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, Taggert 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 ≤ cut-off; medium: mean prediction ≤ 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., Alphatetra-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**).

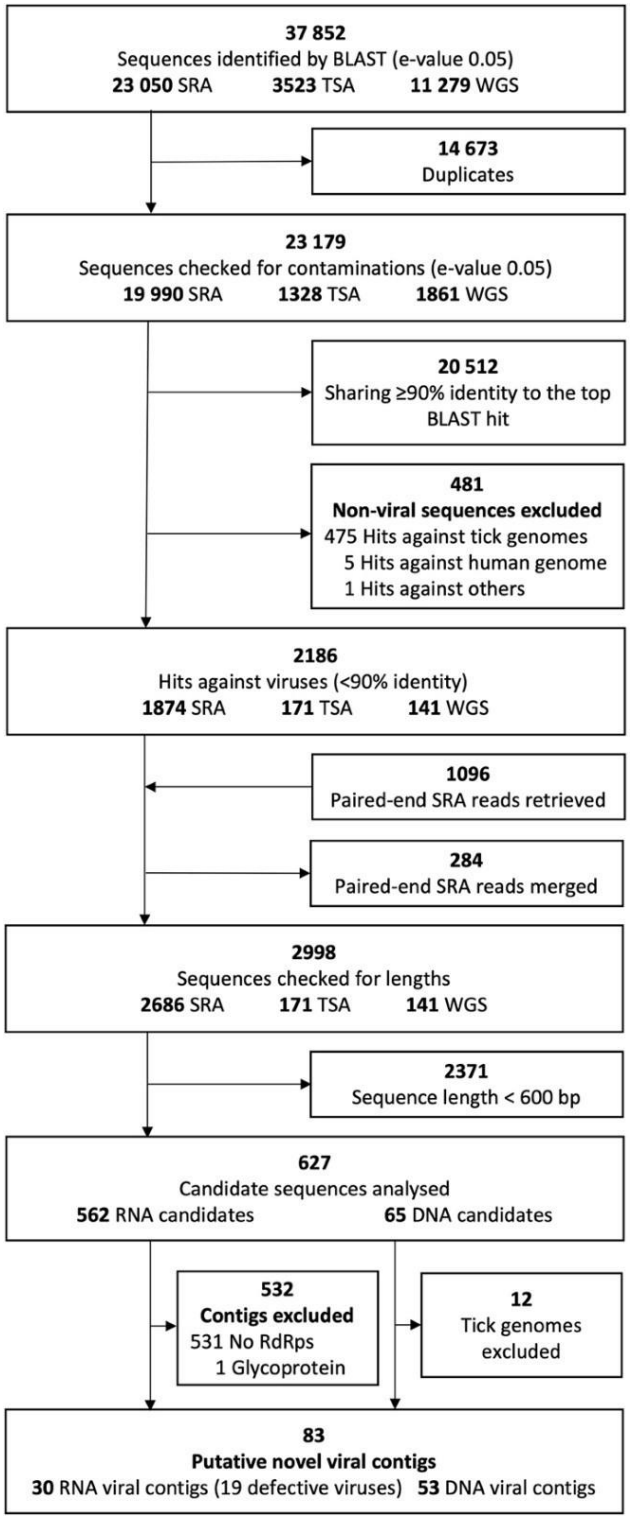

Figure 1 The workflow of identification of novel tick-associated viral contigs. Through BLAST search and curation, 53 DNA sequences (identified as African swine fever like elements) and 30 RNA

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	*Rhipicephalus sanguineus*	Italy	Orthomyxoviridae	ssRNA(-)	2136	Zambezi tick virus 1 (89)	HACP01027211.1 (HACW01024387.1)
Orthomyxo-like tick virus 2	*Rhipicephalus sanguineus*	Italy	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (73)	HACP01022575.1
Orthomyxo-like tick virus 3	*Rhipicephalus sanguineus*	Italy	Orthomyxoviridae	ssRNA(-)	1290	Zambezi tick virus 1 (88)	HACW01018819.1
Orthomyxo-like tick virus 4	*Rhipicephalus haemaphysaloides*	China	Orthomyxoviridae	ssRNA(-)	2357	Zambezi tick virus 1 (89)	GIJA01018702.1
Alphatetra-like tick virus 1	*Ixodes ricinus*	China	Alphatetraviridae	ssRNA(+)	5496	Bulatov virus (44)	GIXL01013119.1
Alphatetra-like tick virus 2	*Ixodes persulcatus*	USA	Alphatetraviridae	ssRNA(+)	1056	Vovk virus (60)	GBXQ01012426.1
Alphatetra-like tick virus 3	*Ornithodoros moubata*	Spain	Alphatetraviridae	ssRNA(+)	5452	Bulatov virus (40)	GIXP02005464.1
Alphatetra-like tick virus 4	*Ornithodoros moubata*	Spain	Alphatetraviridae	ssRNA(+)	3873	Bulatov virus (41)	GFJQ02007921.1
Alphatetra-like tick virus 5	*Rhipicephalus microplus*	USA	Alphatetraviridae	ssRNA(+)	1488	Hepelivirales sp. (80)	GEMR01004364.1
Chu-like tick virus 1	*Ixodes scapularis*	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 Quaranfil 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) Alphatetraviridae-like contigs

Members of the *Alphatetraviridae* are non-enveloped positive-sense single-stranded RNA viruses (57). The identified Alphatetra-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 *Alphatetraviridae* had been previously believed to infect predominantly moths and butterflies (57), but the recent discovery of several Alphatetra-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 Alphatetra-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 Alphatetra-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 *Alphatetraviridae* 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 Alphatetra-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	*Wellfleet Bay virus*	No known human infections	0.368	0.213-0.636	High
	Araguari virus	No known human infections	0.222	0.102-0.372	Medium
	Johnston Atoll quaranjavirus	No known human infections	0.513	0.311-0.802	Very high
	Lake Chad virus	No known human infections	0.184	0.081-0.334	Medium
	Tjuloc virus	No known human infections	0.352	0.141-0.607	High
	Quaranfil quaranjavirus	Human virus (54)	0.561	0.128-0.863	High
Alphatetra-like viral contigs	*Nudaurelia capensis beta virus*	No known human infections	0.302	0.153-0.497	High
	Dendrolimus punctatus virus	No known human infections	0.234	0.128-0.352	Medium
	Helicoverpa armigera stunt virus	No known human infections	0.243	0.135-0.387	Medium
Chu-like viral contigs	*Mivirus suffolkense*	No known human infections	0.309	0.151-0.562	High

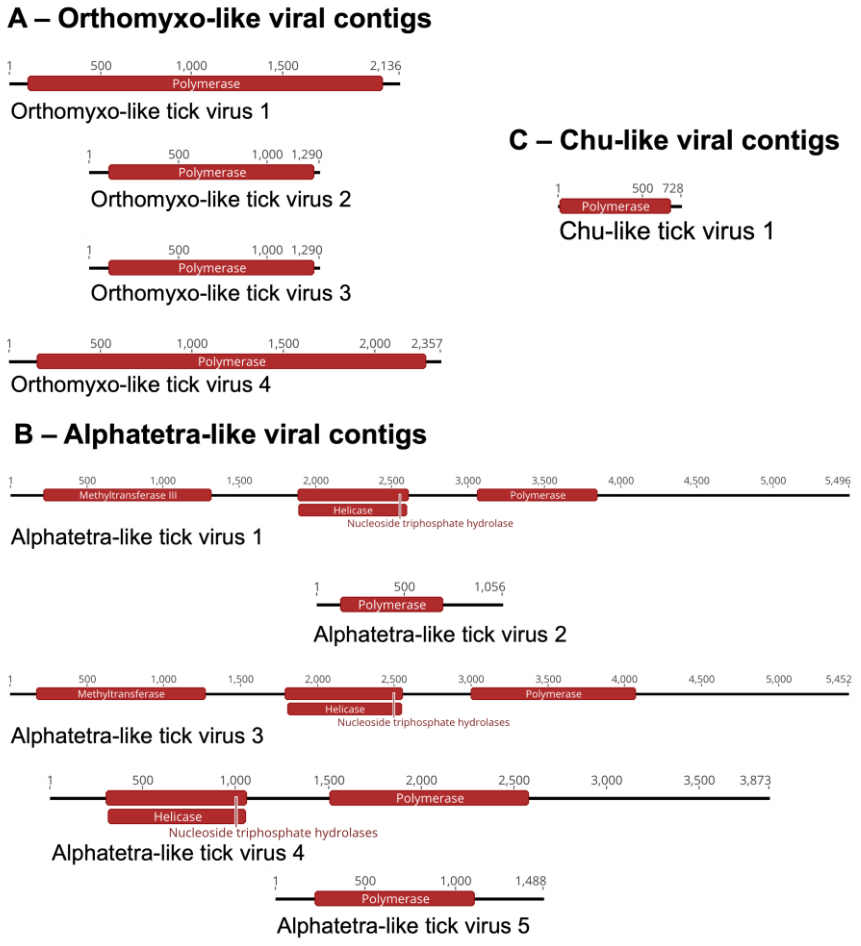

Figure 2 Genome structures of novel viral contigs.

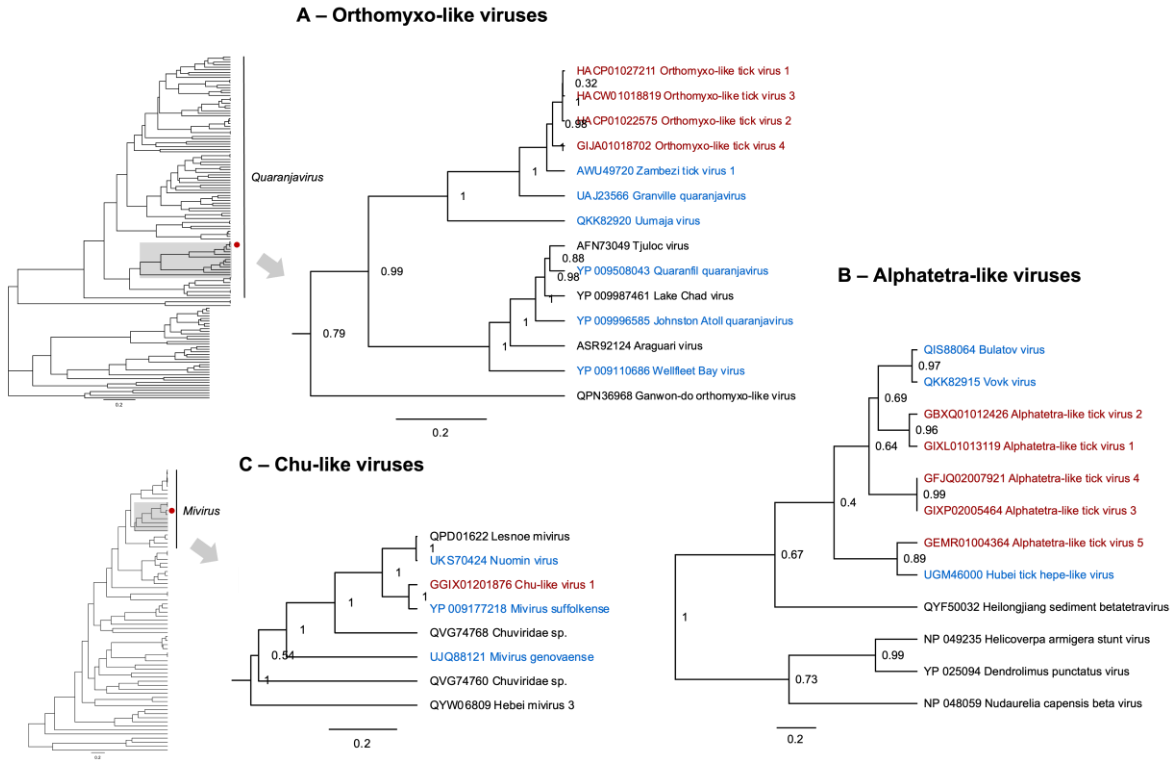

Figure 3 Phylogenetic relationship of the novel viral contigs. Maximum clade credibility trees were inferred from the Bayesian posterior sample. Posterior clade probabilities are shown at the nodes, and the scale is given in amino-acid substitutions per site. Putative novel viral contigs found in the 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, Taggert 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.

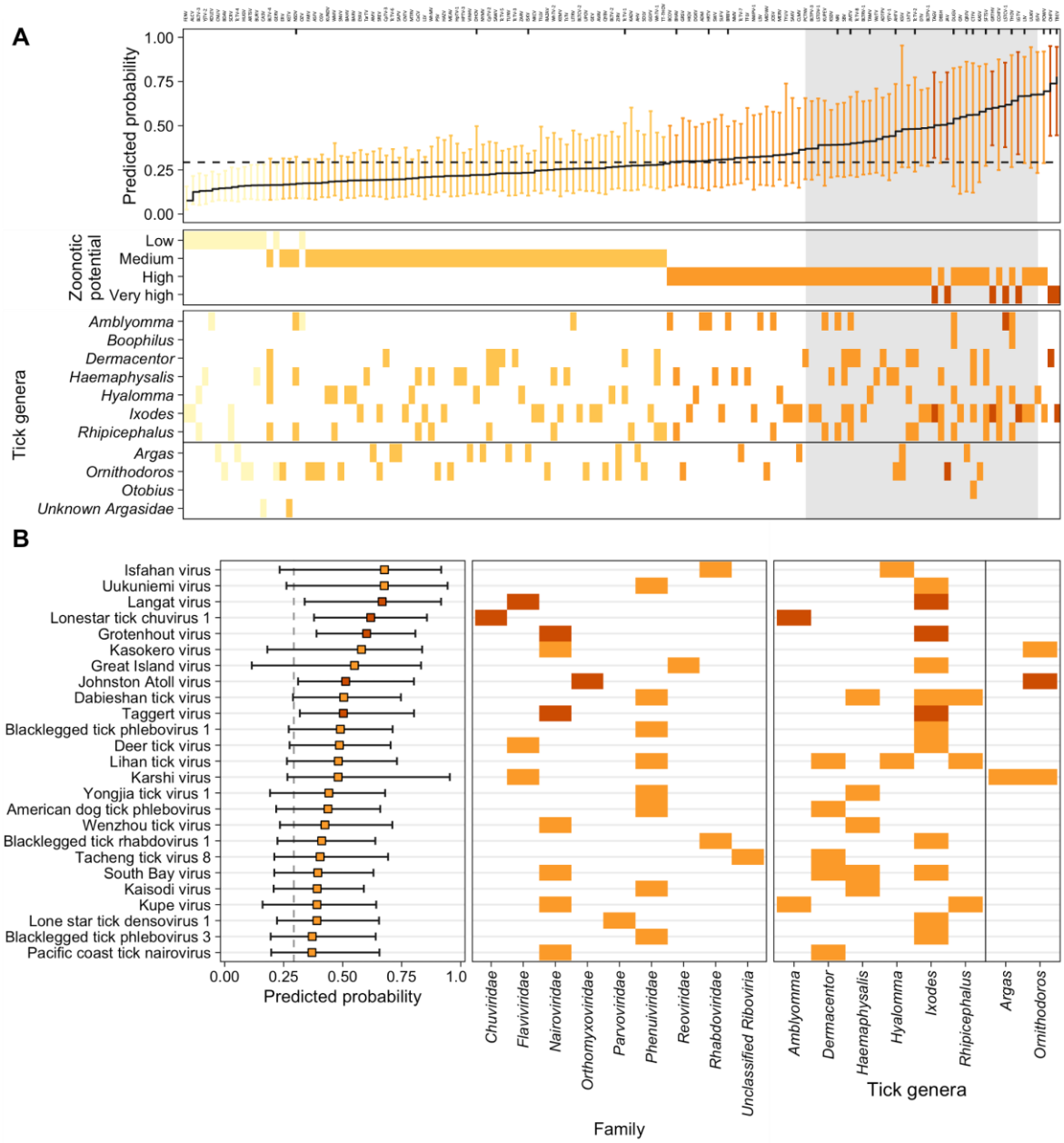

Figure 4 Predicted probability of human infection for tick viruses based on genome composition-based model. (**A**) Predicted probability of human infection for 136 tick viruses with complete genomes. Colour scale show the assigned zoonotic potential categories. Tick marks along the top edge of the first 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	Available sequence	Human infection	First description	Tick vectors	Distribution
African swine fever virus	*African swine fever virus*	*Asfivirus*	*Asfarviridae*	dsDNA	NC_044942	Complete genome	?	1921 (Montgomery et al., 1921)	*O. erraticus, O. moubata* (Shi et al., 2018)	Sub-Saharan Africa, South America, Southern Europe (Shi et al., 2018)
Canine circovirus	*Canine circovirus*	*Circovirus*	*Circoviridae*	ssDNA (+/-)	NC_020904	Complete genome	?	2012 (Kapoor et al., 2012)	*Haemaphysalis spp., Rhipicephalus spp.* (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	*Tick associated circovirus 1*	*Circovirus*	*Circoviridae*	ssDNA (+/-)	NC_030199	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Nayun tick torquevirus	Unclassified	*Thetatorquevirus*	*Anelloviridae*	ssDNA (+/-)	KP141758	Partial genome	?	2015 (Xia et al., 2015)	*Rhipicephalus* spp. (Xia et al., 2015)	China (Xia et al., 2015)
Lone star tick densovirus 1	Unclassified	Unclassified	*Parvoviridae*	ssDNA (+/-)	KX774632	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Colorado tick fever virus	*Colorado tick fever coltivirus*	*Coltivirus*	*Reoviridae*	dsRNA	NC_004191, NC_004181, NC_004182, NC_004183,	Complete genome	Y (Shi et al., 2018)	1946 (Florio et al., 1946)	*D. andersoni*, *D. albipictus*, *D. arumapertus*, D. occidentali	USA (Shi et al., 2018)

					NC_004184, NC_004185, NC_004186, NC_004187, NC_004188, NC_004180, NC_004189, NC_004190				s, *H. leporispalustris*, I. sculptus, I. spinipalpis, *Ot. lagophilus* (Shi et al., 2018)	
Eyach virus	*Eyach coltivirus*	*Coltivirus*	*Reoviridae*	dsRNA	NC_003696, NC_003697, NC_003698, NC_003699, NC_003700, NC_003701, NC_003702, NC_003703, NC_003704, NC_003705, NC_003706, NC_003707	Complete genome	?	1976 (Rehse-Kupper et al., 1976)	*I. ricinus*, *I. ventalloi* (Shi et al., 2018)	France, Germany (Shi et al., 2018)
Kundal virus	*Kundal coltivirus*	*Coltivirus*	*Reoviridae*	dsRNA	NC_055248, NC_055249, NC_055247,	Complete genome	?	2019 (Yadav et al., 2019)	*Hy. antolicum* (Yadav et al., 2019)	India (Yadav et al., 2019)

					NC_055240, NC_055250, NC_055239, NC_055242, NC_055245, NC_055241, NC_055246, NC_055243, NC_055244					
Tarumizu tick virus	*Tarumizu coltivirus*	*Coltivirus*	*Reoviridae*	dsRNA	NC_055255, NC_055254, NC_055261, NC_055259, NC_055262, NC_055251, NC_055260, NC_055258, NC_055252, NC_055257, NC_055253, NC_055256	Complete genome	?	2017 (Fujita et al., 2017)	*H. flava* (Fujita et al., 2017)	Japan (Fujita et al., 2017)
Chenuda virus	*Chenuda virus*	*Orbivirus*	*Reoviridae*	dsRNA	NC_027534, NC_027535,	Complete genome	?	1978 (Karabatsos, 1978)	*A. hermanni* (Shi et al., 2018)	Egypt, Uzbekistan (Shi et al., 2018)

					NC_027536, NC_027537, NC_027538, NC_027548, NC_027549, NC_027550, NC_027551, NC_027552					
Chobar Gorge virus	*Chobar Gorge virus*	*Orbivirus*	*Reoviridae*	dsRNA	NC_027553, NC_027554, NC_027555, NC_027556, NC_027557, NC_027558, NC_027559, NC_027560, NC_027561, NC_027562	Complete genome	?	1978 (Karabatsos, 1978)	*Ornithodoros* spp. (Shi et al., 2018)	Nepal (Shi et al., 2018)
Great Island virus	*Great Island virus*	*Orbivirus*	*Reoviridae*	dsRNA	NC_014522, NC_014523, NC_014524, NC_014525, NC_014526,	Complete genome	?	1981 (Nuttall et al., 1981)	*I. uriae* (Shi et al., 2018)	Canada (Shi et al., 2018)

					NC_014527, NC_014528, NC_014529, NC_014530, NC_014531					
Kemerovo virus	*Great Island virus*	*Orbivirus*	*Reoviridae*	dsRNA	MF939555, MF939556, MF939557, MF939558, MF939559, MF939560, MF939561, MF939562, MF939563, MF939564, KJ010787	Complete genome	?	1970 (Libikova et al., 1970)	*I. persulcatus*, *I. ricinus* (Shi et al., 2018)	Russia, Slovakia (Shi et al., 2018)
Lipovnik virus	*Great Island virus*	*Orbivirus*	*Reoviridae*	dsRNA	HM543475, HM543476, HM543477	Partial genome	?	1964 (Libikova et al., 1964)	*I. ricinus* (Shi et al., 2018)	Czech Republic, Slovakia (Shi et al., 2018)
Tribec virus	*Great Island virus*	*Orbivirus*	*Reoviridae*	dsRNA	HQ266581, HQ266582, HQ266583, HQ266584,	Partial genome	?	1964 (Libikova et al., 1964)	*H. punctata, I. ricinus* (Shi et al., 2018)	Belorussia, Italy, Slovakia (Shi et al., 2018)

					HQ266585, HQ266586, HQ266587, HQ266588, HQ266589, HQ266590					
St Croix River virus	*St Croix River virus*	*Orbivirus*	*Reoviridae*	dsRNA	NC_006006, NC_005998, NC_005999, NC_006000, NC_006001, NC_006002, NC_006003.1, NC_006004, NC_006005, NC_005997	Complete genome	?	2001 (Attoui et al., 2001)	*I. scapularis*, *R. appendiculatus* (Shi et al., 2018)	Kenya, USA (Alberdi et al., 2012)
Baku virus	Unclassified	*Orbivirus*	*Reoviridae*	dsRNA	KY023349, KY023350, KY023351, KY023352, KY023353, KY023354, KY023	Partial genome	?	1978 (Karabatsos, 1978)	*O. maritimus* (Shi et al., 2018)	Caspian Sea, Uzbekistan (Shi et al., 2018)

					355, KY023356, KY023357, KY023358					
Matucare virus	Unclassified	*Orbivirus*	*Reoviridae*	dsRNA	HQ397640	Partial genome	?	1970 (Justines et al., 1970)	*Ot. megnini (Palacios et al., 2011)*	
Okhotskiy virus	Unclassified	*Orbivirus*	*Reoviridae*	dsRNA	KY023329, KY023330, KY023331, KY023332, KY023333, KY023334, KY023335, KY023336, KY023337, KY023338, KF981623, KF981624, KF981625, KF981626, KF981627, KF981628, KF981629,	Partial genome	?	1878 (L'vov et al., 1878)	*I. uriae* (Pettersson et al., 2020)	Northern Sweden, Okhotsk (Pettersson et al., 2020)

					KF981630, KF981631, KF981632, MN830241, MN830242, MN830243, MN830244, MN830245					
Wad Medani virus	*Wad Medani virus*	*Orbivirus*	*Reoviridae*	dsRNA	NC_027533, NC_027539, NC_027540, NC_027541, NC_027542, NC_027543, NC_027544, NC_027545, NC_027546, NC_027547	Complete genome	?	1966 (Taylor et al., 1966)	*Hyalomma spp., R. sanguineus* (Shi et al., 2018)	Asia, East Africa, Jamaica (Shi et al., 2018)
Norway partiti-like virus 1	Unclassified	Unclassified	*Partitiviridae*	dsRNA	MF141076	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Lonestar tick totivirus	Unclassified	Unclassified	*Totiviridae*	dsRNA	MG647775, MZ567079	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis* (Tokarz et al., 2018)	USA (Tokarz et al., 2018)

Fennes virus	Unclassified	Unclassified	*Unclassified Riboviria*	dsRNA	MT025166, MT025167, MT025168, MT025169, MN830240	Partial genome	?	2020 (Wille et al., 2020)	*I. uriae* (Wille et al., 2020)	Antarctica (Wille et al., 2020)
Shelly Beach virus	Unclassified	Unclassified	*Unclassified Riboviria*	dsRNA	MK026600, MK026601, MK026602, MK026603, MK026604, MK026605	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Shelly headland virus	Unclassified	Unclassified	*Unclassified Riboviria*	dsRNA	OL452144, OL452150, OL452158, OL452171, OL452185, OL452194, OL452203, OL452214, OL452222, OL452151, OL452172, OL452215,	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)

OL452
223,
OL452
173,
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216,
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219,
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230,
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180,
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220,
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231,
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232,
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181,

					OL452221, OL452233, OL452182, OL452234, OL452235, MK026577, MK026581, MK026582					
Lonestar tick chuvirus 1	*Mivirus amblyommae*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_030204	Complete genome	?	2018 (Tokarz et al., 2018)	*Am. americanum (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Bole tick virus 3	*Mivirus boleense*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_028259	Complete genome	?	2015 (Li et al., 2015)	*Hy. Asiaticum, Hy. Aegyptium, R. turanicus, R. bursa (Li et al., 2015; Brinkmann et al., 2018; Ergunay et al., 2020)*	China, Turkey (Li et al., 2015; Brinkmann et al., 2018; Ergunay et al., 2020)
Changping tick virus 2	*Mivirus changpingense*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_028260	Complete genome	?	2015 (Li et al., 2015)	*Dermacentor spp., H. parva, R. sanguineus (Li et al., 2015; Temmam et al., 2019)*	China, Thailand, Turkey, Trinidad, Tobago (Li et al., 2015; Brinkmann et al., 2018; Temmam et al., 2019)

Changping tick virus 3	*Mivirus dermacentoris*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_028261	Complete genome	?	2015 (Li et al., 2015)	*Dermacentor spp. (Li et al., 2015)*	China (Li et al., 2015)
Genoa virus	*Mivirus genovaense*	*Mivirus*	*Chuviridae*	ssRNA(-)	OL452069	Complete genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Suffolk virus	*Mivirus suffolkense*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_028243	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Wuhan tick virus 2	*Mivirus wuhanense*	*Mivirus*	*Chuviridae*	ssRNA(-)	NC_028266	Complete genome	?	2015 (Li et al., 2015)	*H. longicornis, R. microplus* (Gómez et al., 2020; Xu et al., 2021)	Brazil, China, Colombia, Guadeloupe, Thailand, Trinidad, Tobago (Gomez et al., 2020; Xu et al., 2021)
Wuhan mivirus	*Wuhan mivirus*	*Mivirus*	*Chuviridae*	ssRNA(-)	MZ244267	Complete genome	?	2015 (Li et al., 2015)	*H. longicornis, R. microplus, R. sanguineus* (Sameroff et al., 2019)	China, Thailand, Trinidad and Tobago (Sameroff et al., 2019)
Tacheng tick virus 4	*Morsusvirus argatis*	*Morsusvirus*	*Chuviridae*	ssRNA(-)	NC_028263	Complete genome	?	2015 (Li et al., 2015)	*A. miniatus (Li et al., 2015)*	China (Li et al., 2015)
Blacklegged tick chuvirus 2	*Nigecruvirus ixodes*	*Nigecruvirus*	*Chuviridae*	ssRNA(-)	MF360789	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis* (Tokarz et al., 2018)	USA (Tokarz et al., 2018)
Amblyomma dissimile mivirus*	Unclassified	*Mivirus*	*Chuviridae*	ssRNA(-)	MZ502309.1	Complete genome	?	2021 (Sameroff et al., 2021)	*Am. dissimile (Sameroff et al., 2021)*	Trinidad and Tobago (Sameroff et al., 2021)
Nuomin virus*	Unclassified	Unclassified	*Chuviridae*	ssRNA(-)	MW029986.1	Partial	Y (Quan	2020 (Quan	*I. persulcatus, I.*	China (Quan et al., 2020)

						genome	et al., 2020)	et al., 2020)	*crenulatus, H. conicinna, H. longicornis (Quan et al., 2020)*	
Tacheng tick virus 6	*Tacheng arlivirus*	*Arlivirus*	*Lispiviridae*	ssRNA(-)	NC_031270	Complete genome	?	2015 (Li et al., 2015)	*A. miniatus* (Li et al., 2015)	China (Li et al., 2015)
Grotenhout virus	*Grotenhout norwavirus*	*Norwavirus*	*Nairoviridae*	ssRNA(-)	KY700684, KY700683	Complete genome	?	2017 (Vanmechelen et al., 2017)	*I. ricinus* (Vanmechelen et al., 2017)	Belgium (Vanmechelen et al., 2017)
Abu Hammad virus	*Abu Hammad orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925434, KU925435, KU925436	Complete genome	?	1976 (Darwish et al., 1976)	*A. hermanni* (Darwish et al., 1976)	Egypt (Darwish et al., 1976)
Abu Mina virus	*Abu Mina orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925437, KU925438, KU925439	Complete genome	?	1976 (Darwish et al., 1976)	*A. streptopelia* (Darwish et al., 1976)	Egypt (Darwish et al., 1976)
Artashat virus	*Artashat orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_043440, NC_043442, NC_043441	Complete genome	?	2014 (Al'khovskii et al., 2014)	*O. alactagalis* (Al'khovskii et al., 2014)	Armenia, Azerbaijan (Al'khovskii et al., 2014)
Avalon virus	*Avalon orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_040460, NC_040459, NC_040458	Complete genome	?	1976 (Main et al., 1976)	*I. uriae* (Pettersson et al., 2020)	Canada, France, Sweden (Pettersson et al., 2020)
Burana virus	*Burana orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_043439, NC_043438,	Complete genome	?	2014 (L'vov et al., 2014)	*H. punctate* (L'vov et al., 2014)	Kyrgyzstan (L'vov et al., 2014)

					NC_043437					
Chim virus	*Chim orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_043434, NC_043436, NC_043435	Complete genome	?	2014 (L'vov et al., 2014)	*O. tartakovskyi* (L'vov et al., 2014)	Uzbekistan (L'vov et al., 2014)
Crimean-Congo hemorrhagic fever virus	*Crimean-Congo hemorrhagic fever orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_005301, NC_005300, NC_005302	Complete genome	Y (Garrison et al., 2020)	1945 (Grashchenkov et al., 1945)	*Hy. asiaticum, Hy. marginatum*, *ixodid* spp., *R. rossicus* (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)
Dera Ghazi Khan virus	*Dera Ghazi Khan orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034520, NC_034510, NC_034521	Complete genome	?	1970 (Begum et al., 1970)	*Hy. dromedarii* (Begum et al., 1970)	Pakistan (Begum et al., 1970)
Dugbe virus	*Dugbe orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_004159, NC_004158, NC_004157	Complete genome	Y (Garrison et al., 2020)	1973 (David-West et al., 1973)	*Am. variegatum*, B. decoloratus, *Hy. truncatum*, and *R. appendiculatus* (Shi et al., 2018)	Sub-Saharan Africa (Shi et al., 2018)
Estero Real virus	*Estero Real orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MH017280, MH017286, MH017274	Complete genome	?	1985 (Malkova et al., 1985)	*O. tadaridae* (D Malkova et al., 1985*)*	Cuba (D Malkova et al., 1985)
Hazara virus	*Hazara orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_038709, NC_038710,	Complete genome	?	1970 (Begum et al., 1970)	*I. redikorzevi* (Begum et al., 1970)	Japan, Pakistan (Begum et al., 1970;

					NC_038711					Matsumoto et al., 2019)
Huangpi tick virus 1	*Huangpi orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_031135, NC_031136, NC_031137	Complete genome	?	2015 (Li et al., 2015)	*H. doenitzi, H. longicornis* (Shi et al., 2018)	China (Shi et al., 2018)
Caspiy virus	*Hughes orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KP792708, KP792709, KP792710	Complete genome	?	2014 (L'vov et al., 2014)	*Argasidae* (L'vov et al., 2014)	Azerbaijan (L'vov et al., 2014)
Farallon virus	*Hughes orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034502, NC_034494, NC_034503	Complete genome	?	1967 (Radovsky et al., 1967)	*Ornithodorus* spp. (Shi et al., 2018)	USA (Shi et al., 2018)
Great Saltee virus	*Hughes orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925467, KU925468, KU925469	Complete genome	?	1976 (Keirans et al., 1976)	*O. maritimus* (Kuhn et al., 2016)	Ireland (Great Saltee Island) (Kuhn et al., 2016)
Hughes virus	*Hughes orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925470, KU925471, KU925472	Complete genome	?	1964 (Hughes et al., 1964)	*O. denmarki* (Shi et al., 2018)	Cuba, Trinidad, USA, Venezuela (Shi et al., 2018)
Raza virus	*Hughes orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925479, KU925480, KU925481	Complete genome	?	1968 (Clifford et al., 1968)	*O. denmarki* (Kuhn et al., 2016)	Mexico (Kuhn et al., 2016)
Issyk-kul virus	*Issyk-kul orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KF892055, KF892056, KF892057	Complete genome	?	1973 (L'vov et al, 1973)	*A. vespertlionis* (L'vov et al, 1973)	Kyrgyzstan (Atkinson et al., 2015)

Kasokero virus	*Kasokero orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_036636, NC_029933, NC_029932	Complete genome	?	1986 (Kalunda M et al., 1986)	*O. faini* (Amy et al., 2020)	Uganda (Walker et al., 2015)
Keterah virus	*Keterah orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034392, NC_034388, NC_034389	Complete genome	?	1976 (Varma et al., 1976)	*Argasidae* (Varma et al., 1976)	Malaysia (Varma et al., 1976)
Kupe virus	*Kupe orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	EU257628, EU257627, EU257626	Complete genome	?	2009 (Crabtree et al., 2009)	*Am. gemma, R. pulchellus* (Crabtree et al., 2009)	Kenya (Crabtree et al., 2009)
Meram virus	*Meram orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MN972594, MN972595, MN972596	Complete genome	?	2020 (Ergunay et al., 2020)	*Hy. aegyptium* (Ergunay et al., 2020)	Turkey (Ergunay et al., 2020)
Nairobi sheep disease virus	*Nairobi sheep disease orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034387, NC_034391, NC_034386	Complete genome	Y (Yadav et al., 2011)	1969 (Dandawate et al., 1969)	*Am. variegatum, H. longicornis, H. intermedia, R. appendiculatus, R. hemaphysaloides* (Krasteva et al., 2020)	China, Kenya, India (Krasteva et al., 2020)
Pacific coast tick nairovirus	*Pacific Coast orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU933933, KU933934, KU933935	Complete genome	?	2017 (Bouquet et al., 2017)	*D. occidentalis* (Bouquet et al., 2017)	USA (Bouquet et al., 2017)

Punta Salinas virus	*Punta orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925473, KU925474, KU925475	Complete genome	?	1981 (Converse et al., 1981)	*O. amblus* (Kuhn et al., 2016)	Peru (Kuhn et al., 2016)
Bandia virus	*Qalyub orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925446, KU925447, KU925448	Complete genome	?	1967 (Bres et al., 1967)	*O. sonrai* (Kuhn et al., 2016)	Senegal (Kuhn et al., 2016)
Geran virus	*Qalyub orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KP792714, KP792715, KP792716	Complete genome	?	2014 (L'vov et al., 2014)	*O. asperus* (Kuhn et al., 2016)	Azerbaijan (Kuhn et al., 2016)
Qalyub virus	*Qalyub orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034511, NC_034522, NC_034512	Complete genome	?	1952 (Kuhn et al., 2016)	*O. asperus, O. erraticus* (Walker et al., 2016; Kuhn et al., 2016)	Azerbaijan, Egypt, Senegal (Kuhn et al., 2016; Walker et al., 2016)
Clo Mor virus	*Sakhalin orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_034561, NC_034554, NC_034562	Complete genome	?	1976 (Main et al., 1976)	*A. cooleyi, I. uriae* (Walker et al., 2016)	UK, USA (Walker et al., 2016)
Sakhalin virus	*Sakhalin orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925482, KU925483, KU925484	Complete genome	?	1972 (L'vov et al., 1972)	*I. uriae* (Kuhn et al., 2016)	Antarctica, Australia, Russia, USA (L'vov et al., 2014; Kuhn et al., 2016; Pettersson et al., 2020)
Taggert virus	*Sakhalin orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925491, KU925492, KU925493	Complete genome	?	1985 (Doherty et al., 1985)	*I. uriae* (Pettersson et al., 2020; Wille et al., 2020)	Antarctica, Australia (Pettersson et al., 2020; Wille et al., 2020)

Tillamook virus	*Sakhalin orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925494, KU925495, KU925496	Complete genome	?	1973 (Thomas et al., 1973)	*I. uriae* (Kuhn et al., 2016)	USA (Kuhn et al., 2016)
Soldado virus	*Soldado orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	KU925488, KU925489, KU925490	Complete genome	?	1973 (Jonkers et al., 1973)	*O. maritimus* (Shi et al., 2018)	France, Great Britain, Indian Ocean, North Wales, Seychelles (Shi et al., 2018)
Tacheng tick virus 1	*Tacheng orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_031284, NC_031285, NC_031286	Complete genome	Y	2015 (Li et al., 2015)	*D. marginatus, D. nuttalli, D. silvarum, Hy. asiaticum* (Shi et al., 2018)	China, Kazakhstan (Shi et al., 2018)
Tamdy virus	*Tamdy orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MN792651, MN792652, MN792653	Complete genome	Y (Moming et al., 2021)	2014 (L'vov et al., 2014)	*Hy. asiaticum (L'vov et al., 1984; Moming et al., 2021)*	China, Uzbekistan (Moming et al., 2021)
Tofla virus	*Tofla orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_029124, NC_029123, NC_029122	Complete genome	?	2016 (Shimada et al., 2016)	*H. flava, H. formsensis* (Shimada et al., 2016)	Japan (Shimada et al., 2016)
Tunis virus	*Tunis orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_040770, NC_040771, NC_040772	Complete genome	?	1994 (Chastel et al., 1994)	*A. hermanni* (Chastel et al., 1994)	Tunisia (Chastel et al., 1994)
Vinegar Hill virus	*Vinegar Hill orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MF176881, MF176	Complete	?	2017 (Gauci	*A. robertsi* (Gauci et al., 2017)	Australia (Gauci et al., 2017)

					882, MF176883	genome		et al., 2017)		
Wenzhou tick virus	*Wenzhou orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	NC_031291, NC_031288, NC_031289	Complete genome	?	2015 (Li et al., 2015)	*H. hystricis* (Li et al., 2015)	China (Li et al., 2015)
South Bay virus	*South Bay sabavirus*	*Sabavirus*	*Nairoviridae*	ssRNA(-)	KJ746878, KJ746877	Complete genome	?	2014 (Tokarz et al., 2014)	*D. nuttalli, H. concinna, H. longicornis, I. persulcatus, I. scapularis (Tokarz et al., 2014; Zhao et al., 2021)*	China, USA (Tokarz et al., 2014; Zhao et al., 2021)
Midway virus	*Midway nyavirus*	*Nyavirus*	*Nyamiviridae*	ssRNA(-)	NC_012702	Complete genome	?	1982 (Takahashi et al., 1982)	*Ornithodoros* spp. (Shi et al., 2018)	Central Pacific, Japan (Shi et al., 2018)
Nyamanini virus	*Nyamanini nyavirus*	*Nyavirus*	*Nyamiviridae*	ssRNA(-)	NC_012703	Complete genome	?	1966 (Taylor et al., 1966)	*A. arborerus, A. walkerae* (Shi et al., 2018)	Egypt, India, Nigeria, South Africa, Thailand (Shi et al., 2018)
Sierra Nevada virus	*Sierra Nevada nyavirus*	*Nyavirus*	*Nyamiviridae*	ssRNA(-)	NC_024376	Complete genome	?	2014 (Rogers et al., 2014)	*O. coriaceus* (Rogers et al., 2014)	USA (Rogers et al., 2014)
Johnston Atoll virus	*Johnston Atoll quaranjavirus*	*Quaranjavirus*	*Orthomyxoviridae*	ssRNA(-)	NC_052925, NC_052926, NC_052927, NC_052928, NC_05	Complete genome	?	2009 (Presti et al., 2009)	*O. capensis* (Shi et al., 2018)	Australia, Central Pacific, New Zealand and Hawaii (Shi et al., 2018)

					2929, NC_052930, NC_052931, FJ861696, FJ861697					
Quaranfil virus	*Quaranfil quaranjavirus*	*Quaranjavirus*	*Orthomyxoviridae*	ssRNA(-)	NC_038817, NC_038818, NC_038819, NC_038820, NC_038821, NC_038822	Complete genome	Y (Mourya et al., 2019)	1966 (Taylor et al., 1966)	*A. arboreus* (Shi et al., 2018)	Afghanistan, Egypt, Iraq, Kuwait, Nigeria, South Africa, Yemen and Iran (Shi et al., 2018)
Granville quaranjavirus*	*Granville quaranjavirus*	*Quaranjavirus*	*Orthomyxoviridae*	ssRNA(-)	MZ502307, MZ502306, MZ502305, MZ502304, MZ502308	Partial genome	?	2021 (Sameroff et al., 2021)	*Am. dissimile (Sameroff et al., 2021)*	Trinidad and Tobago (Sameroff et al., 2021)
Dhori virus	*Dhori thogotovirus*	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	NC_034254, NC_034255, NC_034256, NC_034261, NC_034262, NC_034263	Complete genome	Y (Kosoy et al., 2015)	1973 (Anderson et al., 1973)	*Hyalomma* spp. (Shi et al., 2018)	China, Egypt, India, Kyrgyzstan, Russia (Shi et al., 2018)
Jos virus	*Thogoto thogotovirus*	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	HM627170, HM627	Complete	?	1974 (Lee et	*Amblyomma* spp., *Rhipicepha*	Central Africa Republic,

					171, HM627172, HM627173, HM627174, HM627175	genome		al., 1974)	*lus* spp. (Shi et al., 2018)	Guinea, Côte d'Ivoire, Nigeria, Senegal (Shi et al., 2018)
Thogoto virus	*Thogoto thogotovirus*	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	NC_006495, NC_006496, NC_006504, NC_006506, NC_006507, NC_006508	Complete genome	Y (Kosoy et al., 2015)	1965 (Haig et al., 1965)	*Am. Variegatum, Boophilus spp., Hyalomma spp., Rhipicephalus* spp.(Shi et al., 2018)	Central and East Africa, Southern Europe, Southern Portugal (Shi et al., 2018)
Ngari virus	*Bunyamwera orthobunyavirus*	*Orthobunyavirus*	*Peribunyaviridae*	ssRNA(-)	KC608152, KC608153, KC608154	Complete genome	Y (Groseth et al., 2012)	1996 (Zeller et al., 1996)	*Am. variegatum, R. pulchellus* (Groseth et al., 2012)	Guinea, Kenya, Mauritania, Senegal, Somalia, Sudan (Groseth et al., 2012; Makenov et al., 2021)
Matruh virus	*Matruh orthobunyavirus*	*Orthobunyavirus*	*Peribunyaviridae*	ssRNA(-)	KP792693, KP792692, KP792691	Complete genome	?	1973 (Balducci et al., 1973)	*Hy. Marginatum* (Balducci et al., 1973)	Italy (Balducci et al., 1973)
Bahig virus	*Tete orthobunyavirus*	*Orthobunyavirus*	*Peribunyaviridae*	ssRNA(-)	KP792654, KP792653, KP792652	Complete genome	?	1973 (Balducci et al., 1973)	*Hy. Marginatum* (Balducci et al., 1973)	Italy (Balducci et al., 1973)
Bhanja virus	*Bhanja bandavirus*	*Bandavirus*	*Phenuiviridae*	ssRNA(-)	NC_027140, NC_02	Complete	Y (Matsuno et	1977 (Vesenjak-	*H. intermedia, R.*	Africa, Asia, Southern Europe, USA

					7141, NC_027142	genome	al., 2013)	Hirjan et al., 1977)	*decoloratus* (Matsuno et al., 2013)	(Shi et al., 2018)
Heartland virus	*Heartland bandavirus*	*Bandavirus*	*Phenuiviridae*	ssRNA(-)	NC_024494, NC_024495, NC_024496	Complete genome	Y (McMullan et al., 2012)	2012 (McMullan et al., 2012)	*Am. americanum (Mansfield et al., 2017)*	USA (Mansfield et al., 2017)
Hunter Island virus	*Hunter Island bandavirus*	*Bandavirus*	*Phenuiviridae*	ssRNA(-)	NC_027715, NC_027716, NC_027717	Complete genome	?	2014 (Wang et al., 2014)	*I. eudyptidis* (Shi et al., 2018)	Australia (Shi et al., 2018)
lone star virus	*Lone star bandavirus*	*Bandavirus*	*Phenuiviridae*	ssRNA(-)	NC_021242, NC_021243, NC_021244	Complete genome	?	1969 (Kokernot et al., 1969)	*Am. Americanum* (Shi et al., 2018)	USA (Shi et al., 2018)
Severe fever with thrombocytopenia syndrome virus	*Dabie bandavirus*	*Bandavirus*	*Phenuiviridae*	ssRNA(-)	NC_043450, NC_043451, NC_043452	Complete genome	Y (Yu et al., 2011)	2011 (Yu et al., 2011)	*Dermacentor spp., Haemaphysalis spp., I. persulcatus, Rhipicephalus spp. (Mansfield et al., 2017; Zhao et al., 2021)*	East Asia, North America (Mansfield et al., 2017; Zhao et al., 2021)
Norway phlebovirus 1	*Norway ixovirus*	*Ixovirus*	*Phenuiviridae*	ssRNA(-)	NC_055433, NC_055434	Complete genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Blacklegged tick phlebovirus 3	*Scapularis ixovirus*	*Ixovirus*	*Phenuiviridae*	ssRNA(-)	NC_055431, NC_055432	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Laurel Lake virus	*Laurel Lake laulavirus*	*Laulavirus*	*Phenuiviridae*	ssRNA(-)	NC_043679,	Complete	?	2018 (Tokar	*I. scapularis*	USA (Tokarz et al., 2018)

					NC_043680, NC_043681	genome		z et al., 2018)	*(Tokarz et al., 2018)*	
Dabieshan tick virus	*Dabieshan uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	MW721887, MW721893	Complete genome	?	2015 (Li et al., 2015)	*H. longicornis, I. persulcatus, R. microplus* (Wang et al., 2021; Zhao et al., 2021)	China (Wang et al., 2021; Zhao et al., 2021)
Kaisodi virus	*Kaisodi uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_040492, NC_040493, NC_040494	Complete genome	?	1966 (Bhatt et al., 1966)	*H. spinigera* (Shi et al., 2018)	South India (Shi et al., 2018)
Lihan tick virus	*Lihan uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_055423, NC_055424	Complete genome	?	2015 (Li et al., 2015)	*D. nitens, Hy. marginatum, R. microplus, R. sanguineus* (Temmam et al., 2019)	Brazil, China, USA, Guadeloupe, Thailand, Turkey, Trinidad. Tobago (Temmam et al., 2019; Gondard et al., 2020)
Silverwater virus	*Silverwater uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_055369, NC_055370, NC_055371	Complete genome	?	1971 (Hoff et al., 1971)	*H. leporispalustris* (Shi et al., 2018)	Canada, USA (Shi et al., 2018)
Tacheng tick virus 2	*Tacheng uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_055425, NC_055426	Complete genome	Y (Dong et al., 2021)	2015 (Li et al., 2015)	*D. marginatus, D. reticulatus, R. sanguineus, H. marginatum* (Li et al.,	China, Kazakhstan, Romania, Tailand, Turkey (Li et al., 2015; Brinkmann et al., 2018; Temmam et

									2015; Brinkmann et al., 2018; Bratuleanu et al., 2021)	al., 2019; Bratuleanu et al., 2021)
Uukuniemi virus	*Uukuniemi uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_005214, NC_005220, NC_005221	Complete genome	?	2013 (Palacios et al., 2013)	*I. ricinus, I. uriae* (Matsuno et al., 2015)	Czech Republic, Sweden, UK (Matsuno et al., 2015)
Yongjia tick virus 1	*Yongjia uukuvirus*	*Uukuvirus*	*Phenuiviridae*	ssRNA(-)	NC_055427, NC_055428	Complete genome	?	2015 (Li et al., 2015)	*H. hystricis* (Li et al., 2015)	China (Li et al., 2015)
Blanchseco virus	*Blanchseco alpharicinrhavirus*	*Alpharicinrhavirus*	*Rhabdoviridae*	ssRNA(-)	MN025503	Complete genome	?	2019 (Sameroff et al., 2019)	*A. ovale* (Sameroff et al., 2019)	Trinidad and Tobago (Sameroff et al., 2019)
Bole tick virus 2	*Bole alpharicinrhavirus*	*Alpharicinrhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_031079	Complete genome	?	2015 (Li et al., 2015)	*Hy. Asiaticum* (Li et al., 2015)	China (Li et al., 2015)
Wuhan tick virus 1	*Wuhan alpharicinrhavirus*	*Alpharicinrhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_031304	Complete genome	?	2015 (Li et al., 2015)	*D. marginatus, R. microplus, R. annulatus, H. longicornis* (Temmam et al., 2019; Xu et al., 2021)	China, Turkey (Xu et al., 2021)
New Kent County virus	*Kent ephemerovirus*	*Ephemerovirus*	*Rhabdoviridae*	ssRNA(-)	MF615270	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Barur virus	*Barur ledantevirus*	*Ledantevirus*	*Rhabdoviridae*	ssRNA(-)	NC_034535	Complete genome	?	1981 (Butenko et	*Hy. Intermedia* (Shi et al., 2018)	India, Kenya, Somalia (Shi et al., 2018)

								al., 1981)		
Kolente virus	*Kolente ledantevirus*	*Ledantevirus*	*Rhabdoviridae*	ssRNA(-)	NC_025342	Complete genome	?	2013 (Ghedin et al., 2013)	*Am. Variegatum* (Shi et al., 2018)	Guinea (Shi et al., 2018)
Yongjia tick virus 2	*Yongjia ledantevirus*	*Ledantevirus*	*Rhabdoviridae*	ssRNA(-)	NC_031305	Complete genome	?	2015 (Li et al., 2015)	*H. hystricis* (Shi et al., 2018)	China (Shi et al., 2018)
Connecticut virus	*Connecticut sawgrhavirus*	*Sawgrhavirus*	*Rhabdoviridae*	ssRNA(-)	KM205020	Complete genome	?	1978 (Ritter et al., 1978)	*I. dentatus* (Shi et al., 2018)	USA (Shi et al., 2018)
Long Island tick rhabdovirus	*Island sawgrhavirus*	*Sawgrhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_025340	Complete genome	?	2014 (Tokarz et al., 2014)	*Am. americanum (Tokarz et al., 2014)*	USA (Tokarz et al., 2014)
New Minto virus	*Minto sawgrhavirus*	*Sawgrhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_055457	Complete genome	?	1970 (Sather et al., 1970)	*H. leporispalustris* (Shi et al., 2018)	USA (Shi et al., 2018)
Sawgrass virus	*Sawgrass sawgrhavirus*	*Sawgrhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_055461	Complete genome	?	1970 (Sather et al., 1970)	*D. variabilis, H. leporispalustris* (Shi et al., 2018)	USA (Shi et al., 2018)
Isfahan virus	*Isfahan vesiculovirus*	*Vesiculovirus*	*Rhabdoviridae*	ssRNA(-)	NC_020806	Complete genome	?	1977 (Tesh et al., 1977)	*Hy. Asiaticum* (Shi et al., 2018)	Parts of Asia, Turkmenistan (Shi et al., 2018)
Zahedan rhabdovirus	*Zahedan zarhavirus*	*Zarhavirus*	*Rhabdoviridae*	ssRNA(-)	NC_040664	Complete genome	?	2015 (Dilcher et al., 2015)	*Hy. Anatolicum* (Shi et al., 2018)	Iran (Shi et al., 2018)
Beiji nairovirus	Unclassified	*Nairovirus*	*Nairoviridae*	ssRNA(-)	MW315106, MW315112	Partial genome	Y (Wang et al., 2021)	2019 (Meng et al., 2019)	*I. crenulatus, I. persulcatus* (Wang et al., 2021)	China (Wang et al., 2021)
Nayun tick nairovirus	Unclassified	*Nairovirus*	*Nairoviridae*	ssRNA(-)	MW561151,	Partial	?	2015 (Xia et	*R. sanguineus*	China, Romania

					KP141756, KP141755	genome		al., 2015)	(Xia et al., 2015; Bratuleanu et al., 2021)	(Xia et al., 2015; Bratuleanu et al., 2021)
Norway nairovirus 1	Unclassified	*Nairovirus*	*Nairoviridae*	ssRNA(-)	MF141045, MF141044	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Northern Europe (Pettersson et al., 2017)
Paramushir virus	Unclassified	*Nairovirus*	*Nairoviridae*	ssRNA(-)	MH638289, MH124638, MH124637, MH124636, MH124635, MH124634, KF801657, KP792719, KP792718, KP792717	Partial genome	?	1976 (L'vov et al., 1976)	*I. signatus, I. uriae* (L'vov et al., 1976)	Russia (Safonova et al., 2015)
Rondonia orthonairovirus	Unclassified	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MN560621, MN560622, MN560623, MN560624, MN560625, MN560626, MN560627, MN560628,	Partial genome	?	2019 (Blomstrom et al., 2019)	*Antricola* (Blomstrom et al., 2019)	Brazil (Blomstrom et al., 2019)

					MN560629					
Songling virus	Unclassified	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	MT328780, MT328779, MT328778	Partial genome	Y (Ma et al., 2021)	2021 (Ma et al., 2021)	*H. longicornis* (Ma et al., 2021)	China (Ma et al., 2021)
Yezo virus	Unclassified	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	LC621360, LC621359, LC621358	Partial genome	Y (Kodama et al., 2021)	2021 (Kodama et al., 2021)	*H. megaspinosa* (Kodama et al., 2021)	Japan (Kodama et al., 2021)
Zambezi tick virus 1	Unclassified	*Quarjavirus*	*Orthomyxoviridae*	ssRNA(-)	MH267793	Partial genome	?	2018 (Cholleti et al., 2018)	*Rhipicephalus* (Cholleti et al., 2018)	Mozambique (Cholleti et al., 2018)
Aransas Bay virus	Unclassified	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	KC506162, KC506163, KC506164, KC506165, KC506166, KC506167	Partial genome	?	1979 (Yunker et al., 1979)	*Ornithodoros* spp. (Briese et al., 2014)	North America (Briese et al., 2014)
Bourbon virus	Unclassified	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	KU708253, KU708254, KU708255, MH880287, MH880288, MH880289, MH880290, MH880	Complete genome	Y (Kosoy et al., 2015)	2015 (Kosoy et al., 2015)	*Am. Americanum* (Savage et al., 2017)	USA (Kosoy et al., 2015)

					291, MH880292					
Oz virus	Unclassified	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	NC_040730, NC_040731, NC_040732, NC_040733, NC_040734, NC_040735	Complete genome	?	2018 (Ejiri et al., 2018)	*Am. testudinarium* (Ejiri et al., 2018)	Japan (Ejiri et al., 2018)
Thailand tick thogotovirus	Unclassified	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	MN095539, MN095540, MN095541, MN095542, MN095543, MN095544	Complete genome	?	2019 (Temmam et al., 2019)	*R. microplus* (Temmam et al., 2019)	Tailand (Temmam et al., 2019)
Upolu virus	Unclassified	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	KC506156, KC506157, KC506158, KC506159, KC506160, KC506161	Complete genome	?	1968 (Doherty et al., 1968)	*O. capensis* (Briese et al., 2014)	Australia (Briese et al., 2014)
American dog tick phlebovirus	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	KM048312, KM048311	Complete genome	?	2014 (Tokarz et al., 2014)	*D. variabilis (Tokarz et al., 2014)*	USA (Tokarz et al., 2014)
Blacklegged tick	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	KX184200,	Complete	?	2014 (Tokar	*I. scapularis*	USA (Tokarz et al., 2014)

phlebovirus 1					KX184201	genome		z et al., 2014)	*(Tokarz et al., 2014)*	
Blacklegged tick phlebovirus 2	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	KM589357, KM589354	Partial genome	?	2014 (Tokarz et al., 2014)	*I. scapularis (Tokarz et al., 2014)*	USA (Tokarz et al., 2014)
Bole tick virus 1	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MZ244253, MZ244252, KM817731, MH916622, MH916621, MH916620, MH916619, MH688504, MH836620, MH688505, MH688503, MH688501, MH688578, MH688577, MH688576, MH688575, MH688574, MH688573, MH688572, MH688571	Partial genome	?	2015 (Li et al., 2015)	*Hy. Asiaticum* (Li et al., 2015)	China (Li et al., 2015)

Brown dog tick phlebovirus 1	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MZ244261, MZ244260, MZ244259, MZ244256, MN025507, MN025506	Partial genome	?	2019 (Sameroff et al., 2019)	*R. sanguineus* *R. microplus* (Sameroff et al., 2019)	China, Trinidad and Tobago (Sameroff et al., 2019)
Brown dog tick phlebovirus 2	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MW561139, MW561138, MW561137, MW561136, MN025509, MN025508	Partial genome	?	2019 (Sameroff et al., 2019)	*R. microplus, R. sanguineus* (Sameroff et al., 2019)	China, Trinidad and Tobago (Sameroff et al., 2019)
Changping tick virus 1	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MW561146, MW561145, MW561144, MW561143, MW561142, MW561141, MW561140, KM817732, KM817665	Partial genome	?	2015 (Li et al., 2015)	*Dermacentor* spp. (Li et al., 2015)	China, Romania (Matsuno et al., 2013; Li et al., 2015)
Lanjan virus	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	KM370974	Partial genome	?	1967 (Tan et al., 1967)	*D. auratus* (Shi et al., 2018)	Malaysia (Shi et al., 2018)

Palma virus	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	JX961630, JX961629, JX961628	Partial genome	?	1994 (Filipe et al., 1994)	*H. punctate* (Shi et al., 2018)	Portugal (Shi et al., 2018)
Rhipicephalus associated phlebovirus 1	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MZ244255, MZ244254, MH814976, MH814975	Partial genome	?	2021 (Shi et al., 2021)	*R. microplus* (Shi et al., 2021)	China (Shi et al., 2021)
Tick phlebovirus Anatolia 1	Unclassified	*Phlebovirus*	*Phenuiviridae*	ssRNA(-)	MG764522, MG764521	Partial genome	?	2018 (Brinkmann et al., 2018)	*R. sanguineus* (Brinkman n et al., 2018)	Turkey (Brinkmann et al., 2018)
Neke harbour virus	Unclassified	Unclassified	*Orthomyxoviridae*	ssRNA(-)	MN830238	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Antarctica (Pettersson et al., 2020)
Uumaja virus	Unclassified	Unclassified	*Orthomyxoviridae*	ssRNA(-)	MN830237	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Khasan virus	Unclassified	Unclassified	*Peribunyaviridae*	ssRNA(-)	KF892046, KF892047, KF892048	Partial genome	?	1978 (L'vov et al., 1978)	*H. longgicornis* (Shi et al., 2018)	Russia (Shi et al., 2018)
American dog tick rhabdovirus 2	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	MF962659, MF962661	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Blacklegged tick rhabdovirus 1	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	MF360790	Complete genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Dog tick rhabdovirus 1	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	MF360791	Partial	?	2018 (Tokar	*I. scapularis*	USA (Tokarz et al., 2018)

						genome		z et al., 2018)	*(Tokarz et al., 2018)*	
Huangpi tick virus 3	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	NC_031083	Complete genome	?	2015 (Li et al., 2015)	*H. doenitzi* (Li et al., 2015)	China (Li et al., 2015)
Nayun tick rhabdovirus	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	KP141757	Partial genome	?	2015 (Xia et al., 2015)	*Rhipicephalus* spp. (Xia et al., 2015)	China (Xia et al., 2015)
Rhipicephalus associated rhabdo-like virus	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	MH814974	Partial genome	?	2021 (Shi et al., 2021)	*H. longicornis, R. microplus* (Shi et al., 2021)	China (Shi et al., 2021)
Tacheng tick virus 3	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	NC_031268	Complete genome	?	2015 (Li et al., 2015)	*D. marginatus* (Li et al., 2015)	China (Li et al., 2015)
Tacheng tick virus 7	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	NC_031272	Complete genome	?	2015 (Li et al., 2015)	*A. miniatus* (Li et al., 2015)	China (Li et al., 2015)
Taishun tick virus	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	NC_031273	Complete genome	?	2015 (Li et al., 2015)	*H. hystricis* (Li et al., 2015)	China, Russia (Li et al., 2015)
Deer tick mononegavirales-like virus	Unclassified	Unclassified	Unclassified	ssRNA(-)	MG880117, KM048317, KJ746903	Partial genome	?	2014 (Tokarz et al., 2014)	*D. nuttalli, D. silvarum, H. concinna, I. persulcatus, I. scapularis (Tokarz et al., 2014; Zhao et al., 2021)*	China, USA (Tokarz et al., 2014; Zhao et al., 2021)
Bonden virus	Unclassified	Unclassified	*Unclassified Bunyavirales*	ssRNA(-)	MN830227	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)

Bronnoya virus	Unclassified	Unclassified	*Unclassified Bunyavirales*	ssRNA(-)	MF141063, MF141062	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Ubmeje virus	Unclassified	Unclassified	*Unclassified Bunyavirales*	ssRNA(-)	MN830232	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Norway mononegavirus 1	Unclassified	Unclassified	*Unclassified Mononegavirales*	ssRNA(-)	MF141072	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Tick mononegavirus	Unclassified	Unclassified	*Unclassified Mononegavirales*	ssRNA(-)	MZ244310, MH835441, MH835440, MH835439, MH835438	Partial genome	?	2018 (Yang et al., 2018)	*I. scapularis, H. longicornis* (Yang et al., 2018)	China (Yang et al., 2018)
Umea virus	Unclassified	Unclassified	*Unclassified Mononegavirales*	ssRNA(-)	MN830236	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Sweden (Pettersson et al., 2020)
Canne point virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026566	Partial genome	?	2018 (Harvey et al., 2018)	*Am. moreliae (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Fairlight virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026565	Partial genome	?	2018 (Harvey et al., 2018)	*Am. moreliae (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Manly virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026564	Partial genome	?	2018 (Harvey et al., 2018)	*Am. moreliae (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Messner virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MT025174	Partial genome	?	2020 (Wille et al., 2020)	*I. uriae* (Wille et al., 2020)	Antarctica (Wille et al., 2020)

North Shore virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	OL452126	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Old quarry swamp virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026595, MK026596, MK026597, MK026598, MK026599	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Piguzov virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MT025176, MT025177	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Antarctica (Pettersson et al., 2020)
Quarantine Head virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026568	Partial genome	?	2018 (Harvey et al., 2018)	*Am. moreliae (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Ronne virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MT025165, MT025164	Partial genome	?	2020 (Pettersson et al., 2020; Wille et al., 2020)	*I. uriae* (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	*Unclassified Riboviria*	ssRNA(-)	NC_028264	Complete genome	?	2015 (Li et al., 2015)	*D. marginatus (Li et al., 2015)*	China, Kazakhstan (Li et al., 2015)
Timbillica virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(-)	MK026589, MK026590	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Gadgets Gully virus	*Gadgets Gully virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	NC_033723	Complete genome	?	1985 (St St George et al., 1985)	*I. uriae* (Pettersson et al., 2020)	Antarctica, Australia (Pettersson et al., 2020)

Kadam virus	*Kadam virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	NC_033724	Complete genome	?	1970 (Henderson et al., 1970)	*R. pravus* (Shi et al., 2018)	Saudi Arabia, Uganda (Shi et al., 2018)
Alkhumra hemorrhagic fever virus	*Kyasanur Forest disease virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	AF331718	Complete genome	Y (Grard et al., 2007)	1957 (Work et al., 1957)	*H. spinigera, O. savignyi* (Shi et al., 2018)	India, Saudi Arabia (Shi et al., 2018)
Langat virus	*Langat virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	AF253419	Complete genome	?	1956 (Smith et al., 1956)	*I. granulatus* (Shi et al., 2018)	Malaysia (Shi et al., 2018)
Louping ill virus	*Louping ill virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	Y07863	Complete genome	Y (Davidson et al., 1991)	1931 (Greig et al., 1931)	*I. ricinus* (Shi et al., 2018)	England, Ireland, Scotland, Wales (Shi et al., 2018)
Meaban virus	*Meaban virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	NC_033721	Complete genome	?	1985 (Chastel et al., 1985)	*O. maritimus* (Shi et al., 2018)	France (Shi et al., 2018)
Omsk hemorrhagic fever virus	*Omsk hemorrhagic fever virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	AY193805	Complete genome	Y (Grard et al., 2007)	1989 (Gaidamovich et al., 1989)	*Dermacentor spp., I. persculatus* (Ruzek et al., 2010)	Russia (Grard et al., 2007)
Deer tick virus	*Powassan virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	AF311056	Complete genome	?	1997 (Telford et al., 1997)	*I. scapularis (Mansfield et al., 2017; Shi et al., 2018)*	New England, North America (Mansfield et al., 2017; Shi et al., 2018)
Powassan virus	*Powassan virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	L06436	Complete genome	Y (Tokarz et al., 2014)	1959 (McLean and Donohue 1959)	*I. cookei, Ixodes spp. (Tokarz et al., 2014)*	North America, Russia (Mansfield et al., 2017)
Karshi virus	*Royal Farm virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	AY863002	Complete	?	1976 (L'vov	*A. hermanni,*	North of Central Asia,

						genome		et al., 1976)	*O. papillipes* (Shi et al., 2018)	Uzbek (Shi et al., 2018)
Saumarez Reef virus	*Saumarez Reef virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	DQ235150	Complete genome	?	1977 (St George et al., 1977)	*I. eudyptidis, O. capensis* (Shi et al., 2018)	Australia (Shi et al., 2018)
Tick-borne encephalitis virus	*Tick-borne encephalitis virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	NC_001672	Complete genome	Y (Shi et al., 2018)	1931 (Schneider et al., 1931)	*I. ovatus, I. persulcatus, I. ricinus* (Shi et al., 2018)	Northern Asia, Northern Europe, Siberia (Shi et al., 2018)
Tyuleniy virus	*Tyuleniy virus*	*Flavivirus*	*Flaviviridae*	ssRNA(+)	NC_023424	Complete genome	?	1971 (L'vov et al., 1971)	*I. putus* (Shi et al., 2018)	Tuleniy Island (Shi et al., 2018)
Ixodes holocyclus iflavirus	*Ixodes holocyclus iflavirus*	*Iflavirus*	*Iflaviridae*	ssRNA(+)	OL452115	Partial genome	?	2018 (O'Brien et al., 2018)	*I. holocyclus* (O'Brien et al., 2018)	Australia (O'Brien et al., 2018)
Blacklegged tick associated ilarvirus	Unclassified	*Ilarvirus*	*Bromoviridae*	ssRNA(+)	MG647776, MG647777	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Trinbago virus	Unclassified	*Pestivirus*	*Flaviviridae*	ssRNA(+)	MN025505	Partial genome	?	2019 (Sameroff et al., 2019)	*A. ovale, R. microplus, R. sanguineus* (Sameroff et al., 2019)	Trinidad, Tobago (Sameroff et al., 2019)
Cattle tick tymovirus-like virus 1	Unclassified	*Tymovirus*	*Tymoviridae*	ssRNA(+)	MN025504	Partial genome	?	2019 (Sameroff et al., 2019)	*R. microplus* (Sameroff et al., 2019)	Trinidad and Tobago (Sameroff et al., 2019)
Lone star tick dicistrovirus	Unclassified	Unclassified	*Dicistroviridae*	ssRNA(+)	KX774633	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Alongshan virus	Unclassified	Unclassified	*Flaviviridae*	ssRNA(+)	MN648770,	Partial	Y (Wan	2019 (Kuiva	*I. persulcatu*	China, France,

					MN648771, MN648772, MN648773	genome	g et al., 2019)	nen et al., 2019)	*s, I. ricinus* (Kholodilov et al., 2020)	Finland (Kholodilov et al., 2020)
Jingmen tick virus	Unclassified	Unclassified	*Flaviviridae*	ssRNA(+)	MK721629, MK721630, MK721631, MK721632	Complete genome	Y (Jia et al., 2019)	2014 (Qin et al., 2014)	*Am. javanense, D. nuttalli, Haemaphysalis spp., Ixodes spp., Rhipicephalus* spp. (Zhao et al., 2021)	Many countries in Asia, America, and Africa (Vandegrift et al., 2020; Zhao et al., 2021)
Norway luteo-like virus 1	Unclassified	Unclassified	*Luteoviridae*	ssRNA(+)	MF141065	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Norway luteo-like virus 2	Unclassified	Unclassified	*Luteoviridae*	ssRNA(+)	MF141068	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Norway luteo-like virus 3	Unclassified	Unclassified	*Luteoviridae*	ssRNA(+)	MF141069	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Norway luteo-like virus 4	Unclassified	Unclassified	*Luteoviridae*	ssRNA(+)	MF141070	Partial genome	?	2017 (Pettersson et al., 2017)	*I. ricinus* (Pettersson et al., 2017)	Norway (Pettersson et al., 2017)
Lone star tick nodavirus	Unclassified	Unclassified	*Nodaviridae*	ssRNA(+)	KX774635, KX774634	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Paradise bay virus	Unclassified	Unclassified	*Tombusviridae*	ssRNA(+)	MN830247	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Antarctica (Pettersson et al., 2020)

Upmeje virus	Unclassified	Unclassified	*Tombusviridae*	ssRNA(+)	MN830246	Partial genome	?	2020 (Pettersson et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Northern Sweden (Pettersson et al., 2020)
Bagotville virus	Unclassified	Unclassified	*Unclassified Picornavirales*	ssRNA(+)	MW741892	Partial genome	?	2021 (Chandra et al., 2021)	*I. holocyclus* (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Blacklegged tick picorna-like virus 1	Unclassified	Unclassified	*Unclassified Picornavirales*	ssRNA(+)	MG647769, MG647774	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Blacklegged tick picorna-like virus 2	Unclassified	Unclassified	*Unclassified Picornavirales*	ssRNA(+)	MG647773, MG647772, MG647771, MG647770	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Wardell virus	Unclassified	Unclassified	*Unclassified Picornavirales*	ssRNA(+)	MW741896, MW741895, MW741894	Partial genome	?	2021 (Chandra et al., 2021)	*I. holocyclus* (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Woodburn virus	Unclassified	Unclassified	*Unclassified Picornavirales*	ssRNA(+)	MW741893	Partial genome	?	2021 (Chandra et al., 2021)	*I. holocyclus* (Chandra et al., 2021)	Australia (Chandra et al., 2021)
Blue Fish Point virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026570, MK026571	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Bole tick virus 4	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MZ244286	Complete genome	?	2015 (Shi et al., 2015)	*D. marginatus, D. reticulatus, H. asiaticum, Hy. asiaticum, Hy.*	China, Romania, Saudi Arabia, Thailand, Trinidad, Tobago (Temmam et al., 2019;

									detritum, R. microplus, R. sanguineus (Temmam et al., 2019; Bratuleanu et al., 2021; Zakham et al., 2021)	Bratuleanu et al., 2021; Zakham et al., 2021)
Bulatov virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MN830234, MT025173	Partial genome	?	2020 (Pettersson et al., 2020; Wille et al., 2020)	*I. uriae* (Pettersson et al., 2020)	Antarctica (Pettersson et al., 2020)
Collins beach virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026585	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Fairfax Lookout virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026588, MK026587, MK026586	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Gerbovich virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MN830239, MT025175	Partial genome	?	2020 (Pettersson et al., 2020; Wille et al., 2020)	*I. uriae* (Pettersson et al., 2020; Wille et al., 2020)	Antarctica (Pettersson et al., 2020; Wille et al., 2020)
Ingleside virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	OL452105	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Ixodes scapularis	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	LC094965,	Partial	?	2017 (Nakao	*I. scapularis (Tokarz et*	USA, Japan (Tokarz et al., 2018;

associated virus 3					MG677814	genome		et al., 2017)	*al., 2018; Nakao et al., 2017)*	Nakao et al., 2017)
Jump Rock virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026583	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Nadgee virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026592	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Store beach virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026567	Partial genome	?	2018 (Harvey et al., 2018)	*Am. moreliae (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Tacheng tick virus 8	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	NC_028367	Complete genome	?	2015 (Shi et al., 2015)	*D. marginatus (Shi et al., 2015)*	China (Shi et al., 2015)
Vovk virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MN830235, MT025162	Partial genome	?	2020 (Pettersson et al., 2020; Wille et al., 2020)	*I. uriae* (Pettersson et al., 2020; Wille et al., 2020)	Antarctica (Pettersson et al., 2020; Wille et al., 2020)
Wangarabell virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026593	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Yambulla virus	Unclassified	Unclassified	*Unclassified Riboviria*	ssRNA(+)	MK026594	Partial genome	?	2018 (Harvey et al., 2018)	*I. holocyclus (Harvey et al., 2018)*	Australia (Harvey et al., 2018)
Antioquia tymovirus-like 1	Unclassified	Unclassified	*Unclassified Tymovirales*	ssRNA(+)	MK683451	Partial genome	?	2020 (Gomez et al., 2020)	*R. microplus* (Gomez et al., 2020)	Colombia (Gomez et al., 2020)
Guarapuava tymovirus-like 1	Unclassified	Unclassified	*Unclassified Tymovirales*	ssRNA(+)	MH155882	Partial genome	?	2018 (de Souza et al., 2018)	*R. microplus* (de Souza et al., 2018)	Brazil (de Souza et al., 2018)
American dog tick	Unclassified	Unclassified	Unclassified	Unknown	MF962660	Partial	?	2018 (Tokar	*D. variabilis*	USA (Tokarz et al., 2018)

associated virus 1						genome		z et al., 2018)	*(Tokarz et al., 2018)*	
American dog tick associated virus 2	Unclassified	Unclassified	Unclassified	Unknown	MF962662, MF962657	Partial genome	?	2018 (Tokarz et al., 2018)	*D. variabilis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Finch Creek virus	Unclassified	Unclassified	Unclassified	Unknown	EU267169	Partial genome	?	2009 (Major et al., 2009)	*I. uriae* (Major et al., 2009)	Australia (Major et al., 2009)
Ganjam virus	Unclassified	Unclassified	Unclassified	Unknown	KU925466, KU925465, KU925464	Partial genome	?	1969 (Dandawate et al., 1969)	*H. intermedia* (Kuhn et al., 2016)	India (Kuhn et al., 2016)
Ixodes scapularis associated virus 1	Unclassified	Unclassified	Unclassified	Unknown	LC094964, KM048318	Partial genome	?	2014 (Tokarz et al., 2014)	*I. scapularis (Tokarz et al., 2014; Nakao et al., 2017)*	Japan, USA (Tokarz et al., 2014; Nakao et al., 2017)
Ixodes scapularis associated virus 2	Unclassified	Unclassified	Unclassified	Unknown	KM048319	Partial genome	?	2014 (Tokarz et al., 2014)	*I. scapularis (Tokarz et al., 2014)*	USA (Tokarz et al., 2014)
Ixodes scapularis associated virus 4	Unclassified	Unclassified	Unclassified	Unknown	MF962656	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Ixodes scapularis associated virus 5	Unclassified	Unclassified	Unclassified	Unknown	MG256513	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Ixodes scapularis associated virus 6	Unclassified	Unclassified	Unclassified	Unknown	MG256514	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Lone star tick associated virus 1	Unclassified	Unclassified	Unclassified	Unknown	MF962658	Partial genome	?	2018 (Tokarz et al., 2018)	*I. scapularis (Tokarz et al., 2018)*	USA (Tokarz et al., 2018)
Sapphire II virus	Unclassified	Unclassified	Unclassified	Unknown	MK896468, MK896467,	Complete genome	?	1972 (Yunker et al., 1972)	*A. cooleyi* (Yunker et al., 1972)	USA (Yunker et al., 1972)

					MK896466					
Tick borne tetravirus-like virus	Unclassified	Unclassified	Unclassified	Unknown	MW334982, KM048322	Partial genome	?	2014 (Tokarz et al., 2014)	*D. variabilis (Tokarz et al., 2014)*	USA (Tokarz et al., 2014)
Zirqa virus	Unclassified	Unclassified	Unclassified	Unknown	KU925500, KU925501, KU925502	Complete genome	?	1973 (Varma et al., 1973)	*A. cooleyi, Ornithodorus* spp. (Shi et al., 2018)	Abu Dhabi (Shi et al., 2018)
Bovine hepacivirus **	*Hepacivirus N*	*Hepacivirus*	*Flaviviridae*	ssRNA(+)	NC_026797	Complete genome	?	2015 (Baechlein et al., 2015)	Unknown (Temmam et al., 2019)	Brazil, China, Germany, Ghana, US (Baechlein et al., 2019)
HoBi-like pestivirus**	*Pestivirus H*	*Pestivirus*	*Flaviviridae*	ssRNA(+)	MK689376	Partial genome	?	2004 (Schirrmeier et al., 2004)	Unknown (Temmam et al., 2019)	Argentina, Bangladesh, Brazil, China, Germany, India, Italy, Mexico, Thailand, Turkey, USA (Bauermann et al., 2021)
Erve virus**	*Erve orthonairovirus*	*Orthonairovirus*	*Nairoviridae*	ssRNA(-)	JF911697, JF911698, JF911699	Complete genome	?	1989 (Chastel et al., 1989)	Unknown (Dilcher et al., 2012)	Czech Republic, France, Germany, Netherland (Dilcher et al., 2012)
Bovine parvovirus-2**	*Ungulate copiparvovirus 1*	*Copiparvovirus*	*Parvoviridae*	ssDNA(+/-)	KT148961	Complete genome	?	2001 (Allander et al., 2001)	Unknown (Temmam et al., 2019)	Brazil, China, USA (Ng et al., 2015; Cibulski et al., 2016; Wang et al., 2018)
Nkolbisson virus**	*Nkolbisson ledantevirus*	*Ledantevirus*	*Rhabdoviridae*	ssRNA(-)	NC_034539	Complete genome	?	2010 (Dacheux et al., 2010)	Unknown (Temmam et al., 2019)	Cameroon (Dacheux et al., 2010)

Spring viremia of carp virus**	*Carp sprivivirus*	*Sprivivirus*	*Rhabdoviridae*	ssRNA(-)	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**	*Maraba virus*	*Vesiculovirus*	*Rhabdoviridae*	ssRNA(-)	NC_025255	Complete genome	?	2010 (Brun et al., 2010)	Unknown (Temmam et al., 2019)	Brazil (Brun et al., 2010)
Wellfleet Bay virus**	Unclassified	*Quaranjavirus*	*Orthomyxoviridae*	ssRNA(-)	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	*Thogotovirus*	*Orthomyxoviridae*	ssRNA(-)	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)

					KX670395					
Eelpout rhabdovirus**	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	KR612230	Partial genome	?	2017 (Axen et al., 2017)	Unknown (Temmam et al., 2019)	Sweden (Axen et al., 2017)
Wuhan redfin culter dimarhabodovirus**	Unclassified	Unclassified	*Rhabdoviridae*	ssRNA(-)	MG600013	Complete genome	?	2018 (Shi et al., 2018)	Unknown (Temmam et al., 2019)	China (Shi et al., 2018)
Bat nairovirus/ Ahun nairovirus**	Unclassified	*Nairovirus*	*Nairoviridae*	ssRNA(-)	KF170224	Partial genome	?	2014 (Dacheux et al., 2014)	Unknown (Dacheux et al., 2014)	France (Dacheux et al., 2014)
Essaouira virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1993 (Chastel et al., 1993)	*O. maritimus* (Chastel et al., 1993)	Morocco (Chastel et al., 1993)
Huacho virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1967 (Belaganahalli et al., 2015)	*C. amblus* (Belaganahalli et al., 2015)	Peru (Belaganahalli et al., 2015)
Kala Iris virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1993 (Chastel et al., 1993)	*O. maritimus* (Chastel et al., 1993)	Morocco (Chastel et al., 1993)
Mono Lake virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1988 (Calisher et al., 1988)	*A. cooleyi* (Calisher et al., 1988)	USA (Calisher et al., 1988)
Sixgun city virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1988 (Calisher et al., 1988)	*A. cooleyi* (Calisher et al., 1988)	USA (Calisher et al., 1988)
Ellidaey virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1986 (Moss et al., 1986)	*I. uriae* (Moss et al., 1986)	Iceland (Elliđaey island) (Moss et al., 1986)

Foula virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1986 (Nuttall et al., 1986)	*I. uriae* (Nuttall et al., 1986)	Scotland (Shetland Islands) (Nuttall et al., 1986)
Grimsey virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1986 (Moss et al., 1986)	*I. uriae* (Moss et al., 1986)	Iceland (Grimsey island) (Moss et al., 1986)
Inner Farne Island virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1986 (Nuttall et al., 1986)	*I. uriae* (Nuttall et al., 1986)	England (Nuttall et al., 1986)
Mykines virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1978 (Main et al., 1978)	*I. uriae* (Main et al., 1978)	Denmark (Faroe Islands) (Main et al., 1978)
Kao Shuan virus**	Unclassified	Unclassified	Unclassified	Unknown	Unavailable	Not available	?	1989 (Moussa et al., 1989)	*A. robertsi* (Moussa et al., 1989)	Indonesia, Taiwan (Moussa et al., 1989)
Pretoria virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1975 (Converse et al., 1975)	*A. africolumbae* (Converse et al., 1975)	South Africa (Converse et al., 1975)
Puffin Island virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1983 (Gould et al., 1983)	*O. maritimus* (Gould et al., 1983)	Puffin Island (Gould et al., 1983)
Seletar virus**	Unclassified	Unclassified	Unclassified	Unknown	Not available	Not available	?	1961 (Shi et al., 2018)	*B. microplus* (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	*Ixodes ricinus*	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 *et al*. 2020, 10.1038/s41598-020-76268-y
Alphatetra-like tick virus 2	GBXQ01012426.1	*Ixodes persulcatus*	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	*Ornithodoros moubata*	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 *et al*. 2021, 10.1371/journal.pntd.0009105
Alphatetra-like tick virus 4	GFJQ02007921.1	*Ornithodoros moubata*	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 *et al*. 2017, 10.1016/j.ttbdis.2017.05.002
Alphatetra-like tick virus 5	GEMR01004364.1	*Rhipicephalus microplus*	Alphatetraviridae	ssRNA(+)	1488	Hepelivirales sp. (MW722078.1)	73	One putative ORF; predicted protein contains homologs of RdRp 2 (PF00978) motif.	Munoz *et al*. 2017, 10.1371/journal.pone.0172326
Orthomyxo-like tick virus 1	HACP01027211.1 (HACW01024387.1)	*Rhipicephalus sanguineus*	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 *et al*. 2015, Unpublished
Orthomyxo-like tick virus 2	HACP01022575.1	*Rhipicephalus sanguineus*	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 *et al*. 2015, Unpublished
Orthomyxo-like tick virus 3	HACW01018819.1	*Rhipicephalus sanguineus*	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 *et al*. 2015, Unpublished
Orthomyxo-like tick virus 4	GIJA01018702.1	*Rhipicephalus haemaphysaloides*	Orthomyxoviridae	ssRNA(-)	2357	Zambezi tick virus 1 (MH267793.1)	77	One putative ORF; predicted protein contains homologs of	Wang *et al*. 2020, 10.3389/fcimb.2020.00093

								Influenza RdRp subunit PB1 (PF00602) motif.		
Chu-like tick virus 1	GGIX01201876.1	*Ixodes scapularis*	Chuviridae	ssRNA(-)	728	Bole tick virus 3 (MH688550.1)	87	One putative ORF; predicted protein contains homologs of Mononegavirales RdRp (PF00946) motif.	Robertson Unpublished	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	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	4383	Bole tick virus 3 (MH688550.1)	84	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.681872.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	4528	Bole tick virus 3 (MH688550.1)	82	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.681877.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	4420	Bole tick virus 3 (MH688550.1)	84	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.681878.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	4440	Bole tick virus 3 (MH688550.1)	86	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.779074.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5286	Bole tick virus 3 (MH688550.1)	84	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.779079.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5379	Bole tick virus 3 (MH688550.1)	85	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.779081.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5334	Bole tick virus 3 (MH688550.1)	83	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.1447289.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5272	Bole tick virus 3 (MH688550.1)	85	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.1447293.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5001	Bole tick virus 3 (MH688550.1)	87	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.2865317.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5556	Bole tick virus 3 (MH688550.1)	83	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.2865320.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	5643	Bole tick virus 3 (MH688550.1)	87	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598504.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	8170	Bole tick virus 3 (MH688550.1)	88	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598510.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	8206	Bole tick virus 3 (MH688550.1)	87	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.4598511.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	8182	Bole tick virus 3 (MH688550.1)	85	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.7000060.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	4986	Bole tick virus 3 (MH688550.1)	84	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.10341027.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	2448	Bole tick virus 3 (MH688550.1)	86	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.10526706.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	6273	Bole tick virus 3 (MH688550.1)	87	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR10549473.10526708.1	*Hy. asiaticum*	*Chuviridae*	ssRNA(-)	6276	Nuomin virus (MW029964.1)	78	Yuan *et al*. 2020, 10.1016/j.jip.2020.107481
SRR17281102.635386.1	*I. scapualris*	*Chuviridae*	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	*Ornithodoros moubata*	dsDNA	2232	DdRp subunit 3 (encoded by *H359L*); ATP-dependent RNA helicase (encoded by *Q706L*); ATP-dependent RNA helicase (encoded by *QP509L*)	Oleaga *et al*. 2021, 10.1371/journal.pntd.0009105
GIXP02006837.1	*Ornithodoros moubata*	dsDNA	1450	DdRp subunit 3 (encoded by *H359L*); Uncharacterized protein (encoded by *H171R)*	Oleaga *et al*. 2021, 10.1371/journal.pntd.0009105
CAJHNL010000002.1	*Ornithodoros porcinus*	dsDNA	7421	DdRp subunit 2 (encoded by *EP1242L*); Helicase (encoded by *F1055L*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000003.1	*Ornithodoros porcinus*	dsDNA	6757	Transcription factor SII homolog (encoded by *I243L*); pI226R; RPB7 homolog; Uncharacterized protein (encoded by *D339L)*; Uncharacterized protein (encoded by *D129L*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000004.1	*Ornithodoros porcinus*	dsDNA	6577	Primase (encoded by *C962R*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000005.1	*Ornithodoros porcinus*	dsDNA	3455	TATA-binding protein (encoded by *B263R*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000006.1	*Ornithodoros porcinus*	dsDNA	3089	DdRp subunit 2 (encoded by *EP1242L*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000007.1	*Ornithodoros porcinus*	dsDNA	1557	DdDp (encoded by *G1211R*)	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNL010000008.1	*Ornithodoros porcinus*	dsDNA	629	Ribonucleotide reductase large subunit (encoded by *F778R*); Uncharacterized protein p360 15R	Forth *et al*. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000002.1	*Ornithodoros moubata*	dsDNA	7383	DdRp subunit 2 (encoded by *EP1242L*); Ribonucleotide reductase large subunit (encoded by *F778R*); Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000004.1	*Ornithodoros moubata*	dsDNA	670	DdRp subunit 3 (encoded by *H359L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000005.1	*Ornithodoros moubata*	dsDNA	5156	Viral histone-like protein (encoded by *A104R*); Inhibitor of apoptosis protein (encoded by *A224L*); Thymidylate kinase (encoded by *A240L*); Uncharacterized protein (encoded by *A151R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000006.1	*Ornithodoros moubata*	dsDNA	3634	DdRp subunit 3 (encoded by *H359L*); Uncharacterized protein *CP123L*; ATP-dependent RNA helicase (encoded by *QP509L*); DNA topoisomerase 2 (encoded by *P1192R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000007.1	*Ornithodoros moubata*	dsDNA	2713	Early transcription factor large subunit (encoded by *D1133L*); Uncharacterized protein (encoded by *H124R*); Uncharacterized protein (encoded by *H171R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNP010000017.1	*Ornithodoros moubata*	dsDNA	1007	Primase (encoded by *C962R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNQ010000010.1	*Ornithodoros moubata*	dsDNA	636	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNQ010000014.1	*Ornithodoros moubata*	dsDNA	679	DdRp subunit 2 (encoded by *EP1242L*); Ribonucleotide reductase large subunit (encoded by *F778R*); Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNQ010000015.1	*Ornithodoros moubata*	dsDNA	1193	Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNQ010000016.1	*Ornithodoros moubata*	dsDNA	1697	DdRp subunit 2 (encoded by *EP1242L*); Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000004.1	*Ornithodoros moubata*	dsDNA	16841	DdRp subunit 2 (encoded by *EP1242L*); Ribonucleotide reductase large subunit (encoded by *F778R*); Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000005.1	*Ornithodoros moubata*	dsDNA	15286	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000006.1	*Ornithodoros moubata*	dsDNA	13138	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6

CAJHNR010000011.1	*Ornithodoros moubata*	dsDNA	8352	Helicase (encoded by *A859L*); Uncharacterized protein p360 15R; Uncharacterized protein 5ELp28; IkB-like protein (encoded by *A238L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000013.1	*Ornithodoros moubata*	dsDNA	7718	Early transcription factor large subunit (encoded by *D1133L*); DdRp subunit 3 (encoded by *H359L*); Uncharacterized protein H171R	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000014.1	*Ornithodoros moubata*	dsDNA	7045	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000015.1	*Ornithodoros moubata*	dsDNA	6370	TATA-binding protein (encoded by *B263R*); Early transcription factor large subunit (encoded by *G1340L*); Primase (encoded by *C962R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000016.1	*Ornithodoros moubata*	dsDNA	5808	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000017.1	*Ornithodoros moubata*	dsDNA	5688	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000018.1	*Ornithodoros moubata*	dsDNA	5489	DdRp subunit 3 (encoded by *H359L*); Uncharacterized protein (encoded by *CP123L*); DNA topoisomerase II (encoded by *P1192R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000019.1	*Ornithodoros moubata*	dsDNA	5396	Uncharacterized protein p360 15R	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000020.1	*Ornithodoros moubata*	dsDNA	5152	Histone-like protein (encoded by *A104R*); Inhibitor of apoptosis protein (encoded by *A224L*); Thymidylate kinase (encoded by *A240L*); Uncharacterized protein (encoded by *A151R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000021.1	*Ornithodoros moubata*	dsDNA	4920	DdRp subunit 10 (encoded by *CP80R*); Uncharacterized protein (encoded by *CP312R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000023.1	*Ornithodoros moubata*	dsDNA	4152	Primase (encoded by *C962R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000024.1	*Ornithodoros moubata*	dsDNA	3824	DdRp subunit 2 (encoded by *EP1242L*); Transmembrane protein (encoded by *EP84R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000025.1	*Ornithodoros moubata*	dsDNA	3339	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000026.1	*Ornithodoros moubata*	dsDNA	2712	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000027.1	*Ornithodoros moubata*	dsDNA	2653	Putative poly(A) polymerase catalytic subunit (encoded by *C475L*); Primase (encoded by *C962R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000028.1	*Ornithodoros moubata*	dsDNA	2475	DdRp subunit 3 (encoded by *H359L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000029.1	*Ornithodoros moubata*	dsDNA	2196	Ribonucleotide reductase large subunit (encoded by *F778R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000030.1	*Ornithodoros moubata*	dsDNA	2179	Uncharacterized protein (encoded by CP123L); mRNA-capping enzyme (encoded by *NP868R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNR010000032.1	*Ornithodoros moubata*	dsDNA	1763	Ribonucleotide reductase large subunit (encoded by *F778R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNS010000026.1	*Ornithodoros moubata*	dsDNA	1078	Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000002.1	*Ornithodoros porcinus*	dsDNA	3380	DdRp subunit 2 (encoded by *EP1242L*); Helicase (encoded by *F1055L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000003.1	*Ornithodoros porcinus*	dsDNA	641	Ribonucleotide reductase large subunit (encoded by *F778R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000004.1	*Ornithodoros porcinus*	dsDNA	1803	TATA-binding protein (encoded by *B263R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000009.1	*Ornithodoros porcinus*	dsDNA	776	Transcription factor S-II-related protein (encoded by *I243L*); Late protein (encoded by *I226R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000011.1	*Ornithodoros porcinus*	dsDNA	2551	Primase (encoded by *C962R*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNU010000014.1	*Ornithodoros porcinus*	dsDNA	3100	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV010000002.1	*Ornithodoros porcinus*	dsDNA	4758	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6

CAJHNV010000004.1	*Ornithodoros porcinus*	dsDNA	3378	Transcription factor SII homolog (encoded by *I243L*); Late protein (encoded by *I226R*); Uncharacterized protein (encoded by *D79L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV010000005.1	*Ornithodoros porcinus*	dsDNA	2605	DdRp subunit 2 (encoded by *EP1242L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNV010000007.1	*Ornithodoros porcinus*	dsDNA	777	Transcription factor SII homolog (encoded by *I243L*)	Forth et al. 2020, 10.1186/s12915-020-00865-6
CAJHNW010000016.1	*Ornithodoros moubata*	dsDNA	1078	Helicase (encoded by *F1055L*)	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	*Nudaurelia capensis beta virus*	NC_001990.1
		NC_005898.1; NC_005899.1
	Helicoverpa armigera stunt virus	NC_001981.1; NC_001982.1
Orthomyxo-like viral contigs	*Wellfleet Bay virus*	NC_025798.1; NC_025797.1; NC_025796.1; NC_025795.1; NC_025794.1; NC_025793.1; NC_025799.1
	Araguari virus	KX670389.1; KX670390.1; KX670391.1; KX670392.1; KX670393.1; KX670394.1; KX670395.1
	Johnston Atoll quaranjavirus	NC_052931.1; NC_052930.1; NC_052929.1; NC_052928.1; NC_052927.1; NC_052926.1; NC_052925.1
	Lake Chad virus	NC_052682.1; NC_052686.1; NC_052685.1; NC_052684.1; NC_052683.1; NC_052681.1; NC_052680.1
	Tjuloc virus	JQ928941.1; JQ928942.1; JQ928943.1; JQ928944.1; JQ928945.1; JQ928946.1; MT774252.1
	Quaranfil quaranjavirus	NC_038821.1; NC_038822.1; NC_038820.1; NC_038819.1; NC_038818.1; NC_038817.1
Chu-like viral contigs	*Mivirus suffolkense*	NC_028243

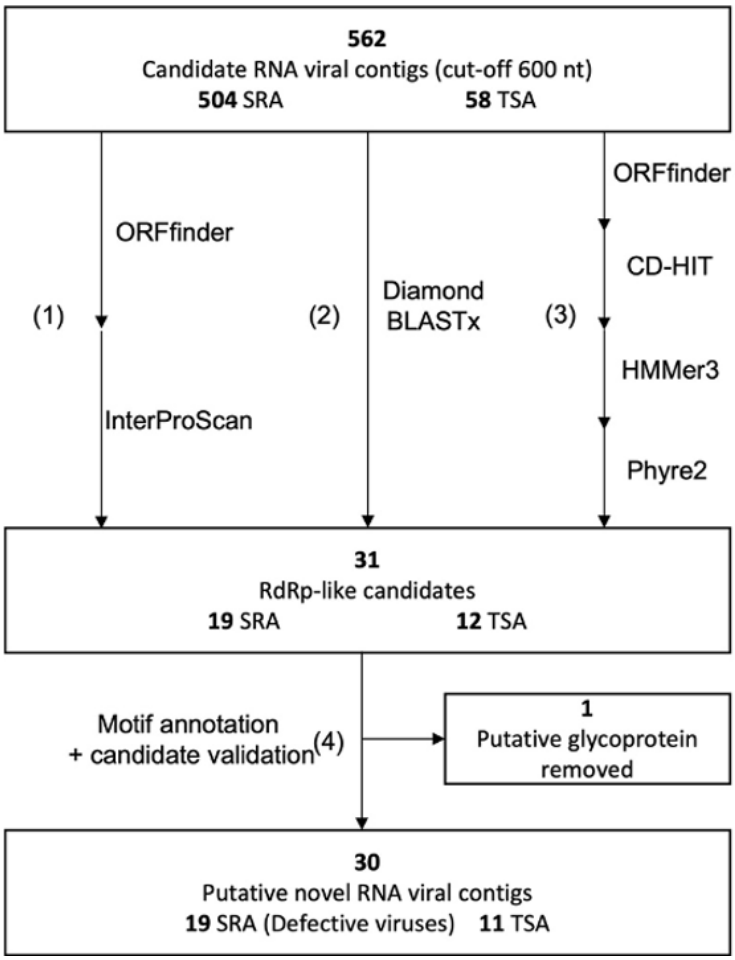
Appendix Table 6. Zoonotic ranking of 136 known tick-borne viruses with complete genomes. Zoonotic risks of virus sequences (in GenBank format) were predicted using the GCB model.

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

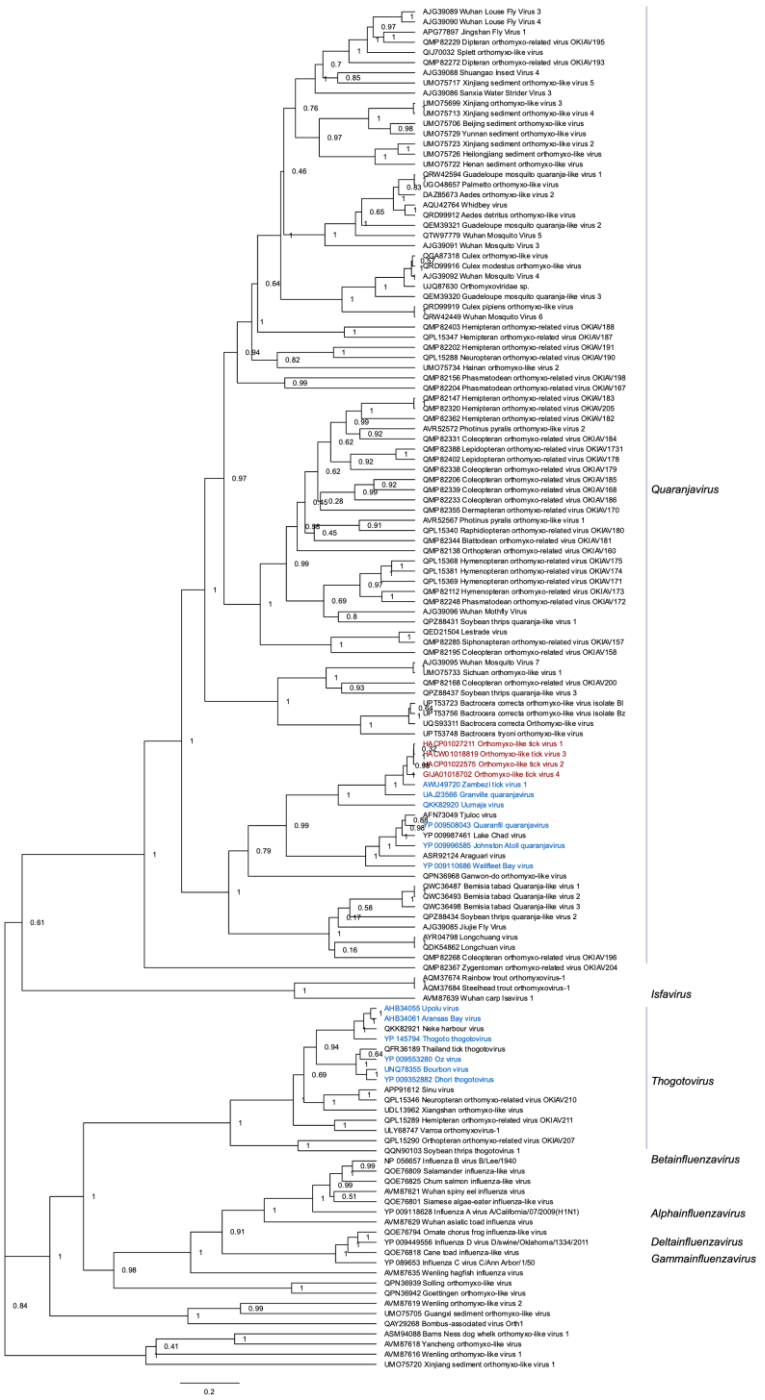
Blacklegged tick rhabdovirus 1	0.411	0.223	0.638	31	High
Tacheng tick virus 8	0.404	0.210	0.692	32	High
Jingmen tick virus	0.401	0.219	0.663	33	High
South Bay virus	0.395	0.210	0.630	34	High
Ngari virus	0.393	0.214	0.624	35	High
Kaisodi virus	0.392	0.208	0.590	36	High
Kupe virus	0.391	0.160	0.642	37	High
Lone star tick densovirus 1	0.391	0.221	0.654	38	High
Blacklegged tick phlebovirus 3	0.371	0.195	0.640	39	High
Pacific coast tick nairovirus	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 tick thogotovirus	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

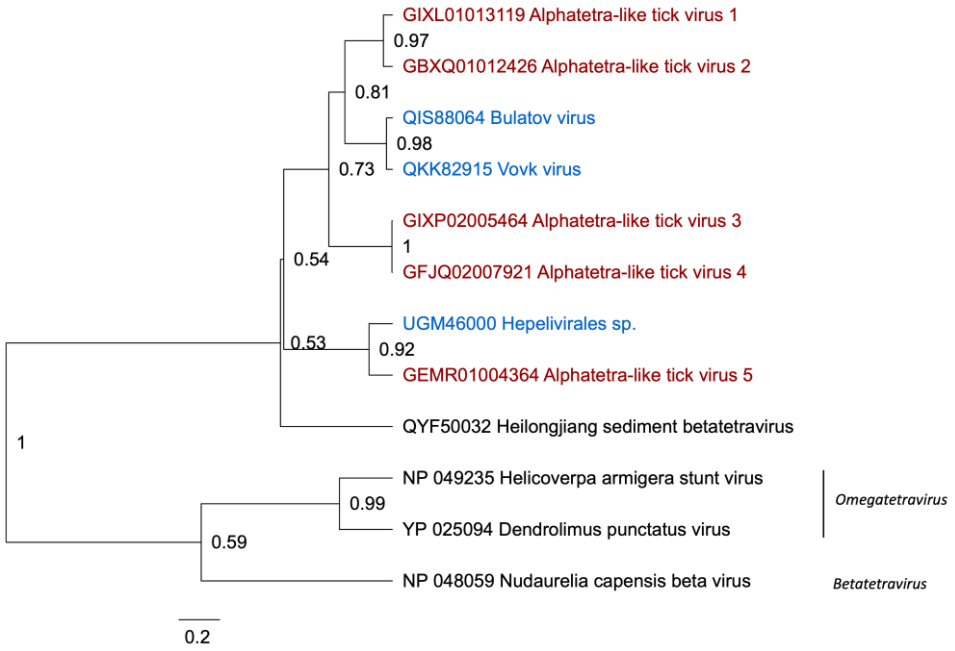
Wad Medani virus	0.186	0.105	0.401	112	Medium
Kundal virus	0.184	0.095	0.312	113	Medium
Chobar Gorge virus	0.178	0.096	0.337	114	Medium
African swine fever virus	0.175	0.082	0.311	115	Medium
Farallon virus	0.175	0.088	0.312	116	Medium
Oz virus	0.174	0.089	0.283	117	Low
Nairobi sheep disease virus	0.173	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



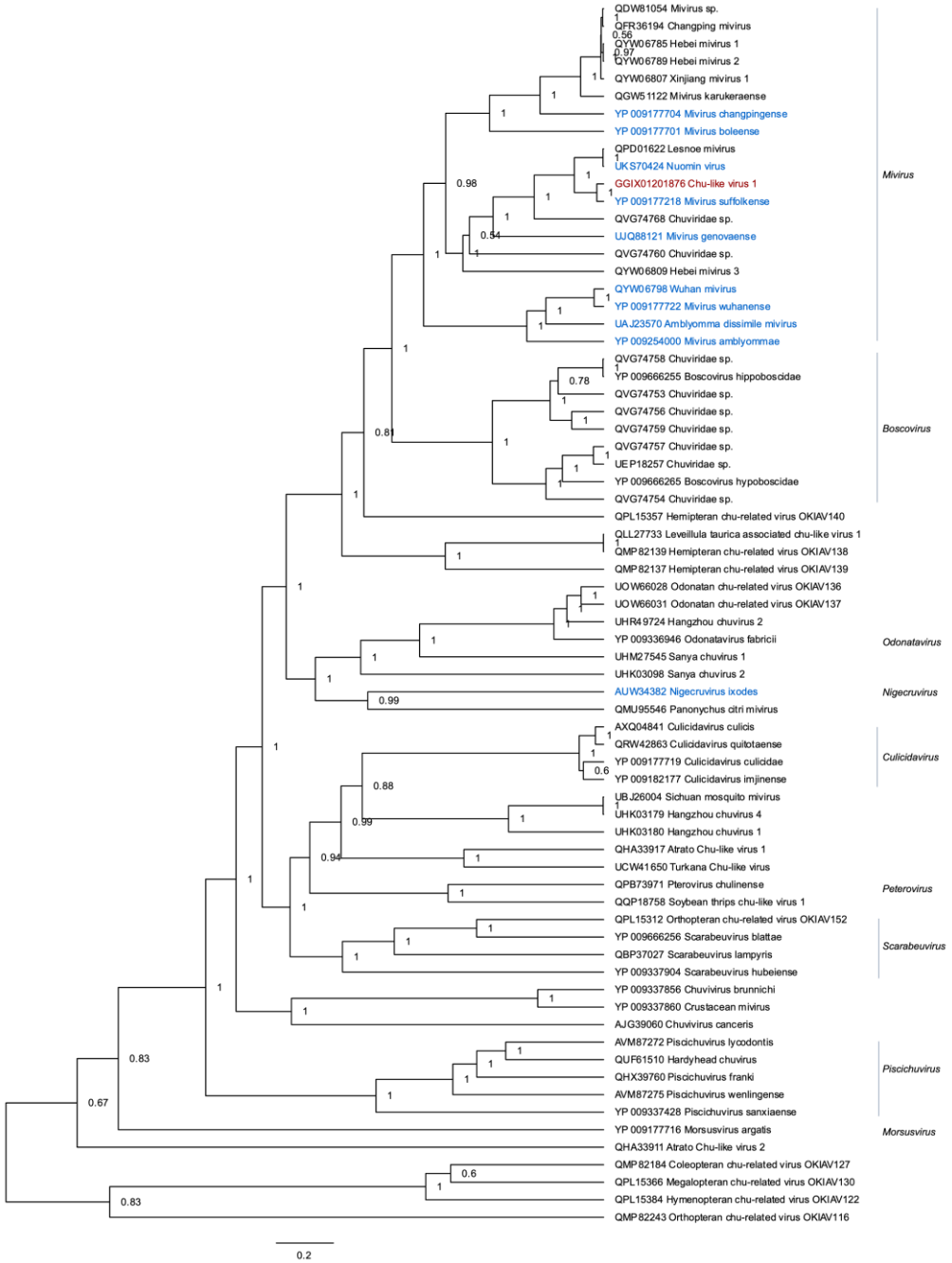
Appendix Figure 1. Workflow of detecting viral RNA-dependent RNA polymerase sequences. (1) ORFs were translated using ORFfinder (cut-off 200 aa). The translated sequences were predicted using the InterProScan-5.55-88.0 (--minsize 600; -goterms). (2) BLASTx using Diamond v2.0.14.152 against both non-redundant 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 Alphatetra-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.