.D. & Rima, B.K. Nucleotide sequence analysis of the large (L) genes of phocine distemper virus and canine distemper virus (corrected sequence). *J Gen Virol* **78 ( Pt 3)**, 571-576 (1997).
85. Lednicky, J.A., *et al.* Effective primary isolation of wild-type canine distemper virus in MDCK, MV1 Lu and Vero cells without nucleotide sequence changes within the entire haemagglutinin protein gene and in subgenomic sections of the fusion and phospho protein genes. *J Virol Methods* **118**, 147-157 (2004).
86. Lednicky, J.A., Dygas, M.W., Downes, H., Cera, L.M. & and Meehan, T.P. Complete genomic sequence of Canine distemper virus 164071 from blood of a Rottweiler. (National Center for Biotechnology Information, 2008).
87. Fujii, Y., Kiyotani, K., Yoshida, T. & Sakaguchi, T. Conserved and non-conserved regions in the Sendai virus genome: evolution of a gene possessing overlapping reading frames. *Virus Genes* **22**, 47-52 (2001).
88. Shi, L.Y., Li, M., Yuan, L.J., Wang, Q. & Li, X.M. A new paramyxovirus, Tianjin strain, isolated from common cotton-eared marmoset: genome characterization and structural protein sequence analysis. *Arch Virol* **153**, 1715-1723 (2008).
89. Bailly, J.E., McAuliffe, J.M., Skiadopoulos, M.H., Collins, P.L. & Murphy, B.R. Sequence determination and molecular analysis of two strains of bovine parainfluenza virus type 3 that are attenuated for primates. *Virus Genes* **20**, 173-182 (2000).
90. Newman, J.T., *et al.* Sequence analysis of the Washington/1964 strain of human parainfluenza virus type 1 (HPIV1) and recovery and characterization of wild-type recombinant HPIV1 produced by reverse genetics. *Virus Genes* **24**, 77-92 (2002).
91. Stokes, A., Tierney, E.L., Murphy, B.R. & Hall, S.L. The complete nucleotide sequence of the JS strain of human parainfluenza virus type 3: comparison with the Wash/47885/57 prototype strain. *Virus Res* **25**, 91-103 (1992).
92. Qiao, D., Janke, B.H. & Elankumaran, S. Complete genome sequence and pathogenicity of two swine parainfluenzavirus 3 isolates from pigs in the United States. *Journal of virology* **84**, 686-694.
93. Yea, C., *et al.* The Complete Sequence of a Human Parainfluenzavirus 4 Genome. *Viruses* **1**, 26-41 (2009).
94. Parks, G.D., Ward, C.D. & Lamb, R.A. Molecular cloning of the NP and L genes of simian virus 5: identification of highly conserved domains in paramyxovirus NP and L proteins. *Virus Res* **22**, 259-279 (1992).
95. Ogawa, M., *et al.* Nucleotide sequence analysis of the simian virus 41 gene encoding the large (L) protein and construction of a phylogenetic tree for the L proteins of paramyxoviruses. *J Gen Virol* **73 ( Pt 10)**, 2743-2750 (1992).
96. Philbey, A.W., *et al.* An apparently new virus (family Paramyxoviridae) infectious for pigs, humans, and fruit bats. *Emerg Infect Dis* **4**, 269-271 (1998).
97. Wang, L.F., *et al.* Full-length genome sequence and genetic relationship of two paramyxoviruses isolated from bat and pigs in the Americas. *Arch Virol* **152**, 1259-1271 (2007).
98. Zeller, H.G., *et al.* Electron microscopy and antigenic studies of uncharacterized viruses. I. Evidence suggesting the placement of viruses in families Arenaviridae, Paramyxoviridae, or Poxviridae. *Arch Virol* **108**, 191-209 (1989).
99. Jin, L., Beard, S., Hale, A., Knowles, W. & Brown, D.W. The genomic sequence of a contemporary wild-type mumps virus strain. *Virus Res* **70**, 75-83 (2000).
100. Santak, M., *et al.* Mumps virus strains isolated in Croatia in 1998 and 2005: Genotyping and putative antigenic relatedness to vaccine strains. *J Med Virol* **78**, 638-643 (2006).

101. Young, D.F., *et al.* Mumps virus Enders strain is sensitive to interferon (IFN) despite encoding a functional IFN antagonist. *J Gen Virol* **90**, 2731-2738 (2009).
102. Neverov, A.A., Agafonov, A.P., Kameneva, S.N., Ignatyev, I.M. & and Chumakov, K.M. Characterization of Mumps viruses isolated in Novosibirsk (Western Siberia) during 1994-2003. (National Center for Biotechnology Information, 2004).
103. Lee, J.Y., *et al.* Complete nucleotide sequence of a mumps virus genotype I strain isolated in Korea. *Virus Genes* **28**, 201-205 (2004).
104. Amexis, G., Rubin, S., Chatterjee, N., Carbone, K. & Chumakov, K. Identification of a new genotype H wild-type mumps virus strain and its molecular relatedness to other virulent and attenuated strains. *J Med Virol* **70**, 284-286 (2003).
105. Moreno-Lopez, J., Correa-Giron, P., Martinez, A. & Ericsson, A. Characterization of a paramyxovirus isolated from the brain of a piglet in Mexico. *Arch Virol* **91**, 221-231 (1986).
106. Chanock, R.M. Association of a new type of cytopathogenic myxovirus with infantile croup. *J Exp Med* **104**, 555-576 (1956).
107. Kattenbelt, J.A., Stevens, M.P. & Gould, A.R. Sequence variation in the Newcastle disease virus genome. *Virus Res* **116**, 168-184 (2006).
108. Subbiah, M., Xiao, S., Collins, P.L. & Samal, S.K. Complete sequence of the genome of avian paramyxovirus type 2 (strain Yucaipa) and comparison with other paramyxoviruses. *Virus Res* **137**, 40-48 (2008).
109. Kumar, S., Nayak, B., Collins, P.L. & Samal, S.K. Complete genome sequence of avian paramyxovirus type 3 reveals an unusually long trailer region. *Virus Res* **137**, 189-197 (2008).
110. Nayak, B., Kumar, S., Collins, P.L. & Samal, S.K. Molecular characterization and complete genome sequence of avian paramyxovirus type 4 prototype strain duck/Hong Kong/D3/75. *Virol J* **5**, 124 (2008).
111. Samuel, A.S., Paldurai, A., Kumar, S., Collins, P.L. & Samal, S.K. Complete genome sequence of avian paramyxovirus (APMV) serotype 5 completes the analysis of nine APMV serotypes and reveals the longest APMV genome. *PLoS ONE* **5**, e9269 (2010).
112. Chang, P.C., *et al.* Complete nucleotide sequence of avian paramyxovirus type 6 isolated from ducks. *J Gen Virol* **82**, 2157-2168 (2001).
113. Xiao, S., *et al.* Complete genome sequence of avian paramyxovirus type 7 (strain Tennessee) and comparison with other paramyxoviruses. *Virus Res* **145**, 80-91 (2009).
114. Paldurai, A., Subbiah, M., Kumar, S., Collins, P.L. & Samal, S.K. Complete genome sequences of avian paramyxovirus type 8 strains goose/Delaware/1053/76 and pintail/Wakuya/20/78. *Virus Res* **142**, 144-153 (2009).
115. Samuel, A.S., Kumar, S., Madhuri, S., Collins, P.L. & Samal, S.K. Complete sequence of the genome of avian paramyxovirus type 9 and comparison with other paramyxoviruses. *Virus Res* (2009).
116. Miller, P.J., *et al.* Evidence for a new avian paramyxovirus serotype 10 detected in rockhopper penguins from the Falkland Islands. *J Virol* **84**, 11496-11504 (2010).
117. Herfst, S., *et al.* Recovery of human metapneumovirus genetic lineages a and B from cloned cDNA. *J Virol* **78**, 8264-8270 (2004).
118. van den Hoogen, B.G., *et al.* A newly discovered human pneumovirus isolated from young children with respiratory tract disease. *Nat Med* **7**, 719-724 (2001).
119. Bennett, R.S., *et al.* Evidence of avian pneumovirus spread beyond Minnesota among wild and domestic birds in central North America. *Avian Dis* **48**, 902-908 (2004).
120. Alvarez, R. & Seal, B.S. Avian metapneumovirus type C polymerase gene. (National Center for Biotechnology Information, 2004).
121. Sugiyama, M., Ito, H., Hata, Y., Ono, E. & Ito, T. Complete nucleotide sequences of avian metapneumovirus subtype B genome. *Virus Genes* **41**, 389-395 (2010).
122. Giraud, P., Bennejean, G., Guittet, M. & Toquin, D. Turkey rhinotracheitis in France: preliminary investigations on a ciliostatic virus. *Vet Rec* **119**, 606-607 (1986).
123. Naylor, C.J., Ling, R., Edworthy, N., Savage, C.E. & Easton, A.J. Avian metapneumovirus SH gene end and G protein mutations influence the level of protection of live-vaccine candidates. *J Gen Virol* **88**, 1767-1775 (2007).

124. Tennant, R.W. & Ward, T.G. Pneumonia virus of mice (PVM) in cell culture. *Proc Soc Exp Biol Med* **111**, 395-398 (1962).
125. Thorpe, L.C. & Easton, A.J. Genome sequence of the non-pathogenic strain 15 of pneumonia virus of mice and comparison with the genome of the pathogenic strain J3666. *J Gen Virol* **86**, 159-169 (2005).
126. Mohanty, S.B., Ingling, A.L. & Lillie, M.G. Experimentally induced respiratory syncytial viral infection in calves. *Am J Vet Res* **36**, 417-419 (1975).
127. Lewis, F.A., Rae, M.L., Lehman, N.I. & Ferris, A.A. A syncytial virus associated with epidemic disease of the lower respiratory tract in infants and young children. *Med J Australia* **2**, 932-933 (1961).
128. Hierholzer, J.C. & Hirsch, M.S. Croup and pneumonia in human infants associated with a new strain of respiratory syncytial virus. *J Infect Dis* **140**, 826-828 (1979).
129. Tolley, K.P., *et al.* Identification of mutations contributing to the reduced virulence of a modified strain of respiratory syncytial virus. *Vaccine* **14**, 1637-1646 (1996).
130. Lambeth, L.S., *et al.* Complete genome sequence of Nariva virus, a rodent paramyxovirus. *Arch Virol* **154**, 199-207 (2009).
131. Falk, K., *et al.* Molecular characterisation of Atlantic salmon paramyxovirus (ASPV): a novel paramyxovirus associated with proliferative gill inflammation. *Virus Res* **133**, 218-227 (2008).
132. Tidona, C.A., Kurz, H.W., Gelderblom, H.R. & Darai, G. Isolation and molecular characterization of a novel cytopathogenic paramyxovirus from tree shrews. *Virology* **258**, 425-434 (1999).
133. Miller, P.J., Boyle, D.B., Eaton, B.T. & Wang, L.F. Full-length genome sequence of Mossman virus, a novel paramyxovirus isolated from rodents in Australia. *Virology* **317**, 330-344 (2003).
134. Li, Z., *et al.* Beilong virus, a novel paramyxovirus with the largest genome of non-segmented negative-stranded RNA viruses. *Virology* **346**, 219-228 (2006).
135. Jack, P.J., Boyle, D.B., Eaton, B.T. & Wang, L.F. The complete genome sequence of J virus reveals a unique genome structure in the family Paramyxoviridae. *J Virol* **79**, 10690-10700 (2005).
136. Kurath, G., Batts, W.N., Ahne, W. & Winton, J.R. Complete genome sequence of Fer-de-Lance virus reveals a novel gene in reptilian paramyxoviruses. *J Virol* **78**, 2045-2056 (2004).
137. Rima, B.K., Wishaupt, R.G., Welsh, M.J. & Earle, J.A. The evolution of morbilliviruses: a comparison of nucleocapsid gene sequences including a porpoise morbillivirus. *Vet Microbiol* **44**, 127-134 (1995).
138. Banyard, A.C., Grant, R.J., Romero, C.H. & Barrett, T. Sequence of the nucleocapsid gene and genome and antigenome promoters for an isolate of porpoise morbillivirus. *Virus Res* **132**, 213-219 (2008).
139. Taubenberger, J.K., *et al.* Molecular genetic evidence of a novel morbillivirus in a long-finned pilot whale (Globicephalus melas). *Emerg Infect Dis* **6**, 42-45 (2000).
140. Belliere, E.N., *et al.* Phylogenetic analysis of a new Cetacean morbillivirus from a short-finned pilot whale stranded in the Canary Islands. *Res Vet Sci* **90**, 324-328 (2011).
141. Nollens, H.H., *et al.* Characterization of a parainfluenza virus isolated from a bottlenose dolphin (Tursiops truncatus). *Vet Microbiol* **128**, 231-242 (2008).
142. Simmons, J.H., *et al.* Characterization of a novel parainfluenza virus, caviid parainfluenza virus 3, from laboratory guinea pigs (Cavia porcellus). *Comp Med* **52**, 548-554 (2002).
143. Lyon, M., *et al.* Presence of a unique parainfluenza virus 3 strain identified by RT-PCR in visna-maedi virus infected sheep. *Vet Microbiol* **57**, 95-104 (1997).
144. Klenk, C. & Klenk, H.D. Sequence characterization of the fusion protein of porcine parainfluenza virus (SER). (National Center for Biotechnology Information, 2000).
145. Chatziandreou, N., *et al.* Relationships and host range of human, canine, simian and porcine isolates of simian virus 5 (parainfluenza virus 5). *J Gen Virol* **85**, 3007-3016 (2004).

146. Meng, Q., Qiao, J. & Guo, X. Cloning and sequence analysis of fusion protein gene of canine parainfluenza virus wildtype strain. (National Center for Biotechnology Information, 2003).
147. Yan, X.J., Xia, X.Z. & Wang, F.X. Cloning and sequence analysis of fusion protein gene of CPIV. (National Center for Biotechnology Information, 2007).
148. Goswami, K.K., Lange, L.S., Mitchell, D.N., Cameron, K.R. & Russell, W.C. Does simian virus 5 infect humans? *J Gen Virol* **65 ( Pt 8)**, 1295-1303 (1984).
149. Bayon-Auboyer, M.H., Arnauld, C., Toquin, D. & Eterradossi, N. Nucleotide sequences of the F, L and G protein genes of two non-A/non-B avian pneumoviruses (APV) reveal a novel APV subgroup. *J Gen Virol* **81**, 2723-2733 (2000).
150. Renshaw, R., Laverack, M., Zylich, N., Glaser, A. & Dubovi, E. Genomic analysis of a pneumovirus isolated from dogs with acute respiratory disease. *Vet Microbiol* **150**, 88-95 (2011).
151. Batts, W.N., Falk, K. & Winton, J.R. Genetic analysis of paramyxovirus isolates from Pacific salmon reveals two independently co-circulating lineages. *J Aquat Anim Health* **20**, 215-224 (2008).
152. Renshaw, R.W., Glaser, A.L., Van Campen, H., Weiland, F. & Dubovi, E.J. Identification and phylogenetic comparison of Salem virus, a novel paramyxovirus of horses. *Virology* **270**, 417-429 (2000).
153. Kusagawa, S.*, et al.* Antigenic and molecular properties of Murayama virus isolated from cynomolgus monkeys: the virus is closely related to avian paramyxovirus type 2. *Virology* **194**, 828-832 (1993).
154. Marschang, R.E., Papp, T. & Frost, J.W. Comparison of paramyxovirus isolates from snakes, lizards and a tortoise. *Virus Res* **144**, 272-279 (2009).
155. Kurath, G. Fish paramyxoviruses: one new species in new genus Aquaparamyxovirus. (International Committee on Taxonomy of Viruses (ICTV), 2009).
156. Kurath, G. Reptile paramyxoviruses: 1 new species and new genus, Ferlavirus. (International Committee on Taxonomy of Viruses (ICTV), 2009).