

# Supplementary Information

## The Viromes of Six Ecosystem Service Providers Parasitoid Wasps

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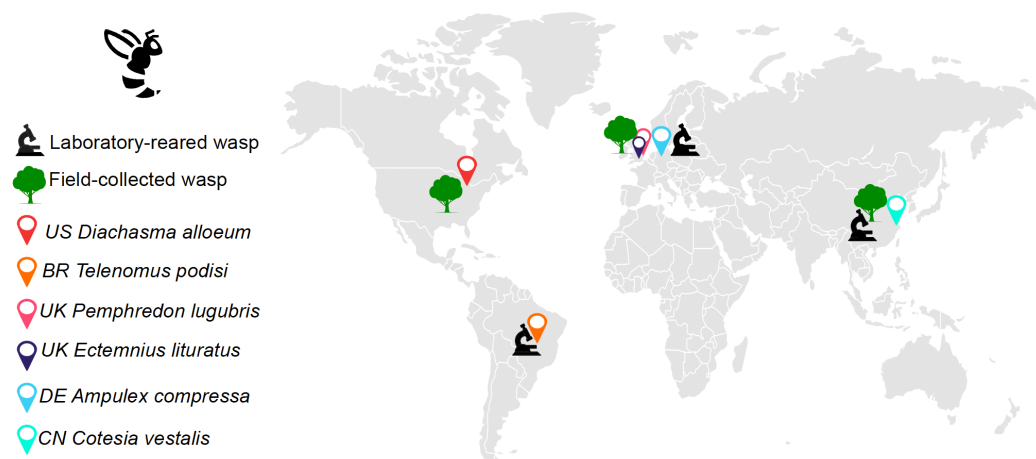
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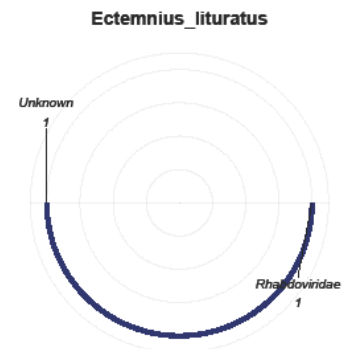
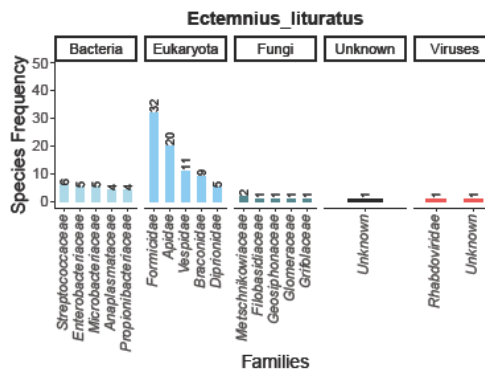
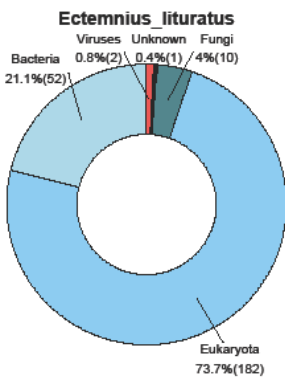
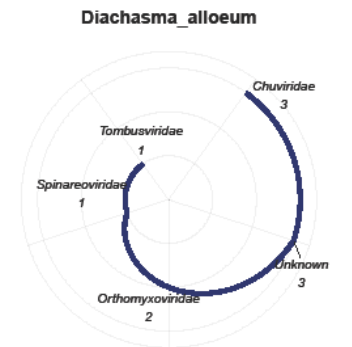
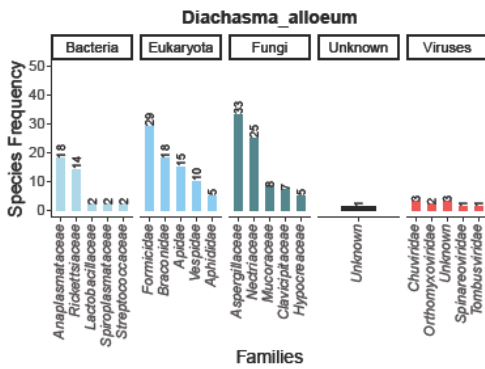
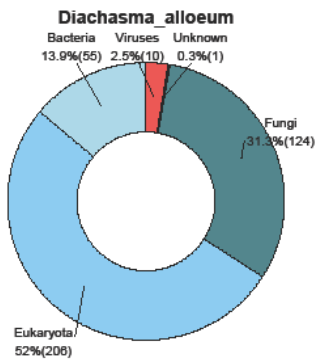
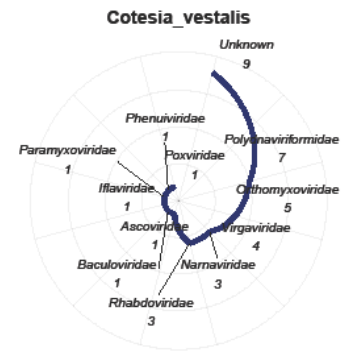
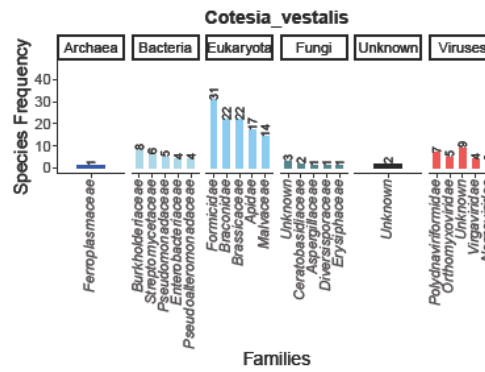
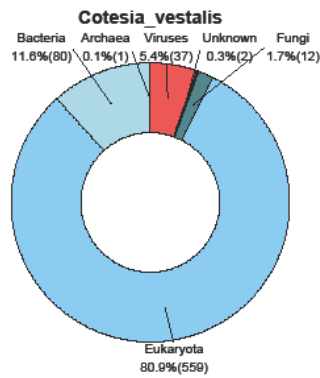
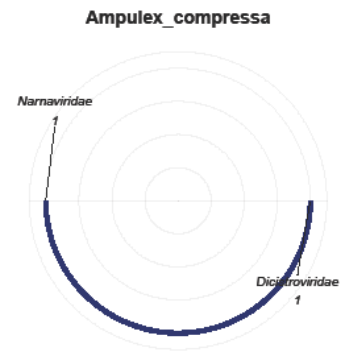
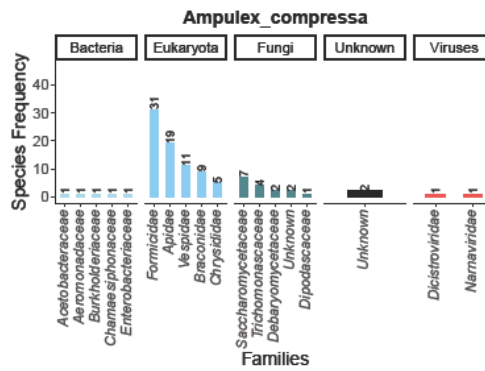
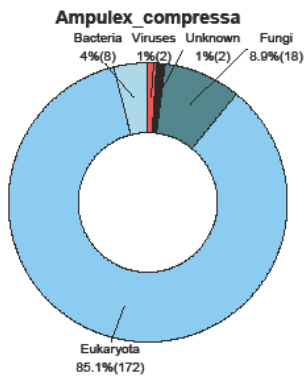
<sup>3</sup> Department of Genetics, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte 30270-901, Brazil

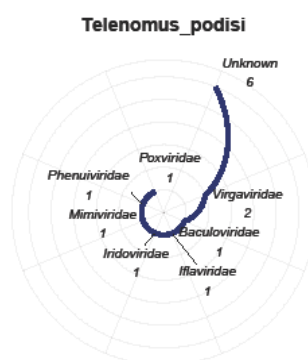
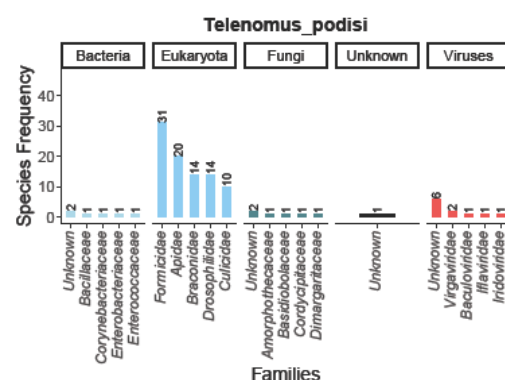
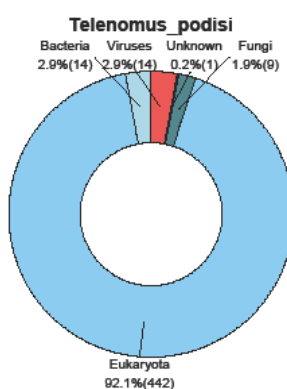
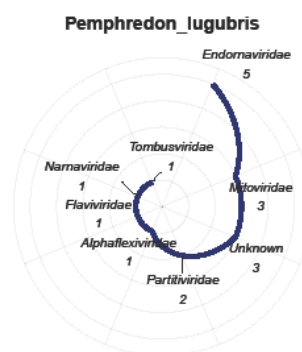
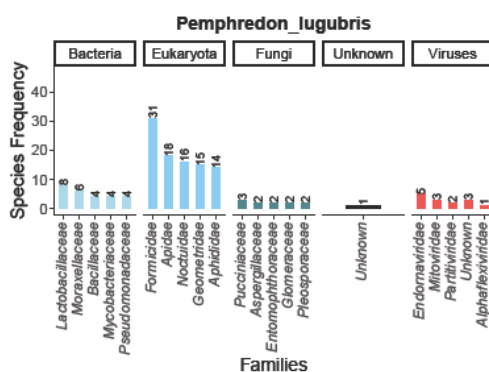
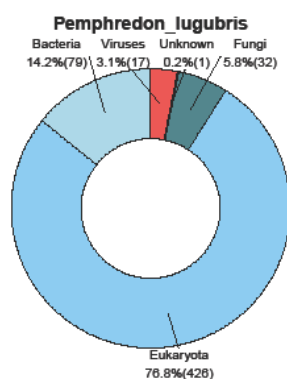
<sup>4</sup> Departament of Biological Sciences, Universidade Estadual de Santa Cruz, Ilhéus 45662-900, Brazil; costama@uesc.br

\* Correspondence: ericgdp@gmail.com



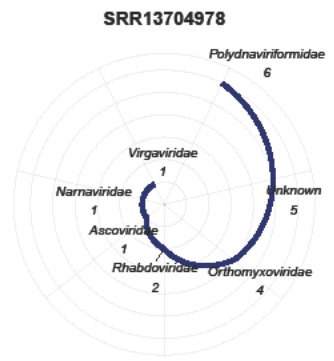
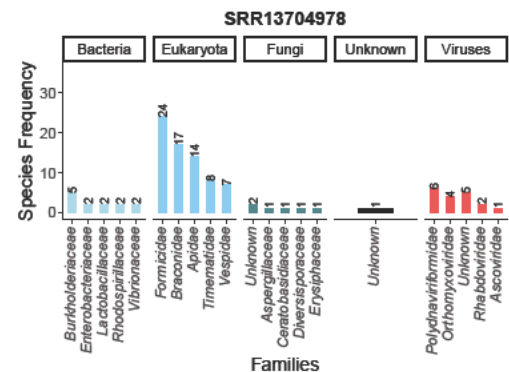
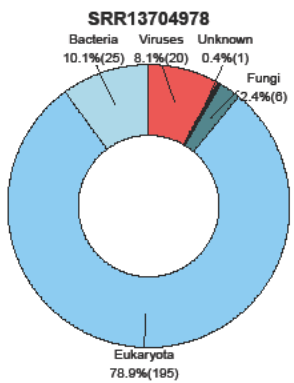
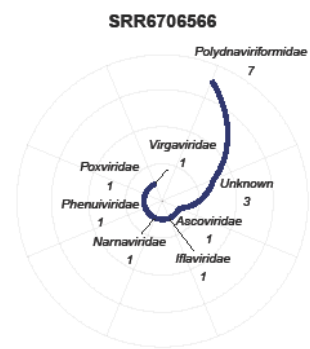
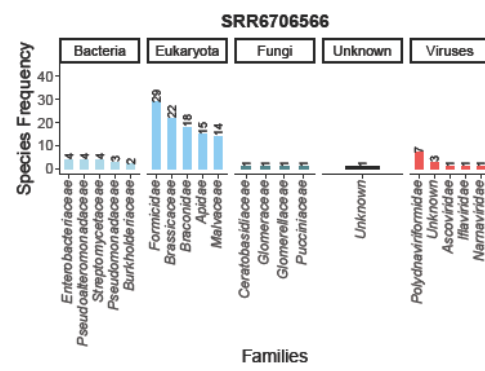
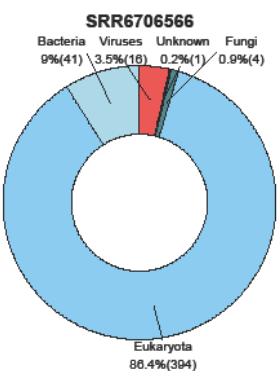
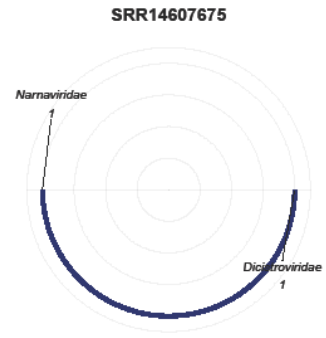
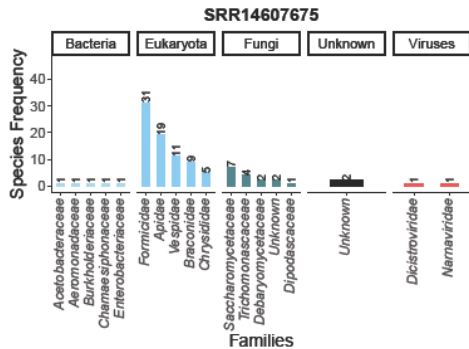
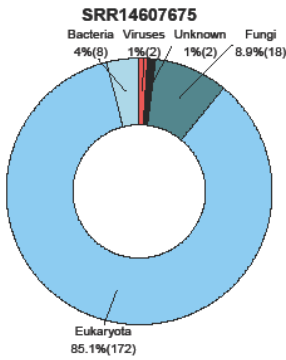
**Supplementary Figure S1. Geographical distribution of libraries used in the study classified by wasp species.**

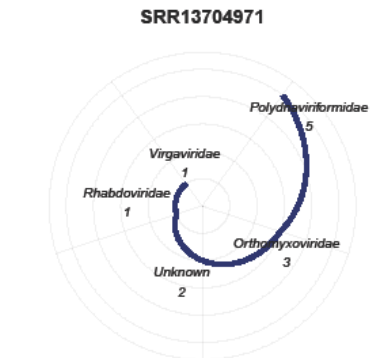
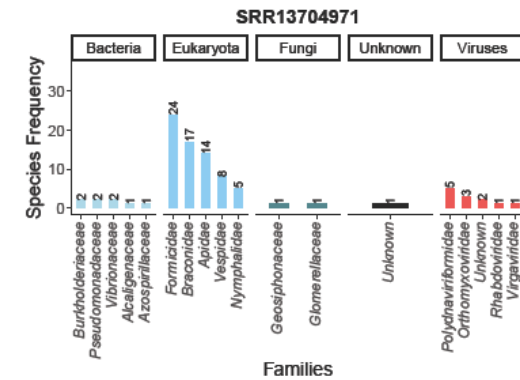
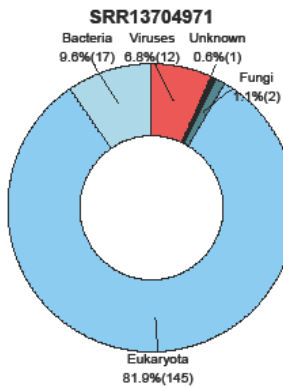
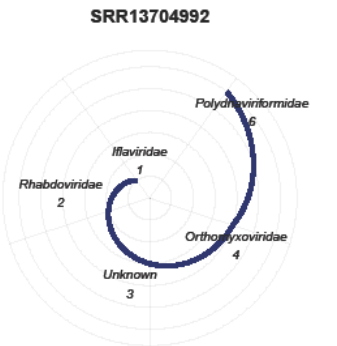
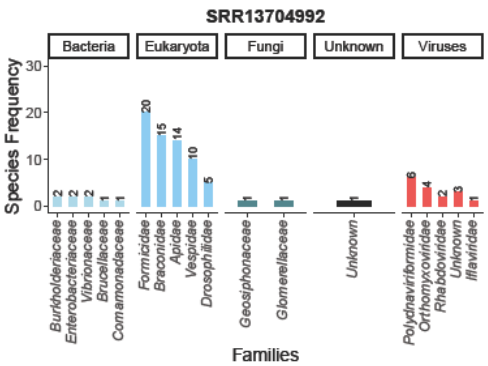
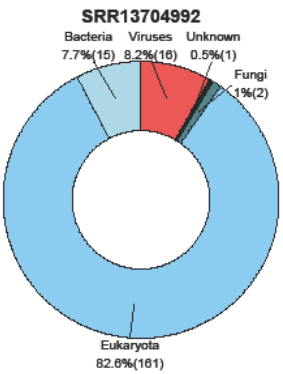
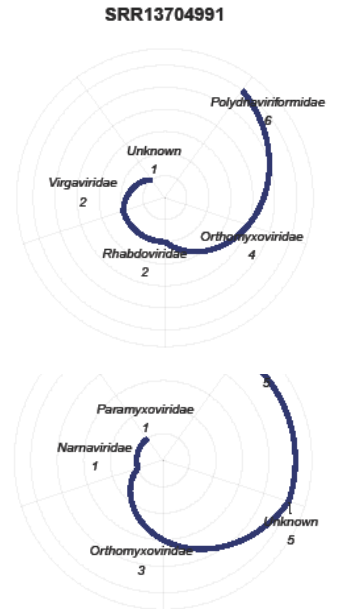
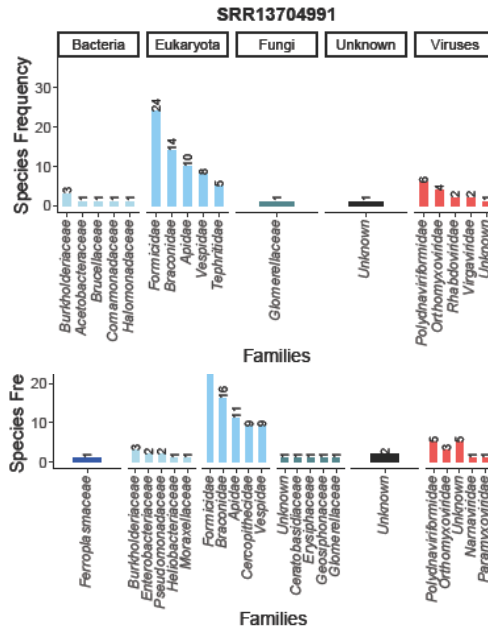
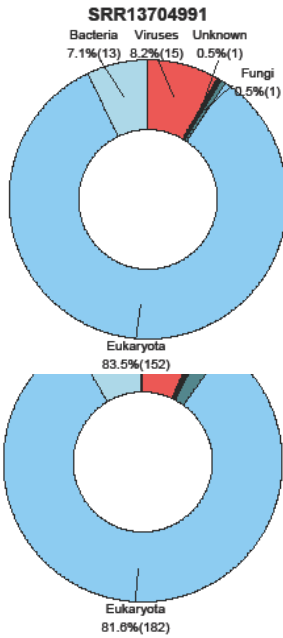


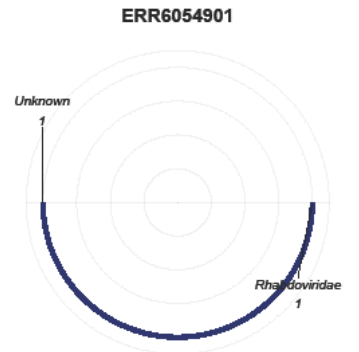
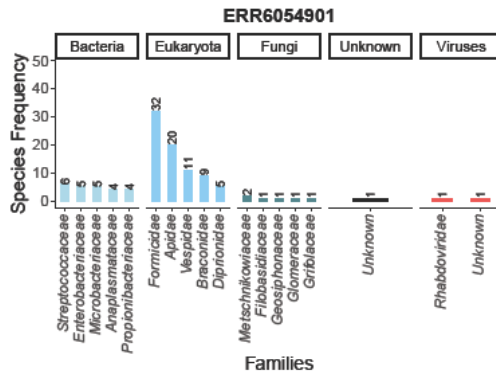
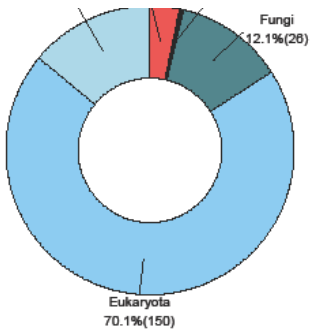


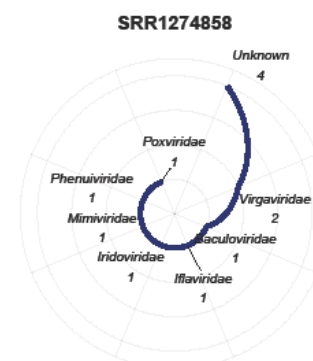
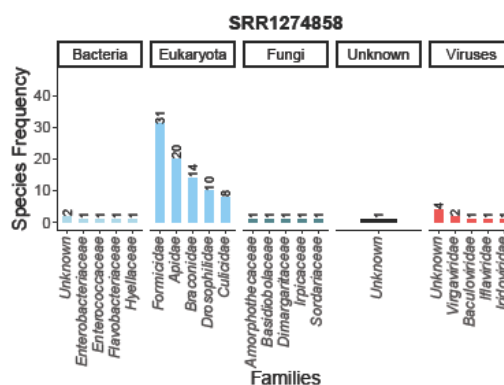
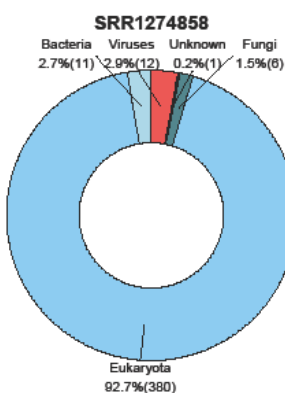
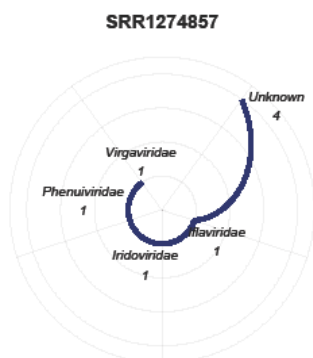
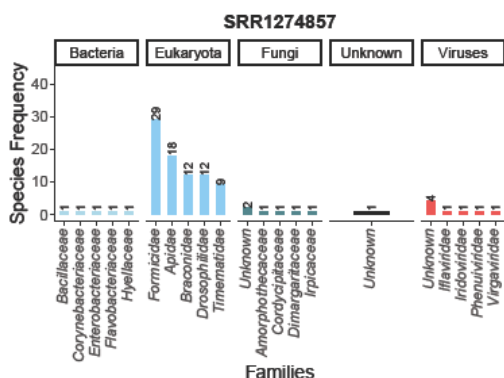
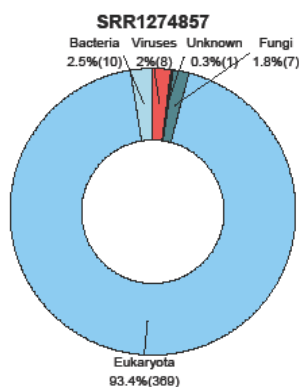
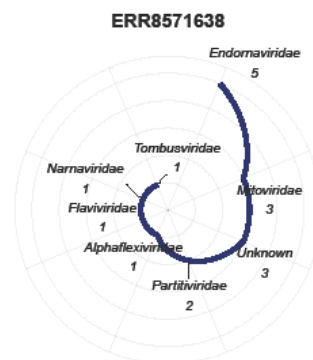
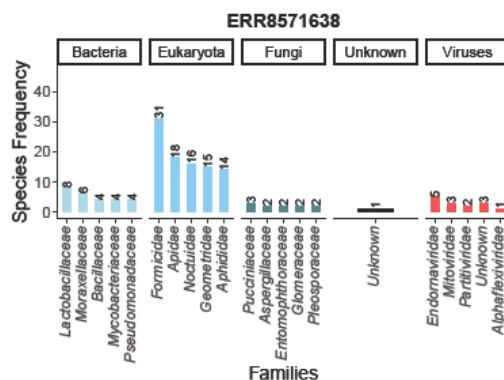
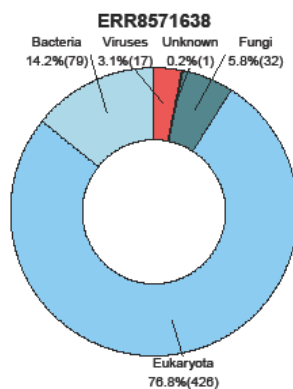
### Supplementary Figure S2. Metagenomics analysis grouped by species of parasitoid wasps.

In order: *A. compressa*, *C. vestalis*, *D. allozum*, *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.





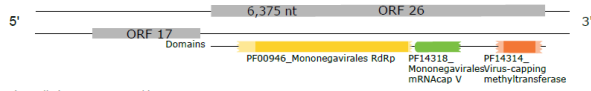




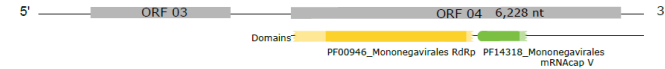
**Supplementary Figure S3. Metagenomics analysis for each RNA-seq library included in the study.** In order: SRR14607675 (*A. compressa*); SRR6706566, SRR13704978, SRR13704979, SRR13704980, SRR13704991, SRR13704992, SRR13704971 (*C. vestalis*); SRR2041626, SRR2040481 (*D. alloeum*); ERR6054901 (*E. lituratus*); 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.



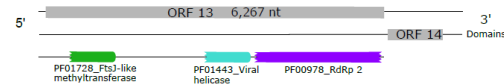
Lasius neglectus virus 2 12,041 nt



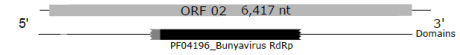
Gudgenby Calliphora mononega-like virus 12,763 nt



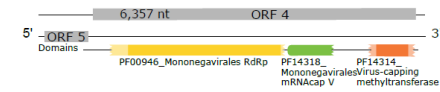
Sanya virga-like virus 1 7,145 nt



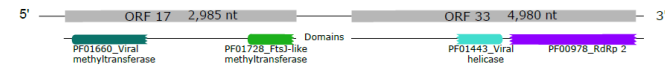
Wuhan insect virus 16 6,684 nt



Wuhan ant virus 7,202 nt



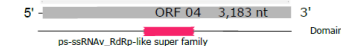
Megastigmus ssRNA, partial genome 12,061 nt



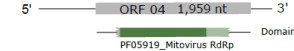
Hymenopteran chu-related virus OKIAV147 7,082 nt



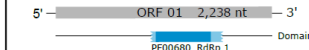
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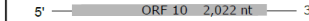
Hangzhou mitovirus 4 2,376 nt



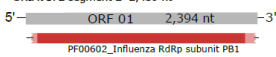
Dill cryptic virus 2 segment RNA 1 2,430 nt



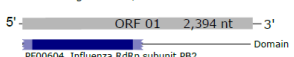
Dill cryptic virus segment RNA 2 2,354 nt



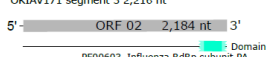
Phasmatodean orthomyxo-related virus OKIAV172 segment 2 2,439 nt



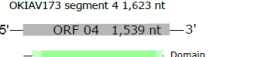
Phasmatodean orthomyxo-related virus OKIAV172 segment 1 2,504 nt



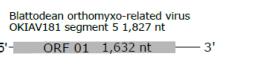
Hymenopteran orthomyxo-related virus OKIAV171 segment 3 2,216 nt



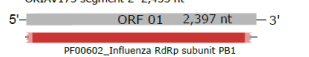
Hymenopteran orthomyxo-related virus OKIAV173 segment 4 1,623 nt



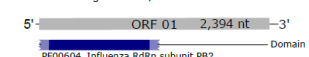
Blattodean orthomyxo-related virus OKIAV181 segment 5 1,827 nt



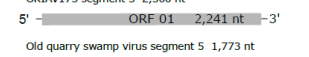
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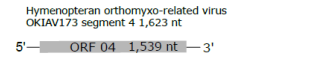
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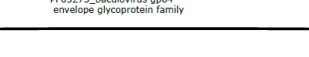
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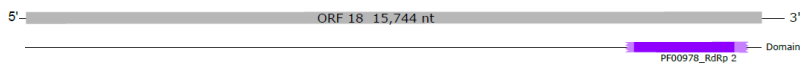
Old quarry swamp virus segment 5 1,773 nt



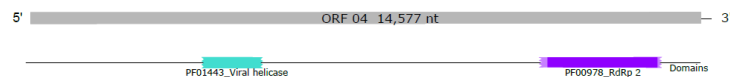
Hymenopteran orthomyxo-related virus OKIAV173 segment 4 1,623 nt



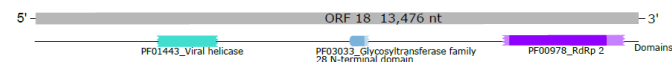
Lily alphaendornavirus isolate B1, complete genome 16,483 nt



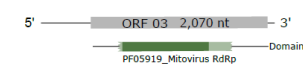
Geranium carolinianum endornavirus 14,625 nt



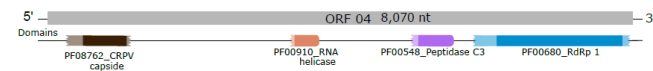
Hallsjon virus, complete genome 13,476 nt



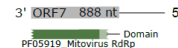
Entomophthora muscae mitovirus 2 RdRp 2,408 nt



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



Pemphredon lugubris 1,143nt: Hubei narna-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.