

Uncovering a Complex Virome Associated with the Cacao Pathogens *Ceratocystis cacaofunesta* and *Ceratocystis fimbriata*

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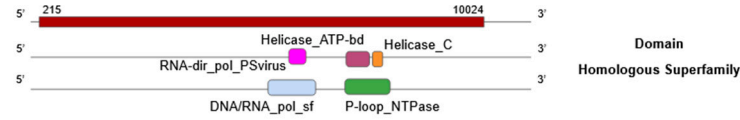
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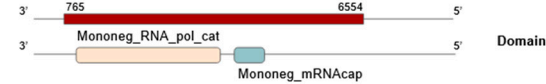
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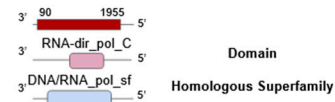
MK231018.1 - *Mycosphaerella hypovirus A*



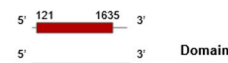
MK584852.1 - *Alternaria tenuissima negative-stranded RNA virus 1*



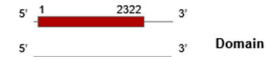
NC_006440.1 - *A. cherry disease-associated mycovirus**



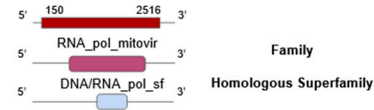
NC_006440.1 - *A. cherry disease associated partitivirus CP*



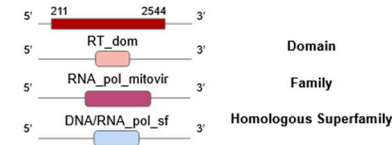
MN619799.1 - *Botrytis cinerea binarnavirus 5*



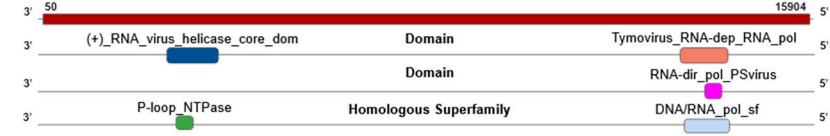
NC_004046.1 - *Cryphonectria parasitica mitovirus 1*



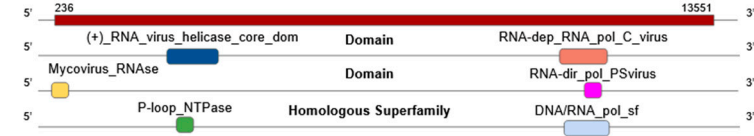
NC_012585.1 - *Thielaviopsis basicola mitovirus*



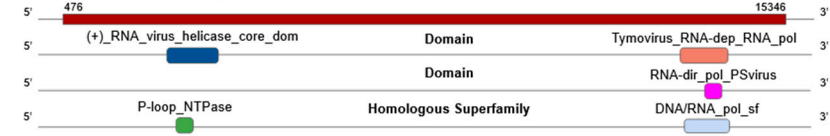
ON955056.1 - *Tvarminne alphaendornavirus*



MW788771.1 - *Alphaendornavirus sp.*



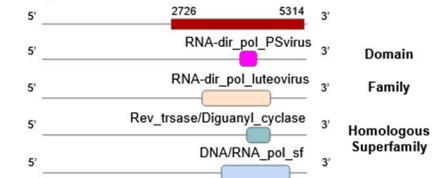
MK279478.1 - *Morchella importuna endornavirus 2*



MZ218601.1 - *Totiviridae sp.*



NC_040653.1 - *Colletotrichum eremochloae totivirus 1*



* *Amasya cherry disease-associated mycovirus* is a below-species classification of *Cherry chlorotic rusty spot associated partitivirus*

Figure S1. Conserved structures of the hit organisms for e-value of the studied sequences based on BlastX similarity analysis. The ORFfinder program was used to identify the largest ORF and InterProScan program was used to identify conserved structures.



Figure S2. Conserved motifs and catalytic site in the *Hypovirus cacaofunestae* viral contig. A. Superfamily cl40470 similar to ps-ssRNAV_RdRp located in the interval 2079-2303, conserved polymerase motif A, located at position 2149-2163, conserved polymerase motif B, located at position 2217-2233 and 2235-2240, conserved polymerase motif C, located at position 2255-2258 and 2259-2269 B. Species of the family *Hypoviridae* with similarity of motifs conserved with HVC, Catalytic site (Yellow), Motif A (Light Grey), Motif B (Light Green), Motif C (Lemon Green).

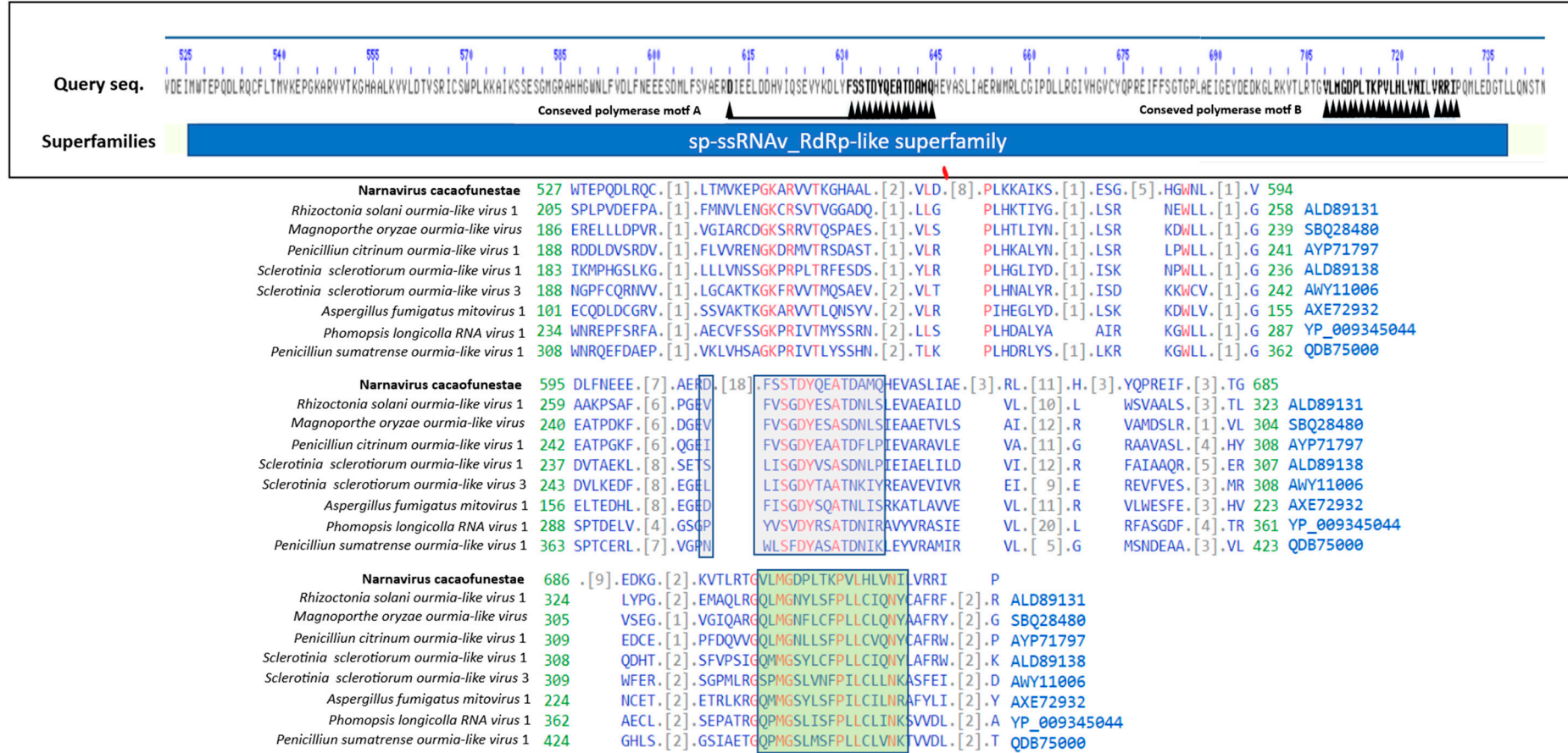


Figure S3. Conserved motifs and catalytic site in the Narnavirus cacaofunestae viral contig. A. Superfamily cl40470 similar to ps-ssRNAv_RdRp located in the interval 527-736, conserved polymerase motif A, located at positions 612 and 631-644, conserved polymerase motif B, located at positions 698-724 and 726-729. B. Species of the family Botourmiaviridae and Mitoviridae with similarity of motifs conserved with NVf, Motif A (light grey), Motif B (light green).

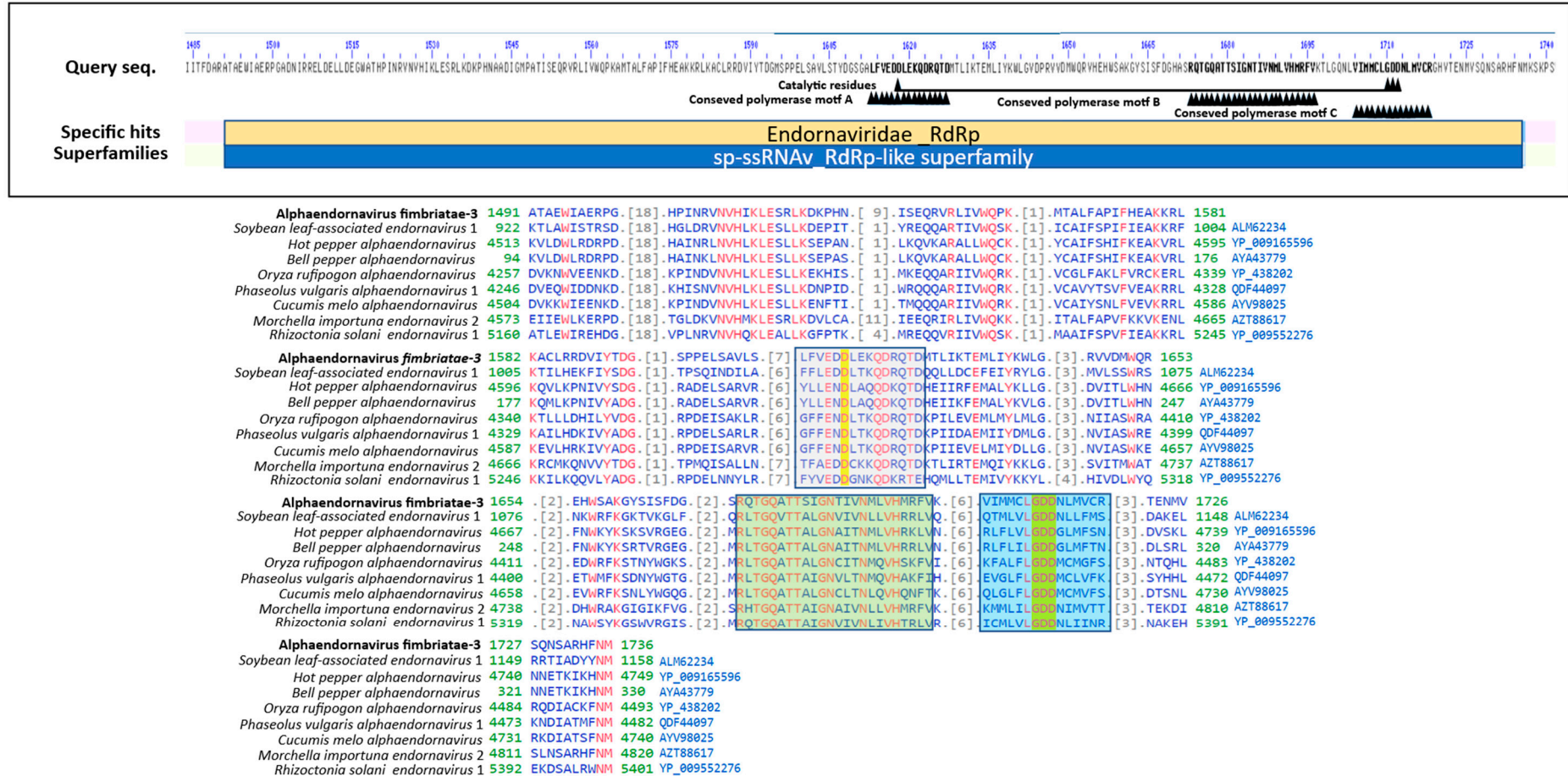


Figure S4. Conserved motifs and catalytic site in the Alphaendornavirus fimbriatae-3 viral contig. A. Superfamily cl40470 similar to ps-ssRNAV_RdRp located in the interval 1491-1736, conserved polymerase motif A, located at position 1613-1627, conserved polymerase motif B, located at position 1673-1696, conserved polymerase motif C, located at position 1704-1718 B. Species of the family *Endornaviridae* with similarity of motifs conserved with AEVf-3, Catalytic site (Yellow), Motif A (Light Grey), Motif B (Light Green), Motif C (Blue).

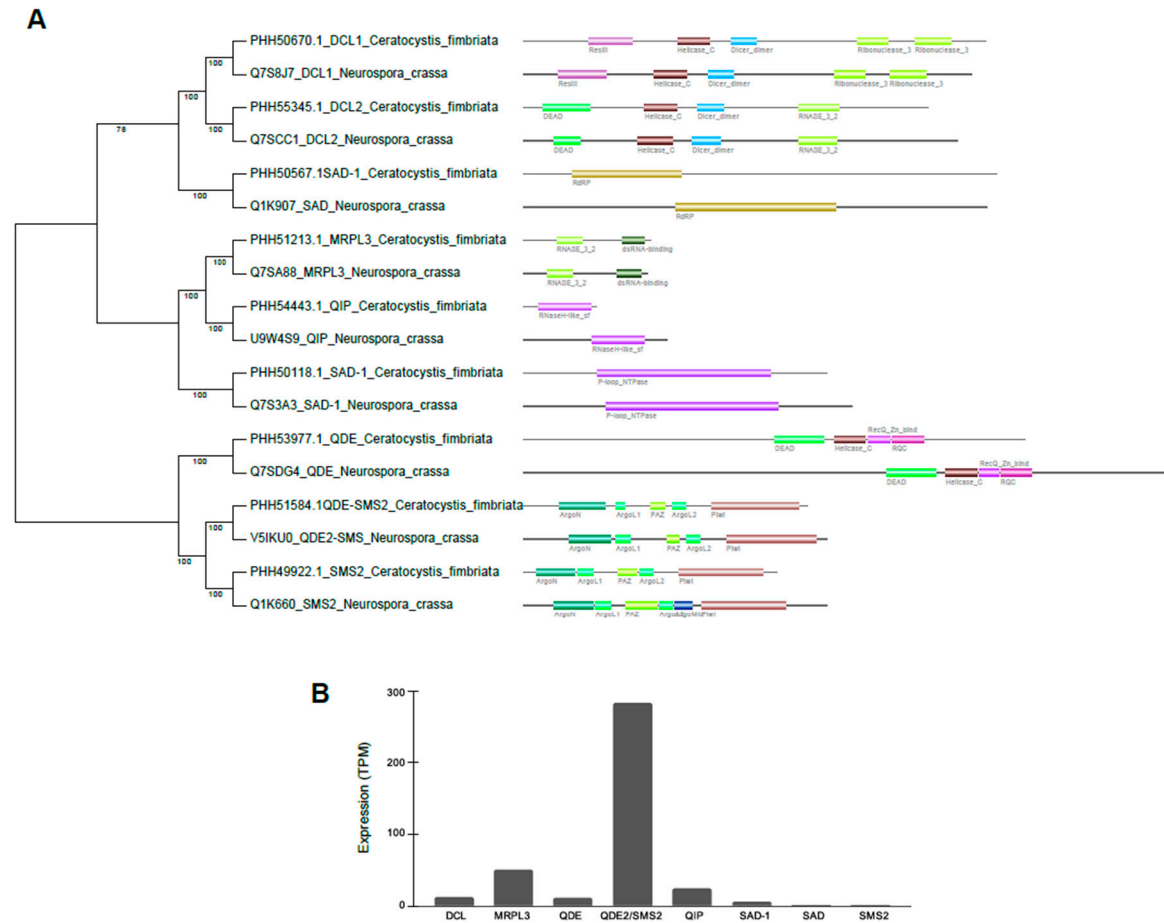


Figure S5. Characterization of RNAi-related genes in *Ceratocystis fimbriata*. (A) Dendrogram based on sequence similarity. (B) Evaluation of RNAi-related genes transcriptional activity. Quantification was normalized by Transcripts Per Million (TPM).