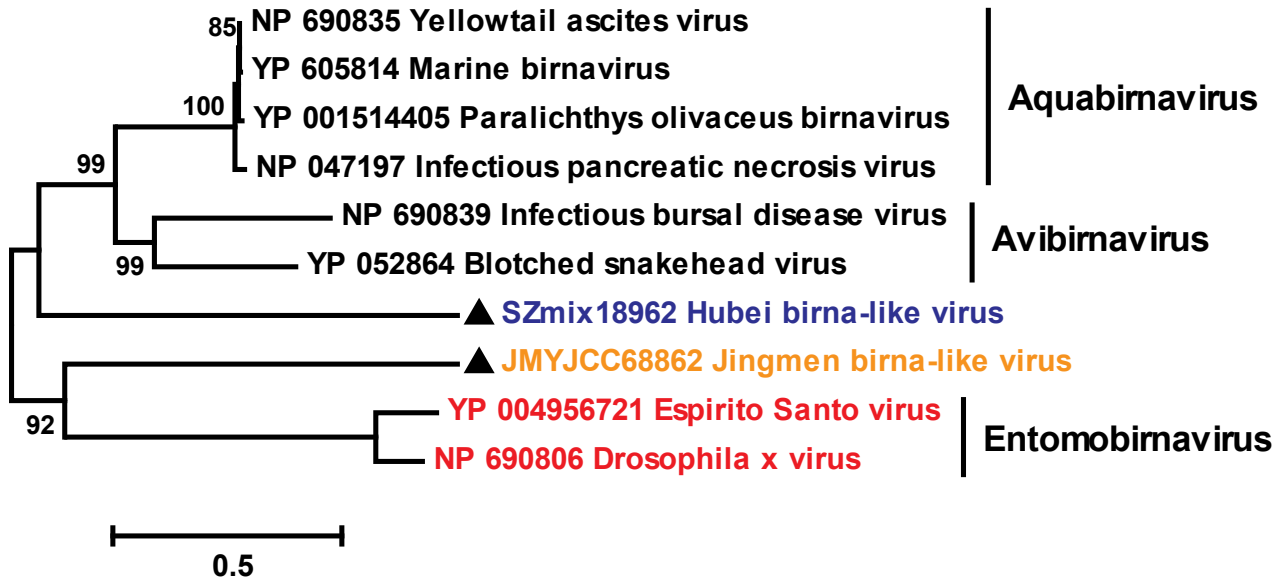


Supplementary Data 1. Maximum likelihood phylogeny of the “Astro” clade. Each phylogeny provided in this and the other Supplementary Data is based on an analysis of the viral RdRp domain. The names of the viruses are marked with different colours based on their host taxonomy. The newly identified viruses are distinguished from previously published viruses with black solid triangle at the beginning of their names. The silhouetted animal denotes host taxa that contain endogenous virus copies (i.e. EVEs), labelled next to its exogenous relative(s). The star symbol signifies viral frequency, subdivided as follows: no star (< 0.1% non-rRNA reads), one star (0.1% ~ 1%), two stars (> 1%). The grey tick symbol indicates viruses whose genome is shown as a representative in Supplementary Data 22.



Red: Phylum Arthropoda, Class Insecta

Light blue: Phylum Arthropoda, Subphylum Crustacea

Purple: Phylum Arthropoda, Subphylum Myriapoda

Yellow: Phylum Arthropoda, Subphylum Chelicerata

Orange: Phylum Nematoda

Dark blue: Superphylum Lophotrochozoa

Black: Subphylum Vertebrata

Green: Kingdom Viridiplantae

Dark green: Kingdom Fungi

Grey: other hosts or undertermined

EVE vertebrates

EVE arthropods

EVE nematodes

EVE protists

EVE flatworms

EVE plants

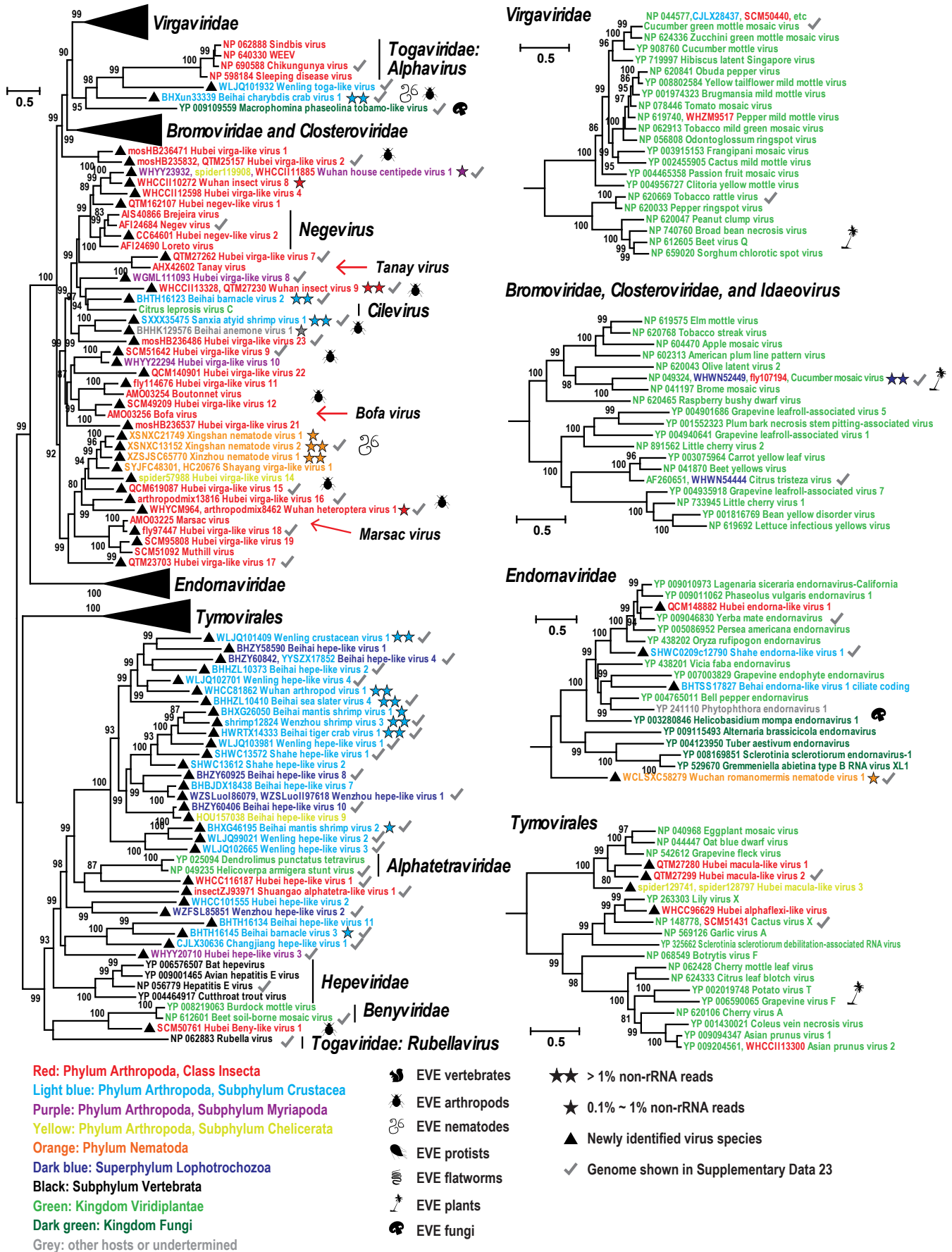
EVE fungi

★★ > 1% non-rRNA reads

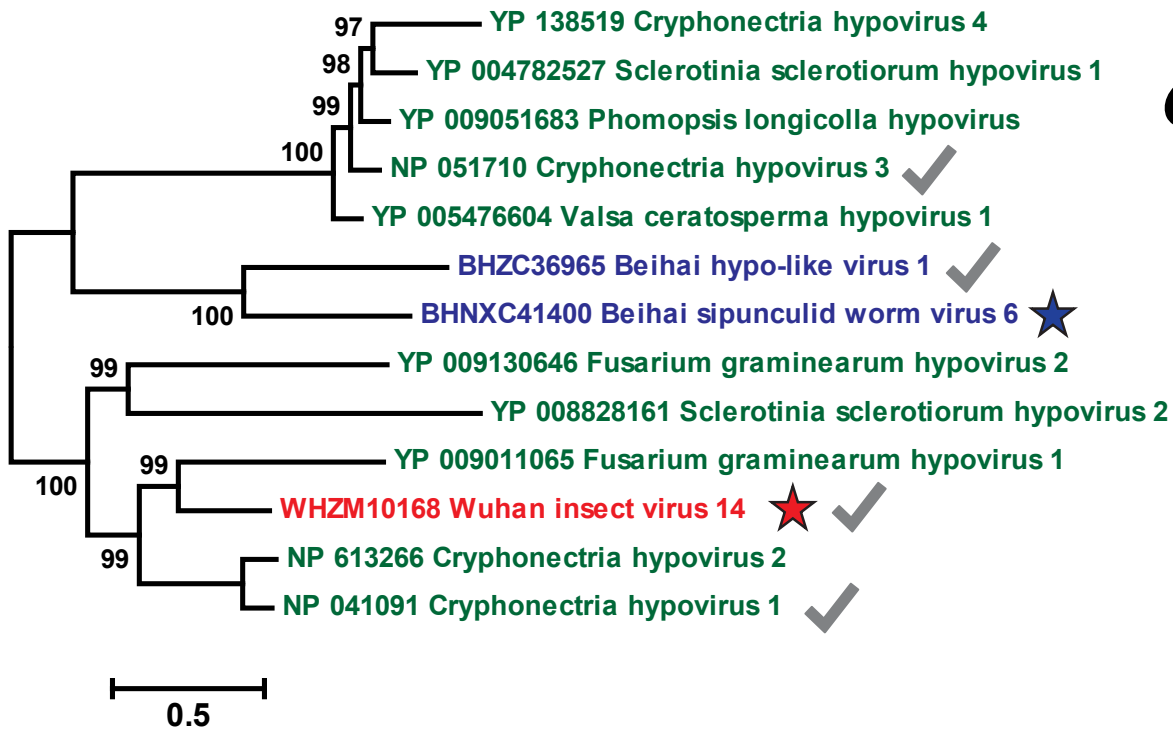
★ 0.1% ~ 1% non-rRNA reads

▲ Newly identified virus species

Supplementary Data 2. Maximum likelihood phylogeny of the “Birna” clade. Figure legend follows Supplementary Data 1.

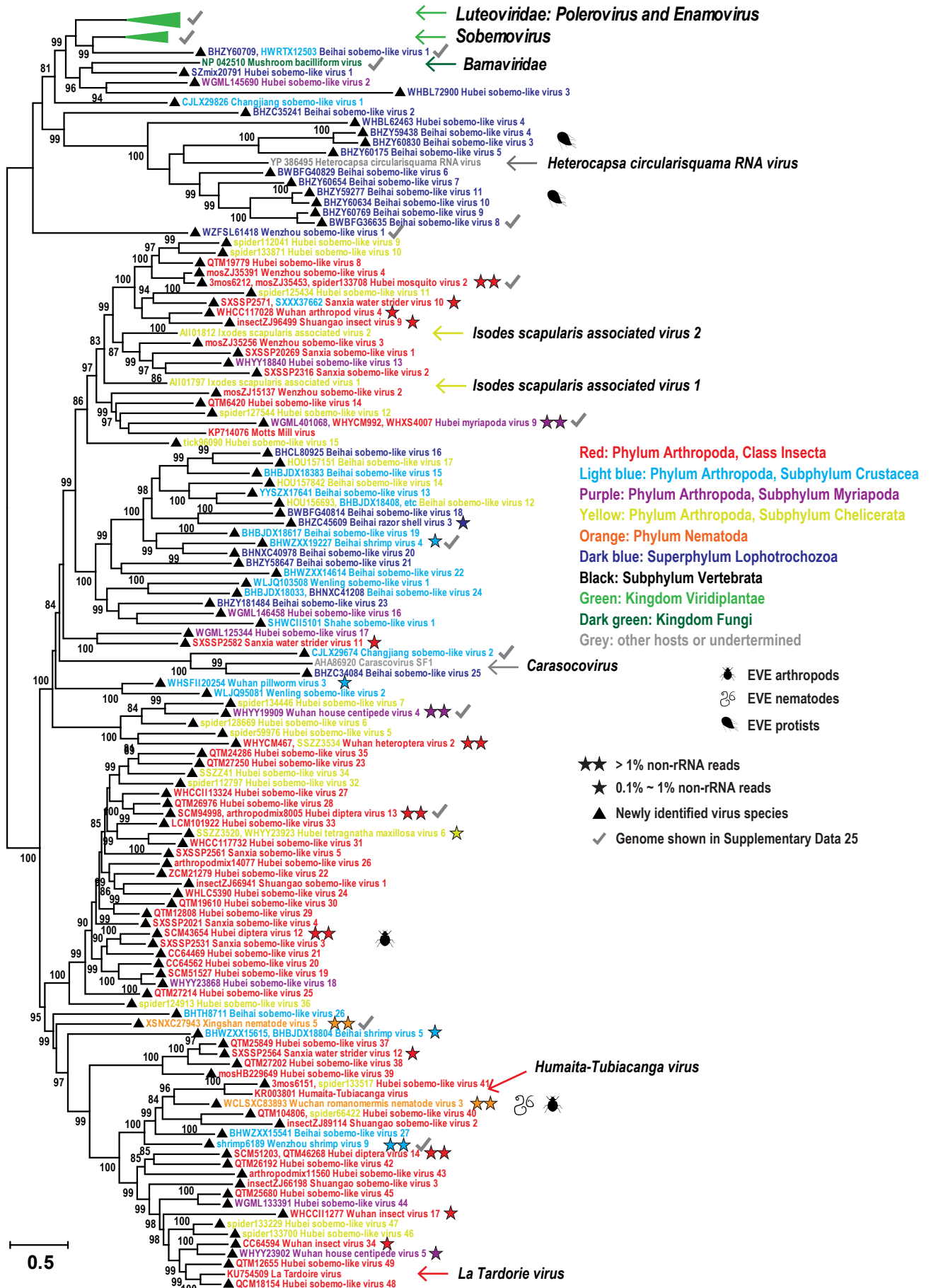


Supplementary Data 3. Maximum likelihood phylogeny of the “Hepe-Virga” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 23.

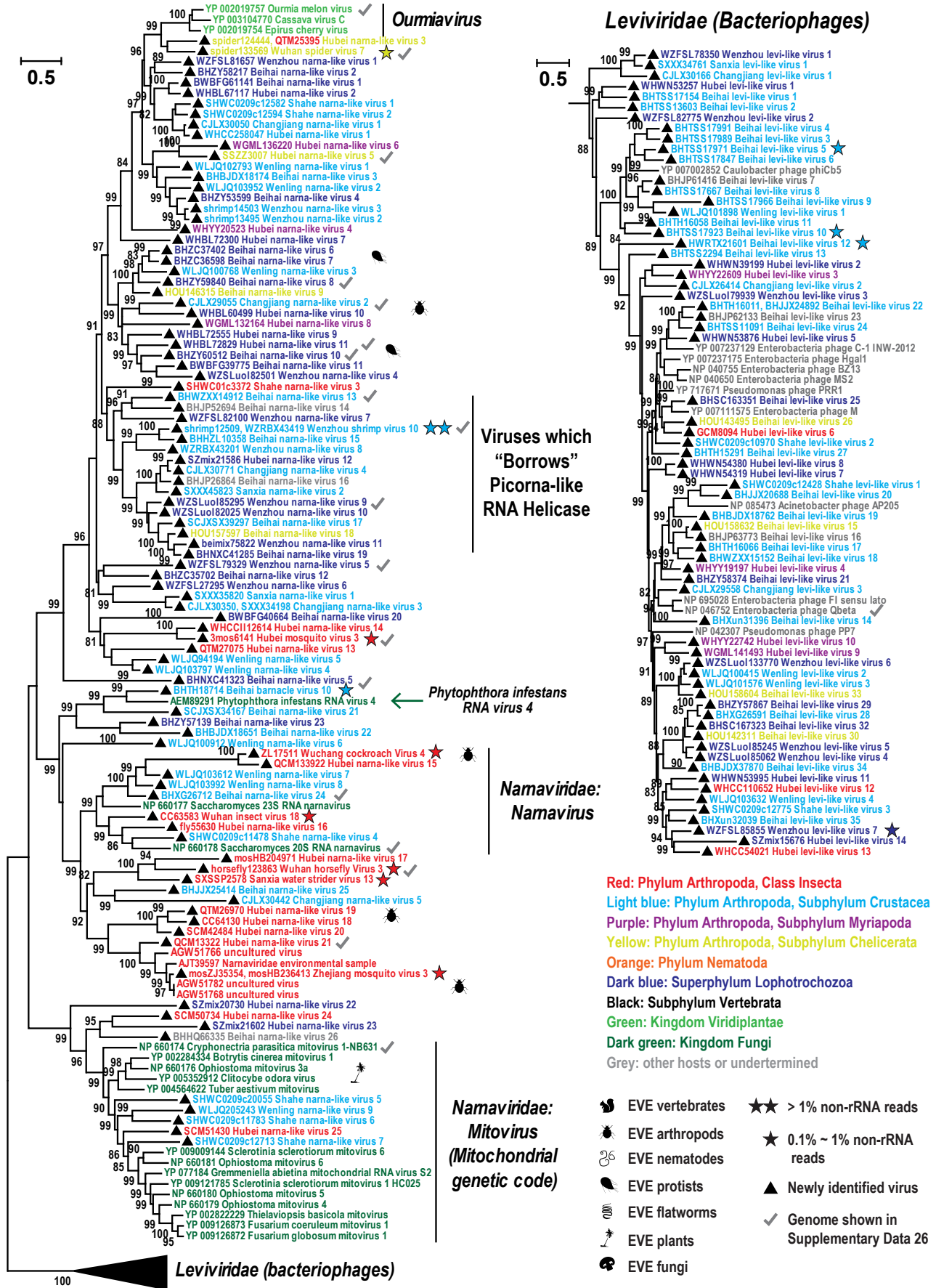


- | | | |
|--|-----------------|---|
| Red: Phylum Arthropoda, Class Insecta | EVE vertebrates | ★★ > 1% non-rRNA reads |
| Light blue: Phylum Arthropoda, Subphylum Crustacea | EVE arthropods | ★ 0.1% ~ 1% non-rRNA reads |
| Purple: Phylum Arthropoda, Subphylum Myriapoda | EVE nematodes | ▲ Newly identified virus species |
| Yellow: Phylum Arthropoda, Subphylum Chelicerata | EVE protists | ✓ Genome shown in Supplementary Data 24 |
| Orange: Phylum Nematoda | EVE flatworms | |
| Dark blue: Superphylum Lophotrochozoa | EVE plants | |
| Black: Subphylum Vertebrata | EVE fungi | |
| Green: Kingdom Viridiplantae | | |
| Dark green: Kingdom Fungi | | |
| Grey: other hosts or undertermined | | |

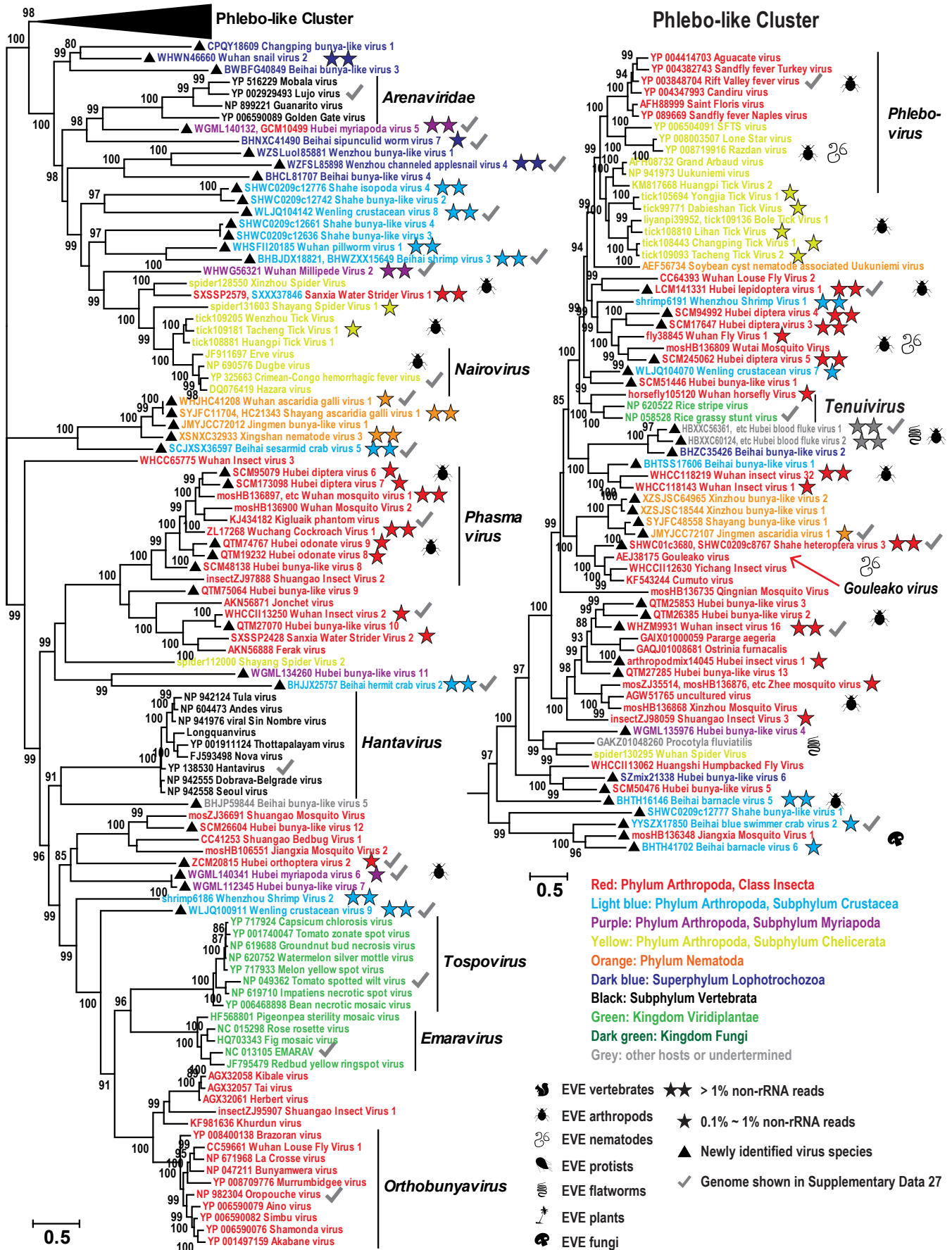
Supplementary Data 4. Maximum likelihood phylogeny of the “Hypo” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 24.



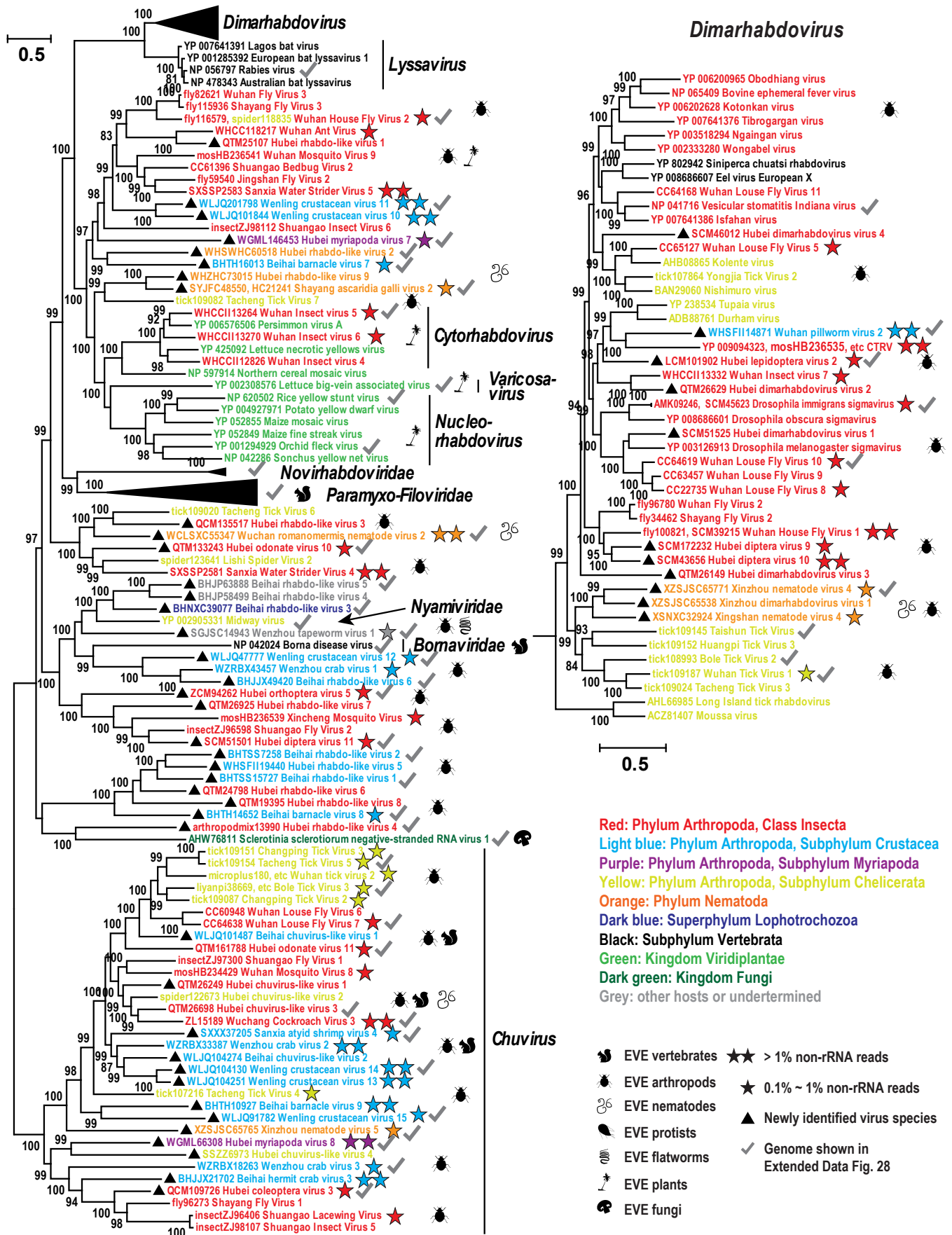
Supplementary Data 5. Maximum likelihood phylogeny of the “Luteo-Sobemo” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 25.



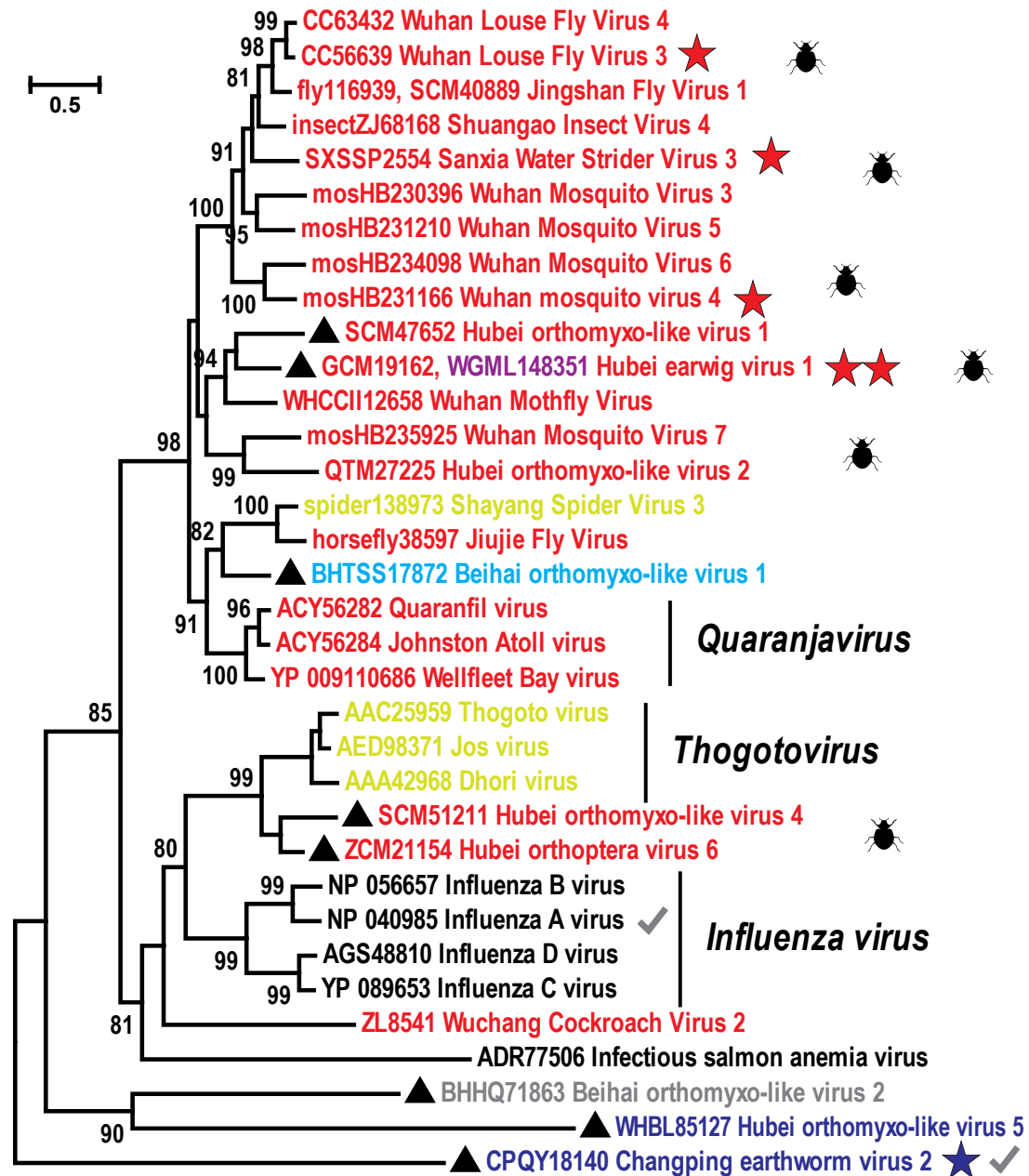
Supplementary Data 6. Maximum likelihood phylogeny of the "Narna-Levi" clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 26.



Supplementary Data 7. Maximum likelihood phylogeny of the “Bunya-Arena” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 27.

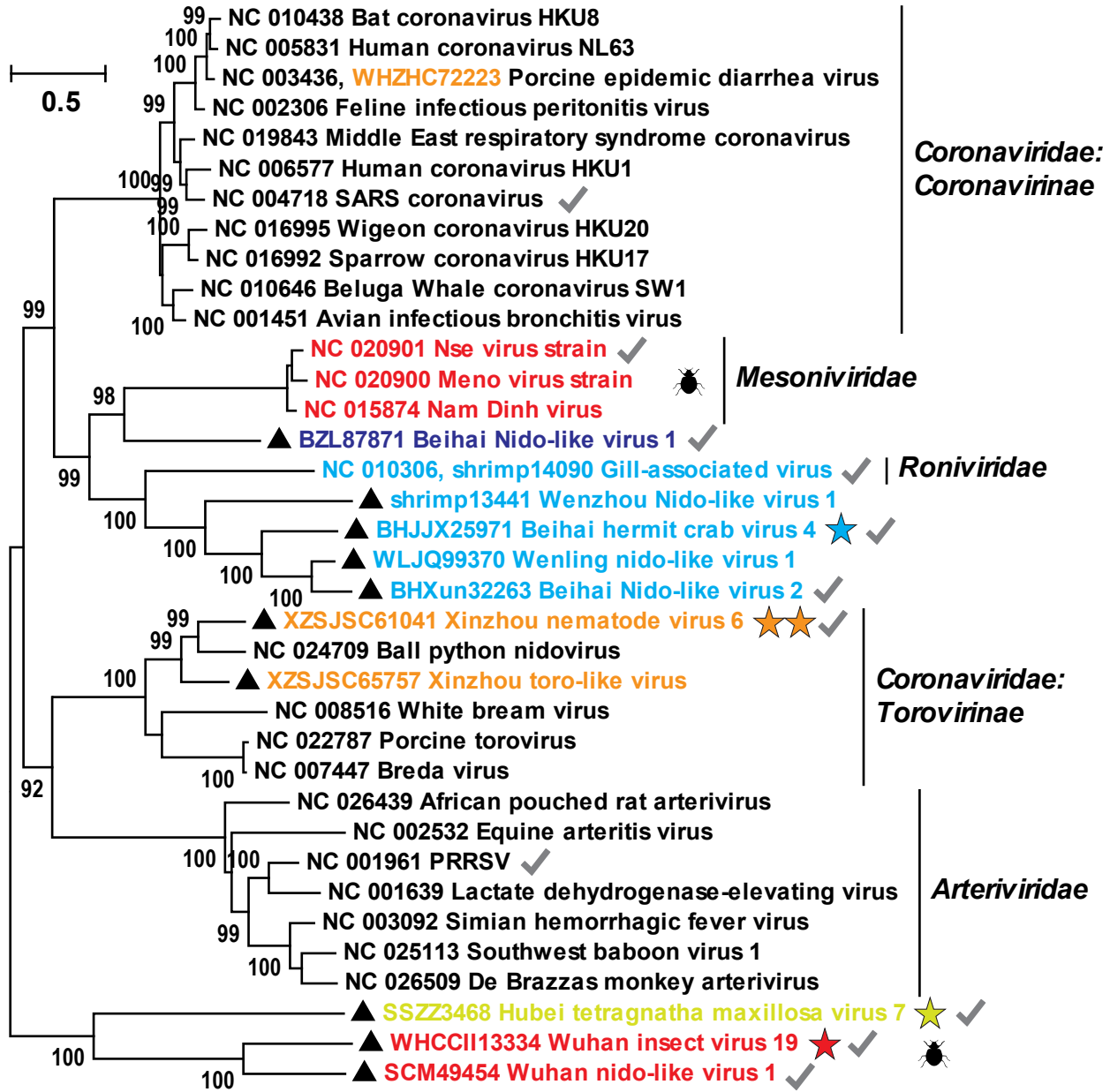


Supplementary Data 8. Maximum likelihood phylogeny of the “Mono-Chu” clade. Figure legend follows Extended Data Fig. 1. Matching virus genomes are shown in Extended Data Fig. 28.



- Red: Phylum Arthropoda, Class Insecta
 - Light blue: Phylum Arthropoda, Subphylum Crustacea
 - Purple: Phylum Arthropoda, Subphylum Myriapoda
 - Yellow: Phylum Arthropoda, Subphylum Chelicerata
 - Orange: Phylum Nematoda
 - Dark blue: Superphylum Lophotrochozoa
 - Black: Subphylum Vertebrata
 - Green: Kingdom Viridiplantae
 - Dark green: Kingdom Fungi
 - Grey: other hosts or undetermined
- EVE vertebrates
 - EVE arthropods
 - EVE nematodes
 - EVE protists
 - EVE flatworms
 - EVE plants
 - EVE fungi
- ★★ > 1% non-rRNA reads
 - ★ 0.1% ~ 1% non-rRNA reads
 - ▲ Newly identified virus species
 - ✓ Genome shown in Extended Data Fig. 29

Supplementary Data 9. Maximum likelihood phylogeny of the “Orthomyxo” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 29.



Red: Phylum Arthropoda, Class Insecta

Light blue: Phylum Arthropoda, Subphylum Crustacea

Purple: Phylum Arthropoda, Subphylum Myriapoda

Yellow: Phylum Arthropoda, Subphylum Chelicerata

Orange: Phylum Nematoda

Dark blue: Superphylum Lophotrochozoa

Black: Subphylum Vertebrata

Green: Kingdom Viridiplantae

Dark green: Kingdom Fungi

Grey: other hosts or undetermined

☾ EVE vertebrates

🐜 EVE arthropods

🪱 EVE nematodes

🐛 EVE protists

🐛 EVE flatworms

🌱 EVE plants

🍄 EVE fungi

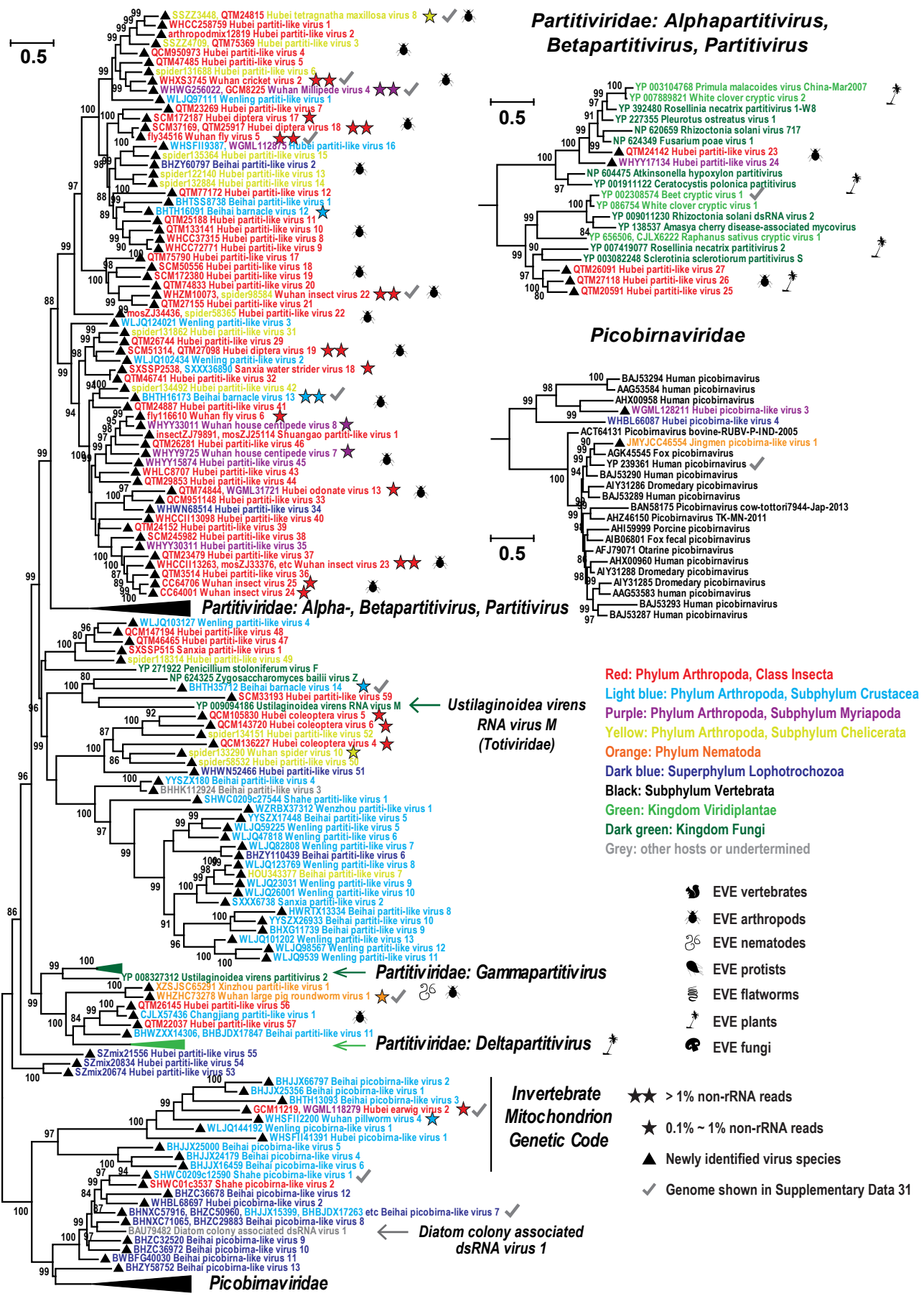
★★ > 1% non-rRNA reads

★ 0.1% ~ 1% non-rRNA reads

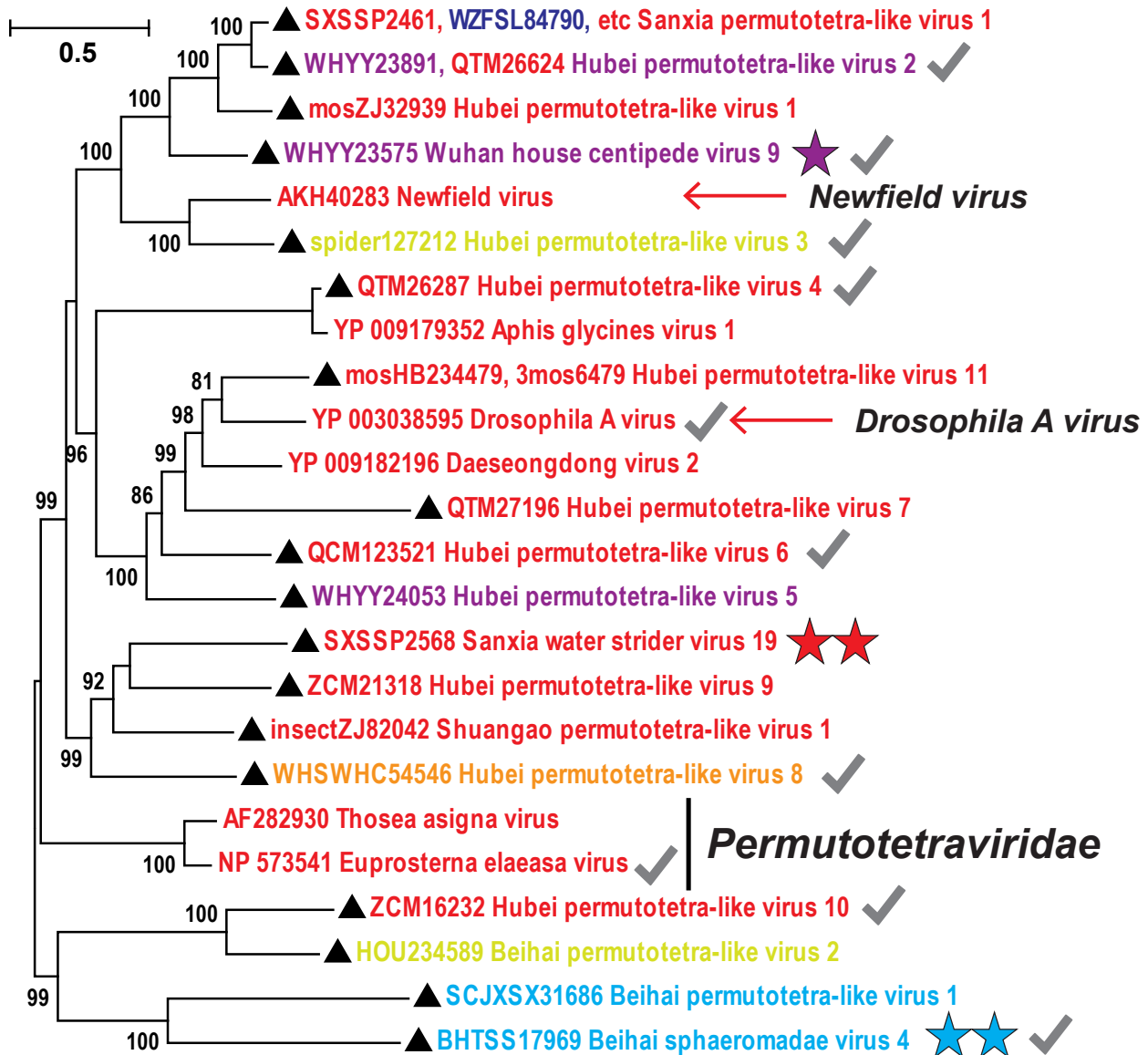
▲ Newly identified virus species

✓ Genome shown in Supplementary Data 30

Supplementary Data 10. Maximum likelihood phylogeny of the “Nido” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 30.



Supplementary Data 11. Maximum likelihood phylogeny of the “Partitvi-Picobirna” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 31.



Red: Phylum Arthropoda, Class Insecta

Light blue: Phylum Arthropoda, Subphylum Crustacea

Purple: Phylum Arthropoda, Subphylum Myriapoda

Yellow: Phylum Arthropoda, Subphylum Chelicerata

Orange: Phylum Nematoda

Dark blue: Superphylum Lophotrochozoa

Black: Subphylum Vertebrata

Green: Kingdom Viridiplantae

Dark green: Kingdom Fungi

Grey: other hosts or undetermined



EVE vertebrates

★★ > 1% non-rRNA reads



EVE arthropods

★ 0.1% ~ 1% non-rRNA reads



EVE nematodes

▲ Newly identified virus species



EVE protists

✓ Genome shown in Supplementary Data 32



EVE flatworms

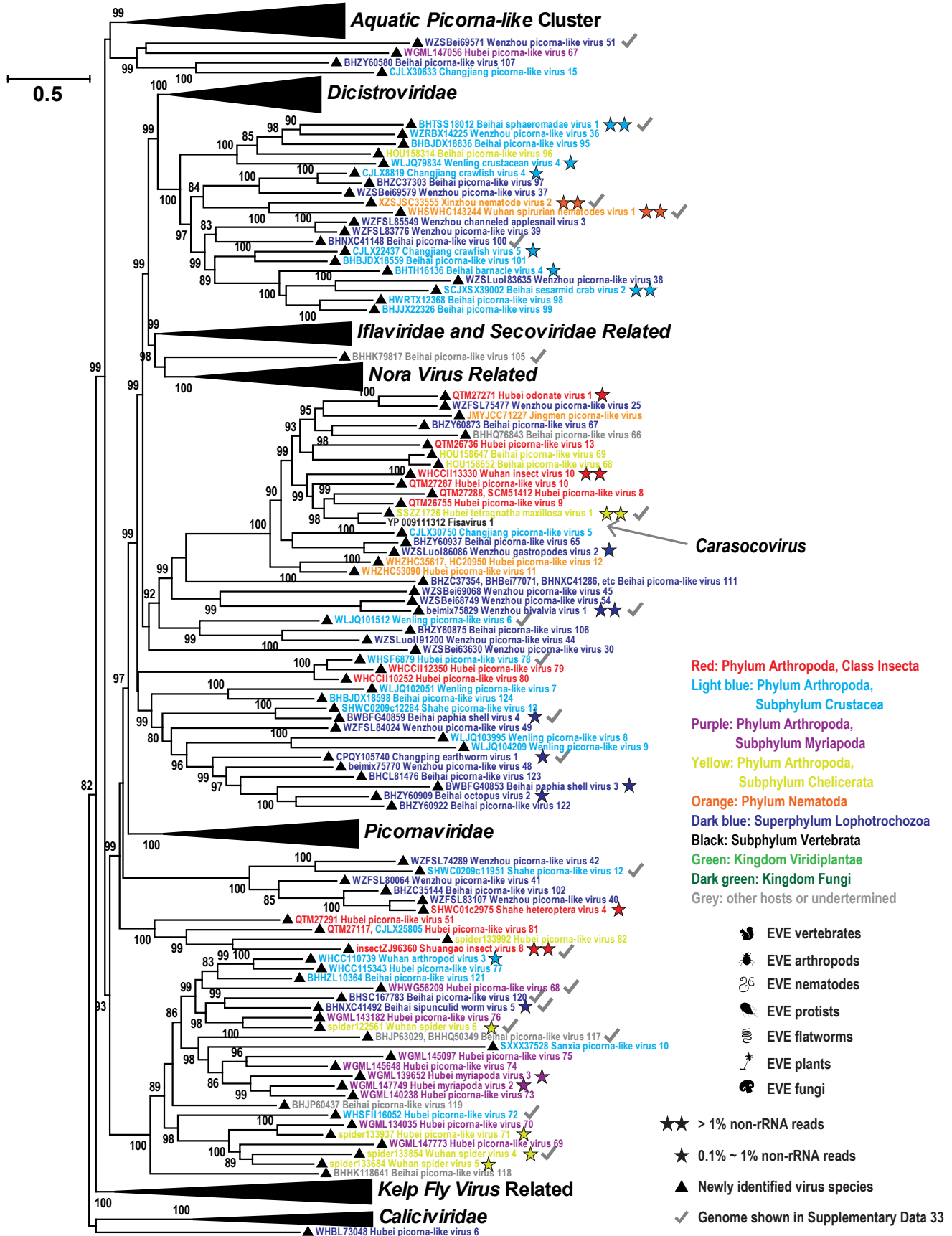


EVE plants

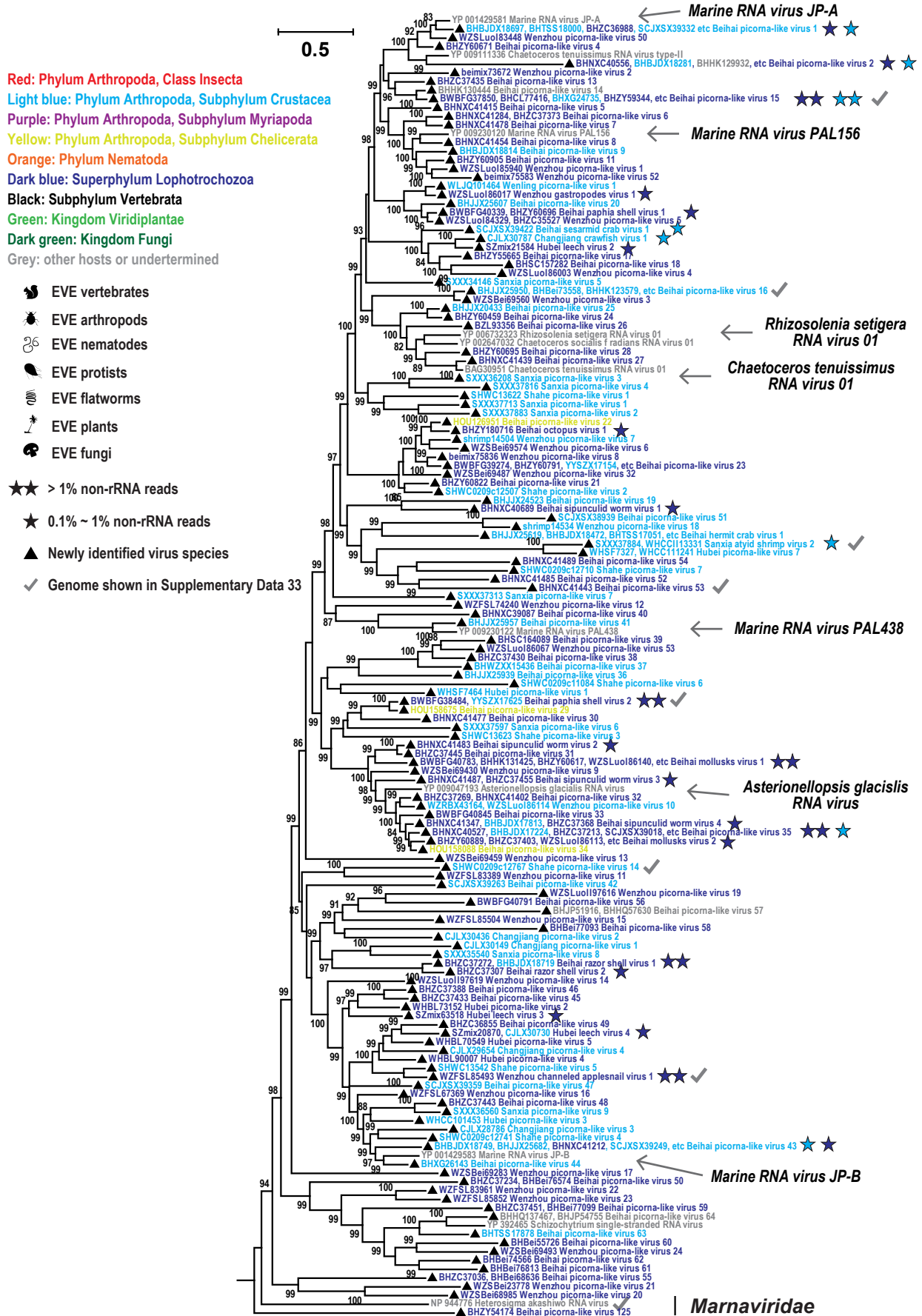


EVE fungi

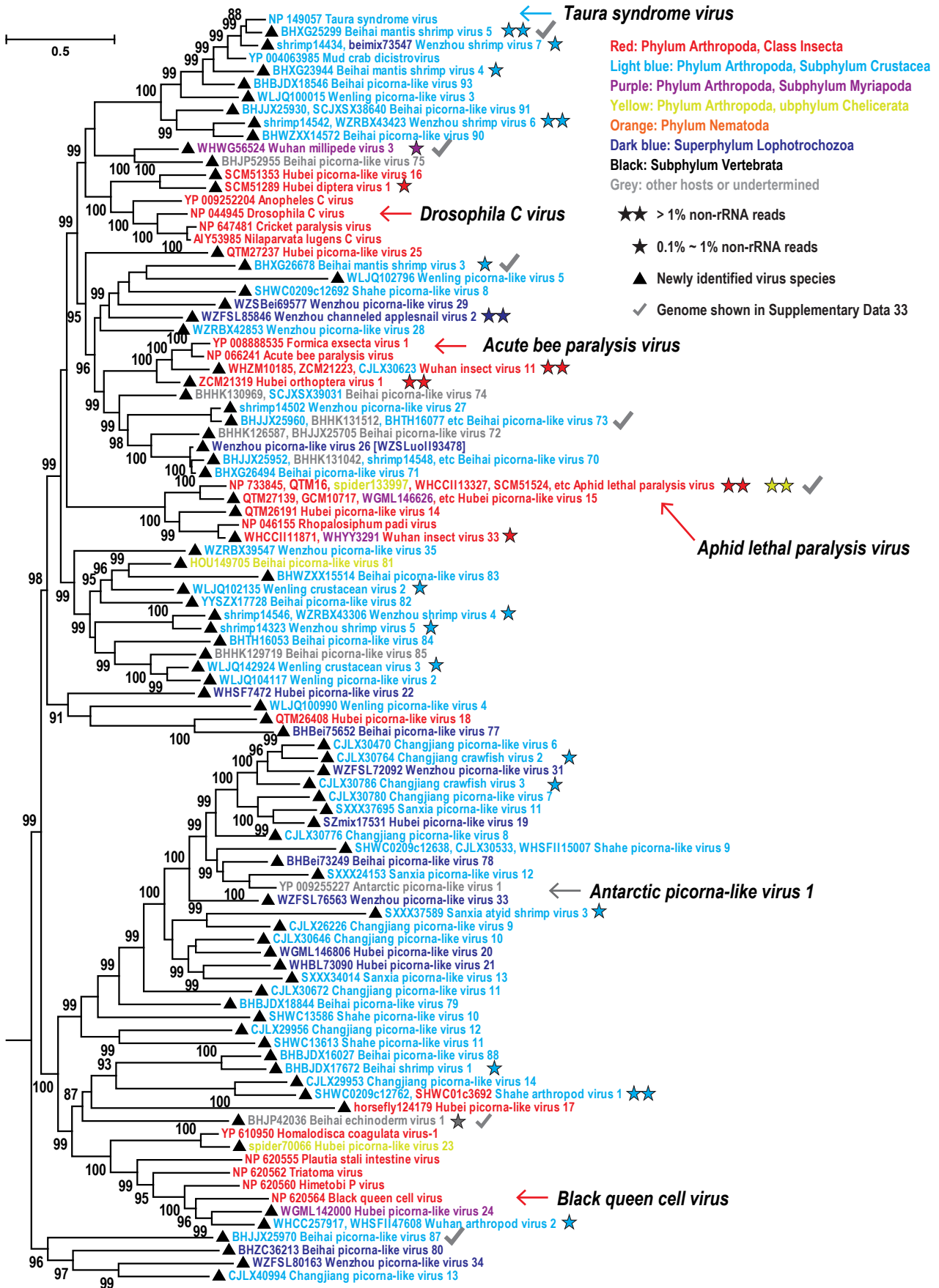
Supplementary Data 12. Maximum likelihood phylogeny of the “Permutotetra” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 32.



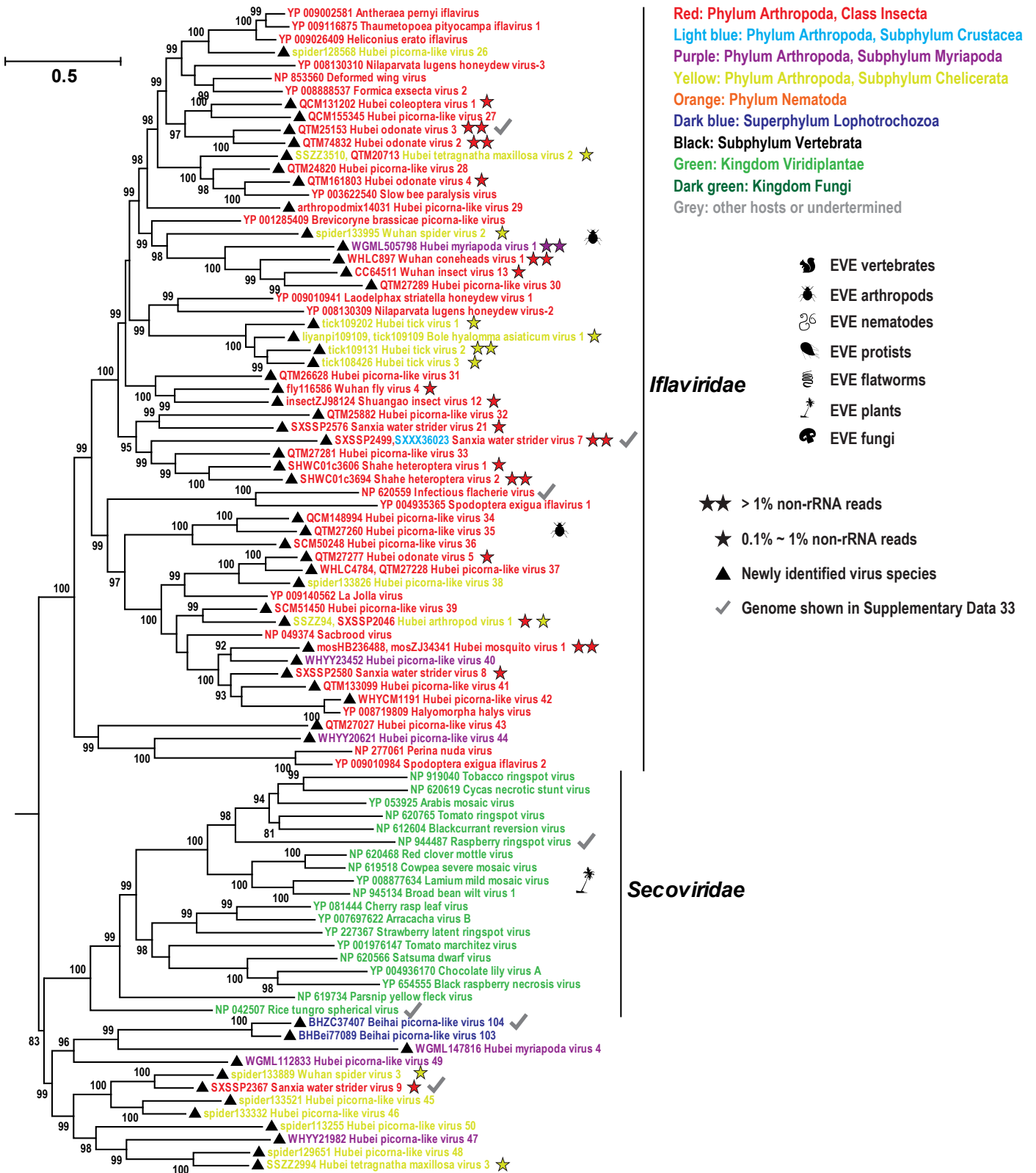
Supplementary Data 13. Maximum likelihood phylogeny of the “Picorna-Calici” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Extended Data Fig. 33. Part of the diversity not shown in this figure can be found in Supplementary Data 14-17.



Supplementary Data 14. Maximum likelihood phylogeny of the “Aquatic picorna-like cluster” within the “Picorna-Calici” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 33.

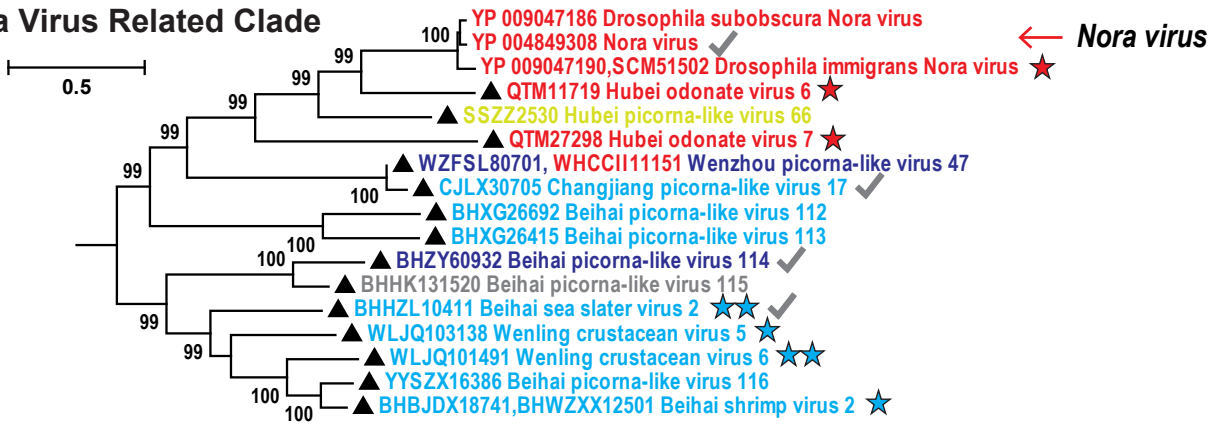


Supplementary Data 15. Maximum likelihood phylogeny of the “Dicistroviridae cluster” within the “Picorna-Calici” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 33.

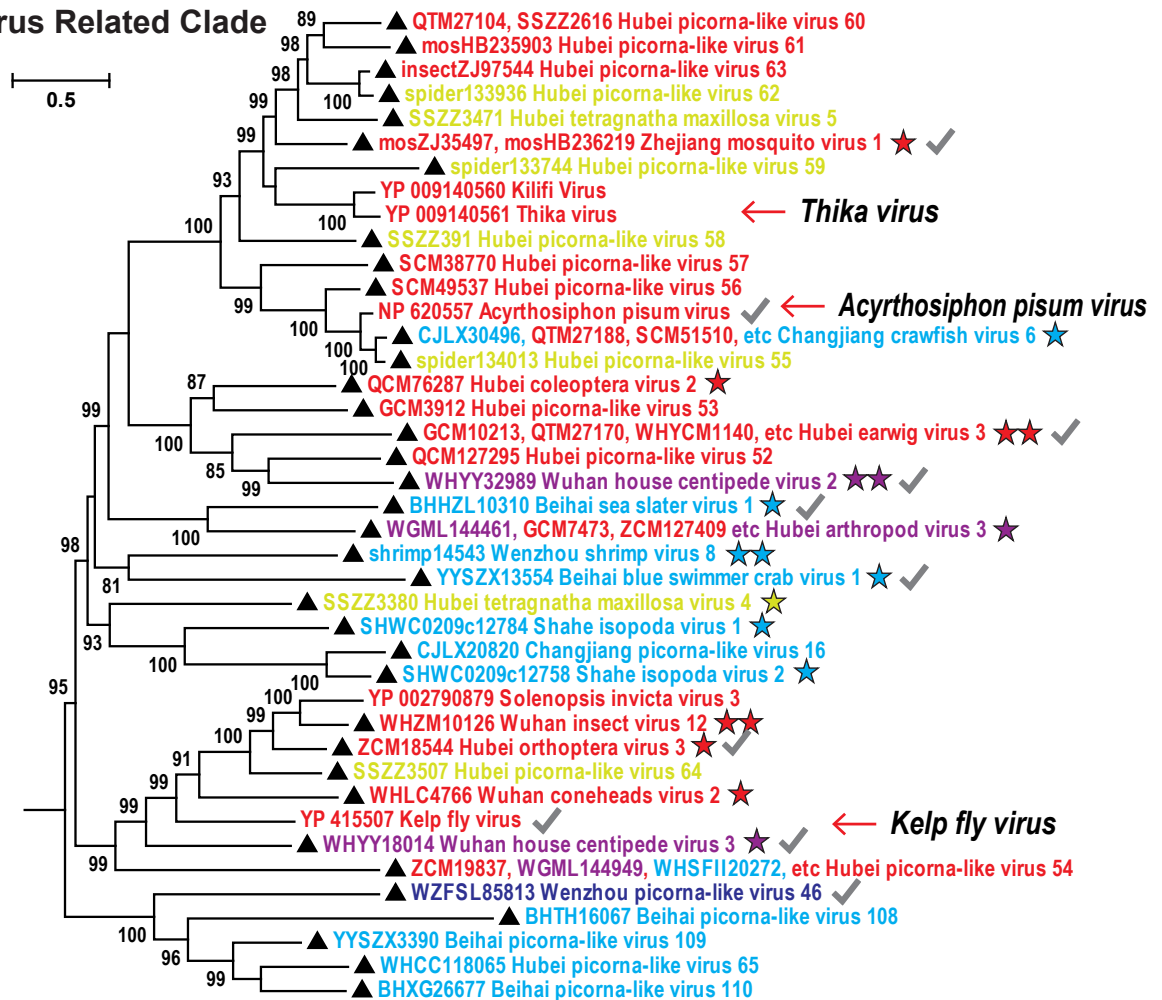


Supplementary Data 16. Maximum likelihood phylogeny of the “Iflaviridae-Secoviridae related cluster” within the “Picorna-Calici” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 33.

Nora Virus Related Clade

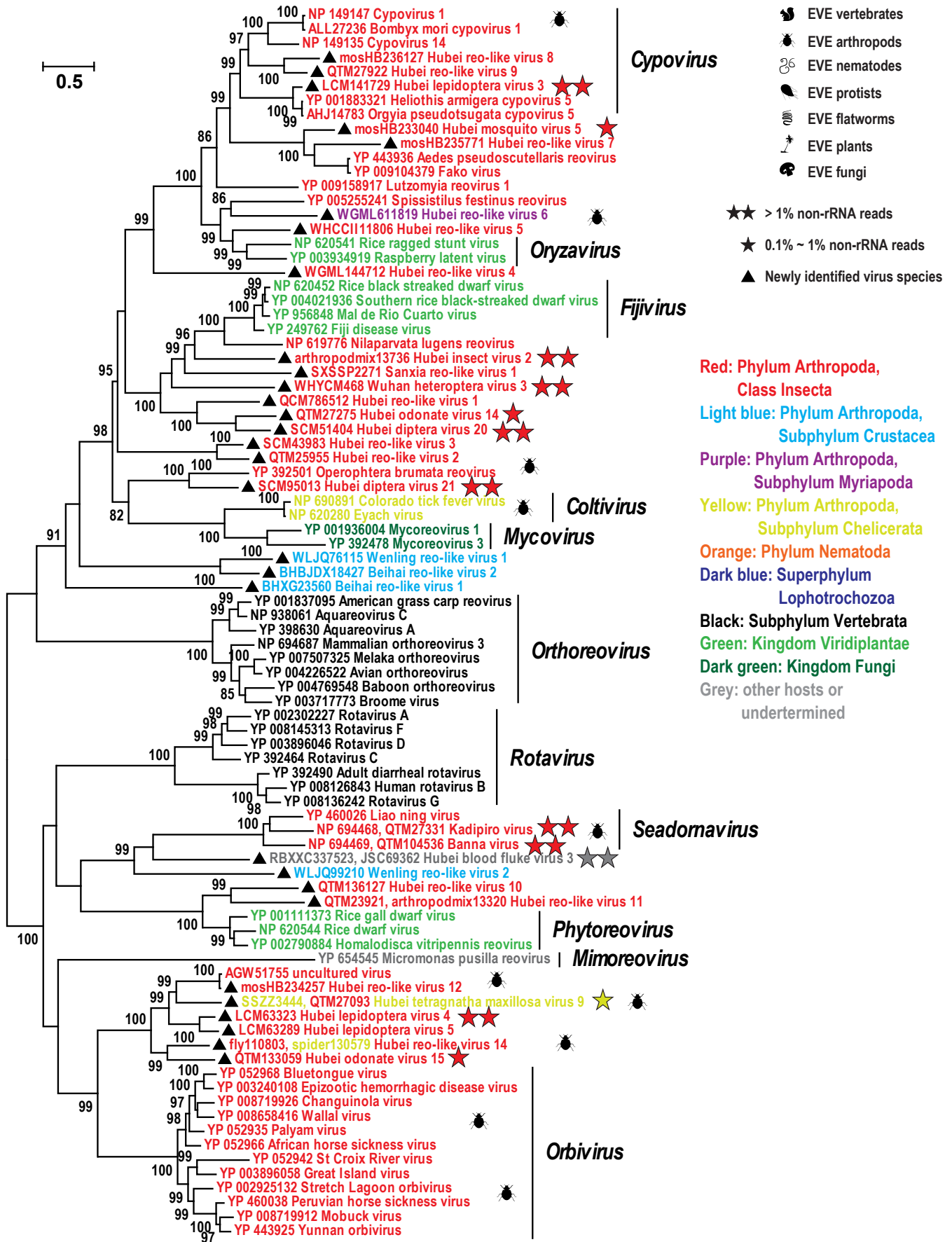


Kelp Fly Virus Related Clade

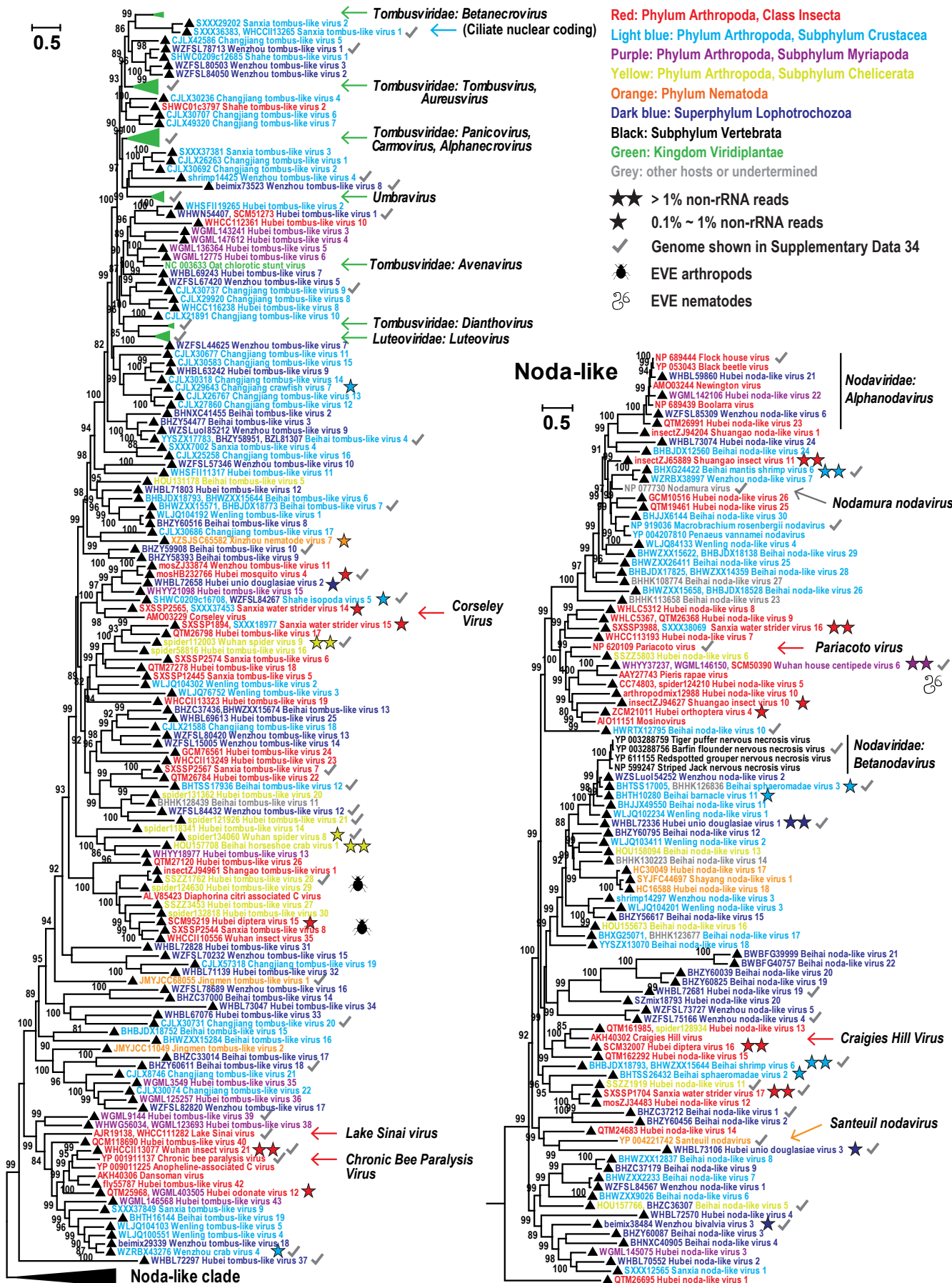


- Red: Phylum Arthropoda, Class Insecta
 - Light blue: Phylum Arthropoda, Subphylum Crustacea
 - Purple: Phylum Arthropoda, Subphylum Myriapoda
 - Yellow: Phylum Arthropoda, Subphylum Chelicerata
 - Orange: Phylum Nematoda
 - Dark blue: Superphylum Lophotrochozoa
 - Black: Subphylum Vertebrata
 - Green: Kingdom Viridiplantae
 - Grey: other hosts or undetermined
- EVE vertebrates
 - EVE arthropods
 - EVE nematodes
 - EVE protists
 - EVE flatworms
 - EVE plants
 - EVE fungi
- ★★★ > 1% non-rRNA reads
 - ★ 0.1% ~ 1% non-rRNA reads
 - ▲ Newly identified virus species
 - ✓ Genome shown in Supplementary Data 23

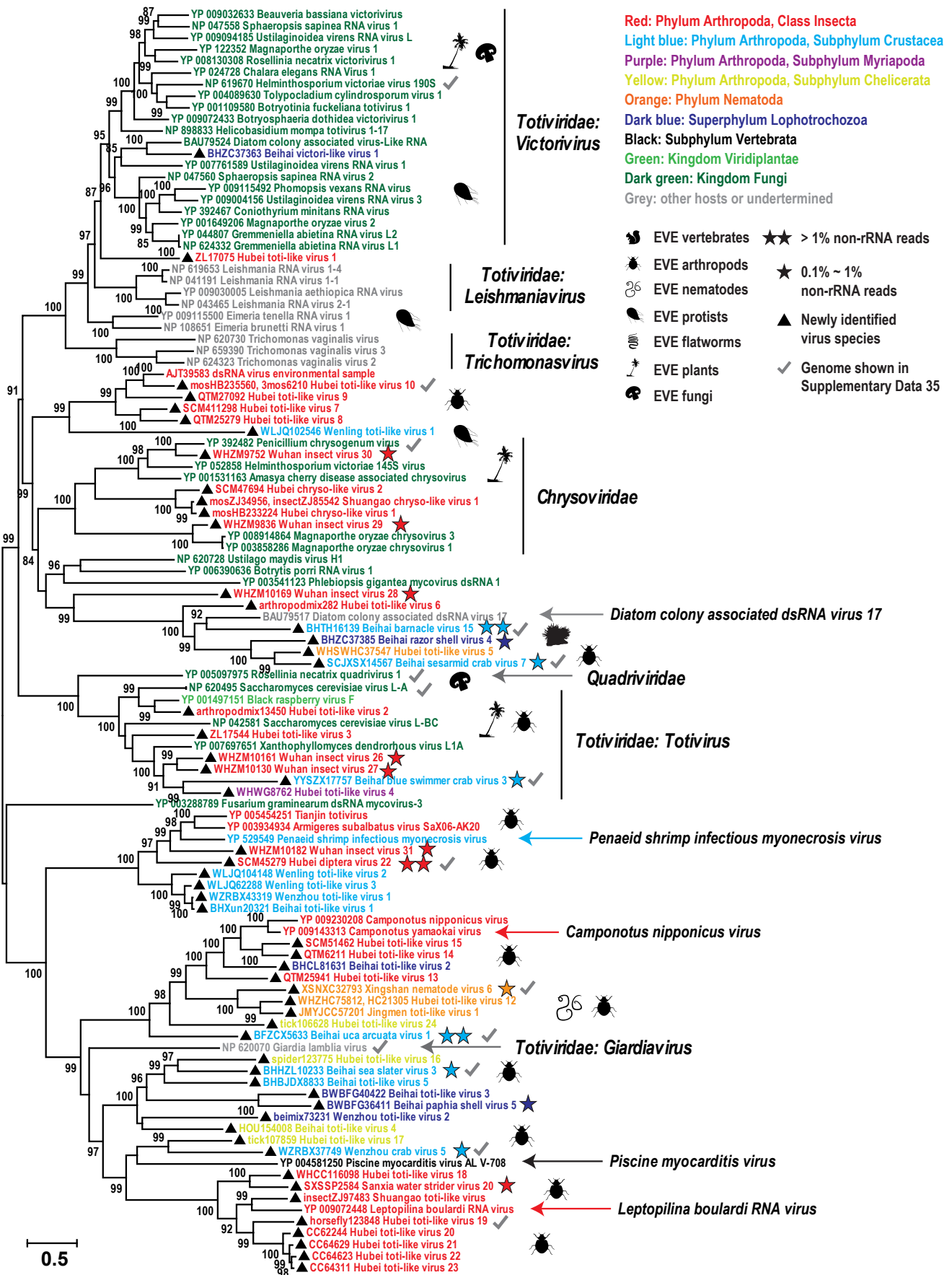
Supplementary Data 17. Maximum likelihood phylogenies of the “Kelp Fly Virus Related Cluster” and “Noravirus Related Cluster” within the “Picorna-Calici” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 33.



Supplementary Data 18. Maximum likelihood phylogeny of the “Reo” clade. Figure legend follows Supplementary Data 1.

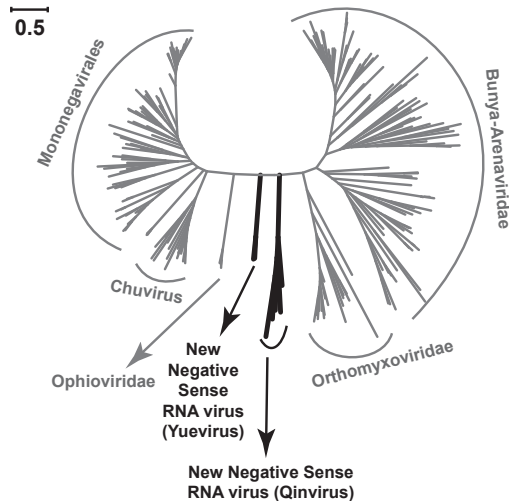


Supplementary Data 19. Maximum likelihood phylogenies of the “Tombus-noda” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 34.

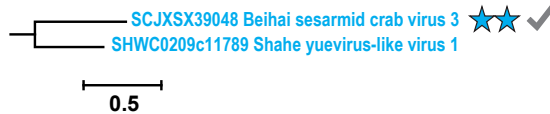


Supplementary Data 20. Maximum likelihood phylogeny of the “Toti-Chryso” clade. Figure legend follows Supplementary Data 1. Matching virus genomes are shown in Supplementary Data 35.

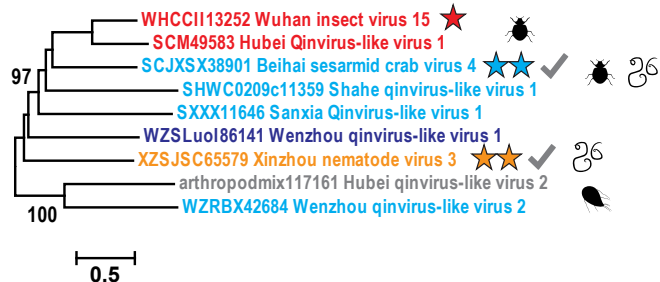
Putative negative-sense (-ve) RNA viruses



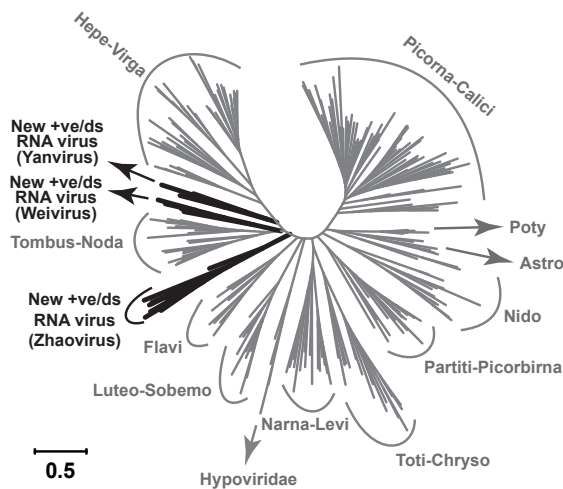
New negative-sense RNA virus (Yuevirus)



New negative-sense RNA virus (Qinivirus)



Putative positive-sense (+ve) or Double-strand (ds) RNA viruses

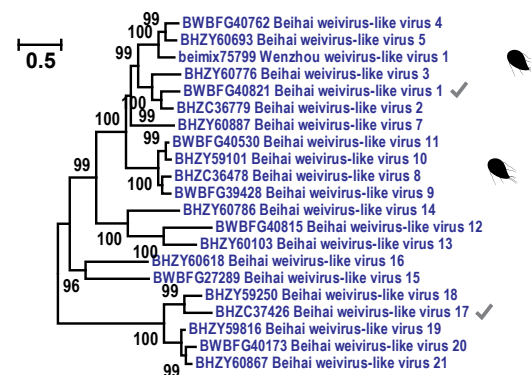


New +ve/ds RNA virus (Zhaovirus)

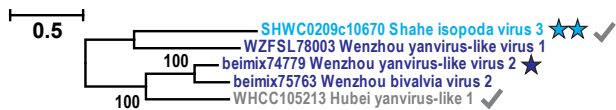
(Ciliate, dasycladacean and hexamita nuclear coding)



New +ve/ds RNA virus (Weivirus)



New +ve/ds RNA virus (Yanvirus)



Red: Phylum Arthropoda, Class Insecta

Light blue: Phylum Arthropoda, Subphylum Crustacea

Purple: Phylum Arthropoda, Subphylum Myriapoda

Yellow: Phylum Arthropoda, Subphylum Chelicerata

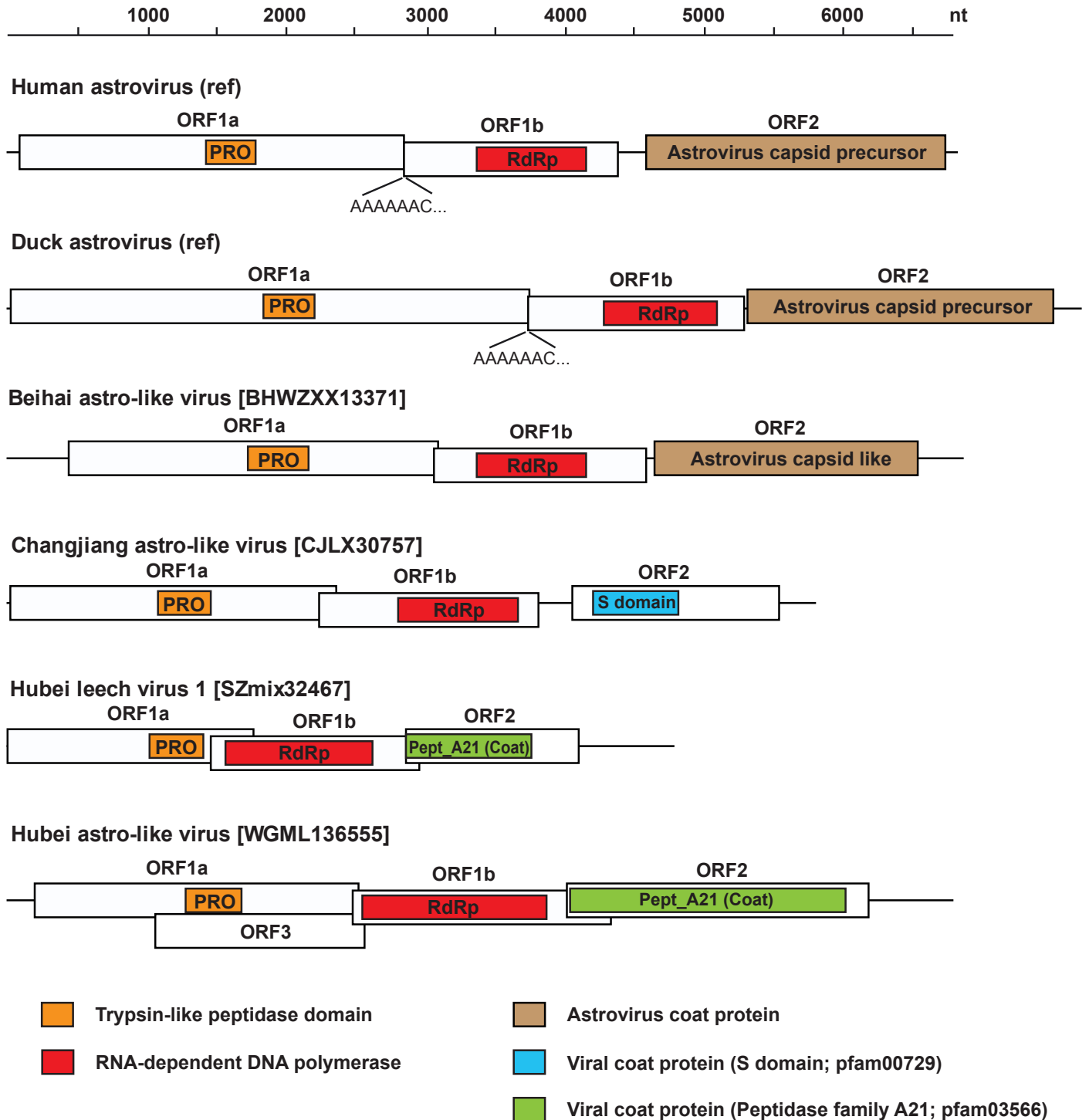
Orange: Phylum Nematoda

Dark blue: Superphylum Lophotrochozoa

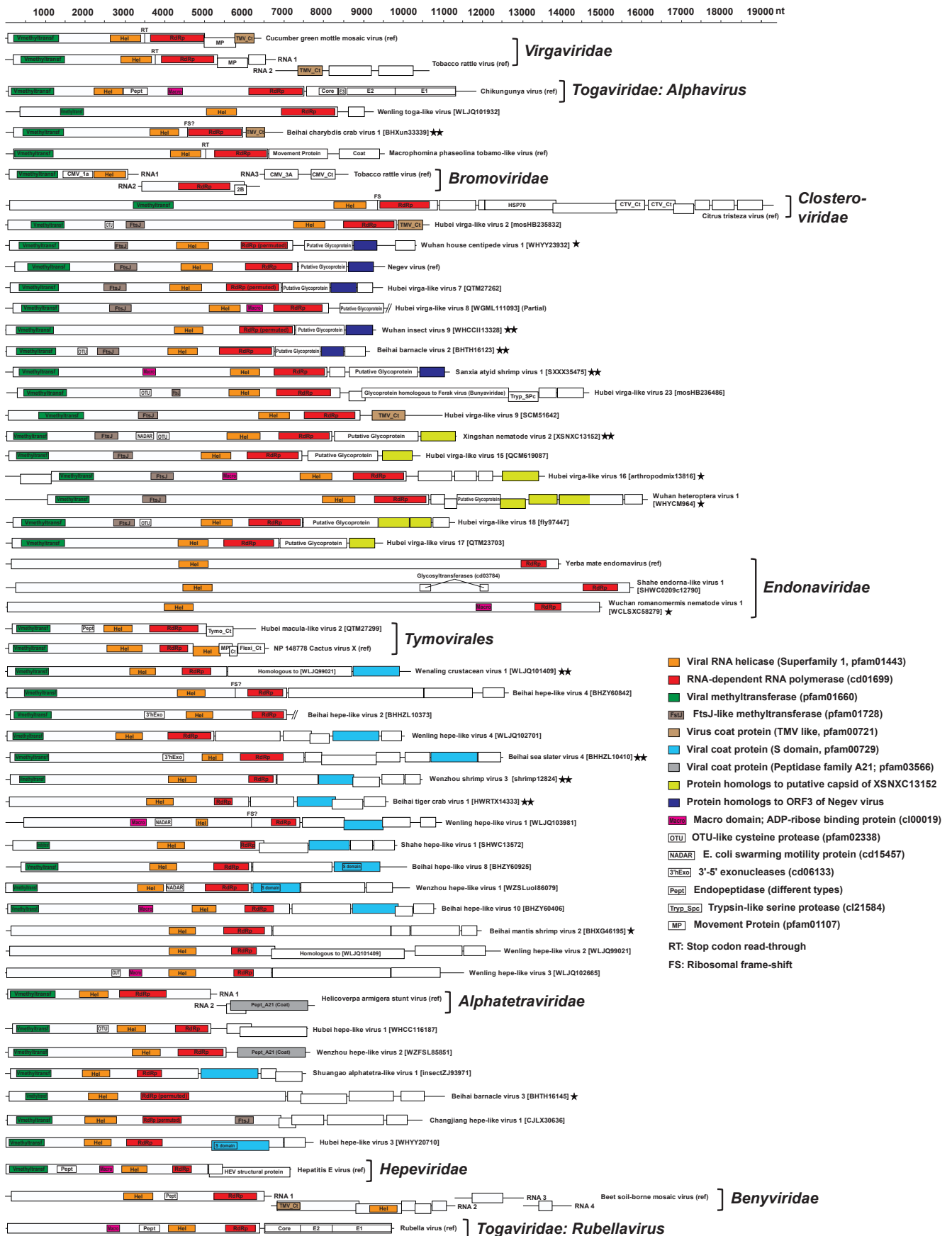
Grey: other hosts or undetermined

- EVE vertebrates ★★ > 1% non-rRNA reads
- EVE arthropods ★ 0.1% ~ 1% non-rRNA reads
- EVE nematodes ✓ Genome shown in Supplementary Data 36
- EVE protists
- EVE flatworms

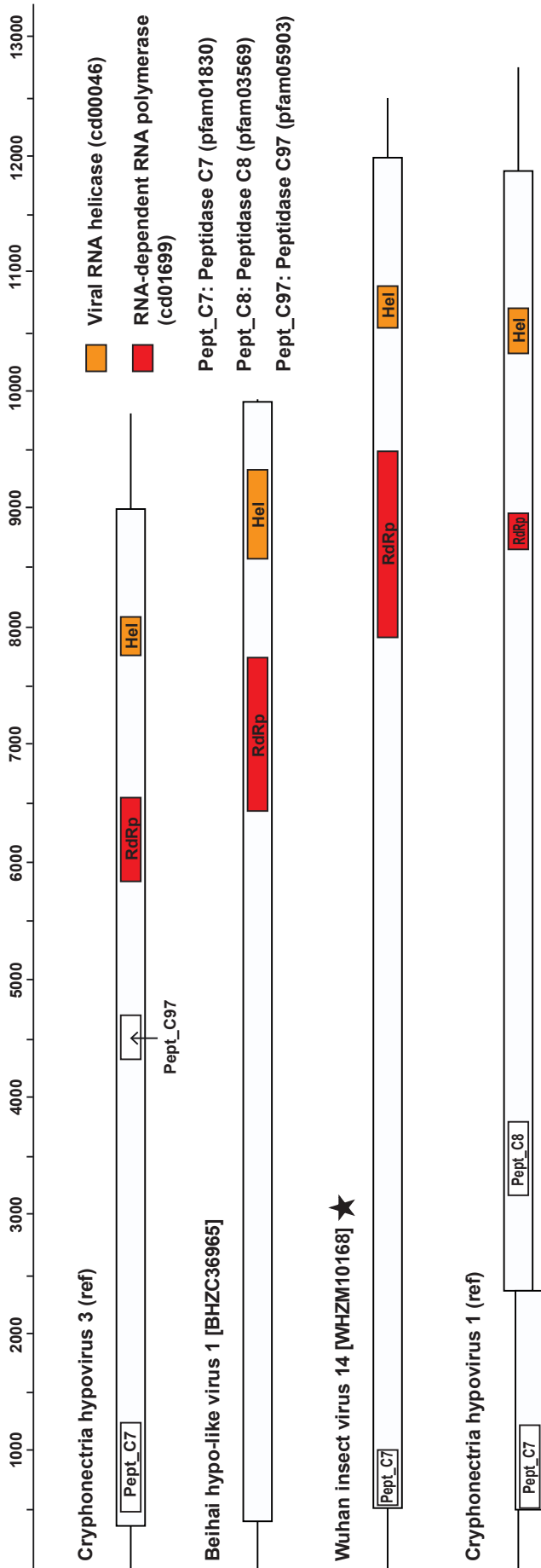
Supplementary Data 21. Five newly identified and highly divergent clades of RNA viruses. Their position is shown within unrooted phylogenetic trees of +ve-sense and -ve sense-RNA viruses (which should be considered as highly tentative because of the difficulties in analysing viruses this divergent). The remaining phylogenies show the evolutionary relationships within each clade. The names of the viruses are marked with different colours based on their host taxonomy. The silhouetted animal denotes host taxa that contain endogenous virus copies, labelled next to its exogenous relative(s). The star symbol signifies viral frequency, subdivided as follows: no star (< 0.1% non-rRNA reads), one star (0.1% ~ 1%), two stars (> 1%). The grey tick symbol indicates viruses whose genome is shown as representative genomes in Supplementary Data 36 (others).



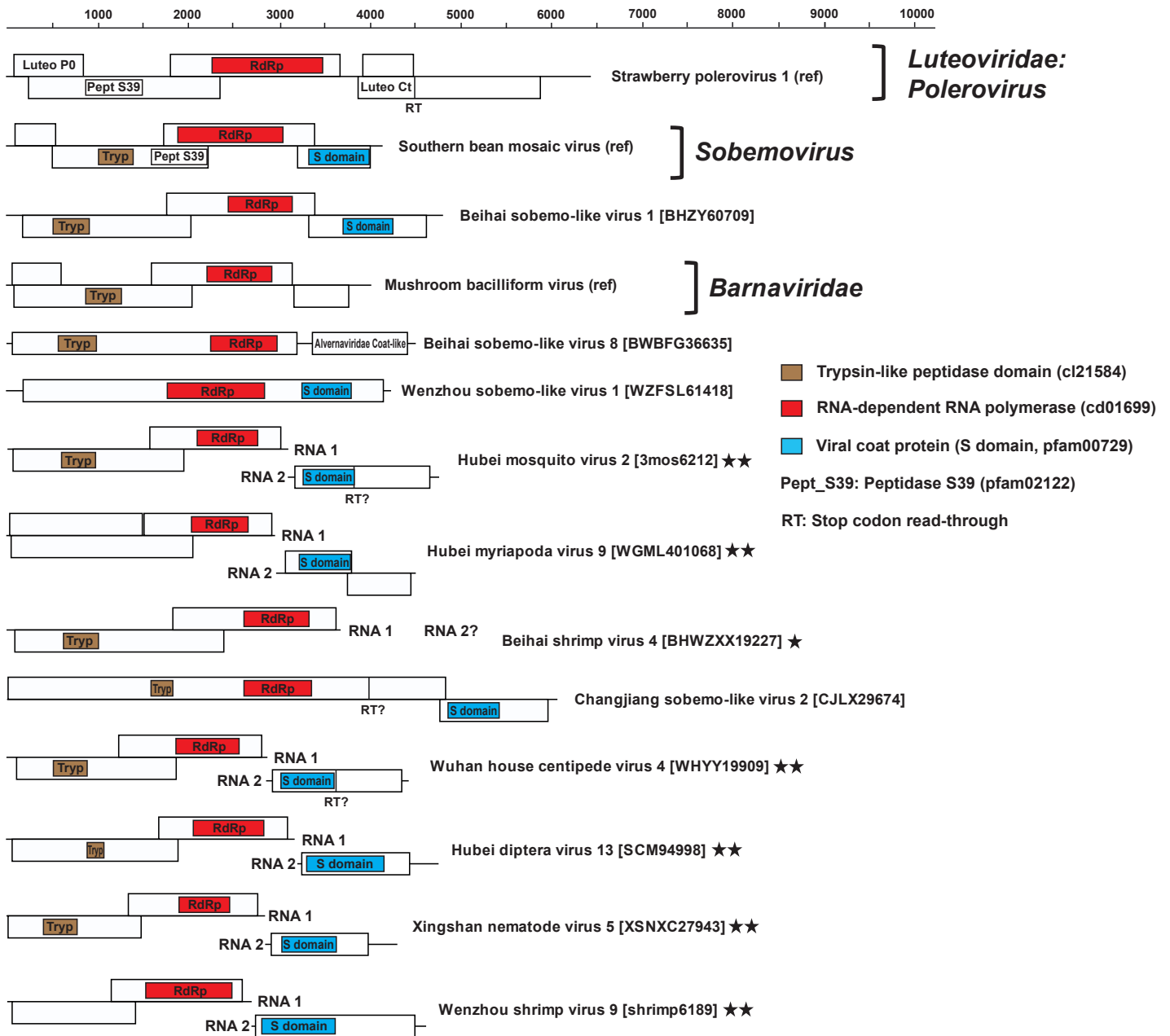
Supplementary Data 22. Representative genome organizations of the “Astro” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 1 and marked with a grey tick symbol. The order of the genomes follows that on the phylogeny. The genomes are drawn to a unified length scale shown at the top. Within each genome, the outer boxes define the ORF boundaries, while the inner boxes define regions with blast matches to a viral protein or a protein domain whose detailed information is provided in the upper/lower right corner of the figure. Each major homologous protein/domain among different genomes is shaded a different colour.



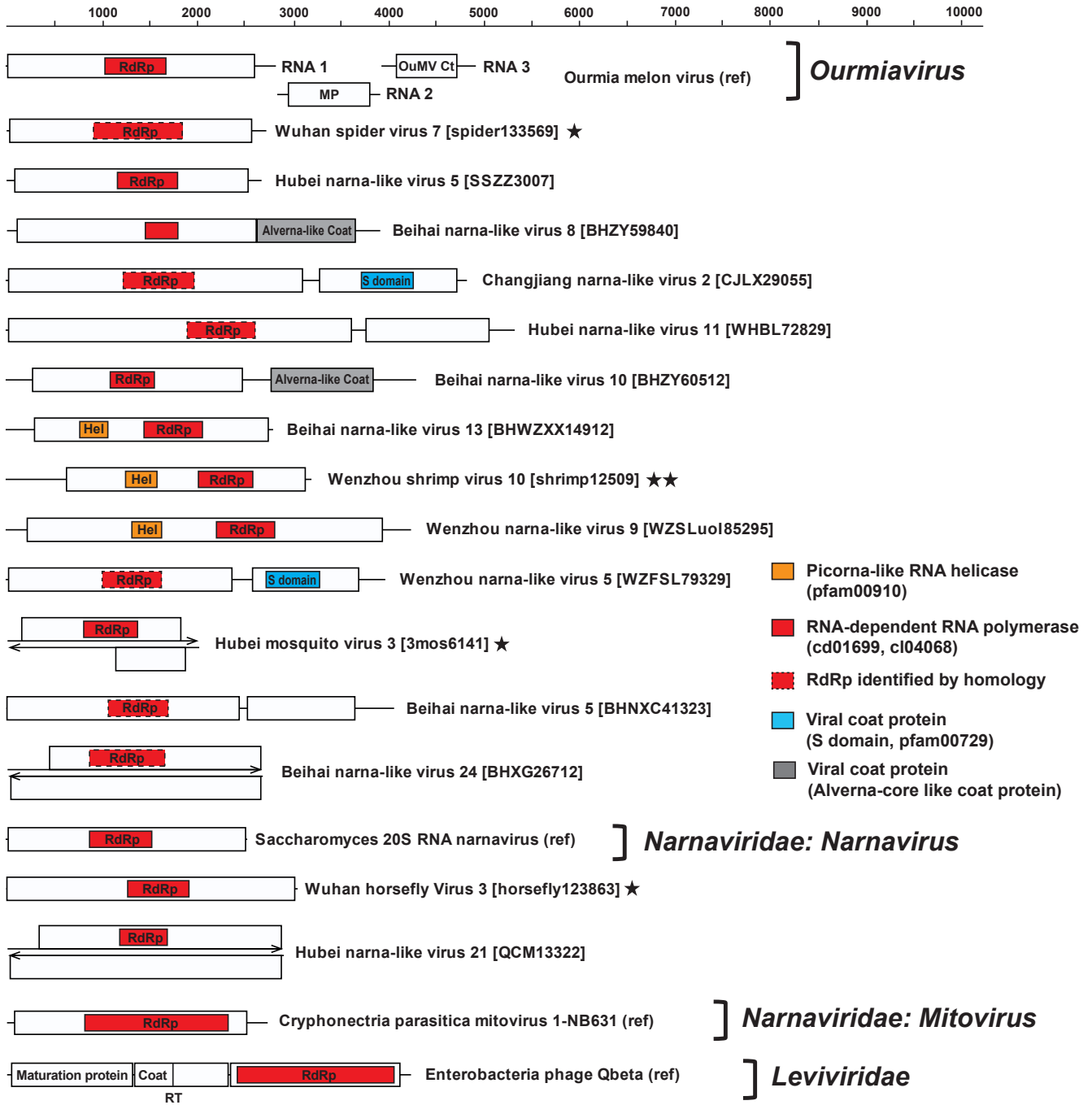
Supplementary Data 23. Representative genome organizations of the “Hepe-Virga” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 3. Figure legend follows Supplementary Data 22.



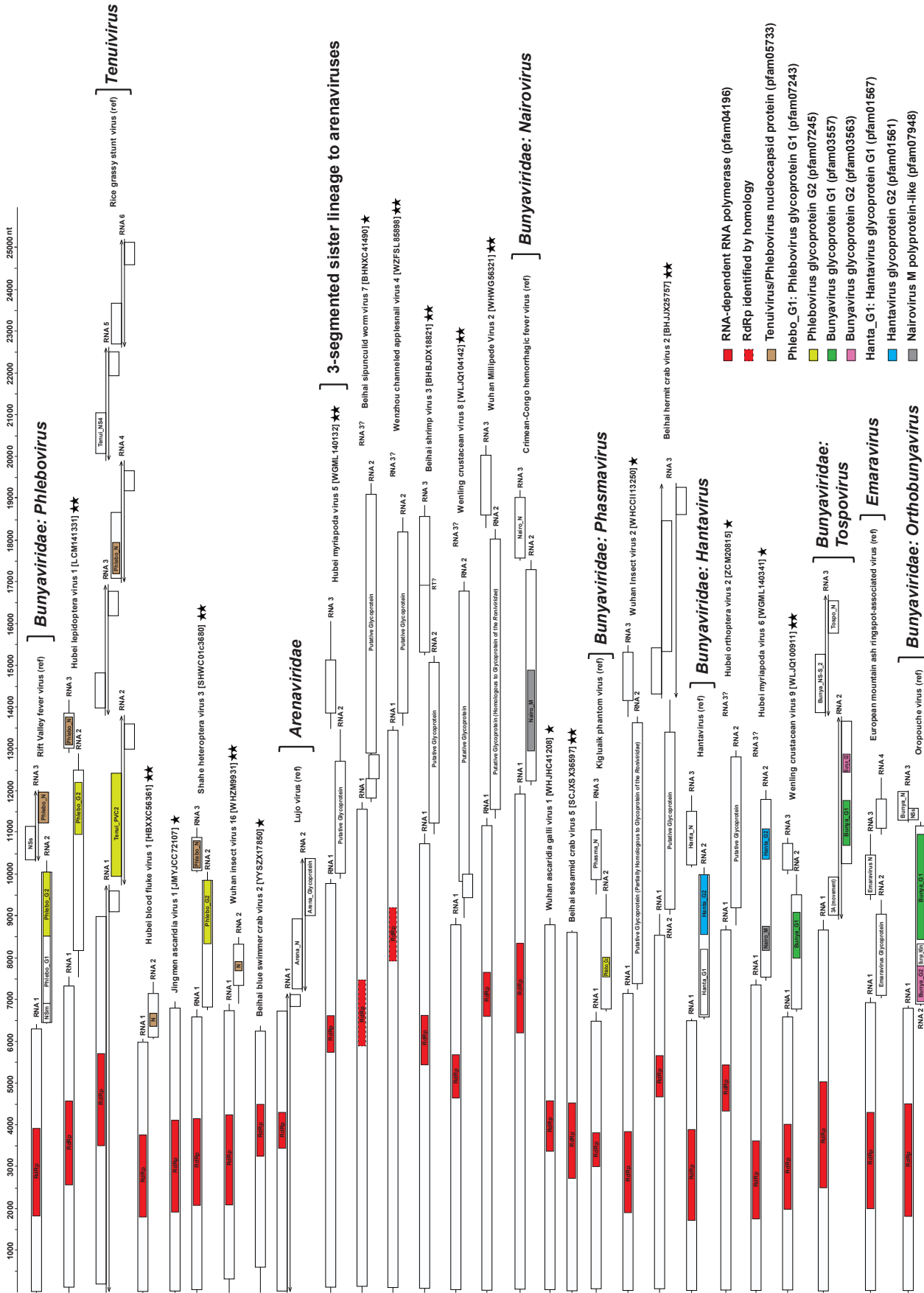
Supplementary Data 24. Representative genome organizations of the “Hypo” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 3. Figure legend follows Supplementary Data 22.



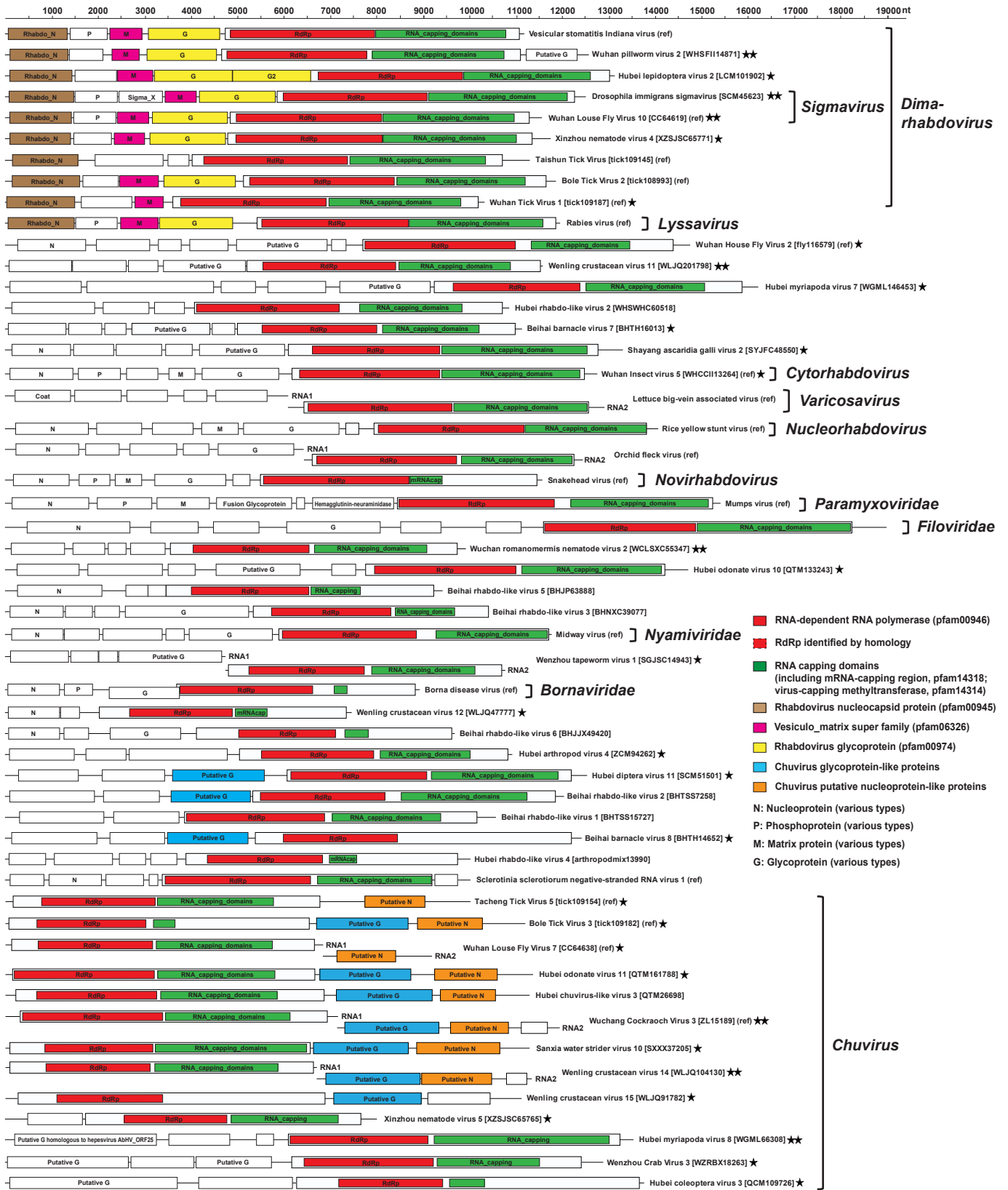
Supplementary Data 25. Representative genome organizations of the “Luteo-Sobemo” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 5. Figure legend follows Supplementary Data 22.



Supplementary Data 26. Representative genome organizations of the “Narna-Levi” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 6. Figure legend follows Supplementary Data 22.

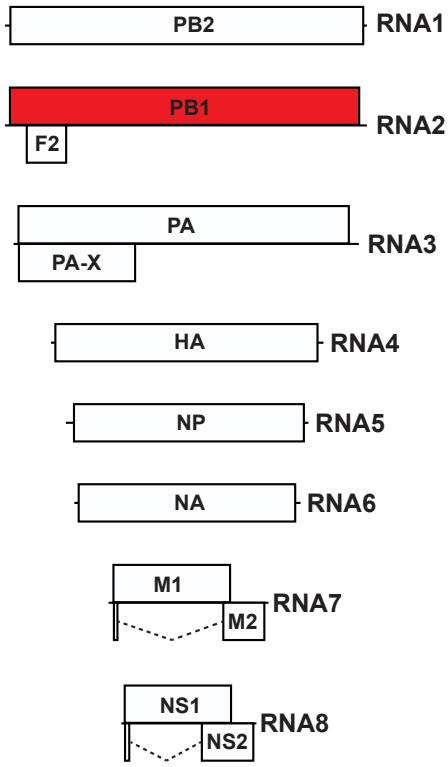


Supplementary Data 27. Representative genome organizations of the “Bunya-Arena” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 7. Figure legend follows Supplementary Data 22.

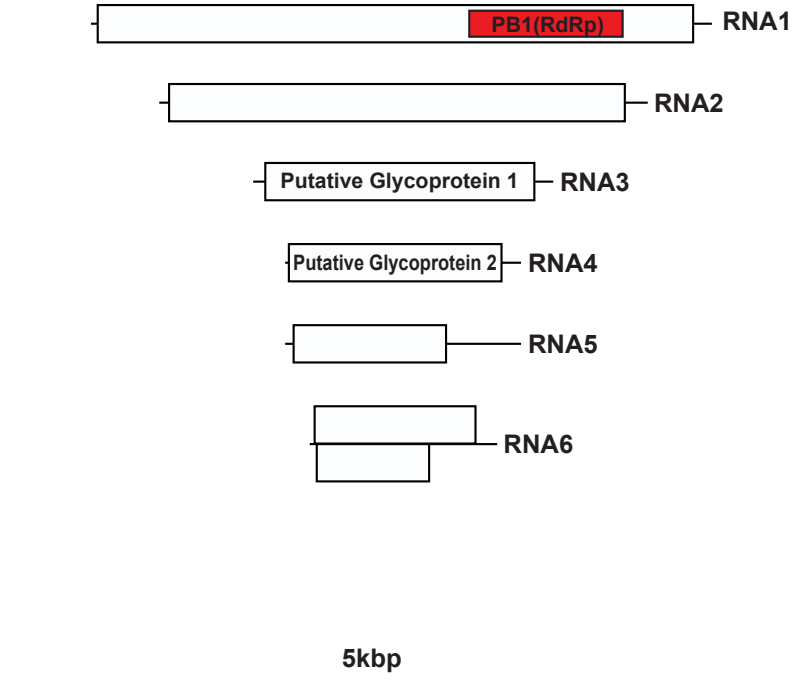


Supplementary Data 28. Representative genome organizations of the “Mono-Chu” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 8. Figure legend follows Supplementary Data 22.

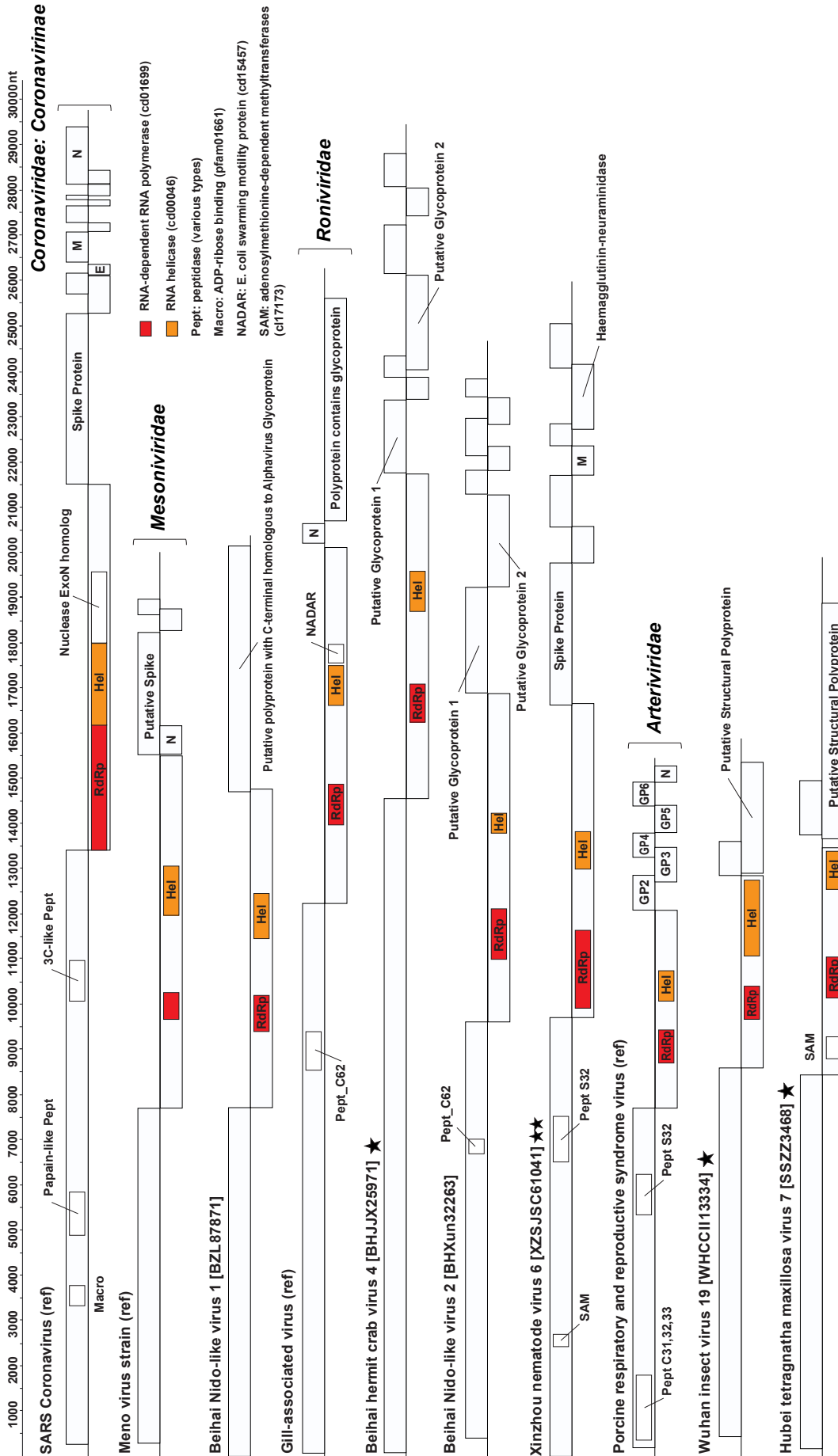
**Influenza A virus
(A/goose/Guangdong/1/1996(H5N1))**



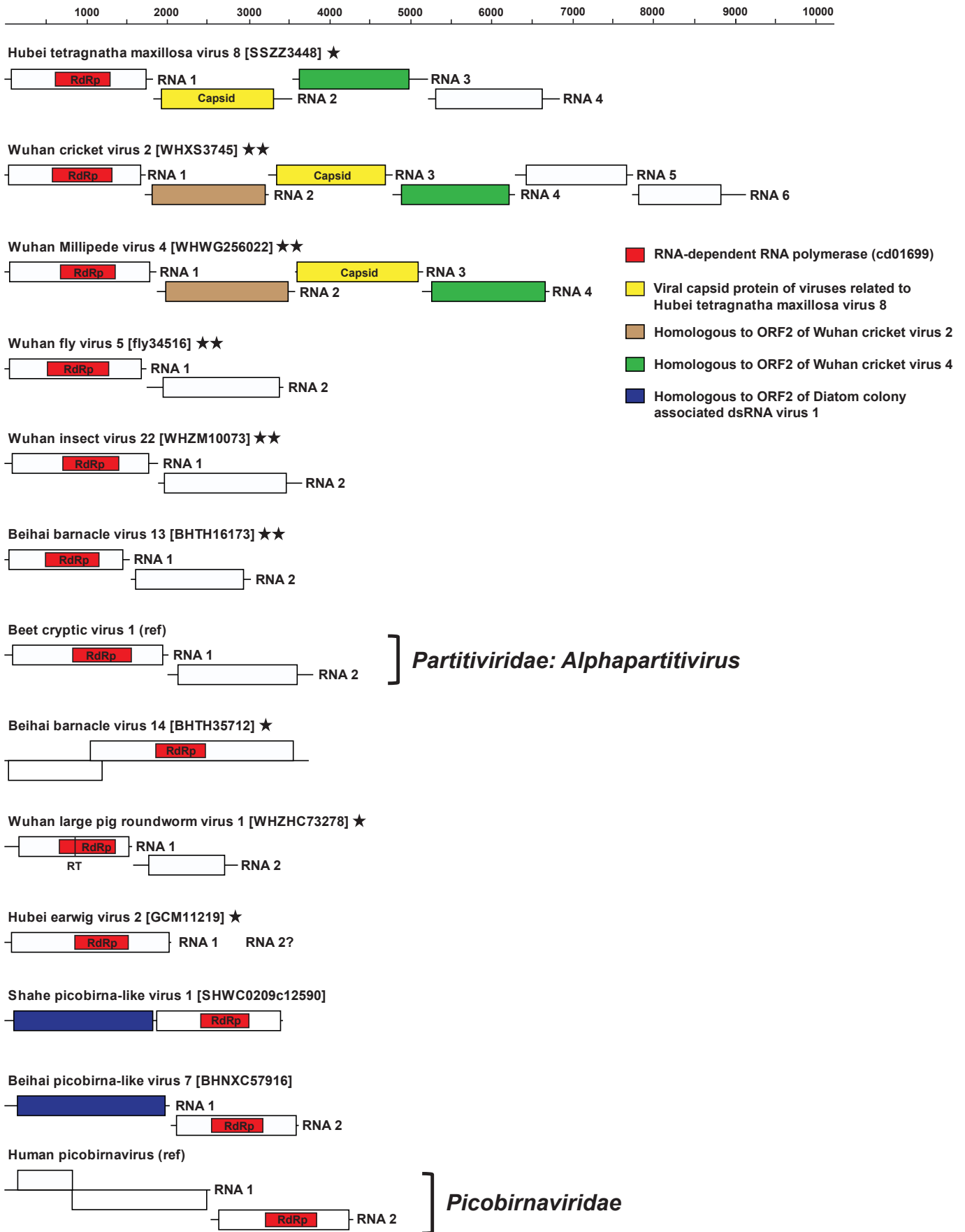
Changping earthworm virus 2 [CPQY18140] ★



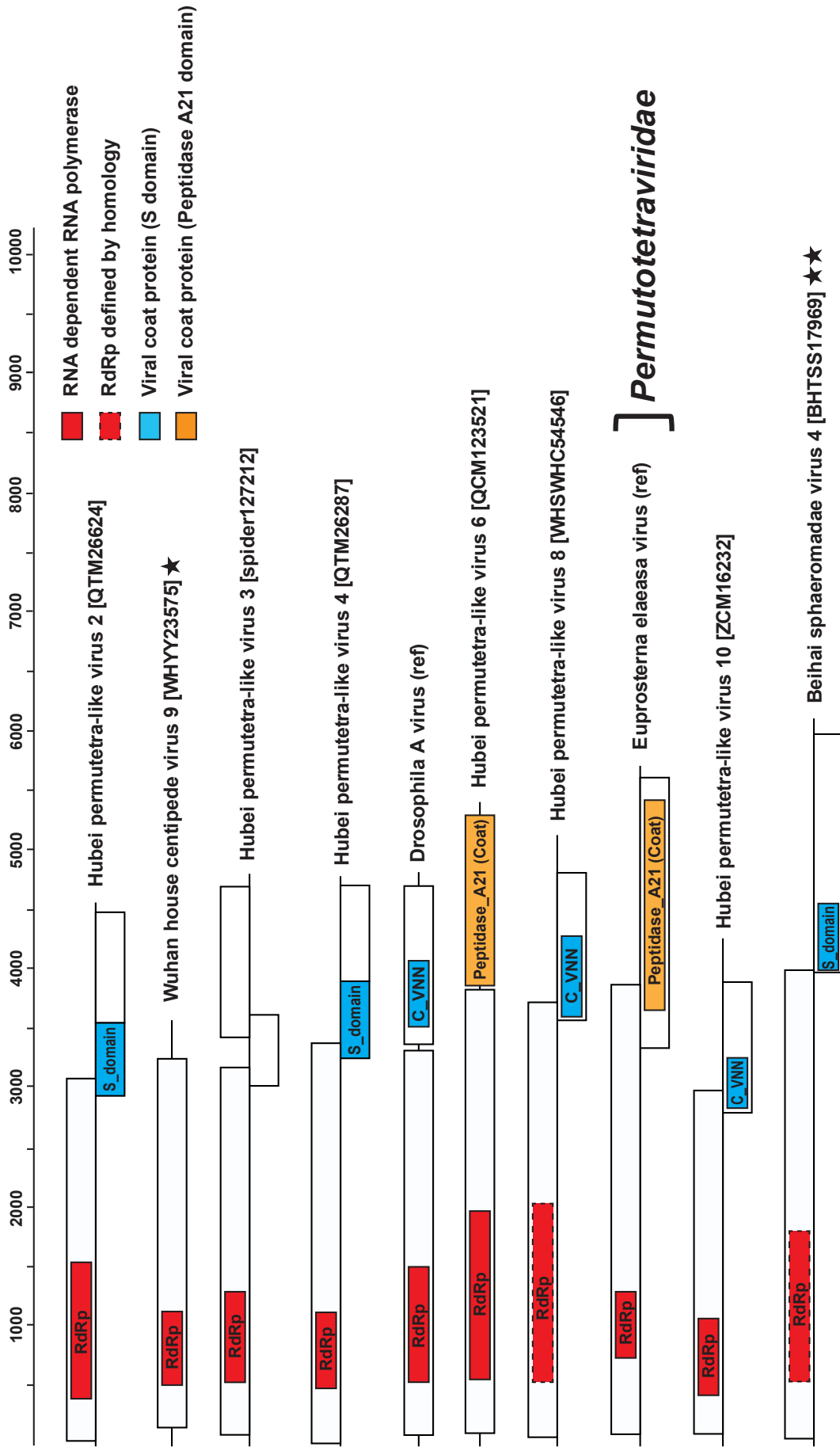
Supplementary Data 29. Representative genome organizations of the “Othomyxo” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 9. Figure legend follows Supplementary Data 22.



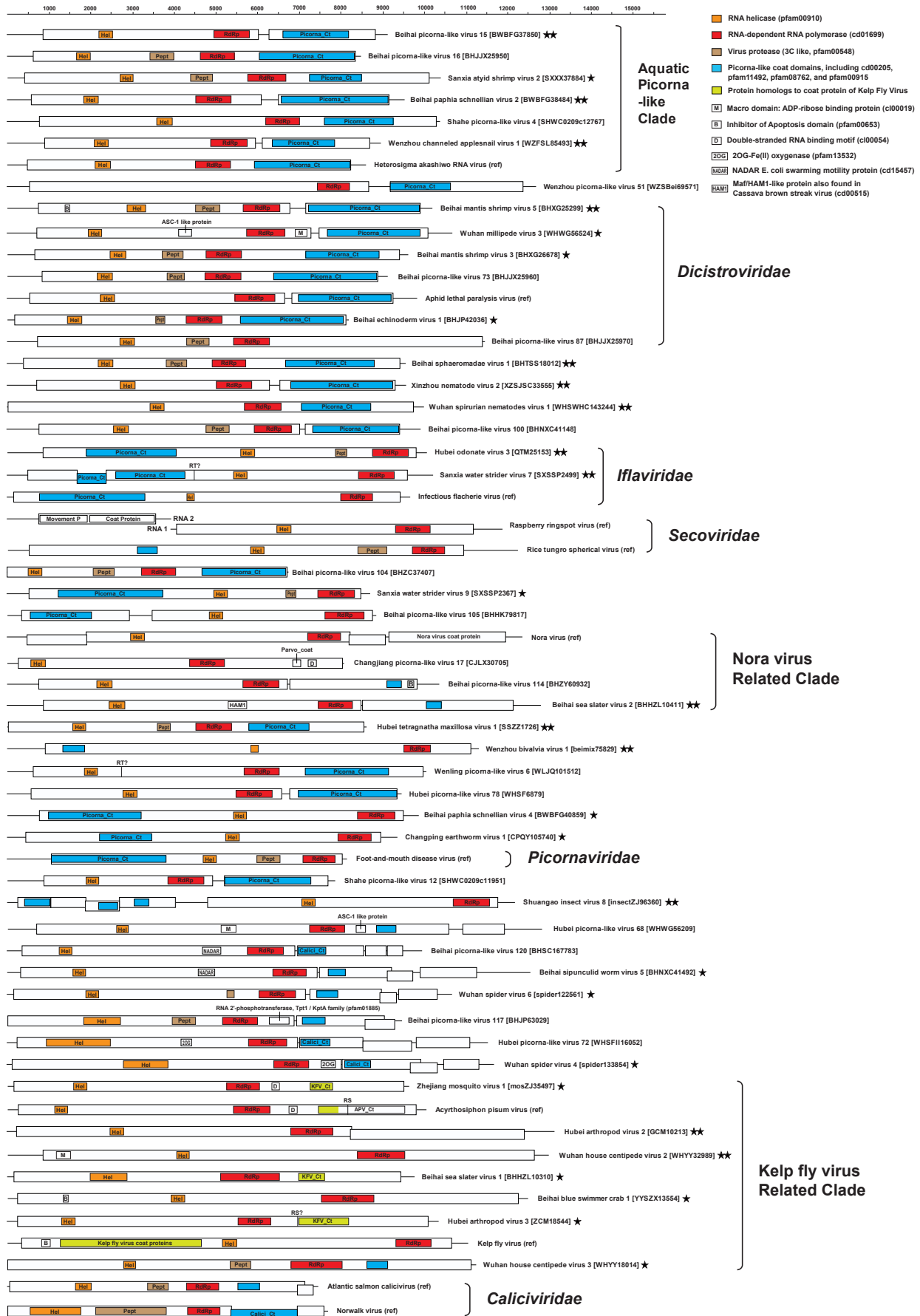
Supplementary Data 30. Representative genome organizations of the “Nido” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 10. Figure legend follows Supplementary Data 22.



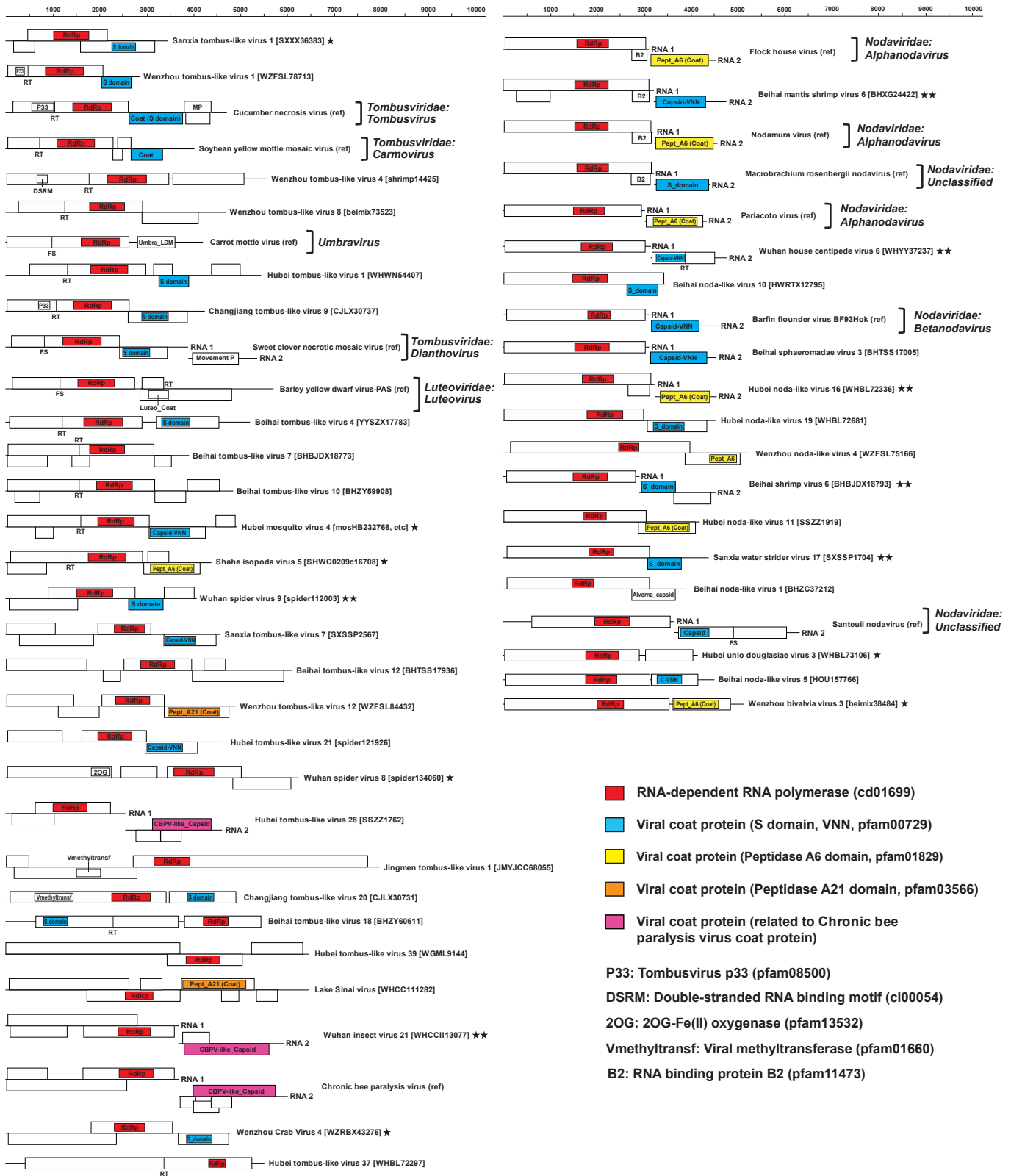
Supplementary Data 31. Representative genome organizations of the “Partiti-Picobirna” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 11. Figure legend follows Supplementary Data 22.



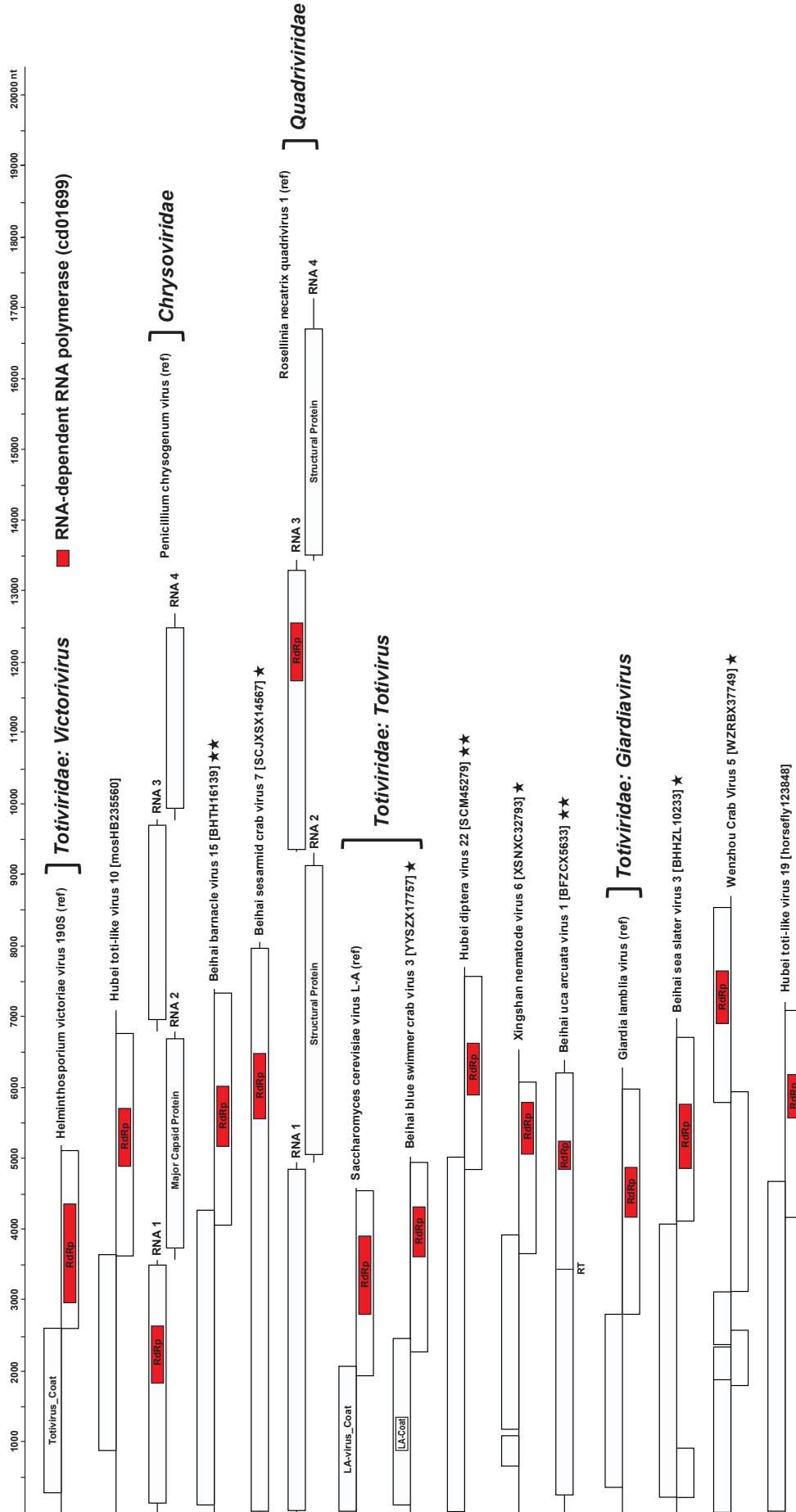
Supplementary Data 32. Representative genome organizations of the “Permutotetra” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 12. Figure legend follows Supplementary Data 22.



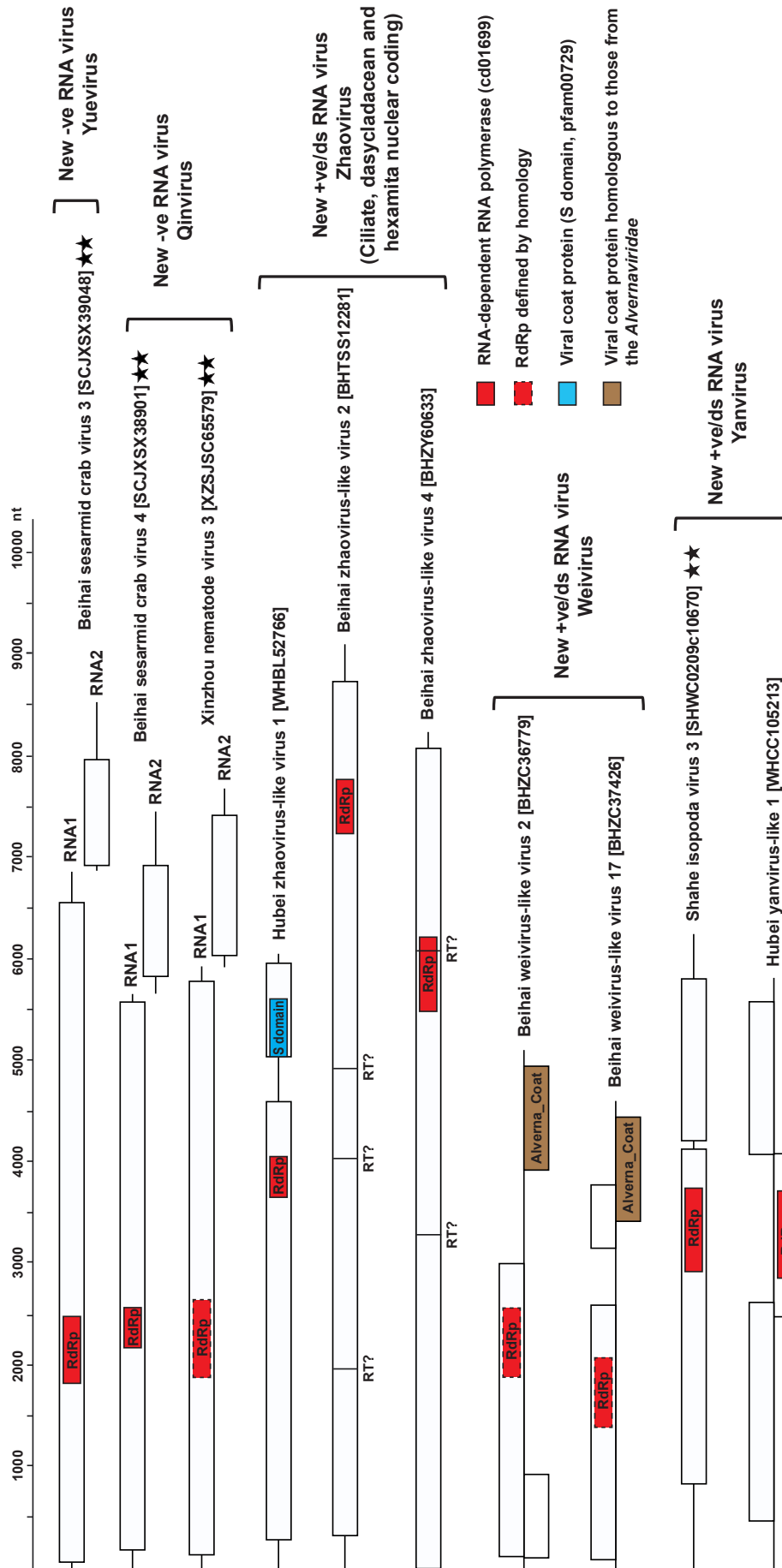
Supplementary Data 33. Representative genome organizations of the “Picorna-Calici” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 13-17. Figure legend follows Supplementary Data 22.



Supplementary Data 34. Representative genome organizations of the “Tombus-Noda” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 19. Figure legend follows Supplementary Data 22.



Supplementary Data 35. Representative genome organizations of the “Toti-Chryso” clade. The matching viruses are shown in the phylogenetic trees in Supplementary Data 20. Figure legend follows Supplementary Data 22.



Supplementary Data 36. Representative genome organizations of the new +ve/ds RNA viruses discovered here. The matching viruses are shown in the phylogenetic trees in Supplementary Data 21. Figure legend follows Supplementary Data 22.