
Characterisation and zoonotic risk of tick viruses in public datasets

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Abstract

Tick-borne viruses remain a substantial zoonotic risk worldwide, so knowledge of the diversity of tick viruses has potential health consequences. Despite their importance, large amounts of sequences in public datasets from tick meta-genomic and –transcriptomic projects remain unannotated, sequence data that could contain undocumented viruses. Through data mining and bioinformatic analyses of more than 37,800 public meta-genomic and -transcriptomic datasets, we found 83 unannotated contigs exhibiting high identity with known tick viruses. These putative viral contigs were classified into three RNA viral families (*Alphatetraviridae*, *Orthomyxoviridae*, *Chuviridae*) and one DNA viral family (*Asfaviridae*). After manual checking of quality and dissimilarity toward other sequences in the dataset, these 83 contigs were reduced to five putative novel Alphatetra-like viral contigs, four putative novel Orthomyxo-like viral contigs, and one Chu-like viral contig which clustered with known tick-borne viruses, forming a separate clade within the viral families. We further attempted to assess which previously known tick viruses likely represent zoonotic risks and thus deserve further investigation. We ranked the human infection potential of 136 known tick-borne viruses using a genome composition-based machine learning model. We found five high-risk tick-borne viruses (Langat virus, Lonestar tick chuvirus 1, Grotenhout virus, Taggart virus, and Johnston Atoll virus) that have not been known to infect human and two viral families (*Nairoviridae* and *Phenuiviridae*) that contain a large proportion of potential zoonotic tick-borne viruses. This adds to the knowledge of tick virus diversity and highlights the importance of surveillance of newly emerging tick-borne diseases.

Importance

Ticks are important hosts of pathogens. Despite this, numerous tick-borne viruses are still unknown or poorly characterised. To overcome this, we re-examined currently known tick-borne viruses and identified putative novel viruses associated with ticks in public datasets. Using genome-based machine learning approach, we predicted five high-risk tick-borne viruses that have not yet been reported to cause human infections. Additionally, we highlighted two viral families, *Nairoviridae* and *Phenuiviridae*, which are potential public health threats. Our analysis also revealed 10 putative novel RNA viral contigs clustered with known tick-borne viruses. Our study highlights the importance of monitoring ticks and the viruses they carry in endemic areas to prevent and control zoonotic infectious disease outbreaks. To achieve this, we advocate for a multidisciplinary approach within a One Health and EcoHealth framework that considers the relationship between zoonotic disease outbreaks and their hosts, humans, and the environment.

Introduction

The role of ticks in the transmission of viruses has been known for over 100 years (1) with ticks being second only to mosquitoes as vectors of pathogens to humans and the primary vector of pathogens to livestock, wildlife, and companion animals (2). Nonetheless, new tick viruses are still being

detected (3). Two recent examples are Yezo virus identified in Japan (4) and Songling virus identified in China (5), which have both been associated with acute human febrile disease.

Prior to the advent of molecular biology, tick-borne viruses were identified through microscopy, isolation in culture or serology (6–11). Over the last two decades, meta-genomics and –transcriptomics tools have revolutionised virus discovery. These approaches employ high-throughput sequencing technologies to capture total viral communities in a relatively unbiased manner (12,13) and have facilitated studies of the tick virome that resulted in the discovery and characterisation of hundreds of new tick-borne viruses globally (14–23). While this has led to dramatic increases in the understanding of tick virus communities, being able to evaluate the human infection potential of the discovered viruses would additionally allow the leveraging of this data to provide public health benefits.

Models of zoonotic risk assessment often rely on the existence of zoonotic viruses in the same viral family or evolutionary relatedness to known zoonoses (24). These models rely on phenotypic information commonly unavailable for novel viruses or of insufficient resolution to estimate different levels of zoonotic potential for closely related viruses (25–27). More recent models based on the genomic features of viruses which do not strictly rely on phylogeny or taxonomy avoid this issue. Such models use genomic features that may individually contain weak signals but can be combined and exploited via machine learning algorithms (28–31). These models, built from genomic data alone, have particular strength in evaluating newly discovered viruses that lack other information sources, but are limited by the need for full viral genomes for accurate assessment.

In this study, we aimed to detect novel viruses that may have been overlooked by previous tick meta-genomic and –transcriptomic studies, and assess the zoonotic risk posed by tick virus diversity as it is currently understood. Thus, we searched publicly available tick sequence data for signs of viruses misidentified as tick sequences and evaluated the zoonotic risk of these and other tick viruses to find those which deserve further investigation.

Materials and methods

Datasets. We collected tick virus data from reports published prior to December 2021 and constructed a tick virus dataset that contained 261 tick-borne viruses from 23 viral families (34 genera) and 12 putative tick-borne viruses sampled from tick pools. Tick-borne viruses with unknown tick vectors (N = 13) or sequences unavailable (N = 13) were excluded from analyses. This resulted in 235 viruses in the final tick virus database, of which 3 of them (*Amblyomma dissimile mivirus*, *Nuomin virus*, and *Granville quaranjavirus*) were added later and not included in the database for virus detection. Among the 235 tick-borne viruses, more than 92% of viruses were RNA viruses, while few other viral sequences were identified (2.2% DNA viruses and 5.6% viruses with unknown genome composition). Among the RNA viruses, most sequences were negative-sense (-) single-stranded RNA (ssRNA) viruses (63.0%), followed by positive-sense (+) single-stranded RNA (ssRNA) (20.8%), double-stranded RNA (dsRNA) (8.5%), and unclassified RNA (5.6%) viruses, depending on version 2020 of the International Committee on Taxonomy of Viruses (ICTV) master species list (<https://talk.ictvonline.org/files/master-species-lists/>). We labelled each virus as being capable of infecting humans or not known to infect humans using published reports as ground truth. In all cases, only viruses detected in humans by either PCR or sequencing were considered to have proven ability to infect humans. See the summary table of currently known tick-borne viruses in **Appendix Table 1**.

Viral identification and annotation. We used representative genomic sequences of the 232 tick-borne viruses as our reference database, with genome segments of segmented viruses concatenated into one. Using the 'blastn_vdb' (corresponding to nucleotide BLAST) executable in the BLAST+ v2.13.0 (32–34), we searched the Sequence Read Archive (SRA), Transcriptome Shotgun Assembly (TSA), and Whole Genome Shotgun (WGS) datasets that derived from ticks and subordinate taxa directly with an expectation cut-off of 0.05. We also performed a 'tBLASTx' search for the TSA database to find distant relationships between nucleotide sequences; SRA and WGS datasets were not suitable for 'tBLASTx' search because it was computationally prohibitive. This resulted in 1328 TSA, 19,990 SRA, and 1861 WGS sequences after removing duplicates. The GenBank accession numbers of the candidate sequences are provided at <https://github.com/ytlin2021/TickVirus.git>.

Candidate sequences were filtered according to the pipeline modified from Webster et al. (35). The thresholds used in each step can be seen in **Figure 1**. To confirm final RNA candidates, we checked the presence of RNA-dependent RNA polymerase (RdRp), an essential protein encoded in the genomes of all replicating RNA viruses without a DNA stage except deltaviruses, and not present in the genome of the eukaryotic or prokaryotic cell. We adopted a combined analysis approach to predict RdRps by using a general protein function prediction software package InterProScan v5.55-88.0 (36) and a new open bioinformatics toolkit - RdRp-scan - that allowed the detection of divergent viral RdRp sequences (37). Candidate sequences less than 600 nucleotides (nt) in length were discarded. The translated candidate sequences were searched according to the RdRp-scan workflow (37) and were also predicted using the InterProScan search function. The conserved RdRp motifs were annotated manually based on the RdRp motif database in RdRp-scan, and final RNA viral candidates were confirmed. The workflow of detecting viral RdRp sequences and the thresholds used in each step can be seen in **Appendix Figure 1**.

Protein functions of putative novel viral contigs were annotated using InterProScan and 'BLASTx'. Open Reading Frames (ORFs) were predicted using ORF Finder tool in NCBI (38) with a 150 nt length cut-off. InterProScan searched for protein function annotations in its available databases, including the Gene Ontology (39,40) and Pfam (41,42) databases. At the same time, 'BLASTx' were used to search against the non-redundant protein database with an expectation cut-off of 1e-5 following Charon et al. (37).

Phylogenetics. We searched for close and distant relatives of the identified novel viral contigs in viruses (NCBI taxa ID: 10239) non-redundant nucleotide and protein databases by performing 'BLASTn' and 'BLASTx' separately with an expectation cut-off of 0.005. For each contig with BLAST hits, the phylogenetic hierarchy of the best hits (top 10 hits from 'BLASTx') was traversed upward to identify the lowest taxonomic classification displaying a 75% majority taxonomic agreement following Webster et al. (35). If the best hits were unclassified viruses, the upper order was identified, and the protein sequences were aligned in each family under the order to determine the classification. This allowed putative novel viral contigs in the study to be classified into three RNA viral families (*Alphatetraviridae*, *Orthomyxoviridae*, *Chuviridae*) and one DNA viral family (*Asfaviridae*). All virus species in the same family, as well as unassigned viruses, were aligned and used to construct phylogenetic trees.

Phylogeny of RNA viruses was inferred on the basis of RNA-dependent RNA polymerase protein sequences. We aligned viral RdRp protein sequences using the ClustalW algorithm (43) embedded in the GUIDANCE2 server v2.02 (44). GUIDANCE2 server removed any sequences with a score of less than 0.6 and columns with a score of less than 0.93, aiming to leave sufficient information in alignments while allowing large taxonomic groups of viruses to be compared.

We performed tree estimation for all trees in BEAST2, averaging over protein models using the OBAMA module (45,46). A lognormal relaxed clock model was applied (56-58), and a Yule tree prior was used (47,48). As convergence repeatedly failed under standard MCMC for the *Chuviridae* and *Orthomyxoviridae* trees, models were fit using BEAST2's Metropolis-coupled MCMC routines with 4 chains and a target cross-chain move acceptance probability of 0.029 for the *Alphatetraviridae* and *Chuviridae* trees, and a fixed heating parameter of 0.3 for the *Orthomyxoviridae* tree (49,50). The Yule process birth rate was given a vague Exponential prior with mean 1000, all other parameters took default prior values. Trees were run for 100,000,000 iterations with 50,000,000 discarded as burn-in, and the posterior then being thinned to 1000 trees. A second run of each tree was used to assess convergence with the R package RWTY (51).

Zoonotic risk analyses. The zoonotic risk (precisely, probability of human infection given biologically relevant exposure) for 136 tick-borne viruses with complete genome sequences were evaluated using the best performing model from Mollentze et al. (31), referred to here as genome composition-based (GCB), which was trained on a range of viral genome features and human similarity features. A representative genome was selected for each virus, giving preference to sequences from NCBI Reference Sequence Database (RefSeq) (www.ncbi.nlm.nih.gov/refseq/) wherever possible. RefSeq sequences that had annotation issues or were not judged to be representative of the naturally circulating virus were replaced with alternative genomes. Following Mollentze et al. (31), the predicted probabilities from the GCB model were used to categorise viruses into four priority categories based on the overlap of confidence intervals (CIs) the value of 0.293 (low: entire 95% CI of predicted probability \leq cut-off; medium: mean prediction \leq cut-off, but CI crosses it; high: mean prediction $>$ cut-off, but CI crosses it; very high: entire CI $>$ cut-off). Since the current GCB model was trained for viruses with complete sequences, 99 tick viruses with only partial genomes available were excluded from the analyses. To characterise the zoonotic potential of the identified novel viral contigs, we did qualitative analyses by evaluating the published complete genomes of known viruses most similar to these incomplete viral sequences as determined by a nucleotide BLAST against GenBank.

Results

Identification of putative novel viruses associated with ticks

We examined contigs that showed nucleotide similarity ($<$ 90% identity) to previously characterised tick virus sequences from an extensive collection of tick meta-genomic and –transcriptomic datasets (23,050 SRA, 3523 TSA, and 11,279 WGS sequences; collected on 3 March 2022). The pipeline of detecting novel tick-associated viral contigs can be found in **Figure 1**. For more information on the tick virus database and tick meta-genomic and –transcriptomic datasets, see Methods.

In total, we identified 83 putative novel viral contigs, including 53 double-stranded DNA viral contigs, 5 positive-sense and 25 negative-sense RNA viral contigs (**Appendix Table 2-4**). The 53 DNA viral contigs belong to the family *Asfaviridae*, with homology to African swine fever virus. These African swine fever virus-like contigs were found in *Ornithodoros porcinus* and *Ornithodoros moubata* ticks (**Appendix Table 4**), and all but two of these contigs derived from a study that had previously reported the integration of African swine fever like elements into the genomes of these soft tick species (52), so they will not be discussed further. The 5 positive-sense RNA viral contigs belong to the family *Alphatetraviridae*. Of the negative-sense RNA viral contigs, 5 belong to the family *Orthomyxoviridae*, and 20 belong to the family *Chuviridae*, including 19 chuviruses believed to be replication defective from tick SRA projects. After filtering duplicate sequences (GenBank IDs:

HACP01027211.1 and HACW01024387.1), we obtained 10 putative RNA viral contigs ranging from 728 bp to 5496 bp (**Table 1**). The putative novel viruses found in this study were named after their host order and related viral family, followed by a number (e.g., Alphetetra-like tick virus 1). All sequences identified in the present study with can be found on GenBank (see accession numbers in **Table 1** and **Appendix Table 2-4**).

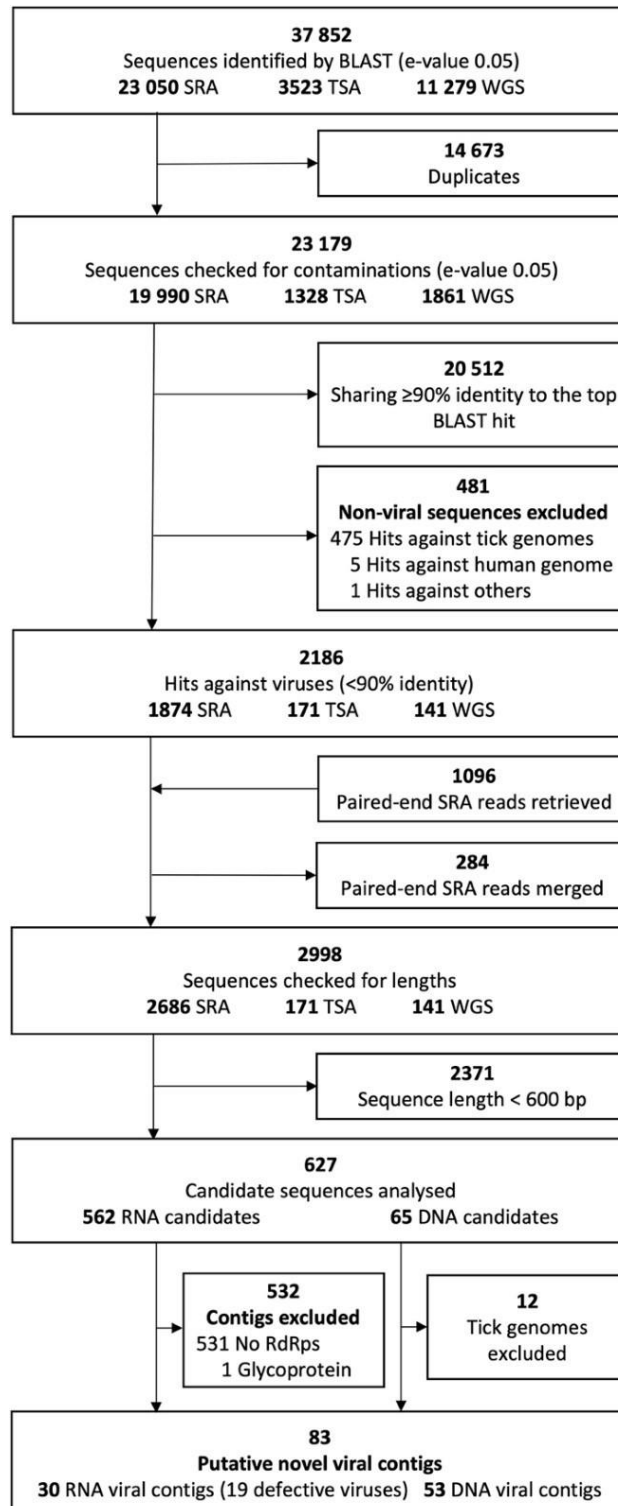


Figure 1 The workflow of identification of novel tick-associated viral contigs. Through BLAST search and curation, 53 DNA sequences (identified as African swine fever like elements) and 30 RNA

sequences (putative viruses in the family *Alphatetraviridae*, *Orthomyxoviridae* and *Chuviridae*) from a collection of tick meta-genomic and –transcriptomic datasets (3 March 2022) were identified as putative novel viral contigs. 10 putative RNA viral contigs were further analysed after filtering. TSA = Transcriptome Shotgun Assembly, SRA = Sequence Read Archive, WGS = Whole Genome Shotgun, E-value = Expectation value.

Table 1 The putative novel RNA viral contigs found after bioinformatic checking.

Putative novel viral contig	Tick species	Geographical location	Provisional family	Genome structure	Sequence length (nt)	Closest BLASTx match (% amino acid identity)	GenBank ID
Orthomyxo-like tick virus 1	<i>Rhipicephalus sanguineus</i>	Italy	Orthomyxoviridae	ssRNA(-)	2136	Zambezi tick virus 1 (89)	HACP01027211.1 (HACW01024387.1)
Orthomyxo-like tick virus 2	<i>Rhipicephalus sanguineus</i>	Italy	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (73)	HACP01022575.1
Orthomyxo-like tick virus 3	<i>Rhipicephalus sanguineus</i>	Italy	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (88)	HACW01018819.1
Orthomyxo-like tick virus 4	<i>Rhipicephalus haemaphysaloides</i>	China	Orthomyxoviridae	ssRNA(-)	2357	Zambezi tick virus 1 (89)	GIJA01018702.1
Alphatetra-like tick virus 1	<i>Ixodes ricinus</i>	China	Alphatetraviridae	ssRNA(+)	5496	Bulatov virus (44)	GIXL01013119.1
Alphatetra-like tick virus 2	<i>Ixodes persulcatus</i>	USA	Alphatetraviridae	ssRNA(+)	1056	Vovk virus (60)	GBXQ01012426.1
Alphatetra-like tick virus 3	<i>Ornithodoros moubata</i>	Spain	Alphatetraviridae	ssRNA(+)	5452	Bulatov virus (40)	GIXP02005464.1
Alphatetra-like tick virus 4	<i>Ornithodoros moubata</i>	Spain	Alphatetraviridae	ssRNA(+)	3873	Bulatov virus (41)	GFJQ02007921.1
Alphatetra-like tick virus 5	<i>Rhipicephalus microplus</i>	USA	Alphatetraviridae	ssRNA(+)	1488	Hepelivirales sp. (80)	GEMR01004364.1
Chu-like tick virus 1	<i>Ixodes scapularis</i>	USA	Chuviridae	ssRNA(-)	728	Nuomin virus (89)	GGIX01201876.1

(i) Orthomyxoviridae-like contigs

The contigs we found contained homologs of Influenza RdRp subunit PB1, the most conserved of the orthomyxovirus genes (**Appendix Figure 2**). Phylogenetic analysis revealed that the putative novel Orthomyxo-like viral contigs fell into the genus *Quaranjavirus* and formed a separate clade with other tick-borne quaranjaviruses (**Appendix Figure 3; Table 1**). Within PB1, the contigs were phylogenetically closely related to Zambezi tick virus 1 (ZaTV-1) – a highly divergent virus identified in *Rhipicephalus* ticks from Mozambique (53) and shared approximately 77% amino-acids identity (**Appendix Figure 3; Table 1**). Quaranjaviruses are enveloped negative-sense single-stranded segmented RNA viruses, generally with multiple segments (54) which have been recorded in argasid and ixodid ticks, other arachnids, insects and vertebrates (55,56). In the present study, we identified 4 putative novel Orthomyxo-like tick viruses from ixodid tick metagenomic projects, 3 of which derived from sequence sampled from *Rhipicephalus sanguineus* in Italy, and one from *Rhipicephalus haemaphysaloides* in China (**Table 1**).

We note that four of the six the viral species that have complete genomes in this clade were either predicted to have very high ($N = 1$) or high ($N = 3$) zoonotic potential based on the GCB model (**Table 2**; the GenBank ID can be found in **Appendix Table 5**), with Quarantil virus (QRFV), one of the viruses rated to have high zoonotic potential, being confirmed to lead to infections in humans (54). Taken together, these results suggest that the novel Orthomyxo-like viral contigs identified in the current study may represent a potential risk of human infection given exposure (which is possible, as *R. haemaphysaloides* is known to parasitise humans).

(ii) Alphetetraviridae-like contigs

Members of the *Alphetetraviridae* are non-enveloped positive-sense single-stranded RNA viruses (57). The identified Alphetetra-like contigs ranged from 1488 nt to 5496 nt, detected via the presence of a putative RdRp 2 motif; some of the longer sequences also encoded putative nucleoside triphosphate hydrolase, viral RNA helicase, and viral methyltransferase three motifs (**Figure 2B**). Viruses in the family *Alphetetraviridae* had been previously believed to infect predominantly moths and butterflies (57), but the recent discovery of several Alphetetra-like viruses in ticks (23,58) implies that this may have been due to sampling biases. Consistent with this, we found the presence of potential Alphetetra-like viruses in four ixodid tick species (*Ixodes ricinus*, *Ixodes persulcatus*, *Ornithodoros moubata* and *Rhipicephalus microplus*) sampled in three geographically diverse locations (China, Spain, and USA) (**Table 1**). Phylogenetic analysis suggested that the novel Alphetetra-like tick viruses formed a separate clade, being placed with the tick-borne viruses recently identified in ixodid ticks from Antarctica (Vovk virus and Bulatov virus from the seabird tick, *Ixodes uriae*) (58) and China (Hubei tick hepe-like virus found in *R. microplus* and *Haemaphysalis longicornis*) (23), and Heilongjiang sediment betatetravirus of unknown host, but originally sampled from river sediment in China (59) (**Figure 3B**; **Table 1**).

No members of the *Alphetetraviridae* are known to infect humans, and, unfortunately, only partial genomes were available for the previously identified viruses in the proposed new clade (Bulatov virus, Vovk virus and Heilongjiang sediment betatetravirus), thus they were inappropriate for zoonotic risk analysis based on the GCB model. The closest related viruses with full genomes were all isolated from moths. Of these viruses *Nudaurelia capensis* beta virus was predicted to have high zoonotic potential; *Dendrolimus punctatus* virus and *Helicoverpa armigera* stunt virus were predicted to have medium zoonotic potential (**Table 2**; the GenBank IDs can be found in **Appendix Table 5**). This result illustrates a deficiency of the currently available zoonotic risk assessment tools for viruses discovered through meta-genomic or –transcriptomic methods. Zoonotic risk estimation using genome information generally requires complete viral genomes, but viruses found through these methods are often incomplete or exhibit uncertainty in segment linkage for segmented viruses, which impacts the ability to make fast decisions on virus research and surveillance at the earliest stage of virus discovery. Training existing models on features from partial viral genomes provides a potential avenue for future work to help alleviate this issue.

(iii) Chuviridae-like contigs

We identified 20 Chu-like viral contigs from *Ixodes scapularis* and *Hyalomma asiaticum* sampled in the US and China (**Table 1**; **Appendix Table 3**). Members of the *Chuviridae* are negative-sense single-stranded RNA viruses, which display a wide variety of genome organisations, including unsegmented, bi-segmented, and circular forms (15). Only the contig labelled Chu-like tick virus 1 is consistent with a live virus, as all other contigs showed signs of mutational degradation with many stop codons present in the region with homology to the RdRp. All but one of the contigs exhibiting

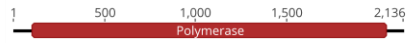
evidence of degradation were generated from a laboratory population of *Hy. asiaticum*, maintained under controlled conditions (60). As such, we speculate that they likely result from the presence of an integrated Chu-like virus in the *Hy. asiaticum* genome present in this laboratory population, and, likely, more broadly.

The viral sequence of Chu-like tick virus 1 was 728 nt in length, comprising one putative ORF that encodes a 240-amino acid protein containing the potential RdRp domain, nucleoside triphosphate hydrolase, viral RNA helicase, and viral methyltransferase 3 (**Figure 2C**). Chu-like tick virus 1 was clustered with other miviruses and was phylogenetically closely related to Suffolk virus, originally sampled in USA (20), with approximately 87% nucleotide identity (**Figure C; Table 1**). With regards to the human infection potential of Chu-like tick virus 1, it is notable that it showed a RdRp amino-acid identity of around 90% with Nuomin virus which has recently been associated with human febrile illness in China (61). The prediction results also classified Suffolk virus into the high zoonotic potential category (**Table 2**; the GenBank IDs can be found in **Appendix Table 5**). These results suggest that Chu-like tick virus 1 may pose a zoonotic risk. This may be especially relevant as the sequence was detected in *I. scapularis*, an important vector of other human pathogens, and so the potential for human exposure is high. However, given the small number of known species in the family *Chuviridae* when the GCB model was trained (31), caution must be applied, as the model might not be able to accurately predict the zoonotic potential viruses in this family. There would therefore seem to be a definite need for characterising viruses in the family *Chuviridae* in terms of their viability in human cell lines with these results feeding through to future zoonotic modelling efforts.

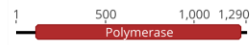
Table 2 Zoonotic risks of virus species closely related to the putative novel Alphetetra-like viral contigs. Zoonotic risks of sequences in GenBank format were predicted using the GCB model.

Putative novel viral contigs	Relative viral species	Current status	Predicted probability	95% Confidence interval	Zoonotic potential
Orthomyxo-like viral contigs	<i>Wellfleet Bay virus</i>	No known human infections	0.368	0.213-0.636	High
	<i>Araguari virus</i>	No known human infections	0.222	0.102-0.372	Medium
	<i>Johnston Atoll quaranjavirus</i>	No known human infections	0.513	0.311-0.802	Very high
	<i>Lake Chad virus</i>	No known human infections	0.184	0.081-0.334	Medium
	<i>Tjuloc virus</i>	No known human infections	0.352	0.141-0.607	High
	<i>Quaranfil quaranjavirus</i>	Human virus (54)	0.561	0.128-0.863	High
Alphetetra-like viral contigs	<i>Nudaurelia capensis beta virus</i>	No known human infections	0.302	0.153-0.497	High
	<i>Dendrolimus punctatus virus</i>	No known human infections	0.234	0.128-0.352	Medium
	<i>Helicoverpa armigera stunt virus</i>	No known human infections	0.243	0.135-0.387	Medium
Chu-like viral contigs	<i>Mivirus suffolkense</i>	No known human infections	0.309	0.151-0.562	High

A – Orthomyxo-like viral contigs



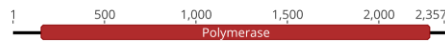
Orthomyxo-like tick virus 1



Orthomyxo-like tick virus 2



Orthomyxo-like tick virus 3



Orthomyxo-like tick virus 4

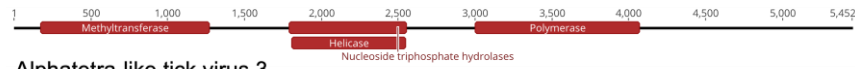
B – Alphatetra-like viral contigs



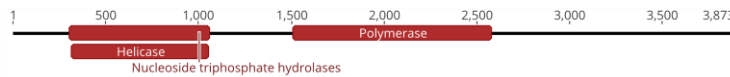
Alphatetra-like tick virus 1



Alphatetra-like tick virus 2



Alphatetra-like tick virus 3

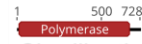


Alphatetra-like tick virus 4



Alphatetra-like tick virus 5

C – Chu-like viral contigs



Chu-like tick virus 1

Figure 2 Genome structures of novel viral contigs.

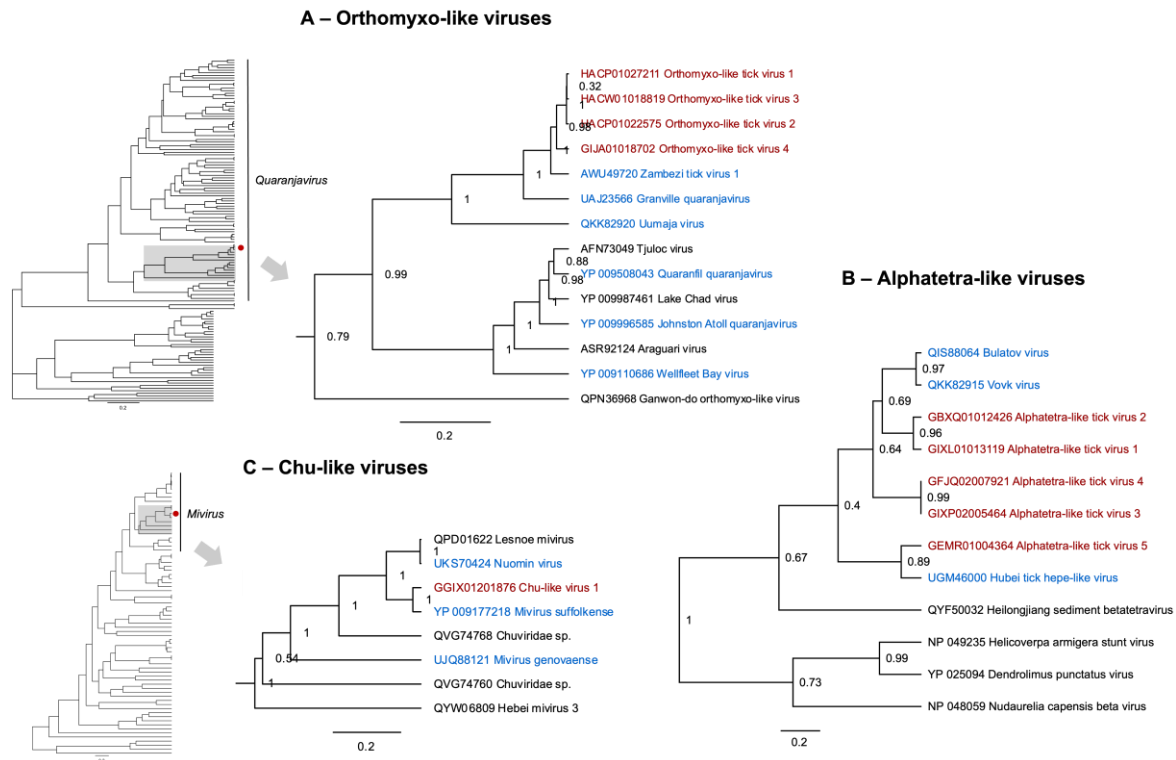


Figure 3 Phylogenetic relationship of the novel viral contigs. Maximum clade credibility trees were inferred from the Bayesian posterior sample. Posterior clade probabilities are shown at the nodes, and the scale is given in amino-acid substitutions per site. Putative novel viral contigs found in the present study are shown in red, and previously known tick-borne viruses are shown in blue. GenBank ID can be found at **Appendix Figure 2-4**. Alignments using ClustalW and maximum clade credibility trees are provided in at <https://github.com/ytlin2021/TickVirus.git>.

Zoonotic ranking of known tick-borne viruses

We used the prediction framework illustrated by Mollentze and colleagues (31) to rank 136 known tick-borne viruses with complete genomes. The viruses here were ranked based on predicted mean probability of zoonotic potential and further converted into four zoonotic potential categories, describing the overlap of confidence intervals (CIs) with the 0.293 cut-off (see Methods). The zoonotic prediction results were given in **Appendix Table 6**. This subset dataset contained representatives from 13 viral families (29 genera) and unassigned viruses, including 21 viruses that were known to infect humans by our criteria.

In total, 5.1% of tick-borne viruses were identified as having very high zoonotic potential (N = 7), 39.7% having high zoonotic potential (N = 54), 44.1% having medium zoonotic potential (N = 60) and 11.0% having low zoonotic potential (N = 15; **Appendix Figure 4**). Among the 22 currently known human-infecting tick-borne viruses, 81.8% were correctly identified as having either very high (N = 2) or high zoonotic potential (N = 16), and the remaining human-associated viruses were classified as medium zoonotic potential (N = 4; **Appendix Figure 4**). Among the tick-borne viruses with unknown human infectivity that were sequenced from nonhuman animal or tick samples, 37.7% were predicted to have either very high (N = 5) or high zoonotic potential (N = 38; **Appendix Figure 4**), including viruses in the family *Chuviridae*, *Nyamiviridae* and *Parvoviridae* that currently do not contain tick-borne viruses known to infect humans. Langat virus, Lonestar tick chuvirus 1, Grotenhout virus, Taggart virus, and Johnston Atoll virus were predicted to have very high zoonotic

risk, although they were not known to infect humans (**Figure 4B**). We therefore recommend these viruses be a high priority for further virological research, in order to assess whether greater surveillance of them in wild tick populations would be warranted.

We noted that the high and very high zoonotic potential categories were dominated by *Nairoviridae* (31.0%) and *Phenuiviridae* (28.6%), consistent with the recent findings of emerging human-infecting tick viruses in these two viral families. For example, among members of the *Nairoviridae* family, two emerging orthonairoviruses called Songling virus and Yezo virus have been recently detected in *Hyalomma* spp. ticks and isolated in patients with the acute febrile disease (4,5). Hospitals in Inner Mongolia and Heilongjiang province, China also reported infections from a novel nairovirus named Beiji nairovirus which mainly circulates in the ixodid ticks *I. crenulatus* and *I. persulcatus* (62). Similarly, among the *Phenuiviridae*, a novel phlebovirus named Tacheng tick virus 2 (TcTV-2) was first sampled from *D. marginatus* ticks in China (15) and later identified in various countries and tick species, primarily circulating in *D. marginatus* and *H. marginatum* ticks (63–65). The risk for human infection from TcTV-2 was not known until 2021 when Dong and colleagues reported on TcTV-2 infection in a patient in China (66). As recently emerged viruses, the geographic ranges of these viruses are poorly understood, and only partial genomes are available. The wide distribution of these tick species suggests that the geographic limits of the emerging tick-borne viruses in the family *Nairoviridae* and *Phenuiviridae* may be larger than presently assumed.

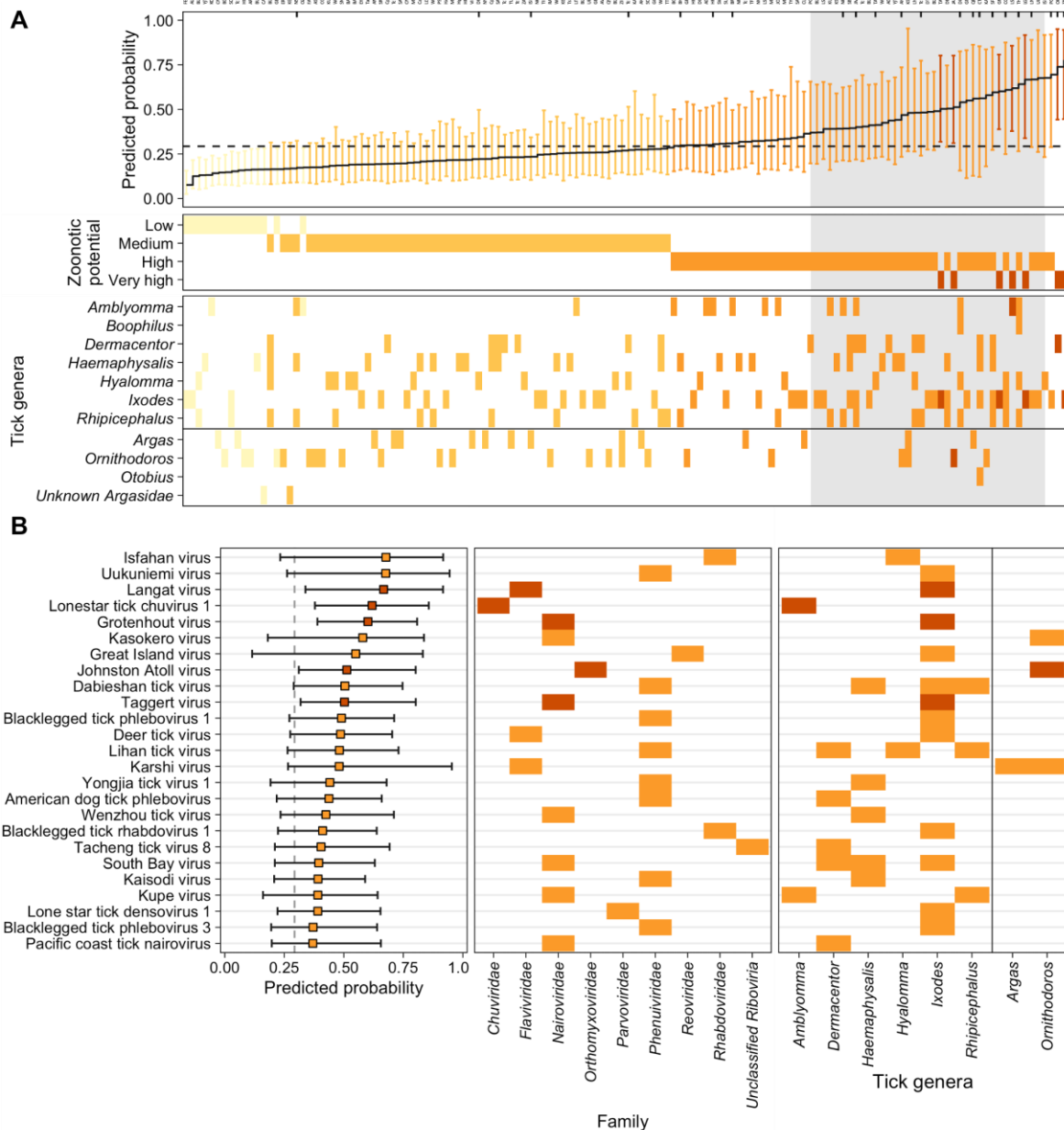


Figure 4 Predicted probability of human infection for tick viruses based on genome composition-based model. **(A)** Predicted probability of human infection for 136 tick viruses with complete genomes. Colour scale show the assigned zoonotic potential categories. Tick marks along the top edge of the first panel show the location of viruses known to infect humans, while a dashed line shows the cut-off 0.293 that balanced sensitivity and specificity according to Mollentze et al. (31). The top 25 viruses that have no known human infection (contained within the grey box) are illustrated in more detail in **(B)** Viruses that have no known human infection are shown in red. Points show the mean calibrated score, with lines indicating 95% confidence intervals. Figures were drawn in R v4.1.1. Zoonotic ranking results can be found in **Appendix Table 6**. Numeric data underlying this figure can be found at <https://github.com/ytlin2021/TickVirus.git>.

Discussion

Here we reanalysed existing tick metagenomic and meta-transcriptomic studies in public datasets to identify potential novel tick-borne viruses, using a tick virus database containing all known tick-borne viruses with genetic sequence available. We then employed the genome composition-based machine learning model of Mollentze et al. (31) to evaluate the zoonotic risk of all published tick viruses with complete genomes.

Novel virus discovery

The presence of undetected viruses in pre-existing meta-genomic and –transcriptomic data illustrate a valuable underutilised data source. A combination of factors, ranging from studies being focused on specific taxa, limitations of the bioinformatic tools being used and incompleteness of reference datasets used within these tools, result the generation of large amounts of unannotated or incorrectly annotated sequence. This provides an opportunity for small studies such as this one, or much larger studies considering wider ranges of or more extensively studied taxa (e.g. (16,35,67)), reanalysing this historical data to detect new viruses (or, equally, other organisms of interest). As a pedagogical aside, as the resource requirements for these studies are low, the scope of the projects limited, the outputs of general scientific interest, and the skills required of particular value to employers, these studies make excellent short projects for late-stage undergraduate or early-stage postgraduate students on ecology or ecology-adjacent courses.

As with all studies that base viral detection around similarity to known viruses, our ability to detect novel viruses was limited by our reference dataset. Hence, some putative novel tick-borne viruses may have been missed due to the absence of similar viruses for comparison.

Zoonotic risk assessment

The model applied showed promising results in distinguishing the zoonotic potential of closely related viruses within a genus. For instance, *Mivirus boleense* (15) was ranked as low zoonotic potential, while *Mivirus suffolkense* (20) was deemed high zoonotic potential. Given the validation of the methodology previously performed, this adds to the evidence suggesting the use of such models in providing targets for further research in a quick and low-cost way. However, caution must be exercised when interpreting the results of the genome composition-based model, as demonstrated in Figure 4B. The predicted probability interval was often large, leading to low confidence in the actual zoonotic risk of these viruses, and some viruses' zoonotic risks were inaccurately estimated. For example, Issyk-kul virus had low predicted probability and associated "medium" risk, although it has been indicated as a likely human pathogen (68). Moreover, the model training did not include any virus in the recently described viral family *Chuviridae*, reminding that while these tools are powerful, predictions of zoonotic risks from viral families with limited data should be treated with an abundance of caution and greater weight should be given to other clinical or epidemiological sources of evidence. Despite these limitations, good performance was observed in the family *Nairoviridae*, which included only 13 viruses in the dataset with the model predicting high risks of zoonotic potential for viruses with the group, consistent with recent findings of new and emerging tick-borne viral diseases associated with nairoviruses and orthonairoviruses (4,5,62,69).

A significant proportion of tick-borne viruses with high or very high zoonotic potential were sampled from ixodid ticks, which may reflect sampling bias towards viruses infecting hard ticks (family *Ixodidae*) in previous studies or be true representation of differences in intrinsic zoonotic risk between the viral communities of argasid and ixodid ticks. The ecology of argasid and ixodid ticks are different, with ixodid ticks generally having longer blood meals (70). The longer feeding time of ixodid ticks may make them on average more favourable for viral transmission, and thus more likely

to harbour communities of viruses capable of infecting mammals. However, it also means that ixodid ticks are more likely to be detected on a host, and thus more likely to be associated with resulting viral infections (i.e. a virus that might cause a fever of unknown origin if transmitted by an argasid tick may be able to be explicitly linked to a tick bite given the greater detection probability if transmitted by an ixodid tick). A more systematic approach that samples both hard and soft ticks would increase our knowledge of the diversity of tick-borne viruses carried by each type and allow us to assess whether they truly do differ in human infection risk.

As the model was trained on complete genomes (31), it is inappropriate for the use on viruses for which only partial genomes are available. This is a particularly important limitation for viruses found purely through bioinformatic means, where only single contigs or disconnected viral segments may be available. We attempted to assess the zoonotic risk of the putative novel viruses detected in this study by using the genomes of the closest related virus with a complete genome as a proxy. However, while this was unavoidable in this case, it does fall prey to one of the same biases the use of genome-based composition methods was originally intended to avoid, the assumption that zoonotic risk is conserved across the phylogeny. Hence, the zoonotic risks of these viruses ought to be reassessed should full genomes become available.

Conclusion

Despite ticks being important vectors of pathogens, the human infection risks of most tick-borne viruses remain uncertain (71). In this study we have both identified new tick viruses in previously collected data and assessed the zoonotic potential of known tick virus diversity, identifying certain high risk viral families deserving of further study and, potentially, surveillance. Cataloging viruses and assessing their human infection risk, as we have done here, represents only a first step in the risk management of zoonoses. Further research into the ecological processes that underlie the geographical distribution and interspecific transmission of ticks and their viruses is necessary to gain a comprehensive understanding of the ecology of this system. It is this eventual ecological knowledge that may allow us to formulate more effective strategies for managing human exposure to vectors, preventing zoonoses at the source.

Data accessibility statement

All novel viral sequences identified in this study have been submitted to Third Party Annotation Section of the DDBJ/ENA/GenBank databases under the accession numbers TPA: BK062905-BK062914. These sequence records will be held confidential until the data or accession numbers appear in print. Data and scripts used to generate the analyses are provided in at <https://github.com/ytlin2021/TickVirus.git>.

Competing interests statement

The authors have no conflict of interest to declare.

Author Contributions

Yuting Lin: Project administration (lead); methodology (equal); data curation (lead); investigation (lead); formal analysis (equal); visualisation (lead); writing – original draft (lead); writing – review and editing (equal). David J Pascall: Conceptualization (lead); methodology (equal); formal analysis

(equal); resources (lead); funding acquisition (lead); supervision (lead); writing – review and editing (equal).

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Appendices

Appendix Table 1. Summary of currently known tick-borne viruses by December 2021. Information from a wide variety of sources, references in the table.

Virus	Species	Genus	Family	Genome structure	Accession	Availability	Human infection	First description	Tick vectors	Distribution
African swine fever virus	<i>African swine fever virus</i>	<i>Asfivirus</i>	<i>Asfarviridae</i>	dsDNA	NC_04942	Complete genome	?	1921 (Montgomery et al., 1921)	<i>O. erraticus</i> , <i>O. moubata</i> (Shi et al., 2018)	Sub-Saharan Africa, South America, Southern Europe (Shi et al., 2018)
Canine circovirus	<i>Canine circovirus</i>	<i>Circovirus</i>	<i>Circoviridae</i>	ssDNA A (+/-)	NC_020904	Complete genome	?	2012 (Kapoor et al., 2012)	<i>Haemaphysalis spp.</i> , <i>Rhipicephalus spp.</i> (Kapoor et al., 2012)	Australia, Brazil, China, Columbia, Croatia, Germany, Iran, Italy, Norway, Thailand, Turkey, UK, USA, Viet Nam (Urbani et al., 2021)
Avian-like circovirus	<i>Tick associated circovirus 1</i>	<i>Circovirus</i>	<i>Circoviridae</i>	ssDNA A (+/-)	NC_030199	Complete genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Nayun torquevirus	Unclassified	<i>Thetatorquevirus</i>	<i>Anelloviridae</i>	ssDNA A (+/-)	KP141758	Partial genome	?	2015 (Xia et al., 2015)	<i>Rhipicephalus spp.</i> (Xia et al., 2015)	China (Xia et al., 2015)
Lone star tick densovirus 1	Unclassified	Unclassified	<i>Parvoviridae</i>	ssDNA A (+/-)	KX774632	Complete genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Colorado tick fever virus	<i>Colorado tick fever coltivirus</i>	<i>Coltivirus</i>	<i>Reoviridae</i>	dsRNA A	NC_004191, NC_004181, NC_004182, NC_004183,	Complete genome	Yes (Shi et al., 2018)	1946 (Florio et al., 1946)	<i>D. andersoni</i> , <i>D. albipictus</i> , <i>D. arumapertus</i> , <i>D. occidentalis</i>	USA (Shi et al., 2018)

					NC_00				s, H.	
					4184,				<i>leporispalu</i>	
					NC_00				<i>stris</i> , I.	
					4185,				<i>sculptus</i> , I.	
					NC_00				<i>spinipalpis</i> ,	
					4186,				<i>Ot.</i>	
					NC_00				<i>lagophilus</i>	
					4187,				(Shi et al.,	
					NC_00				2018)	
					4188,					
					NC_00					
					4180,					
					NC_00					
					4189,					
					NC_00					
					4190					
Eyach virus	<i>Eyach coltivirus</i>	<i>Coltivirus</i>	<i>Reoviridae</i>	dsRN A	NC_00 3696,	Com plete	?	1976 (Rehse	<i>I. ricinus</i> , <i>I. ventalloi</i>	France, Germany (Shi et al., 2018)
					NC_00 3697,	geno me		- Kuppe	(Shi et al., 2018)	(Shi et al., 2018)
					NC_00 3698,			r et al., 1976)		
					NC_00 3699,					
					NC_00 3700,					
					NC_00 3701,					
					NC_00 3702,					
					NC_00 3703,					
					NC_00 3704,					
					NC_00 3705,					
					NC_00 3706,					
					NC_00 3707					
Kundal virus	<i>Kundal coltivirus</i>	<i>Coltivirus</i>	<i>Reoviridae</i>	dsRN A	NC_05 5248,	Com plete	?	2019 (Yadav	<i>Hy. antolicum</i>	India (Yadav et al., 2019)
					NC_05 5249,	geno me		et al., 2019)	(Yadav et al., 2019)	
					NC_05 5247,					

					NC_05					
					5240,					
					NC_05					
					5250,					
					NC_05					
					5239,					
					NC_05					
					5242,					
					NC_05					
					5245,					
					NC_05					
					5241,					
					NC_05					
					5246,					
					NC_05					
					5243,					
					NC_05					
					5244					
Tarumizu	<i>Tarumizu</i>	<i>Coltivirus</i>	<i>Reoviridae</i>	dsRN	NC_05	Com	?	2017	<i>H. flava</i>	Japan (Fujita
tick virus	<i>coltivirus</i>			A	5255,	plete		(Fujita	(Fujita et	et al., 2017)
					NC_05	geno		et al.,	al., 2017)	
					5254,	me		2017)		
					NC_05					
					5261,					
					NC_05					
					5259,					
					NC_05					
					5262,					
					NC_05					
					5251,					
					NC_05					
					5260,					
					NC_05					
					5258,					
					NC_05					
					5252,					
					NC_05					
					5257,					
					NC_05					
					5253,					
					NC_05					
					5256					
Chenuda	<i>Chenuda</i>	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN	NC_02	Com	?	1978	A.	Egypt,
virus	<i>virus</i>			A	7534,	plete		(Karab	<i>hermanni</i>	Uzbekistan
					NC_02	geno		atsos,	(Shi et al.,	(Shi et al.,
					7535,	me		1978)	2018)	2018)

					NC_02					
					7536,					
					NC_02					
					7537,					
					NC_02					
					7538,					
					NC_02					
					7548,					
					NC_02					
					7549,					
					NC_02					
					7550,					
					NC_02					
					7551,					
					NC_02					
					7552					
Chobar	<i>Chobar</i>	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN	NC_02	Com	?	1978	<i>Ornithodoros</i>	Nepal (Shi et
Gorge virus	<i>Gorge virus</i>			A	7553,	plete		(Karab	<i>os</i> spp. (Shi	al., 2018)
					NC_02	geno		atsos,	et al.,	
					7554,	me		1978)	2018)	
					NC_02					
					7555,					
					NC_02					
					7556,					
					NC_02					
					7557,					
					NC_02					
					7558,					
					NC_02					
					7559,					
					NC_02					
					7560,					
					NC_02					
					7561,					
					NC_02					
					7562					
Great Island	<i>Great Island</i>	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN	NC_01	Com	?	1981	<i>I. uriae</i> (Shi	Canada (Shi
virus	<i>virus</i>			A	4522,	plete		(Nuttal	et al.,	et al., 2018)
					NC_01	geno		l et al.,	2018)	
					4523,	me		1981)		
					NC_01					
					4524,					
					NC_01					
					4525,					
					NC_01					
					4526,					

					NC_01						
					4527,						
					NC_01						
					4528,						
					NC_01						
					4529,						
					NC_01						
					4530,						
					NC_01						
					4531						
Kemerovo virus	Great Island virus	Orbivirus	Reoviridae	dsRN A	MF939 555, MF939 556, MF939 557, MF939 558, MF939 559, MF939 560, MF939 561, MF939 562, MF939 563, MF939 564, KJ0107 87	Com plete geno me	?	1970 (Libiko va et al., 1970)	<i>I. persulcatu s, I. ricinus</i> (Shi et al., 2018)	Russia, Slovakia (Shi et al., 2018)	
Lipovnik virus	Great Island virus	Orbivirus	Reoviridae	dsRN A	HM543 475, HM543 476, HM543 477	Parti al geno me	?	1964 (Libiko va et al., 1964)	<i>I. ricinus</i> (Shi et al., 2018)	Czech Republic, Slovakia (Shi et al., 2018)	
Tribec virus	Great Island virus	Orbivirus	Reoviridae	dsRN A	HQ266 581, HQ266 582, HQ266 583, HQ266 584,	Parti al geno me	?	1964 (Libiko va et al., 1964)	<i>H. punctata, I. ricinus</i> (Shi et al., 2018)	Belorussia, Italy, Slovakia (Shi et al., 2018)	

							HQ266						
							585,						
							HQ266						
							586,						
							HQ266						
							587,						
							HQ266						
							588,						
							HQ266						
							589,						
							HQ266						
							590						
St	Croix	St	Croix	Orbivirus	Reoviridae	dsRN	NC_00	Com	?	2001	<i>I.</i>	Kenya, USA	
River virus		<i>River virus</i>				A	6006,	plete		(Attoui	<i>scapularis</i> ,	(Alberdi et	
							NC_00	geno		et al.,	<i>R.</i>	al., 2012)	
							5998,	me		2001)	<i>appendicul</i>		
							NC_00				<i>atus</i> (Shi et		
							5999,				al., 2018)		
							NC_00						
							6000,						
							NC_00						
							6001,						
							NC_00						
							6002,						
							NC_00						
							6003.1						
							,						
							NC_00						
							6004,						
							NC_00						
							6005,						
							NC_00						
							5997						
Baku virus	Unclassified			Orbivirus	Reoviridae	dsRN	KY023	Parti	?	1978	<i>O.</i>	Caspian Sea,	
						A	349,	al		(Karab	<i>maritimus</i>	Uzbekistan	
							KY023	geno		atsos,	(Shi et al.,	(Shi et al.,	
							350,	me		1978)	2018)	2018)	
							KY023						
							351,						
							KY023						
							352,						
							KY023						
							353,						
							KY023						
							354,						
							KY023						

					355,					
					KY023					
					356,					
					KY023					
					357,					
					KY023					
					358					
Matucare virus	Unclassified	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN A	HQ397 640	Parti al geno me	?	1970 (Justin es et al., 1970)	Ot. <i>megnini</i> (<i>Palacios</i> <i>et al.</i> , 2011)	
Okhotskiy virus	Unclassified	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN A	KY023 329, KY023 330, KY023 331, KY023 332, KY023 333, KY023 334, KY023 335, KY023 336, KY023 337, KY023 338, KF9816 23, KF9816 24, KF9816 25, KF9816 26, KF9816 27, KF9816 28, KF9816 29,	Parti al geno me	?	1878 (L'vov et al., 1878)	<i>I. uriae</i> (Pettersso n et al., 2020)	Northern Sweden, Okhotsk (Pettersson et al., 2020)

					KF9816						
					30,						
					KF9816						
					31,						
					KF9816						
					32,						
					MN83						
					0241,						
					MN83						
					0242,						
					MN83						
					0243,						
					MN83						
					0244,						
					MN83						
					0245						
Wad Medani virus	<i>Wad Medani virus</i>	<i>Orbivirus</i>	<i>Reoviridae</i>	dsRN A	NC_02 7533, NC_02 7539, NC_02 7540, NC_02 7541, NC_02 7542, NC_02 7543, NC_02 7544, NC_02 7545, NC_02 7546, NC_02 7547	Complete genome	?	1966 (Taylor et al., 1966)	<i>Hyalomma spp., R. sanguineus</i> (Shi et al., 2018)	Asia, East Africa, Jamaica (Shi et al., 2018)	
Norway partiti-like virus 1	Unclassified	Unclassified	<i>Partitiviridae</i>	dsRN A	MF141 076	Partial genome	?	2017 (Pettersson et al., 2017)	<i>I. ricinus</i> (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)	
Lonestar tick totivirus	Unclassified	Unclassified	<i>Totiviridae</i>	dsRN A	MG647 775, MZ567 079	Partial genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)	

Fennes virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	dsRN A	MT025 166, MT025 167, MT025 168, MT025 169, MN83 0240	Parti al geno me	?	2020 (Wille et al., 2020)	<i>I. uriae</i> (Wille et al., 2020)	Antarctica (Wille et al., 2020)
Shelly Beach virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	dsRN A	MK026 600, MK026 601, MK026 602, MK026 603, MK026 604, MK026 605	Parti al geno me	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Shelly headland virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	dsRN A	OL452 144, OL452 150, OL452 158, OL452 171, OL452 185, OL452 194, OL452 203, OL452 214, OL452 222, OL452 151, OL452 172, OL452 215,	Parti al geno me	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)

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						OL452					
						221,					
						OL452					
						233,					
						OL452					
						182,					
						OL452					
						234,					
						OL452					
						235,					
						MK026					
						577,					
						MK026					
						581,					
						MK026					
						582					
Lonestar tick chuvirus 1	<i>Mivirus amblyomm ae</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_03 0204	Complete genome	?	2018	<i>Am. americanum</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)	
Bole tick virus 3	<i>Mivirus boleense</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8259	Complete genome	?	2015	<i>Hy. Asiaticum</i> , <i>Hy. Aegyptium</i> , <i>R. turanicus</i> , <i>R. bursa</i> (Li et al., 2015)	China, Turkey (Li et al., 2015; Brinkmann et al., 2018; Ergunay et al., 2020)	
Changping tick virus 2	<i>Mivirus changpingense</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8260	Complete genome	?	2015	<i>Dermacentor spp.</i> , <i>H. parva</i> , <i>R. sanguineus</i> (Li et al., 2015)	China, Thailand, Turkey, Trinidad, Tobago (Li et al., 2015; Brinkmann et al., 2018; Temmam et al., 2019)	

Changping tick virus 3	<i>Mivirus dermatensis</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8261	Complete genome	?	2015 (Li et al., 2015)	<i>Dermacentor spp. (Li et al., 2015)</i>	China (Li et al., 2015)
Genoa virus	<i>Mivirus genovaense</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	OL452 069	Complete genome	?	2018 (Harvey et al., 2018)	<i>I. holocyclus (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Suffolk virus	<i>Mivirus suffolkense</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8243	Complete genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis (Tokarz et al., 2018)</i>	USA (Tokarz et al., 2018)
Wuhan tick virus 2	<i>Mivirus wuhanense</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8266	Complete genome	?	2015 (Li et al., 2015)	<i>H. longicornis, R. microplus (Gómez et al., 2020; Xu et al., 2021)</i>	Brazil, China, Colombia, Guadeloupe, Thailand, Trinidad, Tobago (Gomez et al., 2020; Xu et al., 2021)
Wuhan mivirus	<i>Wuhan mivirus</i>	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	MZ244 267	Complete genome	?	2015 (Li et al., 2015)	<i>H. longicornis, R. microplus, R. sanguineus (Sameroff et al., 2019)</i>	China, Thailand, Trinidad and Tobago (Sameroff et al., 2019)
Tacheng tick virus 4	<i>Morsusvirus argatis</i>	<i>Morsusvirus</i>	<i>Chuviridae</i>	ssRN A(-)	NC_02 8263	Complete genome	?	2015 (Li et al., 2015)	<i>A. miniatus (Li et al., 2015)</i>	China (Li et al., 2015)
Blacklegged tick chuvirus 2	<i>Nigecruvirus ixodes</i>	<i>Nigecruvirus</i>	<i>Chuviridae</i>	ssRN A(-)	MF360 789	Complete genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis (Tokarz et al., 2018)</i>	USA (Tokarz et al., 2018)
Amblyomma dissimile mivirus*	Unclassified	<i>Mivirus</i>	<i>Chuviridae</i>	ssRN A(-)	MZ502 309.1	Complete genome	?	2021 (Sameroff et al., 2021)	<i>Am. dissimile (Sameroff et al., 2021)</i>	Trinidad and Tobago (Sameroff et al., 2021)
Nuomin virus*	Unclassified	Unclassified	<i>Chuviridae</i>	ssRN A(-)	MW02 9986.1	Partial	Y (Quan	2020 (Quan	<i>I. persulcatus, I.</i>	China (Quan et al., 2020)

						geno me	et al., 2020)	et al., 2020)	<i>crenulatus</i> , <i>H.</i> <i>conicinna</i> , <i>H.</i> <i>longicornis</i> (<i>Quan et al., 2020</i>)	
Tacheng tick virus 6	<i>Tacheng arlivirus</i>	<i>Arlivirus</i>	<i>Lispiviridae</i>	ssRN A(-)	NC_03 1270	Com plete geno me	?	2015 (Li et al., 2015)	<i>A. miniatus</i> (Li et al., 2015)	China (Li et al., 2015)
Grotenhout virus	<i>Grotenhout norwavirus</i>	<i>Norwavirus</i>	<i>Nairovirida e</i>	ssRN A(-)	KY700 684, KY700 683	Com plete geno me	?	2017 (Vanm echele n et al., 2017)	<i>I. ricinus</i> (Vanmech elen et al., 2017)	Belgium (Vanmechel en et al., 2017)
Abu Hammad virus	<i>Abu Hammad orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KU925 434, KU925 435, KU925 436	Com plete geno me	?	1976 (Darwi sh et al., 1976)	<i>A. hermanni</i> (Darwish et al., 1976)	Egypt (Darwish et al., 1976)
Abu Mina virus	<i>Abu Mina orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KU925 437, KU925 438, KU925 439	Com plete geno me	?	1976 (Darwi sh et al., 1976)	<i>A. streptopeli a</i> (Darwish et al., 1976)	Egypt (Darwish et al., 1976)
Artashat virus	<i>Artashat orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	NC_04 3440, NC_04 3442, NC_04 3441	Com plete geno me	?	2014 (Al'kho vskii et al., 2014)	<i>O. alactagalis</i> (Al'khovski i et al., 2014)	Armenia, Azerbaijan (Al'khovskii et al., 2014)
Avalon virus	<i>Avalon orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	NC_04 0460, NC_04 0459, NC_04 0458	Com plete geno me	?	1976 (Main et al., 1976)	<i>I. uriae</i> (Pettersso n et al., 2020)	Canada, France, Sweden (Pettersson et al., 2020)
Burana virus	<i>Burana orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	NC_04 3439, NC_04 3438,	Com plete geno me	?	2014 (L'vov et al., 2014)	<i>H. punctate</i> (L'vov et al., 2014)	Kyrgyzstan (L'vov et al., 2014)

					NC_04 3437						
Chim virus	<i>Chim orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_04 3434, NC_04 3436,	Com plete geno me	?	2014 (L'vov et al., 2014)	<i>O. tartakovskiy</i> (L'vov et al., 2014)	Uzbekistan (L'vov et al., 2014)	
					NC_04 3435						
Crimean-Congo hemorrhagic fever virus	<i>Crimean-Congo hemorrhagic fever orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_00 5301, NC_00 5300, NC_00 5302	Com plete geno me	Y (Garri son et al., 2020)	1945 (Grash chenk ov et al., 1945)	<i>Hy. asiaticum</i> , <i>Hy. marginatum</i> , <i>ixodid</i> spp., <i>R. rossicus</i> (Shi et al., 2018; Zhao et al., 2021)	Many countries in Asia and Africa; parts of Europe (e.g. Albania, Bulgaria) (Shi et al., 2018) (Shi et al., 2021)	
Dera Ghazi Khan virus	<i>Dera Ghazi Khan orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03 4520, NC_03 4510, NC_03 4521	Com plete geno me	?	1970 (Begu m et al., 1970)	<i>Hy. dromedarii</i> (Begum et al., 1970)	Pakistan (Begum et al., 1970)	
Dugbe virus	<i>Dugbe orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_00 4159, NC_00 4158, NC_00 4157	Com plete geno me	Y (Garri son et al., 2020)	1973 (David -West et al., 1973)	<i>Am. variegatum</i> , <i>B. decoloratus</i> , <i>Hy. truncatum</i> , and <i>R. appendiculatus</i> (Shi et al., 2018)	Sub-Saharan Africa (Shi et al., 2018)	
Estero Real virus	<i>Estero Real orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MH017 280, MH017 286, MH017 274	Com plete geno me	?	1985 (Malko va et al., 1985)	<i>O. tadaridae</i> (D Malkova et al., 1985)	Cuba (D Malkova et al., 1985)	
Hazara virus	<i>Hazara orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03 8709, NC_03 8710,	Com plete geno me	?	1970 (Begu m et al., 1970)	<i>I. redikorzevi</i> (Begum et al., 1970)	Japan, Pakistan (Begum et al., 1970; 1970)	

					NC_03 8711						Matsumoto et al., 2019)
Huangpi tick virus 1	<i>Huangpi orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	NC_03 1135, NC_03 1136, NC_03 1137	Com plete geno me	?	2015 (Li et al., 2015)	<i>H. doenitzi</i> , <i>H. longicornis</i> (Shi et al., 2018)		China (Shi et al., 2018)
Caspiy virus	<i>Hughes orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KP792 708, KP792 709, KP792 710	Com plete geno me	?	2014 (L'vov et al., 2014)	<i>Argasidae</i> (L'vov et al., 2014)		Azerbaijan (L'vov et al., 2014)
Farallon virus	<i>Hughes orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	NC_03 4502, NC_03 4494, NC_03 4503	Com plete geno me	?	1967 (Radov sky et al., 1967)	<i>Ornithodor us</i> spp. (Shi et al., 2018)		USA (Shi et al., 2018)
Great Saltee virus	<i>Hughes orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KU925 467, KU925 468, KU925 469	Com plete geno me	?	1976 (Keira ns et al., 1976)	<i>O. maritimus</i> (Kuhn et al., 2016)		Ireland (Great Saltee Island) (Kuhn et al., 2016)
Hughes virus	<i>Hughes orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KU925 470, KU925 471, KU925 472	Com plete geno me	?	1964 (Hugh es et al., 1964)	<i>O. denmarki</i> (Shi et al., 2018)		Cuba, Trinidad, USA, Venezuela (Shi et al., 2018)
Raza virus	<i>Hughes orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KU925 479, KU925 480, KU925 481	Com plete geno me	?	1968 (Cliffor d et al., 1968)	<i>O. denmarki</i> (Kuhn et al., 2016)		Mexico (Kuhn et al., 2016)
Issyk-kul virus	<i>Issyk-kul orthonairov irus</i>	<i>Orthonairov irus</i>	<i>Nairovirida e</i>	ssRN A(-)	KF8920 55, KF8920 56, KF8920 57	Com plete geno me	?	1973 (L'vov et al., 1973)	<i>A. vespertilion</i> <i>is</i> (L'vov et al., 1973)		Kyrgyzstan (Atkinson et al., 2015)

Kasokero virus	<i>Kasokero orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03_6636, NC_02_9933, NC_02_9932	Complete genome	?	1986	<i>O. faini</i> (Amy et al., 2020)	Uganda (Walker et al., 2015)
Keterah virus	<i>Keterah orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03_4392, NC_03_4388, NC_03_4389	Complete genome	?	1976	<i>Argasidae</i> (Varma et al., 1976)	Malaysia (Varma et al., 1976)
Kupe virus	<i>Kupe orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	EU257_628, EU257_627, EU257_626	Complete genome	?	2009	<i>Am. gemma</i> , <i>R. pulchellus</i> (Crabtree et al., 2009)	Kenya (Crabtree et al., 2009)
Meram virus	<i>Meram orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MN97_2594, MN97_2595, MN97_2596	Complete genome	?	2020	<i>Hy. aegyptium</i> (Ergunay et al., 2020)	Turkey (Ergunay et al., 2020)
Nairobi sheep disease virus	<i>Nairobi sheep disease orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03_4387, NC_03_4391, NC_03_4386	Complete genome	Y (Yadvav et al., 2011)	1969	<i>Am. variegatum</i> , <i>H. longicornis</i> , <i>H. intermedia</i> , <i>R. appendiculatus</i> , <i>R. hemaphysaloides</i> (Dandawate et al., 1969)	China, Kenya, India (Krašteva et al., 2020)
Pacific coast nairovirus	<i>Pacific Coast orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU933_933, KU933_934, KU933_935	Complete genome	?	2017	<i>D. occidentalis</i> (Bouquet et al., 2017)	USA (Bouquet et al., 2017)

Punta Salinas virus	<i>Punta orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 473, KU925 474, KU925 475	Complete genome	?	1981	<i>O. amblus</i> (Kuhn et al., 2016)	Peru (Kuhn et al., 2016)
Bandia virus	<i>Qalyub orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 446, KU925 447, KU925 448	Complete genome	?	1967	<i>O. sonrai</i> (Kuhn et al., 2016)	Senegal (Kuhn et al., 2016)
Geran virus	<i>Qalyub orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KP792 714, KP792 715, KP792 716	Complete genome	?	2014	<i>O. asperus</i> (Kuhn et al., 2016)	Azerbaijan (Kuhn et al., 2016)
Qalyub virus	<i>Qalyub orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03 4511, NC_03 4522, NC_03 4512	Complete genome	?	1952	<i>O. asperus</i> , <i>O. erraticus</i> (Walker et al., 2016)	Azerbaijan, Egypt, Senegal (Kuhn et al., 2016; Walker et al., 2016)
Clo Mor virus	<i>Sakhalin orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03 4561, NC_03 4554, NC_03 4562	Complete genome	?	1976	<i>A. cooleyi</i> , <i>I. uriae</i> (Walker et al., 2016)	UK, USA (Walker et al., 2016)
Sakhalin virus	<i>Sakhalin orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 482, KU925 483, KU925 484	Complete genome	?	1972	<i>I. uriae</i> (Kuhn et al., 2016)	Antarctica, Australia, Russia, USA (L'vov et al., 2014; Kuhn et al., 2016; Pettersson et al., 2020)
Taggert virus	<i>Sakhalin orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 491, KU925 492, KU925 493	Complete genome	?	1985	<i>I. uriae</i> (Pettersson et al., 2020)	Antarctica, Australia (Pettersson et al., 2020; Wille et al., 2020)

Tillamook virus	<i>Sakhalin orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 494, KU925 495, KU925 496	Complete genome	?	1973	<i>I. uriae</i> (Kuhn et al., 2016)	USA (Kuhn et al., 2016)
Soldado virus	<i>Soldado orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	KU925 488, KU925 489, KU925 490	Complete genome	?	1973	<i>O. maritimus</i> (Shi et al., 2018)	France, Great Britain, Indian Ocean, North Wales, Seychelles (Shi et al., 2018)
Tacheng tick virus 1	<i>Tacheng orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_03 1284, NC_03 1285, NC_03 1286	Complete genome	Y	2015	<i>D. marginatus</i> , <i>D. nuttalli</i> , <i>D. silvarum</i> , <i>Hy. asiaticum</i> (Shi et al., 2018)	China, Kazakhstan (Shi et al., 2018)
Tamdy virus	<i>Tamdy orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MN79 2651, MN79 2652, MN79 2653	Complete genome	Y	2014	<i>Hy. asiaticum</i> (L'vov et al., 1984; Moming et al., 2021)	China, Uzbekistan (Moming et al., 2021)
Tofla virus	<i>Tofla orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_02 9124, NC_02 9123, NC_02 9122	Complete genome	?	2016	<i>H. flava</i> , <i>H. formsensis</i> (Shimada et al., 2016)	Japan (Shimada et al., 2016)
Tunis virus	<i>Tunis orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	NC_04 0770, NC_04 0771, NC_04 0772	Complete genome	?	1994	<i>A. hermanni</i> (Chastel et al., 1994)	Tunisia (Chastel et al., 1994)
Vinegar Hill virus	<i>Vinegar Hill orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MF176 881, MF176	Complete genome	?	2017	<i>A. robertsi</i> (Gauci et al., 2017)	Australia (Gauci et al., 2017)

					882,	geno			et al.,		
					MF176	me			2017)		
					883						
Wenzhou	<i>Wenzhou</i>	<i>Orthonairov</i>	<i>Nairovirida</i>	ssRN	NC_03	Com	?	2015	<i>H. hystricis</i>	China (Li et	
tick virus	<i>orthonairov</i>	<i>irus</i>	<i>e</i>	A(-)	1291,	plete		(Li et	(Li et al.,	al., 2015)	
	<i>irus</i>				NC_03	geno		al.,	2015)		
					1288,	me		2015)			
					NC_03						
					1289						
South Bay	<i>South Bay</i>	<i>Sabavirus</i>	<i>Nairovirida</i>	ssRN	KJ7468	Com	?	2014	<i>D. nuttalli</i> ,	China, USA	
virus	<i>sabavirus</i>		<i>e</i>	A(-)	78,	plete		(Tokar	<i>H.</i>	(Tokarz et	
					KJ7468	geno		z et al.,	<i>concinna</i> ,	al., 2014;	
					77	me		2014)	<i>H.</i>	Zhao et al.,	
									<i>longicornis</i>	2021)	
									, <i>I.</i>		
									<i>persulcatu</i>		
									<i>s</i> , <i>I.</i>		
									<i>scapularis</i>		
									(Tokarz et		
									al., 2014;		
									Zhao et al.,		
									2021)		
Midway	<i>Midway</i>	<i>Nyavirus</i>	<i>Nyamivirid</i>	ssRN	NC_01	Com	?	1982	<i>Ornithodor</i>	Central	
virus	<i>nyavirus</i>		<i>ae</i>	A(-)	2702	plete		(Takah	<i>os</i> spp. (Shi	Pacific,	
						geno		ashi et	et al.,	Japan (Shi et	
						me		al.,	2018)	al., 2018)	
								1982)			
Nyamanini	<i>Nyamanini</i>	<i>Nyavirus</i>	<i>Nyamivirid</i>	ssRN	NC_01	Com	?	1966	<i>A.</i>	Egypt, India,	
virus	<i>nyavirus</i>		<i>ae</i>	A(-)	2703	plete		(Taylor	<i>arboreris</i> ,	Nigeria,	
						geno		et al.,	<i>A.</i>	South Africa,	
						me		1966)	<i>walkerae</i>	Thailand (Shi	
									(Shi et al.,	et al., 2018)	
									2018)		
Sierra	<i>Sierra</i>	<i>Nyavirus</i>	<i>Nyamivirid</i>	ssRN	NC_02	Com	?	2014	<i>O.</i>	USA (Rogers	
Nevada	<i>Nevada</i>		<i>ae</i>	A(-)	4376	plete		(Roger	<i>coriaceus</i>	et al., 2014)	
virus	<i>nyavirus</i>					geno		s et al.,	(Rogers et		
						me		2014)	al., 2014)		
Johnston	<i>Johnston</i>	<i>Quarantjavir</i>	<i>Orthomyxo</i>	ssRN	NC_05	Com	?	2009	<i>O. capensis</i>	Australia,	
Atoll virus	<i>Atoll</i>	<i>us</i>	<i>viridae</i>	A(-)	2925,	plete		(Presti	(Shi et al.,	Central	
	<i>quarantjavir</i>				NC_05	geno		et al.,	2018)	Pacific, New	
	<i>us</i>				2926,	me		2009)		Zealand and	
					NC_05					Hawaii (Shi	
					2927,					et al., 2018)	
					NC_05						
					2928,						
					NC_05						

					2929,						
					NC_05						
					2930,						
					NC_05						
					2931,						
					FJ8616						
					96,						
					FJ8616						
					97						
Quaranfil virus	<i>Quaranfil quaranjavirus</i>	<i>Quaranjavirus</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	NC_03 8817, NC_03 8818, NC_03 8819, NC_03 8820, NC_03 8821, NC_03 8822	Complete genome	Y	1966 (Mourya et al., 2019)	A. <i>arboreus</i> (Shi et al., 2018)	Afghanistan, Egypt, Iraq, Kuwait, Nigeria, South Africa, Yemen and Iran (Shi et al., 2018)	
Granville quaranjavirus*	<i>Granville quaranjavirus</i>	<i>Quaranjavirus</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	MZ502 307, MZ502 306, MZ502 305, MZ502 304, MZ502 308	Partial genome	?	2021 (Sameroff et al., 2021)	Am. <i>dissimile</i> (<i>Sameroff et al., 2021</i>)	Trinidad and Tobago (Sameroff et al., 2021)	
Dhori virus	<i>Dhori thogotovirus</i>	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	NC_03 4254, NC_03 4255, NC_03 4256, NC_03 4261, NC_03 4262, NC_03 4263	Complete genome	Y	1973 (Kosoy et al., 2015)	<i>Hyalomma</i> spp. (Shi et al., 2018)	China, Egypt, India, Kyrgyzstan, Russia (Shi et al., 2018)	
Jos virus	<i>Thogoto thogotovirus</i>	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	HM627 170, HM627	Complete genome	?	1974 (Lee et al., 2018)	<i>Amblyomma</i> spp., <i>Rhipicephala</i>	Central Africa Republic,	

					171,	geno		al.,	<i>lus</i>	spp.	Guinea, Côte
					HM627	me		1974)	(Shi et al.,		d'Ivoire,
					172,				2018)		Nigeria,
					HM627						Senegal (Shi
					173,						et al., 2018)
					HM627						
					174,						
					HM627						
					175						
Thogoto virus	<i>Thogoto thogotovirus</i>	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	NC_006495, NC_006496, NC_006504, NC_006506, NC_006507, NC_006508	Complete genome	Y	1965 (Haig et al., 1965)	<i>Am. Variiegatus</i> , <i>Boophilus spp.</i> , <i>Hyalomma spp.</i> , <i>Rhipicephalus</i> spp. (Shi et al., 2018)		Central and East Africa, Southern Europe, Southern Portugal (Shi et al., 2018)
Ngari virus	<i>Bunyamwera orthobunyavirus</i>	<i>Orthobunyavirus</i>	<i>Peribunyaviridae</i>	ssRNA(-)	KC608152, KC608153, KC608154	Complete genome	Y	1996 (Grosseth et al., 2012)	<i>Am. variiegatus</i> , <i>R. pulchellus</i> (Grosseth et al., 2012)		Guinea, Kenya, Mauritania, Senegal, Somalia, Sudan (Grosseth et al., 2012; Makenov et al., 2021)
Matruh virus	<i>Matruh orthobunyavirus</i>	<i>Orthobunyavirus</i>	<i>Peribunyaviridae</i>	ssRNA(-)	KP792693, KP792692, KP792691	Complete genome	?	1973 (Balducci et al., 1973)	<i>Hy. Marginatum</i> (Balducci et al., 1973)		Italy (Balducci et al., 1973)
Bahig virus	<i>Tete orthobunyavirus</i>	<i>Orthobunyavirus</i>	<i>Peribunyaviridae</i>	ssRNA(-)	KP792654, KP792653, KP792652	Complete genome	?	1973 (Balducci et al., 1973)	<i>Hy. Marginatum</i> (Balducci et al., 1973)		Italy (Balducci et al., 1973)
Bhanja virus	<i>Bhanja bandavirus</i>	<i>Bandavirus</i>	<i>Phenuiviridae</i>	ssRNA(-)	NC_027140, NC_02	Complete genome	Y	1977 (Matsuno et al., 2018)	<i>H. intermedia</i> , <i>R.</i>		Africa, Asia, Southern Europe, USA

						7141,	geno	al.,	Hirjan	<i>decoloratu</i>	(Shi et al.,
						NC_02	me	2013)	et al.,	<i>s</i> (Matsuno	2018)
						7142			1977)	et al.,	
										2013)	
Heartland virus	<i>Heartland bandavirus</i>	<i>Bandavirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_02	4494,	Com	Y	2012	<i>Am.</i>	USA
						NC_02	plete	(McM	(McM	<i>americanu</i>	(Mansfield
						4495,	geno	ullan	ullan	<i>m</i>	et al., 2017)
						NC_02	me	et al.,	et al.,	<i>(Mansfield</i>	
						4496		2012)	2012)	<i>et al.,</i>	
										2017)	
Hunter Island virus	<i>Hunter Island bandavirus</i>	<i>Bandavirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_02	7715,	Com	?	2014	<i>l.</i>	Australia
						NC_02	plete		(Wang	<i>eudyptidis</i>	(Shi et al.,
						7716,	geno		et al.,	(Shi et al.,	2018)
						NC_02	me		2014)	2018)	
						7717					
lone star virus	<i>Lone star bandavirus</i>	<i>Bandavirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_02	1242,	Com	?	1969	<i>Am.</i>	USA (Shi et
						NC_02	plete		(Koker	<i>Americanu</i>	al., 2018)
						1243,	geno		not et	<i>m</i> (Shi et	
						NC_02	me		al.,	al., 2018)	
						1244			1969)		
Severe fever with thrombocytopenia syndrome virus	<i>Dabie bandavirus</i>	<i>Bandavirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_04	3450,	Com	Y	2011	<i>Dermacent</i>	East Asia,
						NC_04	plete	et al.,	(Yu et	<i>or spp.,</i>	North
						3451,	geno	2011)	al.,	<i>Haemaphy</i>	America
						NC_04	me		2011)	<i>salis spp., l.</i>	(Mansfield
						3452				<i>persulcatu</i>	et al., 2017;
										<i>s,</i>	Zhao et al.,
										<i>Rhipicepha</i>	2021)
										<i>lus spp.</i>	
										<i>(Mansfield</i>	
										<i>et al.,</i>	
										2017; Zhao	
										<i>et al.,</i>	
										2021)	
Norway phlebovirus 1	<i>Norway ixovirus</i>	<i>Ixovirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_05	5433,	Com	?	2017	<i>l. ricinus</i>	Norway
						NC_05	plete		(Petter	(Pettersso	(Pettersson
						5434	geno		sson et	n et al.,	et al., 2017)
							me		al.,	2017)	
										2017)	
Blacklegged tick phlebovirus 3	<i>Scapularis ixovirus</i>	<i>Ixovirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_05	5431,	Com	?	2018	<i>l.</i>	USA (Tokarz
						NC_05	plete		(Tokar	<i>scapularis</i>	et al., 2018)
						5432	geno		z et al.,	<i>(Tokarz et</i>	
							me		2018)	<i>al., 2018)</i>	
Laurel Lake virus	<i>Laurel Lake laulavirus</i>	<i>Laulavirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_04	3679,	Com	?	2018	<i>l.</i>	USA (Tokarz
							plete		(Tokar	<i>scapularis</i>	et al., 2018)

					NC_04	geno			z et al.,	(Tokarz et	
					3680,	me			2018)	al., 2018)	
					NC_04						
					3681						
Dabieshan	<i>Dabieshan</i>	<i>Uukuvirus</i>	<i>Phenuivirid</i>	ssRN	MW72	Com	?	2015	<i>H.</i>	<i>China</i>	(Wang
tick virus	<i>uukuvirus</i>		<i>ae</i>	A(-)	1887,	plete		(Li et	<i>longicornis</i>	et al., 2021;	
					MW72	geno		al.,	, <i>I.</i>	Zhao et al.,	
					1893	me		2015)	<i>persulcatu</i>	2021)	
									<i>s,</i>		
									<i>R.</i>		
									<i>microplus</i>		
									(Wang et		
									al., 2021;		
									Zhao et al.,		
									2021)		
Kaisodi	<i>Kaisodi</i>	<i>Uukuvirus</i>	<i>Phenuivirid</i>	ssRN	NC_04	Com	?	1966	<i>H.</i>	South India	
virus	<i>uukuvirus</i>		<i>ae</i>	A(-)	0492,	plete		(Bhatt	<i>spinigera</i>	(Shi et al.,	
					NC_04	geno		et al.,	(Shi et al.,	2018)	
					0493,	me		1966)	2018)		
					NC_04						
					0494						
Lihan	tick	<i>Lihan</i>	<i>Uukuvirus</i>	ssRN	NC_05	Com	?	2015	<i>D. nitens,</i>	Brazil, China,	
virus	<i>uukuvirus</i>		<i>ae</i>	A(-)	5423,	plete		(Li et	<i>Hy.</i>	USA,	
					NC_05	geno		al.,	<i>marginatu</i>	Guadeloupe	
					5424	me		2015)	<i>m,</i>	, Thailand,	
									<i>R.</i>	Turkey,	
									<i>microplus,</i>		
									<i>R.</i>	Trinidad.	
									<i>sanguineus</i>	Tobago	
									(Temmam	(Temmam et	
									et al.,	al., 2019;	
									2019)	Gondard et	
										al., 2020)	
Silverwater	<i>Silverwater</i>	<i>Uukuvirus</i>	<i>Phenuivirid</i>	ssRN	NC_05	Com	?	1971	<i>H.</i>	Canada, USA	
virus	<i>uukuvirus</i>		<i>ae</i>	A(-)	5369,	plete		(Hoff	<i>leporispalu</i>	(Shi et al.,	
					NC_05	geno		et al.,	<i>stris</i> (Shi et	2018)	
					5370,	me		1971)	al., 2018)		
					NC_05						
					5371						
Tacheng	<i>Tacheng</i>	<i>Uukuvirus</i>	<i>Phenuivirid</i>	ssRN	NC_05	Com	Y	2015	<i>D.</i>	China,	
tick virus 2	<i>uukuvirus</i>		<i>ae</i>	A(-)	5425,	plete		(Dong	<i>marginatu</i>	Kazakhstan,	
					NC_05	geno		et al.,	<i>s,</i>	Romania,	
					5426	me		2021)	<i>D.</i>	Tailand,	
									<i>reticulatus,</i>		
									<i>R.</i>	Turkey (Li et	
									<i>sanguineus</i>	al., 2015;	
									, <i>H.</i>	Brinkmann	
									<i>marginatu</i>	et al., 2018;	
									<i>m</i> (Li et al.,	Temmam et	

									2015;	al.,	2019;
									Brinkmann	Bratuleanu	
									et al.,	et al.,	2021)
									2018;		
									Bratuleanu		
									et al.,		
									2021)		
Uukuniemi virus	<i>Uukuniemi uukuvirus</i>	<i>Uukuvirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_00 5214, NC_00 5220, NC_00 5221	Complete genome	?	2013	(Palacios et al., 2013)	<i>I. ricinus</i> , <i>I. uriae</i> (Matsuno et al., 2015)	Czech Republic, Sweden, UK (Matsuno et al., 2015)
Yongjia tick virus 1	<i>Yongjia uukuvirus</i>	<i>Uukuvirus</i>	<i>Phenuivirid ae</i>	ssRN A(-)	NC_05 5427, NC_05 5428	Complete genome	?	2015	(Li et al., 2015)	<i>H. hystricis</i> (Li et al., 2015)	China (Li et al., 2015)
Blanchseco virus	<i>Blanchseco alpharicinrhavirus</i>	<i>Alpharicinrhavirus</i>	<i>Rhabdovirid ae</i>	ssRN A(-)	MN02 5503	Complete genome	?	2019	(Sameroff et al., 2019)	<i>A. ovale</i> (Sameroff et al., 2019)	Trinidad and Tobago (Sameroff et al., 2019)
Bole tick virus 2	<i>Bole alpharicinrhavirus</i>	<i>Alpharicinrhavirus</i>	<i>Rhabdovirid ae</i>	ssRN A(-)	NC_03 1079	Complete genome	?	2015	(Li et al., 2015)	<i>Hy. Asiaticum</i> (Li et al., 2015)	China (Li et al., 2015)
Wuhan tick virus 1	<i>Wuhan alpharicinrhavirus</i>	<i>Alpharicinrhavirus</i>	<i>Rhabdovirid ae</i>	ssRN A(-)	NC_03 1304	Complete genome	?	2015	(Li et al., 2015)	<i>D. marginatus</i> , <i>R. microplus</i> , <i>R. annulatus</i> , <i>H. longicornis</i> (Temmam et al., 2019; Xu et al., 2021)	China, Turkey (Xu et al., 2021)
New Kent County virus	<i>Kent ephemerovirus</i>	<i>Ephemerovirus</i>	<i>Rhabdovirid ae</i>	ssRN A(-)	MF615 270	Complete genome	?	2018	(Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Barur virus	<i>Barur ledantevirus</i>	<i>Ledantevirus</i>	<i>Rhabdovirid ae</i>	ssRN A(-)	NC_03 4535	Complete genome	?	1981	(Butenko et al., 2018)	<i>Hy. Intermedia</i> (Shi et al., 2018)	India, Kenya, Somalia (Shi et al., 2018)

									al., 1981)	
Kolente virus	<i>Kolente ledantevirus</i>	<i>Ledantevirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_02 5342	Complete genome	?	2013	<i>Am. Variegatum</i> (Shi et al., 2018)	Guinea (Shi et al., 2018)
Yongjia tick virus 2	<i>Yongjia ledantevirus</i>	<i>Ledantevirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_03 1305	Complete genome	?	2015	<i>H. hystricis</i> (Shi et al., 2018)	China (Shi et al., 2018)
Connecticut virus	<i>Connecticut sawgrhavirus</i>	<i>Sawgrhavirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	KM205 020	Complete genome	?	1978	<i>I. dentatus</i> (Shi et al., 2018)	USA (Shi et al., 2018)
Long Island tick rhabdovirus	<i>Island sawgrhavirus</i>	<i>Sawgrhavirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_02 5340	Complete genome	?	2014	<i>Am. americanum</i> (Tokarz et al., 2014)	USA (Tokarz et al., 2014)
New Minto virus	<i>Minto sawgrhavirus</i>	<i>Sawgrhavirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_05 5457	Complete genome	?	1970	<i>H. leporispalustris</i> (Shi et al., 2018)	USA (Shi et al., 2018)
Sawgrass virus	<i>Sawgrass sawgrhavirus</i>	<i>Sawgrhavirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_05 5461	Complete genome	?	1970	<i>D. variabilis</i> , <i>H. leporispalustris</i> (Shi et al., 2018)	USA (Shi et al., 2018)
Isfahan virus	<i>Isfahan vesiculovirus</i>	<i>Vesiculovirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_02 0806	Complete genome	?	1977	<i>Hy. Asiaticum</i> (Shi et al., 2018)	Parts of Asia, Turkmenistan (Shi et al., 2018)
Zahedan rhabdovirus	<i>Zahedan zarhavirus</i>	<i>Zarhavirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_04 0664	Complete genome	?	2015	<i>Hy. Anatolicum</i> (Shi et al., 2018)	Iran (Shi et al., 2018)
Beiji nairovirus	Unclassified	<i>Nairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MW31 5106, MW31 5112	Partial genome	Y (Wang et al., 2021)	2019	<i>I. crenulatus</i> , <i>I. persulcatus</i> (Wang et al., 2021)	China (Wang et al., 2021)
Nayun tick nairovirus	Unclassified	<i>Nairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MW56 1151,	Partial	?	2015	<i>R. sanguineus</i> (Xia et al., 2018)	China, Romania

					KP141 756, KP141 755	geno me		al., 2015)	(Xia et al., 2015; Bratuleanu et al., 2021)	(Xia et al., 2015; Bratuleanu et al., 2021)
Norway nairovirus 1	Unclassified	<i>Nairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MF141 045, MF141 044	Parti al geno me	?	2017 (Pettersson et al., 2017)	<i>I. ricinus</i> (Pettersson et al., 2017)	Northern Europe (Pettersson et al., 2017)
Paramushir virus	Unclassified	<i>Nairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MH638 289, MH124 638, MH124 637, MH124 636, MH124 635, MH124 634, KF8016 57, KP792 719, KP792 718, KP792 717	Parti al geno me	?	1976 (L'vov et al., 1976)	<i>I. signatus</i> , <i>I. uriae</i> (L'vov et al., 1976)	Russia (Safonova et al., 2015)
Rondonia orthonairovirus	Unclassified	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	MN56 0621, MN56 0622, MN56 0623, MN56 0624, MN56 0625, MN56 0626, MN56 0627, MN56 0628,	Parti al geno me	?	2019 (Blomstrom et al., 2019)	<i>Antricola</i> (Blomstrom et al., 2019)	Brazil (Blomstrom et al., 2019)

					MN56						
					0629						
Songling virus	Unclassified	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRNA(-)	MT328 780, MT328 779, MT328 778	Partial genome	Y (Ma et al., 2021)	2021 (Ma et al., 2021)	<i>H. longicornis</i> (Ma et al., 2021)	China (Ma et al., 2021)	
Yezo virus	Unclassified	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRNA(-)	LC6213 60, LC6213 59, LC6213 58	Partial genome	Y (Kodama et al., 2021)	2021 (Kodama et al., 2021)	<i>H. megaspinosus</i> (Kodama et al., 2021)	Japan (Kodama et al., 2021)	
Zambezi tick virus 1	Unclassified	<i>Quarjavirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	MH267 793	Partial genome	?	2018 (Cholleti et al., 2018)	<i>Rhipicephalus</i> (Cholleti et al., 2018)	Mozambique (Cholleti et al., 2018)	
Aransas Bay virus	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	KC506 162, KC506 163, KC506 164, KC506 165, KC506 166, KC506 167	Partial genome	?	1979 (Yunker et al., 1979)	<i>Ornithodoros</i> spp. (Briese et al., 2014)	North America (Briese et al., 2014)	
Bourbon virus	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	KU708 253, KU708 254, KU708 255, MH880 287, MH880 288, MH880 289, MH880 290, MH880	Complete genome	Y (Kosoy et al., 2015)	2015 (Kosoy et al., 2015)	<i>Americanum</i> (Savage et al., 2017)	USA (Kosoy et al., 2015)	

					291, MH880					
					292					
Oz virus	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	NC_04730, NC_04731, NC_04732, NC_04733, NC_04734, NC_04735	Complete genome	?	2018 (Ejiri et al., 2018)	<i>Am. testudinarius</i> (Ejiri et al., 2018)	Japan (Ejiri et al., 2018)
Thailand tick thogotovirus	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	MN095539, MN095540, MN095541, MN095542, MN095543, MN095544	Complete genome	?	2019 (Temmam et al., 2019)	<i>R. microplus</i> (Temmam et al., 2019)	Tailand (Temmam et al., 2019)
Upolu virus	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRNA(-)	KC506156, KC506157, KC506158, KC506159, KC506160, KC506161	Complete genome	?	1968 (Doherly et al., 1968)	<i>O. capensis</i> (Briese et al., 2014)	Australia (Briese et al., 2014)
American dog tick phlebovirus	Unclassified	<i>Phlebovirus</i>	<i>Phenuiviridae</i>	ssRNA(-)	KM048312, KM048311	Complete genome	?	2014 (Tokarz et al., 2014)	<i>D. variabilis</i> (Tokarz et al., 2014)	USA (Tokarz et al., 2014)
Blacklegged tick	Unclassified	<i>Phlebovirus</i>	<i>Phenuiviridae</i>	ssRNA(-)	KX184200	Complete genome	?	2014 (Tokarz et al., 2014)	<i>I. scapularis</i>	USA (Tokarz et al., 2014)

phlebovirus						KX184	geno		z et al., (Tokarz et	
1						201	me		2014) al., 2014)	
Blacklegged tick	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i>	ssRN		KM589	Parti	?	2014	USA (Tokarz et al., 2014)
			<i>ae</i>	A(-)		357,	al		(Tokar	<i>scapularis</i> et al., 2014)
phlebovirus						KM589	geno		z et al., (Tokarz et	
2						354	me		2014) al., 2014)	
Bole tick virus 1	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i>	ssRN		MZ244	Parti	?	2015	China (Li et al., 2015)
			<i>ae</i>	A(-)		253,	al		(Li et	<i>Asiaticum</i> al., 2015)
						MZ244	geno		al., (Li et al.,	
						252,	me		2015) 2015)	
						KM817				
						731,				
						MH916				
						622,				
						MH916				
						621,				
						MH916				
						620,				
						MH916				
						619,				
						MH688				
						504,				
						MH836				
						620,				
						MH688				
						505,				
						MH688				
						503,				
						MH688				
						501,				
						MH688				
						578,				
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						572,				
						MH688				
						571				

Brown dog tick phlebovirus 1	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	MZ244 261, MZ244 260, MZ244 259, MZ244 256, MN02 5507, MN02 5506	Parti al geno me	?	2019 (Sameroff et al., 2019)	<i>R. sanguineus</i> <i>R. microplus</i> (Sameroff et al., 2019)	China, Trinidad and Tobago (Sameroff et al., 2019)
Brown dog tick phlebovirus 2	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	MW56 1139, MW56 1138, MW56 1137, MW56 1136, MN02 5509, MN02 5508	Parti al geno me	?	2019 (Sameroff et al., 2019)	<i>R. microplus</i> , <i>R. sanguineus</i> (Sameroff et al., 2019)	China, Trinidad and Tobago (Sameroff et al., 2019)
Changping tick virus 1	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	MW56 1146, MW56 1145, MW56 1144, MW56 1143, MW56 1142, MW56 1141, MW56 1140, KM817 732, KM817 665	Parti al geno me	?	2015 (Li et al., 2015)	<i>Dermacentor</i> spp. (Li et al., 2015)	China, Romania (Matsuno et al., 2013; Li et al., 2015)
Lanjan virus	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	KM370 974	Parti al geno me	?	1967 (Tan et al., 1967)	<i>D. auratus</i> (Shi et al., 2018)	Malaysia (Shi et al., 2018)

Palma virus	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	JX9616 30, JX9616 29, JX9616 28	Parti al geno me	?	1994 (Filipe et al., 1994)	<i>H. punctate</i> (Shi et al., 2018)	Portugal (Shi et al., 2018)
Rhipicephalus associated phlebovirus 1	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	MZ244 255, MZ244 254, MH814 976, MH814 975	Parti al geno me	?	2021 (Shi et al., 2021)	<i>R. microplus</i> (Shi et al., 2021)	China (Shi et al., 2021)
Tick phlebovirus Anatolia 1	Unclassified	<i>Phlebovirus</i>	<i>Phenuivirid</i> <i>ae</i>	ssRN A(-)	MG764 522, MG764 521	Parti al geno me	?	2018 (Brink mann et al., 2018)	<i>R. sanguineus</i> (Brinkman n et al., 2018)	Turkey (Brinkmann et al., 2018)
Neke harbour virus	Unclassified	Unclassified	<i>Orthomyxo</i> <i>viridae</i>	ssRN A(-)	MN83 0238	Parti al geno me	?	2020 (Petter sson et al., 2020)	<i>I. uriae</i> (Pettersso n et al., 2020)	Antarctica (Pettersson et al., 2020)
Uumaja virus	Unclassified	Unclassified	<i>Orthomyxo</i> <i>viridae</i>	ssRN A(-)	MN83 0237	Parti al geno me	?	2020 (Petter sson et al., 2020)	<i>I. uriae</i> (Pettersso n et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Khasan virus	Unclassified	Unclassified	<i>Peribunyavi</i> <i>ridae</i>	ssRN A(-)	KF8920 46, KF8920 47, KF8920 48	Parti al geno me	?	1978 (L'vov et al., 1978)	<i>H. longgicornis</i> (Shi et al., 2018)	Russia (Shi et al., 2018)
American dog tick rhabdovirus 2	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	MF962 659, MF962 661	Parti al geno me	?	2018 (Tokar z et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Blacklegged tick rhabdovirus 1	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	MF360 790	Com plete geno me	?	2018 (Tokar z et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Dog tick rhabdovirus 1	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	MF360 791	Parti al	?	2018 (Tokar z et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)

								geno	z et al.,	(Tokarz et	
								me	2018)	al., 2018)	
Huangpi tick virus 3	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	NC_03 1083	Com	?	plete	2015	<i>H. doenitzi</i>	China (Li et al., 2015)
								geno	al.,	(Li et al., 2015)	
								me	2015)		
Nayun tick rhabdovirus	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	KP141 757	Parti	?	al	2015	<i>Rhipicephalus</i> spp.	China (Xia et al., 2015)
								geno	al.,	(Xia et al., 2015)	
								me	2015)		
Rhipicephalus associated rhabdo-like virus	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	MH814 974	Parti	?	al	2021	<i>H. longicornis</i> , <i>R. microplus</i>	China (Shi et al., 2021)
								geno	al.,	(Shi et al., 2021)	
								me	2021)		
Tacheng tick virus 3	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	NC_03 1268	Com	?	plete	2015	<i>D. marginatus</i>	China (Li et al., 2015)
								geno	al.,	(Li et al., 2015)	
								me	2015)		
Tacheng tick virus 7	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	NC_03 1272	Com	?	plete	2015	<i>A. miniatus</i>	China (Li et al., 2015)
								geno	al.,	(Li et al., 2015)	
								me	2015)		
Taishun tick virus	Unclassified	Unclassified	<i>Rhabdovirid</i> <i>ae</i>	ssRN A(-)	NC_03 1273	Com	?	plete	2015	<i>H. hystricis</i>	China, Russia (Li et al., 2015)
								geno	al.,	(Li et al., 2015)	
								me	2015)		
Deer tick mononegavirales-like virus	Unclassified	Unclassified	Unclassified	ssRN A(-)	MG880 117, KM048 317, KJ7469 03	Parti	?	al	2014	<i>D. nuttalli</i> , <i>D. silvarum</i> , <i>H. concinna</i> , <i>I. persulcatus</i> , <i>I. scapularis</i>	China, USA (Tokarz et al., 2014; Zhao et al., 2021)
								geno	z et al.,	(Tokarz et al., 2014; Zhao et al., 2021)	
								me	2014)		
Bonden virus	Unclassified	Unclassified	Unclassified <i>Bunyavirales</i>	ssRN A(-)	MN83 0227	Parti	?	al	2020	<i>I. uriae</i>	Northern Sweden (Pettersson et al., 2020)
								geno	(Pettersson et al., 2020)	(Pettersson et al., 2020)	
								me	2020)		

Bronnoya virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Bunyavirales</i>	ssRN A(-)	MF141 063, MF141 062	Parti al geno me	?	2017 (Pettersson et al., 2017)	<i>I. ricinus</i> (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Ubmeje virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Bunyavirales</i>	ssRN A(-)	MN83 0232	Parti al geno me	?	2020 (Pettersson et al., 2020)	<i>I. uriae</i> (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Norway mononegavirus 1	Unclassified	Unclassified	<i>Unclassified</i> <i>Mononegavirales</i>	ssRN A(-)	MF141 072	Parti al geno me	?	2017 (Pettersson et al., 2017)	<i>I. ricinus</i> (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Tick mononegavirus	Unclassified	Unclassified	<i>Unclassified</i> <i>Mononegavirales</i>	ssRN A(-)	MZ244 310, MH835 441, MH835 440, MH835 439, MH835 438	Parti al geno me	?	2018 (Yang et al., 2018)	<i>I. scapularis</i> , <i>H. longicornis</i> (Yang et al., 2018)	China (Yang et al., 2018)
Umea virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Mononegavirales</i>	ssRN A(-)	MN83 0236	Parti al geno me	?	2020 (Pettersson et al., 2020)	<i>I. uriae</i> (Pettersson et al., 2020)	Sweden (Pettersson et al., 2020)
Canne point virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(-)	MK026 566	Parti al geno me	?	2018 (Harvey et al., 2018)	<i>Am. moreliae</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Fairlight virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(-)	MK026 565	Parti al geno me	?	2018 (Harvey et al., 2018)	<i>Am. moreliae</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Manly virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(-)	MK026 564	Parti al geno me	?	2018 (Harvey et al., 2018)	<i>Am. moreliae</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Messner virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(-)	MT025 174	Parti al geno me	?	2020 (Wille et al., 2020)	<i>I. uriae</i> (Wille et al., 2020)	Antarctica (Wille et al., 2020)

North Shore virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	OL452 126	Partial genome	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Old quarry swamp virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	MK026 595, MK026 596, MK026 597, MK026 598, MK026 599	Partial genome	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Piguzov virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	MT025 176, MT025 177	Partial genome	?	2020 (Pettersson et al., 2020)	<i>I. uriae</i> (Pettersson et al., 2020)	Antarctica (Pettersson et al., 2020)
Quarantine Head virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	MK026 568	Partial genome	?	2018 (Harvey et al., 2018)	<i>Am. moreliae</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Ronne virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	MT025 165, MT025 164	Partial genome	?	2020 (Pettersson et al., 2020; Wille et al., 2020)	<i>I. uriae</i> (Pettersson et al., 2020; Wille et al., 2020)	Antarctica, Northern Sweden (Pettersson et al., 2020; Wille et al., 2020)
Tacheng tick virus 5	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	NC_02 8264	Complete genome	?	2015 (Li et al., 2015)	<i>D. marginatus</i> (Li et al., 2015)	China, Kazakhstan (Li et al., 2015)
Timbillica virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(-)	MK026 589, MK026 590	Partial genome	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Gadgets Gully virus	<i>Gadgets Gully virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_03 3723	Complete genome	?	1985 (St George et al., 1985)	<i>I. uriae</i> (Pettersson et al., 2020)	Antarctica, Australia (Pettersson et al., 2020)

Kadam virus	<i>Kadam virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_03 3724	Com plete geno me	?	1970 (Henderson et al., 1970)	<i>R. pravus</i> (Shi et al., 2018)	Saudi Arabia, Uganda (Shi et al., 2018)
Alkhumra hemorrhagic fever virus	<i>Kyasanur Forest disease virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	AF331 718	Com plete geno me	Y (Grard et al., 2007)	1957 (Work et al., 1957)	<i>H. spinigera</i> , <i>O. savignyi</i> (Shi et al., 2018)	India, Saudi Arabia (Shi et al., 2018)
Langat virus	<i>Langat virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	AF253 419	Com plete geno me	?	1956 (Smith et al., 1956)	<i>I. granulatus</i> (Shi et al., 2018)	Malaysia (Shi et al., 2018)
Louping ill virus	<i>Louping ill virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	Y0786 3	Com plete geno me	Y (Davidson et al., 1991)	1931 (Greig et al., 1931)	<i>I. ricinus</i> (Shi et al., 2018)	England, Ireland, Scotland, Wales (Shi et al., 2018)
Meaban virus	<i>Meaban virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_03 3721	Com plete geno me	?	1985 (Chastel et al., 1985)	<i>O. maritimus</i> (Shi et al., 2018)	France (Shi et al., 2018)
Omsk hemorrhagic fever virus	<i>Omsk hemorrhagic fever virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	AY193 805	Com plete geno me	Y (Grard et al., 2007)	1989 (Gaidamovich et al., 1989)	<i>Dermacentor spp.</i> , <i>I. persculatus</i> (Ruzek et al., 2010)	Russia (Grard et al., 2007)
Deer tick virus	<i>Powassan virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	AF311 056	Com plete geno me	?	1997 (Telford et al., 1997)	<i>I. scapularis</i> (Mansfield et al., 2017; Shi et al., 2018)	New England, North America (Mansfield et al., 2017; Shi et al., 2018)
Powassan virus	<i>Powassan virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	L06436	Com plete geno me	Y (Tokarz et al., 2014)	1959 (McLellan and Donohue, 1959)	<i>I. cookei</i> , <i>Ixodes spp.</i> (Tokarz et al., 2014)	North America, Russia (Mansfield et al., 2017)
Karshi virus	<i>Royal Farm virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	AY863 002	Com plete	?	1976 (L'vov et al., 1976)	<i>A. hermanni</i>	North of Central Asia,

						geno		et al.,	<i>O.</i>	Uzbek (Shi et
						me		1976)	<i>papillipes</i>	al., 2018)
									(Shi et al.,	2018)
Saumarez Reef virus	<i>Saumarez Reef virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	DQ235 150	Complete genome	?	1977 (St Georg e et al., 1977)	<i>I. eudyptidis</i> , <i>O. capensis</i>	Australia (Shi et al., 2018)
Tick-borne encephalitis virus	<i>Tick-borne encephalitis virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_00 1672	Complete genome	Y (Shi et al., 2018)	1931 (Schneider et al., 1931)	<i>I. ovatus</i> , <i>I. persulcatus</i> , <i>I. ricinus</i>	Northern Asia, Northern Europe, Siberia (Shi et al., 2018)
Tyuleniy virus	<i>Tyuleniy virus</i>	<i>Flavivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_02 3424	Complete genome	?	1971 (L'vov et al., 1971)	<i>I. putus</i>	Tuleniy Island (Shi et al., 2018)
Ixodes holocyclus iflavivirus	<i>Ixodes holocyclus iflavivirus</i>	<i>Iflavirus</i>	<i>Iflaviridae</i>	ssRN A(+)	OL452 115	Partial genome	?	2018 (O'Brien et al., 2018)	<i>I. holocyclus</i>	Australia (O'Brien et al., 2018)
Blacklegged tick associated ilarvirus	Unclassified	<i>Iflavirus</i>	<i>Bromoviridae</i>	ssRN A(+)	MG647 776, MG647 777	Partial genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (<i>Tokarz et al., 2018</i>)	USA (Tokarz et al., 2018)
Trinidad virus	Unclassified	<i>Pestivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	MN02 5505	Partial genome	?	2019 (Sameroff et al., 2019)	<i>A. ovale</i> , <i>R. microplus</i> , <i>R. sanguineus</i>	Trinidad, Tobago (Sameroff et al., 2019)
Cattle tick tymovirus-like virus 1	Unclassified	<i>Tymovirus</i>	<i>Tymoviridae</i>	ssRN A(+)	MN02 5504	Partial genome	?	2019 (Sameroff et al., 2019)	<i>R. microplus</i>	Trinidad and Tobago (Sameroff et al., 2019)
Lone star tick dicistroviruses	Unclassified	Unclassified	<i>Dicistroviridae</i>	ssRN A(+)	KX774 633	Partial genome	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (<i>Tokarz et al., 2018</i>)	USA (Tokarz et al., 2018)
Alongshan virus	Unclassified	Unclassified	<i>Flaviviridae</i>	ssRN A(+)	MN64 8770,	Partial genome	Y (Wan	2019 (Kuiva	<i>I. persulcatus</i>	China, France,

					MN64	geno	g et	nen et	<i>s. l. ricinus</i>	Finland
					8771,	me	al.,	al.,	(Kholodilo	(Kholodilov
					MN64		2019)	2019)	v et al.,	et al., 2020)
					8772,				2020)	
					MN64					
					8773					
Jingmen	Unclassified	Unclassified	<i>Flaviviridae</i>	ssRN	MK721	Com	Y (Jia	2014	<i>Am.</i>	Many
tick virus				A(+)	629,	plete	et al.,	(Qin et	<i>javanense,</i>	countries in
					MK721	geno	2019)	al.,	<i>D. nuttalli,</i>	Asia,
					630,	me		2014)	<i>Haemaphy</i>	America,
					MK721				<i>salis spp.,</i>	and Africa
					631,				<i>Ixodes</i>	(Vandegrift
					MK721				<i>spp.,</i>	et al., 2020;
					632				<i>Rhipicepha</i>	Zhao et al.,
									<i>lus spp.</i>	2021)
									(Zhao et	al., 2021)
Norway	Unclassified	Unclassified	<i>Luteovirida</i>	ssRN	MF141	Parti	?	2017	<i>I. ricinus</i>	Norway
luteo-like			<i>e</i>	A(+)	065	al		(Petter	(Pettersso	(Pettersson
virus 1						geno		sson et	n et al.,	et al., 2017)
						me		al.,	2017)	
Norway	Unclassified	Unclassified	<i>Luteovirida</i>	ssRN	MF141	Parti	?	2017	<i>I. ricinus</i>	Norway
luteo-like			<i>e</i>	A(+)	068	al		(Petter	(Pettersso	(Pettersson
virus 2						geno		sson et	n et al.,	et al., 2017)
						me		al.,	2017)	
Norway	Unclassified	Unclassified	<i>Luteovirida</i>	ssRN	MF141	Parti	?	2017	<i>I. ricinus</i>	Norway
luteo-like			<i>e</i>	A(+)	069	al		(Petter	(Pettersso	(Pettersson
virus 3						geno		sson et	n et al.,	et al., 2017)
						me		al.,	2017)	
Norway	Unclassified	Unclassified	<i>Luteovirida</i>	ssRN	MF141	Parti	?	2017	<i>I. ricinus</i>	Norway
luteo-like			<i>e</i>	A(+)	070	al		(Petter	(Pettersso	(Pettersson
virus 4						geno		sson et	n et al.,	et al., 2017)
						me		al.,	2017)	
Lone star	Unclassified	Unclassified	<i>Nodavirida</i>	ssRN	KX774	Parti	?	2018	<i>I.</i>	USA (Tokarz
tick			<i>e</i>	A(+)	635,	al		(Tokar	<i>scapularis</i>	et al., 2018)
nodavirus					KX774	geno		z et al.,	(Tokarz et	
					634	me		2018)	<i>al., 2018)</i>	
Paradise	Unclassified	Unclassified	<i>Tombusviri</i>	ssRN	MN83	Parti	?	2020	<i>I. uriae</i>	Antarctica
bay virus			<i>dae</i>	A(+)	0247	al		(Petter	(Pettersso	(Pettersson
						geno		sson et	n et al.,	et al., 2020)
						me		al.,	2020)	

Upmeje virus	Unclassified	Unclassified	<i>Tombusviri dae</i>	ssRN A(+)	MN83 0246	Parti al	?	2020 (Pettersson et al., 2020)	<i>I. uriae</i> (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Bagotville virus	Unclassified	Unclassified	<i>Unclassified Picornavirales</i>	ssRN A(+)	MW74 1892	Parti al	?	2021 (Chandra et al., 2021)	<i>I. holocyclus</i> (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Blacklegged tick picorna-like virus 1	Unclassified	Unclassified	<i>Unclassified Picornavirales</i>	ssRN A(+)	MG647 769, MG647 774	Parti al	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Blacklegged tick picorna-like virus 2	Unclassified	Unclassified	<i>Unclassified Picornavirales</i>	ssRN A(+)	MG647 773, MG647 772, MG647 771, MG647 770	Parti al	?	2018 (Tokarz et al., 2018)	<i>I. scapularis</i> (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Wardell virus	Unclassified	Unclassified	<i>Unclassified Picornavirales</i>	ssRN A(+)	MW74 1896, MW74 1895, MW74 1894	Parti al	?	2021 (Chandra et al., 2021)	<i>I. holocyclus</i> (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Woodburn virus	Unclassified	Unclassified	<i>Unclassified Picornavirales</i>	ssRN A(+)	MW74 1893	Parti al	?	2021 (Chandra et al., 2021)	<i>I. holocyclus</i> (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Blue Fish Point virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 570, MK026 571	Parti al	?	2018 (Harvey et al., 2018)	<i>I. holocyclus</i> (Harvey et al., 2018)	Australia (Harvey et al., 2018)
Bole tick virus 4	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MZ244 286	Com plete	?	2015 (Shi et al., 2015)	<i>D. marginatus</i> , <i>D. asiaticum</i> , <i>D. asiaticum</i> , <i>D. asiaticum</i> , <i>H. asiaticum</i> , <i>Hy. asiaticum</i> , <i>Hy.</i>	China, Romania, Saudi Arabia, Thailand, Trinidad, Tobago (Temmam et al., 2019);

									<i>detrinum</i> , <i>R.</i> <i>microplus</i> , <i>R.</i> <i>sanguineus</i> (<i>Temmam</i> <i>et al.</i> , 2019; <i>Bratuleanu</i> <i>et al.</i> , 2021; <i>Zakham et</i> <i>al.</i> , 2021)	Bratuleanu et al., 2021; Zakham et al., 2021)
Bulatov virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	MN83 0234, MT025 173	Parti al geno me	?	2020 (Petter sson et al., 2020; Wille et al., 2020)	<i>I. uriae</i> (Pettersso n et al., 2020)	Antarctica (Pettersson et al., 2020)
Collins beach virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	MK026 585	Parti al geno me	?	2018 (Harve y et al., 2018)	<i>I. holocyclus</i> (<i>Harvey et</i> <i>al.</i> , 2018)	Australia (Harvey et al., 2018)
Fairfax Lookout virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	MK026 588, MK026 587, MK026 586	Parti al geno me	?	2018 (Harve y et al., 2018)	<i>I. holocyclus</i> (<i>Harvey et</i> <i>al.</i> , 2018)	Australia (Harvey et al., 2018)
Gerbovich virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	MN83 0239, MT025 175	Parti al geno me	?	2020 (Petter sson et al., 2020; Wille et al., 2020)	<i>I. uriae</i> (Pettersso n et al., 2020; Wille et al., 2020)	Antarctica (Pettersson et al., 2020; Wille et al., 2020)
Ingleside virus	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	OL452 105	Parti al geno me	?	2018 (Harve y et al., 2018)	<i>I. holocyclus</i> (<i>Harvey et</i> <i>al.</i> , 2018)	Australia (Harvey et al., 2018)
Ixodes scapularis	Unclassified	Unclassified	<i>Unclassified</i> <i>Riboviria</i>	ssRN A(+)	LC0949 65,	Parti al	?	2017 (Nakao <i>et al.</i>)	<i>I. scapularis</i> (<i>Tokarz et</i> <i>al.</i> , 2018;	USA, Japan (Tokarz et al., 2018;

associated virus 3					MG677	geno			et al., 2017)	<i>al., 2018; Nakao et al., 2017)</i>	Nakao et al., 2017)
Jump Rock virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 583	Parti al	?	2018	(Harvey et al., 2018)	<i>I. holocyclus (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Nadgee virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 592	Parti al	?	2018	(Harvey et al., 2018)	<i>I. holocyclus (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Store beach virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 567	Parti al	?	2018	(Harvey et al., 2018)	<i>Am. moreliae (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Tacheng tick virus 8	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	NC_02 8367	Complete geno	?	2015	(Shi et al., 2015)	<i>D. marginatus (Shi et al., 2015)</i>	China (Shi et al., 2015)
Vovk virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MN83 0235, MT025 162	Parti al	?	2020	(Pettersson et al., 2020; Wille et al., 2020)	<i>I. uriae (Pettersson et al., 2020; Wille et al., 2020)</i>	Antarctica (Pettersson et al., 2020; Wille et al., 2020)
Wangarabe Il virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 593	Parti al	?	2018	(Harvey et al., 2018)	<i>I. holocyclus (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Yambulla virus	Unclassified	Unclassified	<i>Unclassified Riboviria</i>	ssRN A(+)	MK026 594	Parti al	?	2018	(Harvey et al., 2018)	<i>I. holocyclus (Harvey et al., 2018)</i>	Australia (Harvey et al., 2018)
Antioquia tymovirus-like 1	Unclassified	Unclassified	<i>Unclassified Tymovirales</i>	ssRN A(+)	MK683 451	Parti al	?	2020	(Gomez et al., 2020)	<i>R. microplus (Gomez et al., 2020)</i>	Colombia (Gomez et al., 2020)
Guarapuava tymovirus-like 1	Unclassified	Unclassified	<i>Unclassified Tymovirales</i>	ssRN A(+)	MH155 882	Parti al	?	2018	(de Souza et al., 2018)	<i>R. microplus (de Souza et al., 2018)</i>	Brazil (de Souza et al., 2018)
American dog tick	Unclassified	Unclassified	Unclassified	Unkn own	MF962 660	Parti al	?	2018	(Tokarz et al., 2018)	<i>D. variabilis (Tokarz et al., 2018)</i>	USA (Tokarz et al., 2018)

associated virus 1									geno	z et al., (Tokarz et al., 2018)	
American dog tick associated virus 2	Unclassified	Unclassified	Unclassified	Unkn	MF962	Parti	?	2018	al	(Tokarz et al., 2018)	USA (Tokarz et al., 2018)
					own						
					MF962	geno				z et al., (Tokarz et al., 2018)	
					657	me					
Finch Creek virus	Unclassified	Unclassified	Unclassified	Unkn	EU267	Parti	?	2009	al	(Major et al., 2009)	Australia (Major et al., 2009)
					own						
					169	al					
						geno				et al., 2009)	
						me					
Ganjam virus	Unclassified	Unclassified	Unclassified	Unkn	KU925	Parti	?	1969	al	(Dand et al., 1969)	India (Kuhn et al., 2016)
					own						
					466,	al					
					KU925	geno				awate (Kuhn et al., 2016)	
					465,	me					
					KU925						
					464						
Ixodes scapularis associated virus 1	Unclassified	Unclassified	Unclassified	Unkn	LC0949	Parti	?	2014	al	(Tokarz et al., 2014)	Japan, USA (Tokarz et al., 2014; Nakao et al., 2017)
					own						
					64,	al					
					KM048	geno				z et al., (Tokarz et al., 2014)	
					318	me					
Ixodes scapularis associated virus 2	Unclassified	Unclassified	Unclassified	Unkn	KM048	Parti	?	2014	al	(Tokarz et al., 2014)	USA (Tokarz et al., 2014)
					own						
					319	al					
						geno				z et al., (Tokarz et al., 2014)	
						me					
Ixodes scapularis associated virus 4	Unclassified	Unclassified	Unclassified	Unkn	MF962	Parti	?	2018	al	(Tokarz et al., 2018)	USA (Tokarz et al., 2018)
					own						
					656	al					
						geno				z et al., (Tokarz et al., 2018)	
						me					
Ixodes scapularis associated virus 5	Unclassified	Unclassified	Unclassified	Unkn	MG256	Parti	?	2018	al	(Tokarz et al., 2018)	USA (Tokarz et al., 2018)
					own						
					513	al					
						geno				z et al., (Tokarz et al., 2018)	
						me					
Ixodes scapularis associated virus 6	Unclassified	Unclassified	Unclassified	Unkn	MG256	Parti	?	2018	al	(Tokarz et al., 2018)	USA (Tokarz et al., 2018)
					own						
					514	al					
						geno				z et al., (Tokarz et al., 2018)	
						me					
Lone star tick associated virus 1	Unclassified	Unclassified	Unclassified	Unkn	MF962	Parti	?	2018	al	(Tokarz et al., 2018)	USA (Tokarz et al., 2018)
					own						
					658	al					
						geno				z et al., (Tokarz et al., 2018)	
						me					
Sapphire II virus	Unclassified	Unclassified	Unclassified	Unkn	MK896	Com	?	1972	plete	(Yunker et al., 1972)	USA (Yunker et al., 1972)
					own						
					468,						
					MK896	geno				r et al., 1972)	
					467,	me					

MK896										
466										
Tick borne tetraviruses-like virus	Unclassified	Unclassified	Unclassified	Unkn own	MW33 4982, KM048 322	Parti al geno me	?	2014	D. (Tokar z et al., 2014)	USA (Tokarz et al., 2014)
Zirqa virus	Unclassified	Unclassified	Unclassified	Unkn own	KU925 500, KU925 501, KU925 502	Com plete geno me	?	1973	A. cooleyi, (Varm a et al., 1973)	Abu Dhabi (Shi et al., 2018)
Bovine hepatitis virus**	<i>Hepacivirus N</i>	<i>Hepacivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	NC_02 6797	Com plete geno me	?	2015	Unknown (Baechlein et al., 2015)	Brazil, China, Germany, Ghana, US (Baechlein et al., 2019)
HoBi-like pestivirus*	<i>Pestivirus H</i>	<i>Pestivirus</i>	<i>Flaviviridae</i>	ssRN A(+)	MK689 376	Parti al geno me	?	2004	Unknown (Schirr meier et al., 2004)	Argentina, Bangladesh, Brazil, China, Germany, India, Italy, Mexico, Thailand, Turkey, USA (Bauermann et al., 2021)
Erve virus**	<i>Erve orthonairovirus</i>	<i>Orthonairovirus</i>	<i>Nairoviridae</i>	ssRN A(-)	JF9116 97, JF9116 98, JF9116 99	Com plete geno me	?	1989	Unknown (Chast el et al., 1989)	Czech Republic, France, Germany, Netherland (Dilcher et al., 2012)
Bovine parvovirus-2**	<i>Ungulate copiparvovirus 1</i>	<i>Copiparvovirus</i>	<i>Parvoviridae</i>	ssDN A(+/-)	KT148 961	Com plete geno me	?	2001	Unknown (Allander et al., 2001)	Brazil, China, USA (Ng et al., 2015; Cibulski et al., 2016; Wang et al., 2018)
Nkolbisson virus**	<i>Nkolbisson ledantevirus</i>	<i>Ledantevirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_03 4539	Com plete geno me	?	2010	Unknown (Dacheux et al., 2010)	Cameroon (Dacheux et al., 2010)

Spring viremia of carp virus**	<i>Carp sprivivirus</i>	<i>Sprivivirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_002803	Complete genome	?	1996 (Bjorklund et al., 1996)	Unknown (Temmam et al., 2019)	Austria, China, Czech Republic, Denmark, Hungary, Iran, Italy, Mexico, Moldova, Poland, Serbia, South Korea, Ukraine, UK, USA (Marsella et al., 2021)
Maraba virus**	<i>Maraba virus</i>	<i>Vesiculovirus</i>	<i>Rhabdoviridae</i>	ssRN A(-)	NC_025255	Complete genome	?	2010 (Brun et al., 2010)	Unknown (Temmam et al., 2019)	Brazil (Brun et al., 2010)
Wellfleet Bay virus**	Unclassified	<i>Quarantaviruses</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	NC_025793, NC_025794, NC_025795, NC_025796, NC_025797, NC_025798, NC_025799	Complete genome	?	2015 (Allison et al., 2015)	Unknown (Temmam et al., 2019)	USA (Allison et al., 2015)
Araguari virus**	Unclassified	<i>Thogotovirus</i>	<i>Orthomyxoviridae</i>	ssRN A(-)	KX670389, KX670390, KX670391, KX670392, KX670393, KX670394,	Complete genome	?	1969 (Silva et al., 2005)	Unknown tick vectors (Silva et al., 2005)	Brazil (Silva et al., 2005)

KX670										
395										
Eelpout rhabdovirus**	Unclassified	Unclassified	<i>Rhabdovirid ae</i>	ssRN A(-)	KR612 230	Parti al	?	2017	Unknown (Axen et al., 2017)	Sweden (Axen et al., 2017)
Wuhan redfin culter dimarhabo dovirus**	Unclassified	Unclassified	<i>Rhabdovirid ae</i>	ssRN A(-)	MG600 013	Com plete geno me	?	2018	Unknown (Shi et al., 2018)	China (Shi et al., 2018)
Bat nairovirus/Ahun nairovirus*	Unclassified	<i>Nairovirus</i>	<i>Nairovirida e</i>	ssRN A(-)	KF1702 24	Parti al geno me	?	2014	Unknown (Dacheux et al., 2014)	France (Dacheux et al., 2014)
Essaouira virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1993	<i>O. maritimus</i> (Chastel et al., 1993)	Morocco (Chastel et al., 1993)
Huacho virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1967	<i>C. amblus</i> (Belaganahalli et al., 2015)	Peru (Belaganahalli et al., 2015)
Kala Iris virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1993	<i>O. maritimus</i> (Chastel et al., 1993)	Morocco (Chastel et al., 1993)
Mono Lake virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1988	<i>A. cooleyi</i> (Calisher et al., 1988)	USA (Calisher et al., 1988)
Sixgun city virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1988	<i>A. cooleyi</i> (Calisher et al., 1988)	USA (Calisher et al., 1988)
Ellidaey virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1986	<i>I. uriae</i> (Moss et al., 1986)	Iceland (Ellidaey island) (Moss et al., 1986)

Foula virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1986 (Nuttal l et al., 1986)	<i>I. uriae</i> (Nuttall et al., 1986)	Scotland (Shetland Islands) (Nuttall et al., 1986)
Grimsey virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1986 (Moss et al., 1986)	<i>I. uriae</i> (Moss et al., 1986)	Iceland (Grimsey island) (Moss et al., 1986)
Inner Farne Island virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1986 (Nuttal l et al., 1986)	<i>I. uriae</i> (Nuttall et al., 1986)	England (Nuttall et al., 1986)
Mykines virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1978 (Main et al., 1978)	<i>I. uriae</i> (Main et al., 1978)	Denmark (Faroe Islands) (Main et al., 1978)
Kao Shuan virus**	Unclassified	Unclassified	Unclassified	Unkn own	Unavai lable	Not availa ble	?	1989 (Mous sa et al., 1989)	<i>A. robertsi</i> (Moussa et al., 1989)	Indonesia, Taiwan (Moussa et al., 1989)
Pretoria virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1975 (Conve rse et al., 1975)	<i>A. africanum</i> (Converse et al., 1975)	South Africa (Converse et al., 1975)
Puffin Island virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1983 (Gould et al., 1983)	<i>O. maritimus</i> (Gould et al., 1983)	Puffin Island (Gould et al., 1983)
Seletar virus**	Unclassified	Unclassified	Unclassified	Unkn own	Not availab le	Not availa ble	?	1961 (Shi et al., 2018)	<i>B. microplus</i> (Shi et al., 2018)	Malaysia, Singapore (Shi et al., 2018)

* *Amblyomma dissimile* mivirus, Nuomin virus, and Granville quaranjavirus were later added tick-borne viruses which were not included in the original tick virus database.

** Viruses with unknown tick vectors or that sequences unavailable.

Acronyms: *Argas* (A.); *Amblyomma* (Am.); *Boophilus* (B.); *Dermacentor* (D.); *Haemaphysalis* (H.); *Hyalomma* (Hy.); *Ixodes* (I.); *Ornithodoros* (O.); *Otobius* (Ot.); *Rhipicephalus* (R.).

Appendix Table 2. Putative novel RNV viral contigs identified in this study.

Putative novel viral contig	Genbank ID	Tick species	Provisional family	Genome structure	Sequence length (nt)	Closest BLASTn match (e-value 0.005)	Sequence identity (%)	Notes	Reference
Alphatetra-like tick virus 1	GIXL01013119.1	<i>Ixodes ricinus</i>	Alphatetraviridae	ssRNA(+)	5496	Bulatov virus (MT025173.1)	78	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif, nucleoside triphosphate hydrolase (SSF52540), viral (Superfamily 1) RNA helicase (PF01443) and viral methyltransferase 3 (PF01660) motifs.	Trentalman <i>et al.</i> 2020, 10.1038/s41598-020-76268-y
Alphatetra-like tick virus 2	GBXQ01012426.1	<i>Ixodes persulcatus</i>	Alphatetraviridae	ssRNA(+)	1056	Vovk virus (MN830235.1)	81	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif.	Zhang 2014, Unpublished
Alphatetra-like tick virus 3	GIXP02005464.1	<i>Ornithodoros moubata</i>	Alphatetraviridae	ssRNA(+)	5452	Bulatov virus (MT025173.1)	86	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif, nucleoside triphosphate hydrolase (SSF52540), viral (Superfamily 1) RNA helicase (PF01443) and viral methyltransferase 3 (PF01660) motifs.	Oleaga <i>et al.</i> 2021, 10.1371/journal.pntd.009105
Alphatetra-like tick virus 4	GFJQ02007921.1	<i>Ornithodoros moubata</i>	Alphatetraviridae	ssRNA(+)	3873	Bulatov virus (MT025173.1)	67	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif, nucleoside triphosphate hydrolase (SSF52540) and viral (Superfamily 1) RNA helicase (PF01443) motifs.	Oleaga <i>et al.</i> 2017, 10.1016/j.ttbdis.2017.05.002
Alphatetra-like tick virus 5	GEMR01004364.1	<i>Rhipicephalus microplus</i>	Alphatetraviridae	ssRNA(+)	1488	Hepelivirales sp. (MW722078.1)	73	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif.	Munoz <i>et al.</i> 2017, 10.1371/journal.pone.0172326
Orthomyxo-like tick virus 1	HACP01027211 (HACW01024387.1)	<i>Rhipicephalus sanguineus</i>	Orthomyxoviridae	ssRNA(-)	2136	Zambezi tick virus 1 (MH267793.1)	77	One putative ORF; predicted protein contains homologs of Influenza RdRp subunit PB1 (PF00602) motif.	De Marco <i>et al.</i> 2015, Unpublished
Orthomyxo-like tick virus 2	HACP01022575.1	<i>Rhipicephalus sanguineus</i>	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (MH267793.1)	77	One putative ORF; predicted protein contains homologs of Influenza RdRp subunit PB1 (PF00602) motif.	De Marco <i>et al.</i> 2015, Unpublished
Orthomyxo-like tick virus 3	HACW01018819.1	<i>Rhipicephalus sanguineus</i>	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (MH267793.1)	77	One putative ORF; predicted protein contains homologs of Influenza RdRp subunit PB1 (PF00602) motif.	De Marco <i>et al.</i> 2015, Unpublished
Orthomyxo-like tick virus 4	GIIA01018702.1	<i>Rhipicephalus haemaphysalis oides</i>	Orthomyxoviridae	ssRNA(-)	2357	Zambezi tick virus 1 (MH267793.1)	77	One putative ORF; predicted protein contains homologs of	Wang <i>et al.</i> 2020, 10.3389/fcimb.2020.0093

									Influenza RdRp subunit PB1 (PF00602) motif.		
Chu-like tick virus 1	GGIX01201876 .1	<i>Ixodes</i> <i>scapularis</i>	Chuviridae	ssRNA(-)	728	Bole tick virus 3 (MH688550. 1)	87	One predicted contains Mononegavirales (PF00946) motif.	putative protein homologs of RdRp	ORF; Unpublished	Robertson 2016,

Appendix Table 3. Putative novel RNA viral contigs that represent defective viruses.

SRA project ID	Tick species	Provisional family	Genome structure	Sequence length (nt)	Closest BLASTn match (e-value 0.005)	Sequence identity (%)	Reference
SRR10549473.54432.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	4383	Bole tick virus 3 (MH688550.1)	84	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.681872.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	4528	Bole tick virus 3 (MH688550.1)	82	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.681877.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	4420	Bole tick virus 3 (MH688550.1)	84	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.681878.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	4440	Bole tick virus 3 (MH688550.1)	86	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.779074.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5286	Bole tick virus 3 (MH688550.1)	84	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.779079.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5379	Bole tick virus 3 (MH688550.1)	85	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.779081.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5334	Bole tick virus 3 (MH688550.1)	83	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.1447289.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5272	Bole tick virus 3 (MH688550.1)	85	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.1447293.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5001	Bole tick virus 3 (MH688550.1)	87	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.2865317.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5556	Bole tick virus 3 (MH688550.1)	83	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.2865320.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	5643	Bole tick virus 3 (MH688550.1)	87	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598504.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	8170	Bole tick virus 3 (MH688550.1)	88	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598510.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	8206	Bole tick virus 3 (MH688550.1)	87	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598511.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	8182	Bole tick virus 3 (MH688550.1)	85	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.7000060.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	4986	Bole tick virus 3 (MH688550.1)	84	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.10341027.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	2448	Bole tick virus 3 (MH688550.1)	86	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.10526706.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	6273	Bole tick virus 3 (MH688550.1)	87	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR10549473.10526708.1	<i>Hy. asiaticum</i>	<i>Chuviridae</i>	ssRNA(-)	6276	Nuomin virus (MW029964.1)	78	Yuan <i>et al.</i> 2020, 10.1016/j.jip.2020.107481
SRR17281102.635386.1	<i>I. scapularis</i>	<i>Chuviridae</i>	ssRNA(-)	1390	Suffolk virus (NC_028243.1)	78	University of Minnesota 2021, Unpublished



Appendix Table 4. DNA viral contigs found after bioinformatic checking.

WGS project ID	Tick species	Genome structure	Sequence length (bp)	Predicted protein	Reference
GIXP02029293.1	<i>Ornithodoros moubata</i>	dsDNA	2232	DdRp subunit 3 (encoded by <i>H359L</i>); ATP-dependent RNA helicase (encoded by <i>Q706L</i>); ATP-dependent RNA helicase (encoded by <i>QP509L</i>)	Oleaga <i>et al.</i> 2021, 10.1371/journal.pntd.0009105
GIXP02006837.1	<i>Ornithodoros moubata</i>	dsDNA	1450	DdRp subunit 3 (encoded by <i>H359L</i>); Uncharacterized protein (encoded by <i>H171R</i>)	Oleaga <i>et al.</i> 2021, 10.1371/journal.pntd.0009105
CAJHNL01000000 2.1	<i>Ornithodoros porcinus</i>	dsDNA	7421	DdRp subunit 2 (encoded by <i>EP1242L</i>); Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 3.1	<i>Ornithodoros porcinus</i>	dsDNA	6757	Transcription factor SII homolog (encoded by <i>I243L</i>); p1226R; RPB7 homolog; Uncharacterized protein (encoded by <i>D339L</i>); Uncharacterized protein (encoded by <i>D129L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 4.1	<i>Ornithodoros porcinus</i>	dsDNA	6577	Primase (encoded by <i>C962R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 5.1	<i>Ornithodoros porcinus</i>	dsDNA	3455	TATA-binding protein (encoded by <i>B263R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 6.1	<i>Ornithodoros porcinus</i>	dsDNA	3089	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 7.1	<i>Ornithodoros porcinus</i>	dsDNA	1557	DdDp (encoded by <i>G1211R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNL01000000 8.1	<i>Ornithodoros porcinus</i>	dsDNA	629	Ribonucleotide reductase large subunit (encoded by <i>F778R</i>); Uncharacterized protein p360 15R	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000000 2.1	<i>Ornithodoros moubata</i>	dsDNA	7383	DdRp subunit 2 (encoded by <i>EP1242L</i>); Ribonucleotide reductase large subunit (encoded by <i>F778R</i>); Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000000 4.1	<i>Ornithodoros moubata</i>	dsDNA	670	DdRp subunit 3 (encoded by <i>H359L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000000 5.1	<i>Ornithodoros moubata</i>	dsDNA	5156	Viral histone-like protein (encoded by <i>A104R</i>); Inhibitor of apoptosis protein (encoded by <i>A224L</i>); Thymidylate kinase (encoded by <i>A240L</i>); Uncharacterized protein (encoded by <i>A151R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000000 6.1	<i>Ornithodoros moubata</i>	dsDNA	3634	DdRp subunit 3 (encoded by <i>H359L</i>); Uncharacterized protein <i>CP123L</i> ; ATP-dependent RNA helicase (encoded by <i>QP509L</i>); DNA topoisomerase 2 (encoded by <i>P1192R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000000 7.1	<i>Ornithodoros moubata</i>	dsDNA	2713	Early transcription factor large subunit (encoded by <i>D1133L</i>); Uncharacterized protein (encoded by <i>H124R</i>); Uncharacterized protein (encoded by <i>H171R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNP01000001 7.1	<i>Ornithodoros moubata</i>	dsDNA	1007	Primase (encoded by <i>C962R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNQ0100000 10.1	<i>Ornithodoros moubata</i>	dsDNA	636	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNQ0100000 14.1	<i>Ornithodoros moubata</i>	dsDNA	679	DdRp subunit 2 (encoded by <i>EP1242L</i>); Ribonucleotide reductase large subunit (encoded by <i>F778R</i>); Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNQ0100000 15.1	<i>Ornithodoros moubata</i>	dsDNA	1193	Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNQ0100000 16.1	<i>Ornithodoros moubata</i>	dsDNA	1697	DdRp subunit 2 (encoded by <i>EP1242L</i>); Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNR01000000 4.1	<i>Ornithodoros moubata</i>	dsDNA	16841	DdRp subunit 2 (encoded by <i>EP1242L</i>); Ribonucleotide reductase large subunit (encoded by <i>F778R</i>); Helicase (encoded by <i>F1055L</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNR01000000 5.1	<i>Ornithodoros moubata</i>	dsDNA	15286	TATA-binding protein (encoded by <i>B263R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6
CAJHNR01000000 6.1	<i>Ornithodoros moubata</i>	dsDNA	13138	TATA-binding protein (encoded by <i>B263R</i>)	Forth <i>et al.</i> 2020, 10.1186/s12915-020-00865-6

CAJHNR01000001 1.1	<i>Ornithodoros moubata</i>	dsDNA	8352	Helicase (encoded by <i>A859L</i>); Uncharacterized protein p360 15R; Uncharacterized protein 5ELp28; IκB-like protein (encoded by <i>A238L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 3.1	<i>Ornithodoros moubata</i>	dsDNA	7718	Early transcription factor large subunit (encoded by <i>D1133L</i>); DdRp subunit 3 (encoded by <i>H359L</i>); Uncharacterized protein H171R	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 4.1	<i>Ornithodoros moubata</i>	dsDNA	7045	TATA-binding protein (encoded by <i>B263R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 5.1	<i>Ornithodoros moubata</i>	dsDNA	6370	TATA-binding protein (encoded by <i>B263R</i>); Early transcription factor large subunit (encoded by <i>G1340L</i>); Primase (encoded by <i>C962R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 6.1	<i>Ornithodoros moubata</i>	dsDNA	5808	TATA-binding protein (encoded by <i>B263R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 7.1	<i>Ornithodoros moubata</i>	dsDNA	5688	TATA-binding protein (encoded by <i>B263R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 8.1	<i>Ornithodoros moubata</i>	dsDNA	5489	DdRp subunit 3 (encoded by <i>H359L</i>); Uncharacterized protein (encoded by <i>CP123L</i>); DNA topoisomerase II (encoded by <i>P1192R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000001 9.1	<i>Ornithodoros moubata</i>	dsDNA	5396	Uncharacterized protein p360 15R	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 0.1	<i>Ornithodoros moubata</i>	dsDNA	5152	Histone-like protein (encoded by <i>A104R</i>); Inhibitor of apoptosis protein (encoded by <i>A224L</i>); Thymidylate kinase (encoded by <i>A240L</i>); Uncharacterized protein (encoded by <i>A151R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 1.1	<i>Ornithodoros moubata</i>	dsDNA	4920	DdRp subunit 10 (encoded by <i>CP80R</i>); Uncharacterized protein (encoded by <i>CP312R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 3.1	<i>Ornithodoros moubata</i>	dsDNA	4152	Primase (encoded by <i>C962R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 4.1	<i>Ornithodoros moubata</i>	dsDNA	3824	DdRp subunit 2 (encoded by <i>EP1242L</i>); Transmembrane protein (encoded by <i>EP84R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 5.1	<i>Ornithodoros moubata</i>	dsDNA	3339	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 6.1	<i>Ornithodoros moubata</i>	dsDNA	2712	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 7.1	<i>Ornithodoros moubata</i>	dsDNA	2653	Putative poly(A) polymerase catalytic subunit (encoded by <i>C475L</i>); Primase (encoded by <i>C962R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 8.1	<i>Ornithodoros moubata</i>	dsDNA	2475	DdRp subunit 3 (encoded by <i>H359L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000002 9.1	<i>Ornithodoros moubata</i>	dsDNA	2196	Ribonucleotide reductase large subunit (encoded by <i>F778R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000003 0.1	<i>Ornithodoros moubata</i>	dsDNA	2179	Uncharacterized protein (encoded by <i>CP123L</i>); mRNA-capping enzyme (encoded by <i>NP868R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR01000003 2.1	<i>Ornithodoros moubata</i>	dsDNA	1763	Ribonucleotide reductase large subunit (encoded by <i>F778R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNS01000002 6.1	<i>Ornithodoros moubata</i>	dsDNA	1078	Helicase (encoded by <i>F1055L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000000 2.1	<i>Ornithodoros porcinus</i>	dsDNA	3380	DdRp subunit 2 (encoded by <i>EP1242L</i>); Helicase (encoded by <i>F1055L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000000 3.1	<i>Ornithodoros porcinus</i>	dsDNA	641	Ribonucleotide reductase large subunit (encoded by <i>F778R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000000 4.1	<i>Ornithodoros porcinus</i>	dsDNA	1803	TATA-binding protein (encoded by <i>B263R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000000 9.1	<i>Ornithodoros porcinus</i>	dsDNA	776	Transcription factor S-II-related protein (encoded by <i>I243L</i>); Late protein (encoded by <i>I226R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000001 1.1	<i>Ornithodoros porcinus</i>	dsDNA	2551	Primase (encoded by <i>C962R</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU01000001 4.1	<i>Ornithodoros porcinus</i>	dsDNA	3100	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV01000000 2.1	<i>Ornithodoros porcinus</i>	dsDNA	4758	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6

CAJHNV01000000 4.1	<i>Ornithodoros porcinus</i>	dsDNA	3378	Transcription factor SII homolog (encoded by <i>I243L</i>); Late protein (encoded by <i>I226R</i>); Uncharacterized protein (encoded by <i>D79L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV01000000 5.1	<i>Ornithodoros porcinus</i>	dsDNA	2605	DdRp subunit 2 (encoded by <i>EP1242L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV01000000 7.1	<i>Ornithodoros porcinus</i>	dsDNA	777	Transcription factor SII homolog (encoded by <i>I243L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV01000000 16.1	<i>Ornithodoros moubata</i>	dsDNA	1078	Helicase (encoded by <i>F1055L</i>)	Forth et al. 2020, 10.1186/s12915-020-00865-6

Appendix Table 5. GenBank ID of viruses phylogenetically related to the putative novel viral contigs. Zoonotic risks of virus sequences (in GenBank format) were predicted using the GCB model.

Putative novel viral contigs	Relative viral species	GenBank ID	
Alphatetra-like viral contigs	<i>Nudaurelia capensis</i>	NC_001990.1	
	<i>beta virus</i>	NC_005898.1; NC_005899.1	
	<i>Helicoverpa armigera stunt virus</i>	NC_001981.1; NC_001982.1	
Orthomyxo-like viral contigs	<i>Wellfleet Bay virus</i>	NC_025798.1; NC_025797.1; NC_025796.1; NC_025795.1; NC_025794.1; NC_025793.1; NC_025799.1	
	<i>Araguari virus</i>	KX670389.1; KX670390.1; KX670391.1; KX670392.1; KX670393.1; KX670394.1; KX670395.1	
	<i>Johnston Atoll quaranjavirus</i>	NC_052931.1; NC_052930.1; NC_052929.1; NC_052928.1; NC_052927.1; NC_052926.1; NC_052925.1	
	<i>Lake Chad virus</i>	NC_052682.1; NC_052686.1; NC_052685.1; NC_052684.1; NC_052683.1; NC_052681.1; NC_052680.1	
	<i>Tjuloc virus</i>	JQ928941.1; JQ928942.1; JQ928943.1; JQ928944.1; JQ928945.1; JQ928946.1; MT774252.1	
	<i>Quaranfil quaranjavirus</i>	NC_038821.1; NC_038822.1; NC_038820.1; NC_038819.1; NC_038818.1; NC_038817.1	
	Chu-like viral contigs	<i>Mivirus suffolkense</i>	NC_028243

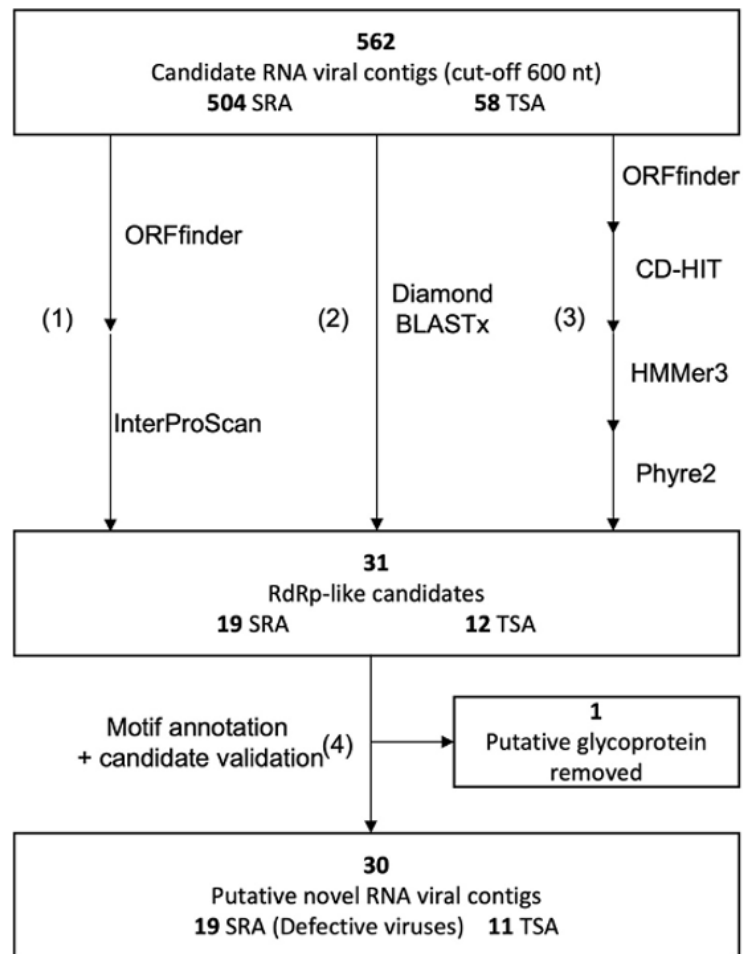
Appendix Table 6. Zoonotic ranking of 136 known tick-borne viruses with complete genomes. Zoonotic risks of virus sequences (in GenBank format) were predicted using the GCB model.

Virus name	Predicted probability mean	Predicted probability lower	Predicted probability upper	Rank	Priority
Tick-borne encephalitis virus	0.777	0.446	0.946	1	Very high
Omsk hemorrhagic fever virus	0.739	0.443	0.951	2	Very high
Powassan virus	0.695	0.288	0.920	3	High
Isfahan virus	0.677	0.233	0.917	4	High
Isfahan virus	0.677	0.233	0.917	4	High
Uukuniemi virus	0.676	0.262	0.944	5	High
Louping ill virus	0.668	0.288	0.890	6	High
Langat virus	0.667	0.339	0.917	7	Very high
Thogoto virus	0.642	0.266	0.899	8	High
Lonestar tick chuvirus 1	0.619	0.379	0.857	9	Very high
Crimean-Congo hemorrhagic fever virus	0.609	0.249	0.875	10	High
Grotenhout virus	0.601	0.389	0.808	11	Very high
Severe fever with thrombocytopenia syndrome virus	0.596	0.273	0.849	12	High
Kasokero virus	0.580	0.180	0.837	13	High
Colorado tick fever virus	0.562	0.121	0.854	14	High
Quaranfil virus	0.561	0.128	0.863	15	High
Great Island virus	0.550	0.115	0.832	16	High
Dugbe virus	0.540	0.157	0.825	17	High
Johnston Atoll virus	0.513	0.311	0.802	18	Very high
Dabieshan tick virus	0.505	0.289	0.747	19	High
Taggert virus	0.503	0.318	0.802	20	Very high
Blacklegged tick phlebovirus 1	0.490	0.271	0.711	21	High
Deer tick virus	0.486	0.275	0.703	22	High
Tacheng tick virus 2	0.482	0.241	0.774	23	High
Lihan tick virus	0.481	0.264	0.730	24	High
Karshi virus	0.481	0.266	0.954	25	High
Alkhumra hemorrhagic fever virus	0.469	0.234	0.736	26	High
Yongjia tick virus 1	0.441	0.192	0.680	27	High
American dog tick phlebovirus	0.438	0.218	0.659	28	High
Wenzhou tick virus	0.425	0.234	0.710	29	High
Tamdy virus	0.413	0.227	0.642	30	High

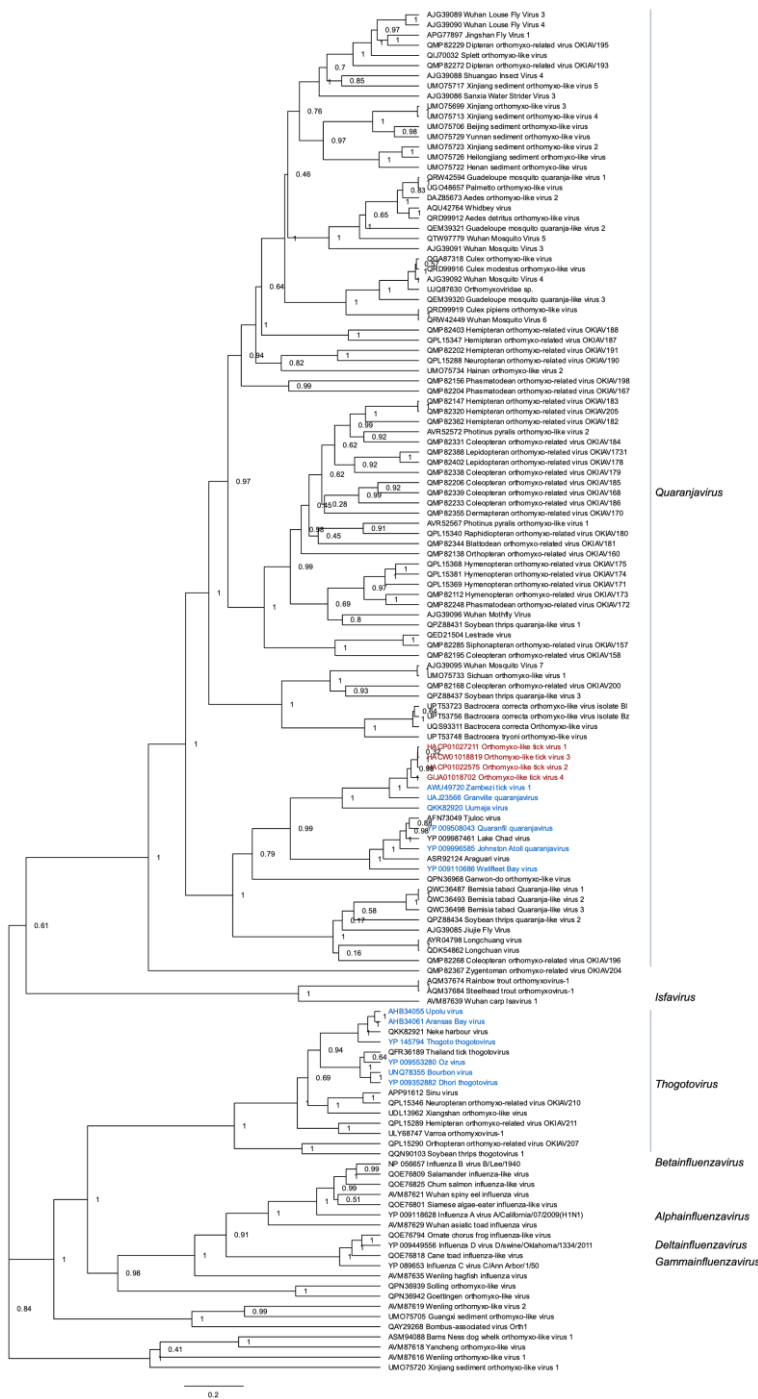
Blacklegged rhabdovirus 1	tick	0.411	0.223	0.638	31	High
Tacheng tick virus 8		0.404	0.210	0.692	32	High
Jingmen tick virus		0.401	0.219	0.663	33	High
South Bay virus		0.395	0.210	0.630	34	High
Ngari virus		0.393	0.214	0.624	35	High
Kaisodi virus		0.392	0.208	0.590	36	High
Kupe virus		0.391	0.160	0.642	37	High
Lone star densovirus 1	tick	0.391	0.221	0.654	38	High
Blacklegged phlebovirus 3	tick	0.371	0.195	0.640	39	High
Pacific coast nairovirus	tick	0.370	0.197	0.656	40	High
Clo Mor virus		0.364	0.149	0.600	41	High
Sakhalin virus		0.345	0.177	0.657	42	High
Tyuleniy virus		0.340	0.160	0.739	43	High
Meram virus		0.335	0.196	0.574	44	High
Jos virus		0.333	0.159	0.579	45	High
Midway virus		0.327	0.163	0.609	46	High
lone star virus		0.326	0.166	0.567	47	High
Norway phlebovirus 1		0.323	0.138	0.559	48	High
Tofla virus		0.323	0.198	0.601	49	High
Tacheng tick virus 7		0.318	0.175	0.511	50	High
New Minto virus		0.318	0.168	0.526	51	High
Bourbon virus		0.311	0.164	0.497	52	High
Suffolk virus		0.309	0.151	0.562	53	High
Silverwater virus		0.307	0.156	0.537	54	High
Heartland virus		0.305	0.135	0.520	55	High
Dera Ghazi Khan virus		0.299	0.150	0.493	56	High
Hunter Island virus		0.299	0.153	0.528	57	High
Great Saltee virus		0.299	0.168	0.543	58	High
Bhanja virus		0.298	0.161	0.446	59	High
Blanchseco virus		0.295	0.153	0.500	60	High
Thailand thogotovirus	tick	0.286	0.135	0.436	61	Medium
Wuhan tick virus 1		0.280	0.145	0.461	62	Medium
Gadgets Gully virus		0.277	0.152	0.583	63	Medium
Soldado virus		0.277	0.164	0.450	64	Medium
Abu Hammad virus		0.275	0.138	0.471	65	Medium
Kadam virus		0.275	0.134	0.602	66	Medium
Tacheng tick virus 1		0.272	0.134	0.514	67	Medium
Zirqa virus		0.269	0.146	0.439	68	Medium
Bole tick virus 2		0.267	0.141	0.466	69	Medium
Qalyub virus		0.264	0.112	0.444	70	Medium

Avalon virus	0.259	0.119	0.449	71	Medium
Genoa virus	0.259	0.131	0.430	72	Medium
Upolu virus	0.258	0.130	0.419	73	Medium
Blacklegged tick chuvirus 2	0.258	0.137	0.453	74	Medium
Long Island tick rhabdovirus	0.257	0.118	0.473	75	Medium
Taishun tick virus	0.256	0.131	0.394	76	Medium
Kemerovo virus	0.255	0.100	0.425	77	Medium
Wuhan tick virus 2	0.253	0.133	0.460	78	Medium
Raza virus	0.250	0.139	0.432	79	Medium
Tillamook virus	0.248	0.118	0.495	80	Medium
New Kent County virus	0.246	0.132	0.359	81	Medium
Issyk-kul virus	0.235	0.105	0.343	82	Medium
Zahedan rhabdovirus	0.234	0.119	0.386	83	Medium
Tacheng tick virus 3	0.232	0.106	0.382	84	Medium
Tunis virus	0.232	0.105	0.369	85	Medium
Tacheng tick virus 5	0.232	0.131	0.359	86	Medium
Sawgrass virus	0.231	0.122	0.403	87	Medium
Changping tick virus 2	0.226	0.111	0.410	88	Medium
Nyamanini virus	0.222	0.123	0.394	89	Medium
Dhori virus	0.222	0.114	0.498	90	Medium
Vinegar Hill virus	0.221	0.118	0.367	91	Medium
Huangpi tick virus 3	0.217	0.106	0.347	92	Medium
Huangpi tick virus 1	0.216	0.102	0.399	93	Medium
Meaban virus	0.216	0.100	0.445	94	Medium
Hazara virus	0.216	0.125	0.419	95	Medium
Punta Salinas virus	0.212	0.102	0.433	96	Medium
Wuhan mivirus	0.212	0.108	0.382	97	Medium
Laurel Lake virus	0.209	0.085	0.324	98	Medium
Canine circovirus	0.208	0.101	0.361	99	Medium
Matruh virus	0.203	0.111	0.311	100	Medium
Connecticut virus	0.201	0.098	0.376	101	Medium
Sapphire II virus	0.197	0.098	0.319	102	Medium
Tacheng tick virus 6	0.197	0.093	0.368	103	Medium
Changping tick virus 3	0.195	0.085	0.331	104	Medium
Saumarez Reef virus	0.194	0.098	0.371	105	Medium
Abu Mina virus	0.193	0.101	0.355	106	Medium
Tarumizu tick virus	0.192	0.104	0.339	107	Medium
Eyach virus	0.192	0.103	0.362	108	Medium
Barur virus	0.191	0.091	0.347	109	Medium
Bahig virus	0.190	0.092	0.324	110	Medium
Sierra Nevada virus	0.186	0.080	0.329	111	Medium

Wad Medani virus	0.186	0.105	0.401	112	Medium
Kundal virus	0.184	0.095	0.312	113	Medium
Chobar Gorge virus	0.178	0.096	0.337	114	Medium
African swine fever virus	0.175	0.082	0.311	115	Medium
Farallon virus	0.175	0.088	0.312	116	Medium
Oz virus	0.174	0.089	0.283	117	Low
Nairobi sheep disease virus	0.173	0.091	0.324	118	Medium
Keterah virus	0.169	0.089	0.314	119	Medium
Estero Real virus	0.167	0.087	0.315	120	Medium
Geran virus	0.165	0.082	0.282	121	Low
Bole tick virus 4	0.164	0.081	0.315	122	Medium
Caspiy virus	0.164	0.081	0.281	123	Low
Burana virus	0.163	0.080	0.279	124	Low
Artashat virus	0.162	0.085	0.278	125	Low
Hughes virus	0.161	0.085	0.267	126	Low
Tacheng tick virus 4	0.158	0.071	0.257	127	Low
St Croix River virus	0.153	0.076	0.264	128	Low
Bandia virus	0.148	0.077	0.245	129	Low
Chenuda virus	0.146	0.079	0.226	130	Low
Kolente virus	0.142	0.072	0.241	131	Low
Yongjia tick virus 2	0.132	0.057	0.219	132	Low
Bole tick virus 3	0.131	0.051	0.231	133	Low
Avian-like circovirus	0.126	0.056	0.216	134	Low
Fennes virus	0.077	0.025	0.157	135	Low

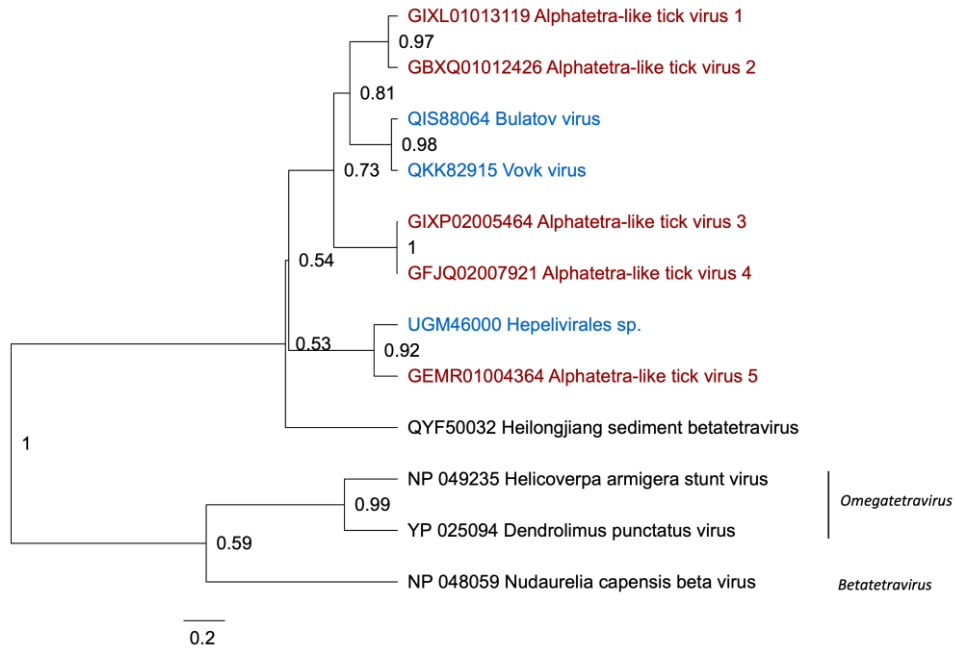


Appendix Figure 1. Workflow of detecting viral RNA-dependent RNA polymerase sequences. (1) ORFs were translated using ORFfinder (cut-off 200 aa). The translated sequences were predicted using the InterProScan-5.55-88.0 (--minsize 600; -goterms). (2) BLASTx using Diamond v2.0.14.152 against both non-redundant protein database and RdRp-scan database (-e 1e-5 --min-orf 600 --very-sensitive). (3) ORFs were translated using ORFfinder (cut-off 200 aa). Redundant sequences were then removed using CD-HIT v4.6.8 at 90% level of identity (-c 0.98 sequence identity threshold). Remaining sequences were scanned using HMMer3 v3.2.1 against RdRp HMM profile database (full sequence e-value 1e-06). HMM-RdRp hits were compared against PDB using Phyre2 server. In total, 31 RdRp-like candidates from SRA and TSA databases were found using RdRp-scan and InterProScan after removing duplicates. (4) RdRp motifs were mapped to candidate sequences using Geneious v2022.1. RdRp-scan database, RdRp HMM profile database, RdRp motifs database and RdRp key word lists were obtained from Charon et al. (77) (<https://github.com/JustineCharon/RdRp-scan>).

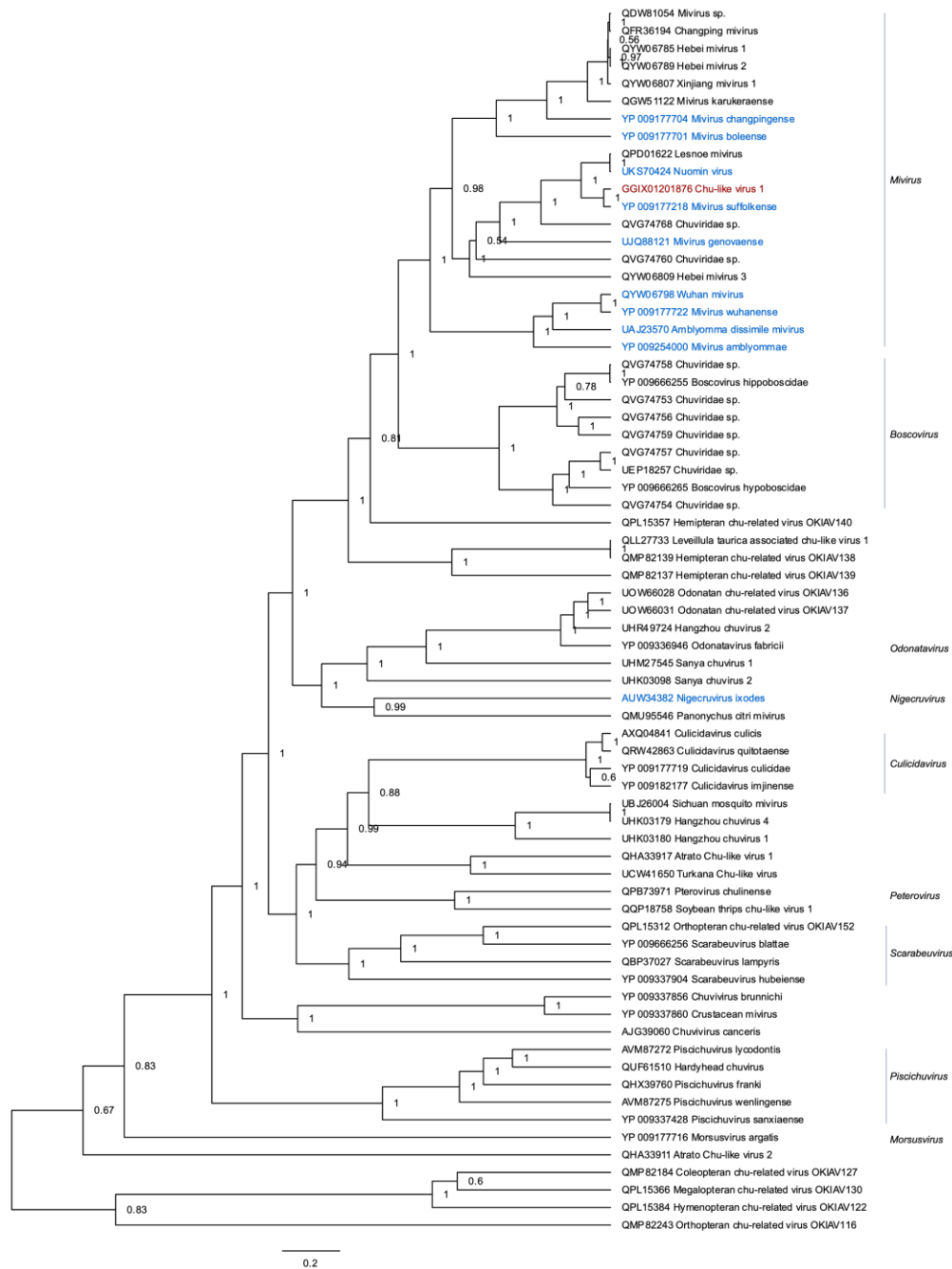


Appendix Figure 2. Phylogenetic relationship of the novel Orthomyxo-like viral contigs. Maximum clade credibility tree was inferred from the Bayesian posterior sample. Putative novel viral contigs found in the present study are shown in red, and previously known tick-borne viruses are shown in blue.





Appendix Figure 3. Phylogenetic relationship of the novel Alphetetra-like viral contigs. Maximum clade credibility tree was inferred from the Bayesian posterior sample. Putative novel viral contigs found in the present study are shown in red, and previously known tick-borne viruses are shown in blue.



Appendix Figure S4. Phylogenetic relationship of the novel Chu-like viral contigs. Maximum clade credibility tree was inferred from the Bayesian posterior sample. Putative novel viral contigs found in the present study are shown in red, and previously known tick-borne viruses are shown in blue.