

Supplementary Information

The Viromes of Six Ecosystem Service Providers Parasitoid Wasps

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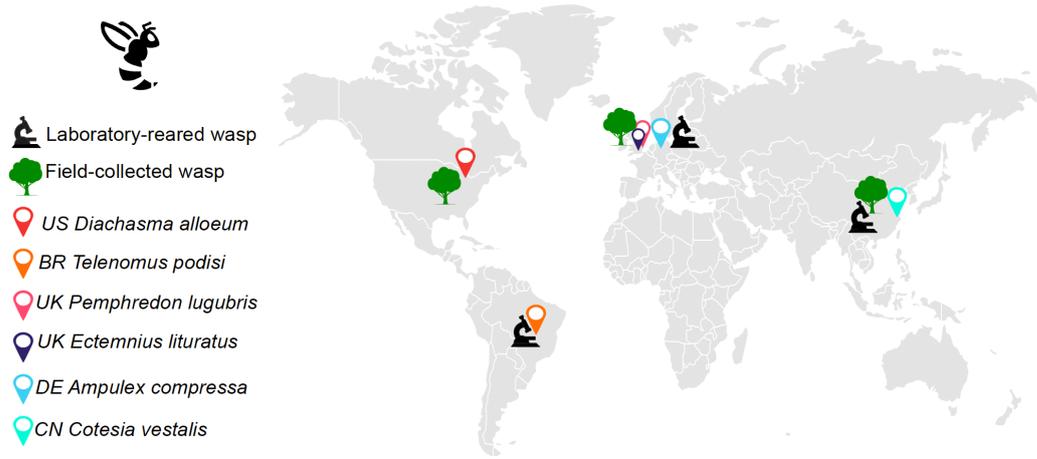
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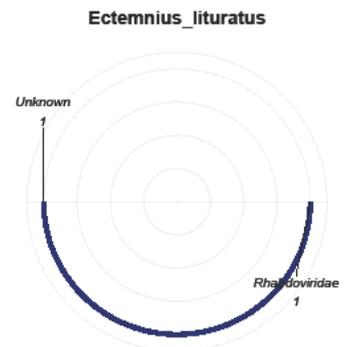
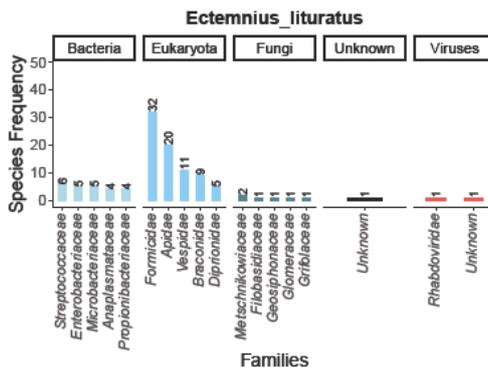
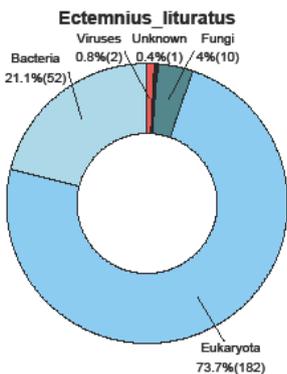
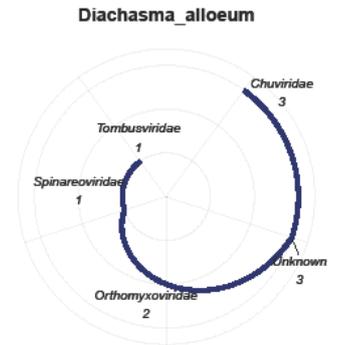
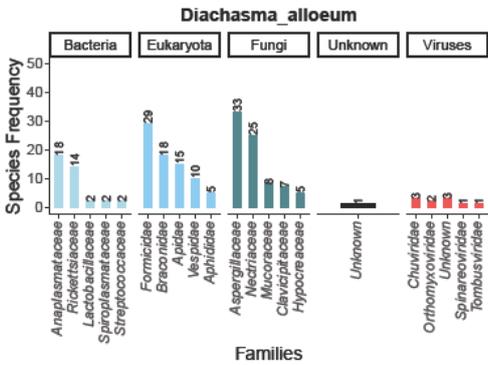
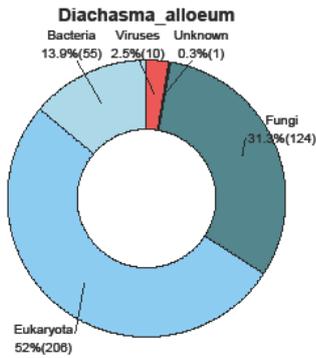
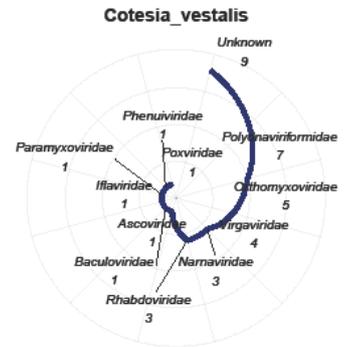
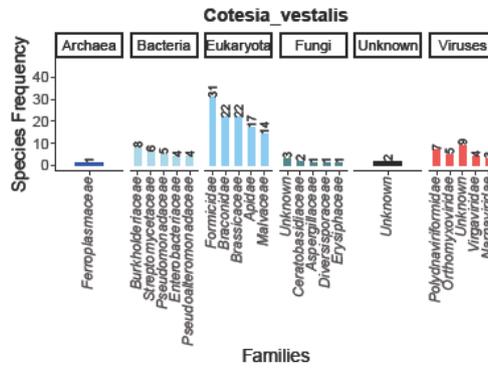
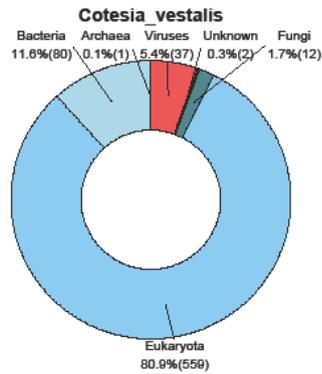
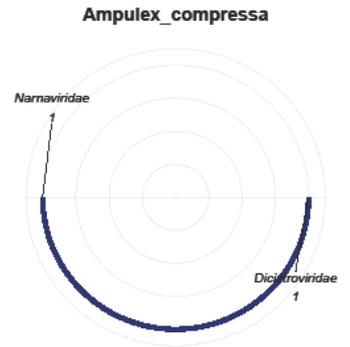
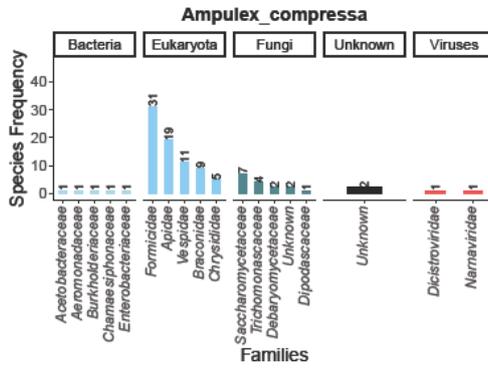
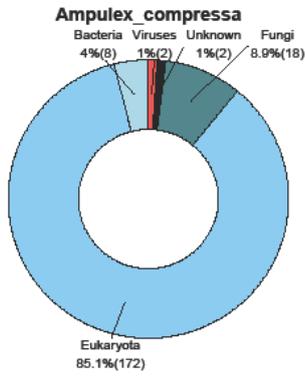
³ Department of Genetics, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte 30270-901, Brazil

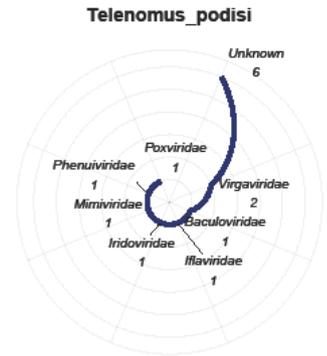
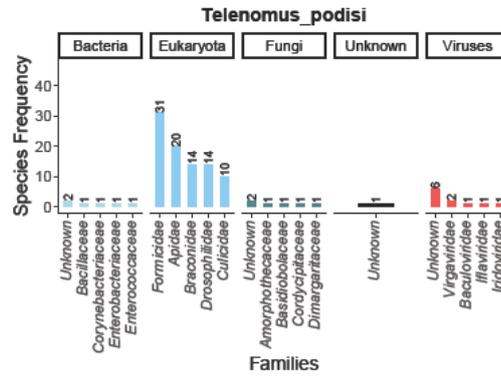
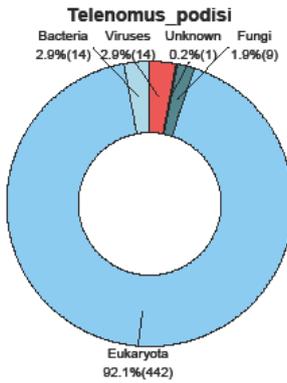
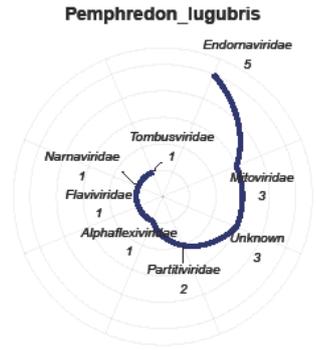
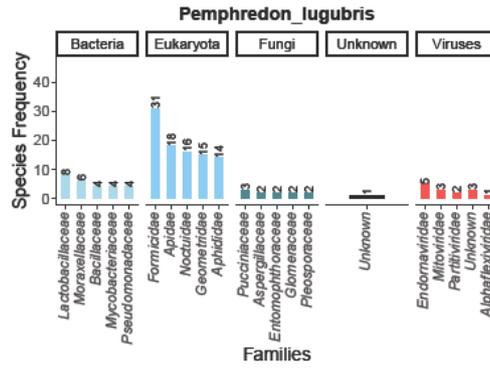
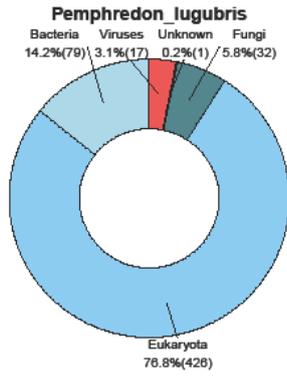
⁴ Department of Biological Sciences, Universidade Estadual de Santa Cruz, Ilhéus 45662-900, Brazil; costama@uesc.br

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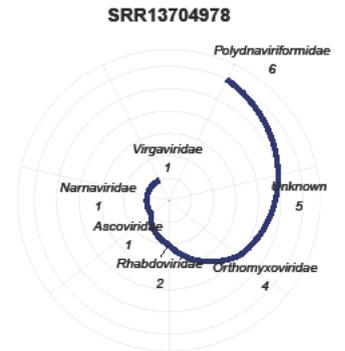
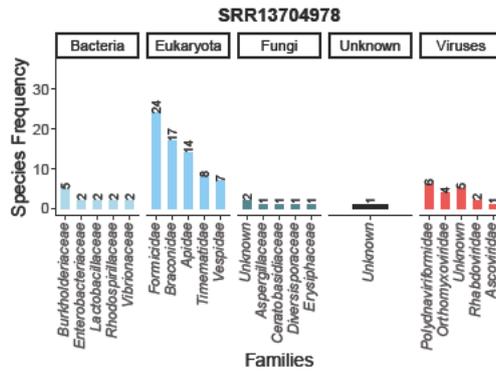
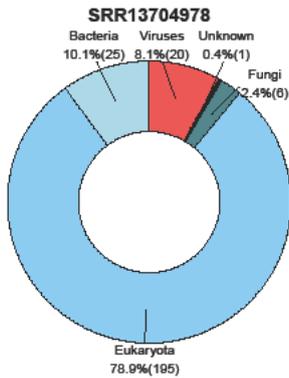
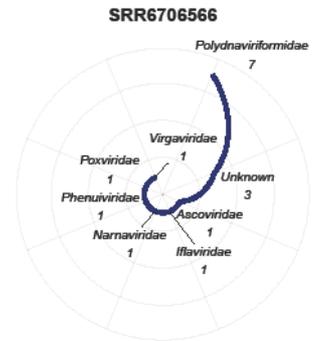
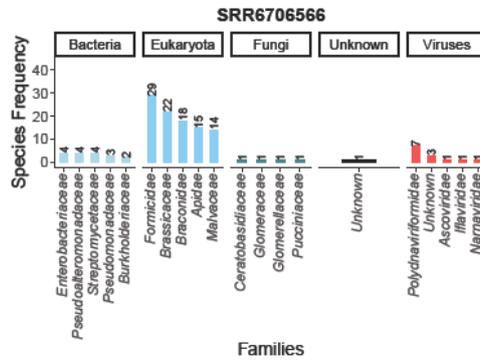
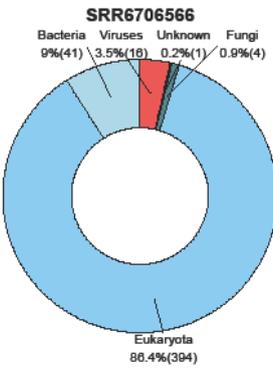
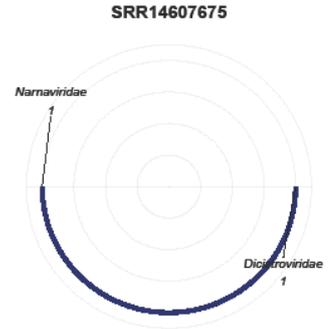
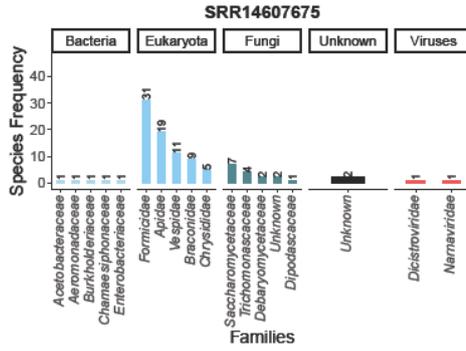
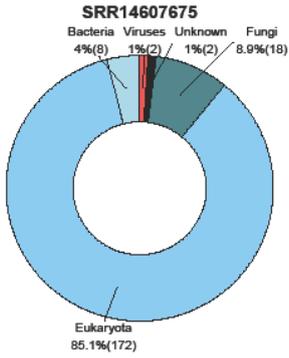
Supplementary Figure S1. Geographical distribution of libraries used in the study classified by wasp species.

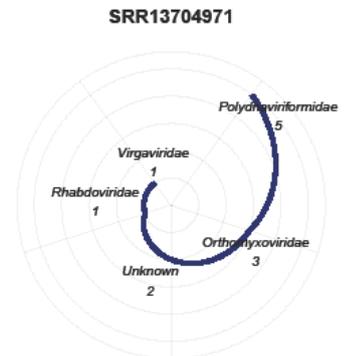
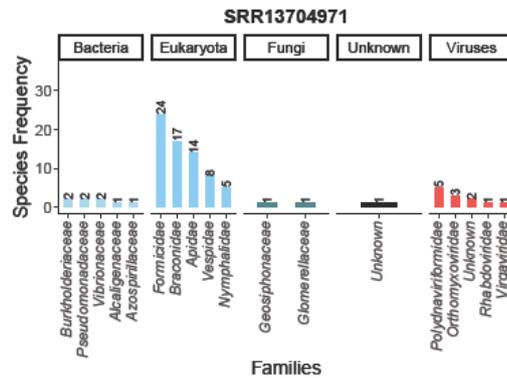
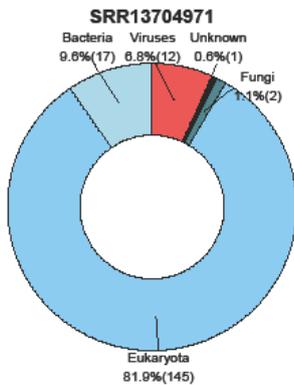
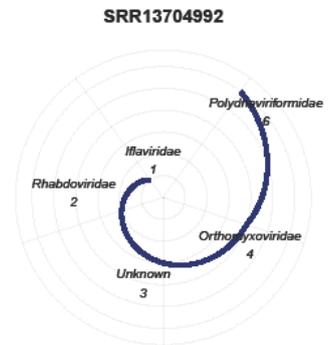
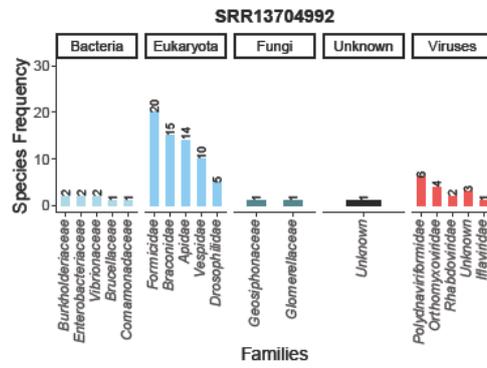
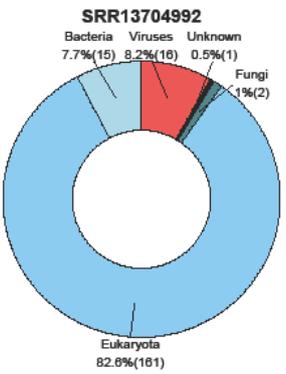
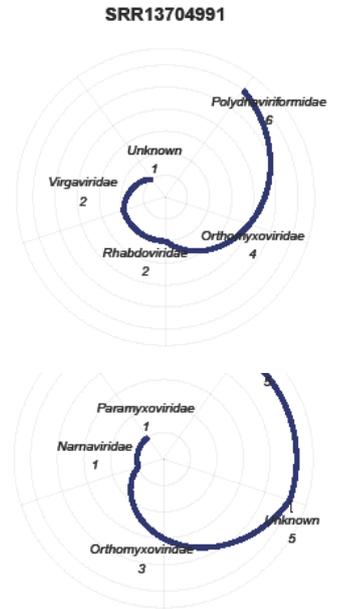
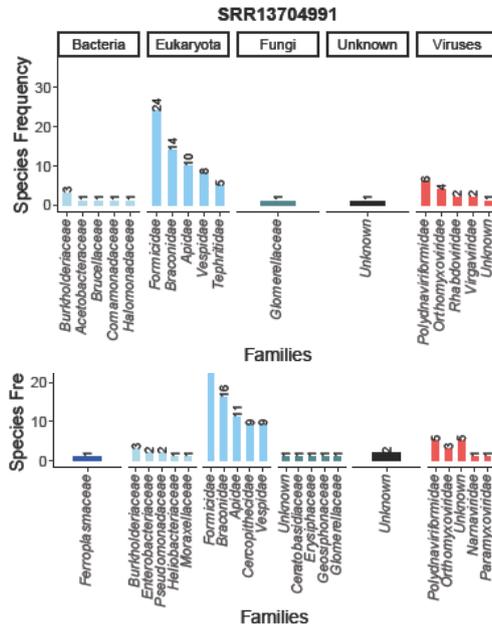
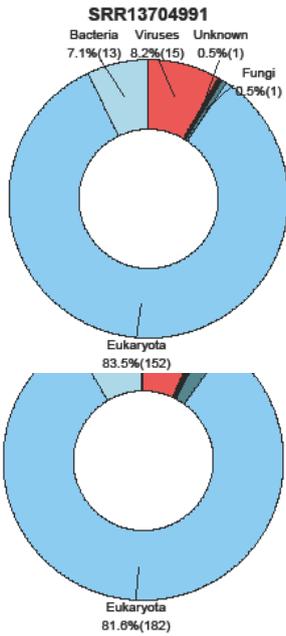


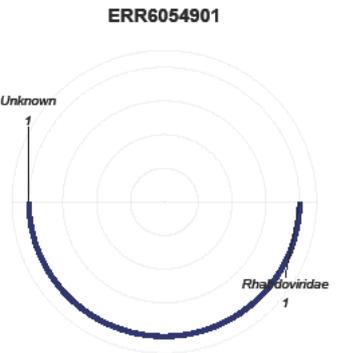
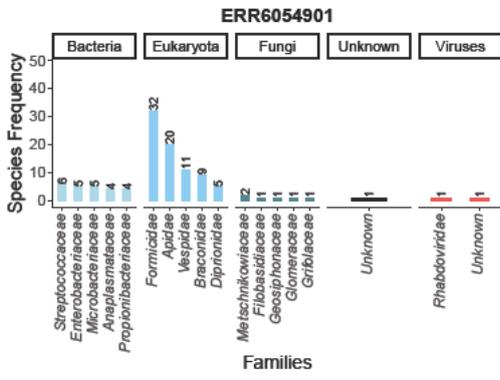
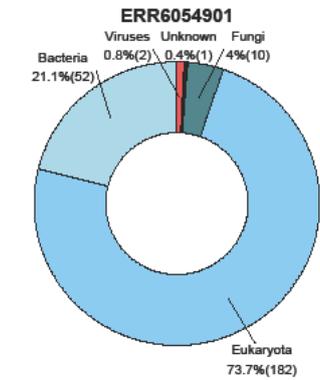
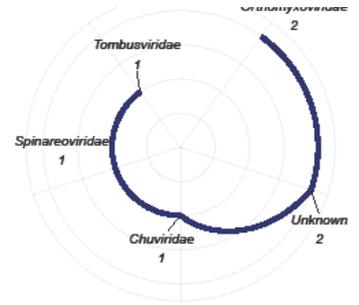
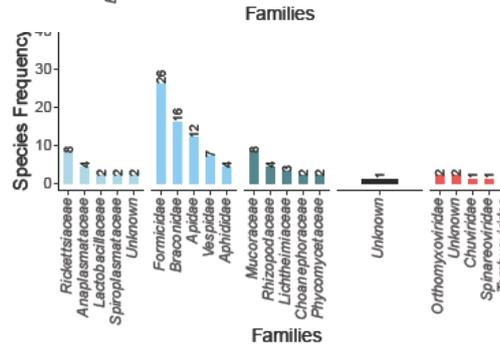
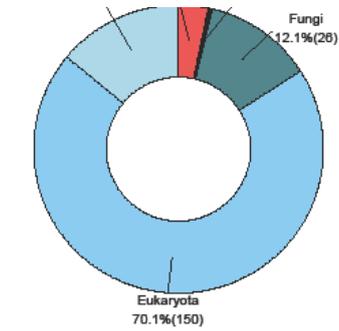
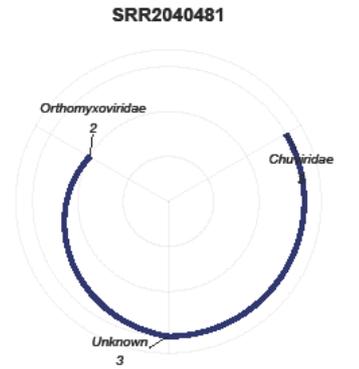
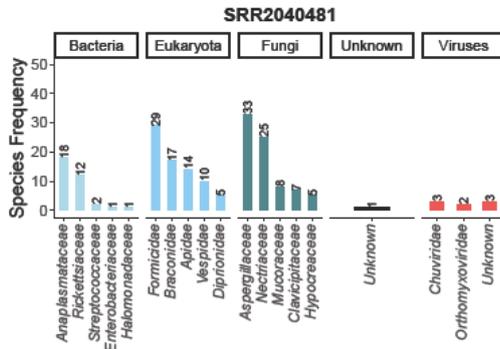
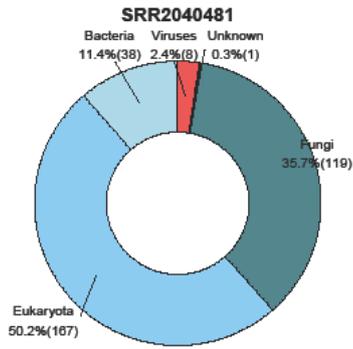


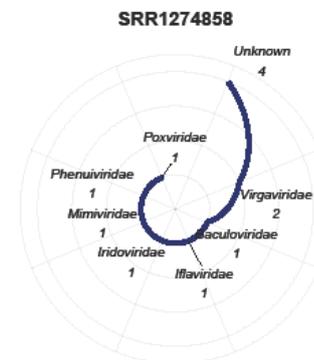
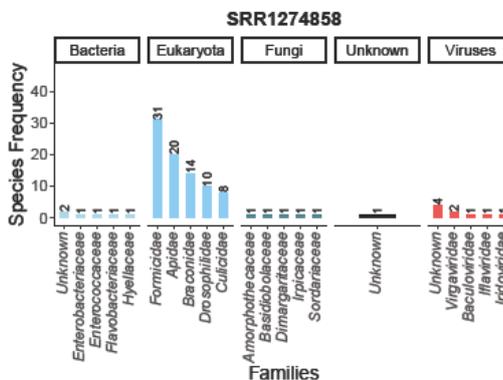
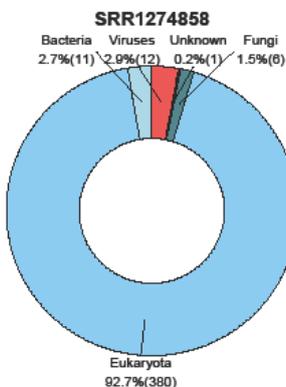
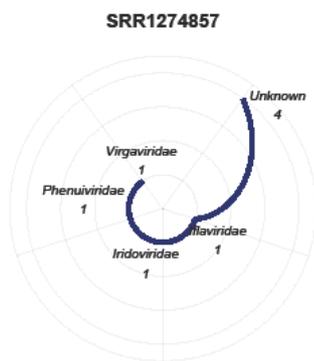
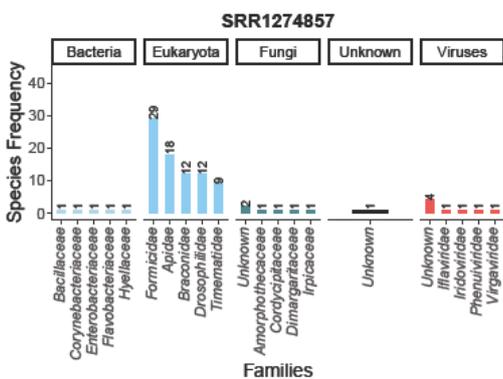
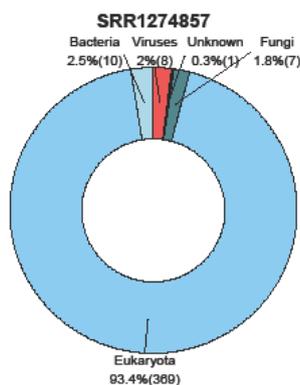
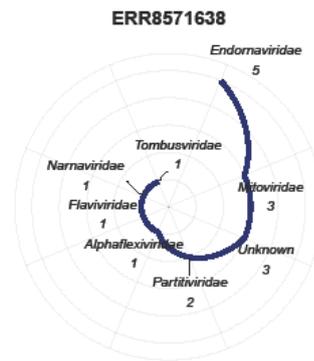
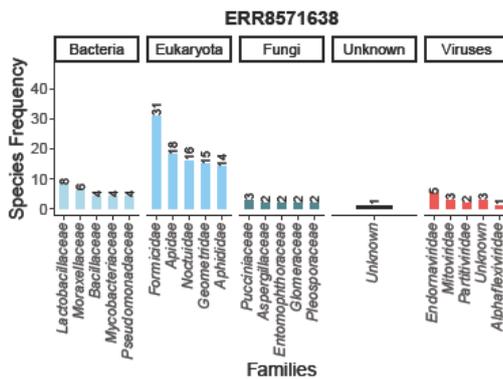
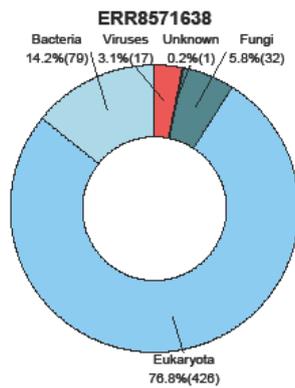
Supplementary Figure S2. Metagenomics analysis grouped by species of parasitoid wasps.

In order: *A. compressa*, *C. vestalis*, *D. alloem*, *E. lituratus*, *P. lugubris*, and *T. podisi*. On the left, donut plot showing percentages of organisms' diversity found by kingdom. The categories are Eukaryota, Bacteria, Fungi, Viruses, and Unknown. On the middle, bar charts with details on the families within each kingdom (x-axis) and the species frequency by family (y-axis). On the right, radar plot showing the diversity of viral families by parasitoid species.



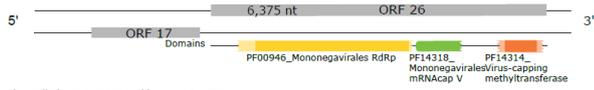




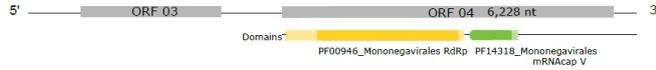


Supplementary Figure S3. Metagenomics analysis for each RNA-seq library included in the study. In order: SRR14607675 (*A. compressa*); SRR6706566, SRR13704978, SRR13704979, SRR13704980, SRR13704991, SRR13704992, SRR13704971 (*C. vestalis*); SRR2041626, SRR2040481 (*D. alloem*); ERR6054901 (*E. lituratus*); ERR8571638 (*P. lugubris*); and SRR1274857, SRR1274858 (*T. podisi*). On the left, donut plot showing percentages of organisms' diversity found by kingdom. The categories are Eukaryota, Bacteria, Fungi, Viruses, and Unknown. On the middle, bar charts with details on the families within each kingdom (x-axis) and the species frequency by family (y-axis). On the right, radar plot showing the diversity of viral families by parasitoid species.

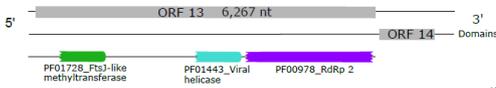
Lasius neglectus virus 2 12,041 nt



Gudgenby Calliphora mononega-like virus 12,763 nt



Sanya virga-like virus 1 7,145 nt



Wuhan insect virus 16 6,684 nt



Wuhan ant virus 7,202 nt



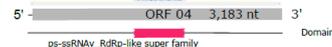
Megastigmus ssRNA, partial genome 12,061 nt



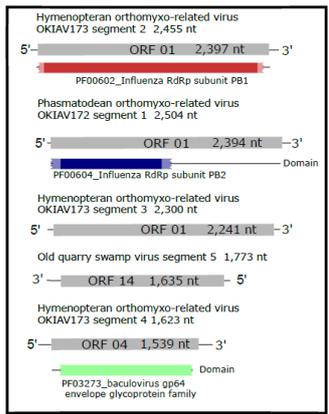
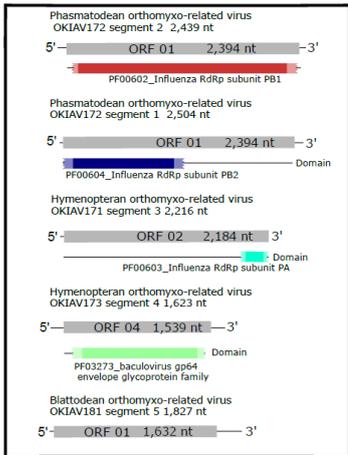
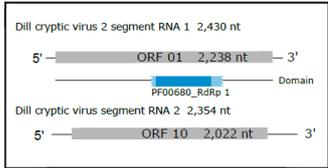
Hymenopteran chu-related virus OKIAV147 7,082 nt



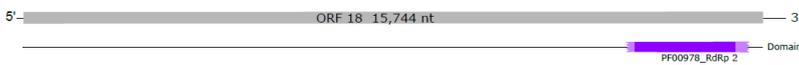
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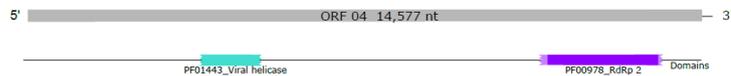
Hangzhou mitovirus 4 2,376 nt



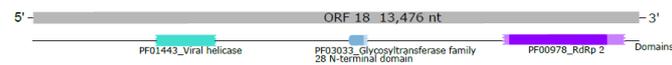
Lily alphaendornavirus isolate B1, complete genome 16,483 nt



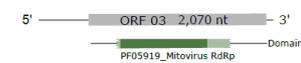
Geranium carolinianum endornavirus 14,625 nt



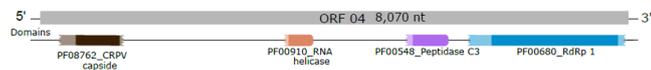
Hallsjon virus, complete genome 13,476 nt



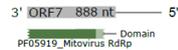
Entomophthora muscae mitovirus 2 RdRp 2,408 nt



Telenomus podisi 8,285 nt: *Halyomorpha halys virus isolate T. podisi*



Pemphredon lugubris 1,143nt: Hubei narva-like virus 25 strain isolate P. lugubris



Supplementary Figure S4. Characterization of segments, ORFs and domains of the closely related sequences to the assembled viral transcripts identified in the work. All viruses represented in this figure are previously described viruses.