

Additional File 1

Supplementary figure legends:

Figure S1 Alignments of 5'-untranslated regions (UTRs) of SsPV-S S-1 and S-2 segments.

The start codon was indicated with red line.

Figure S2 Neighbor-Net analysis of mycovirus-related dsRNA viruses.

The analysis was conducted under the WAG model of substitution. Scale bar corresponds to 1.0 amino acid substitutions per site. The major viral lineages are indicated. The box-like appearance in the basal branches of this phylogeny suggests regions of unresolved branches or conflicting phylogenetic signals. See Table S1 in the supplemental material for abbreviations of virus names and viral protein accession numbers.

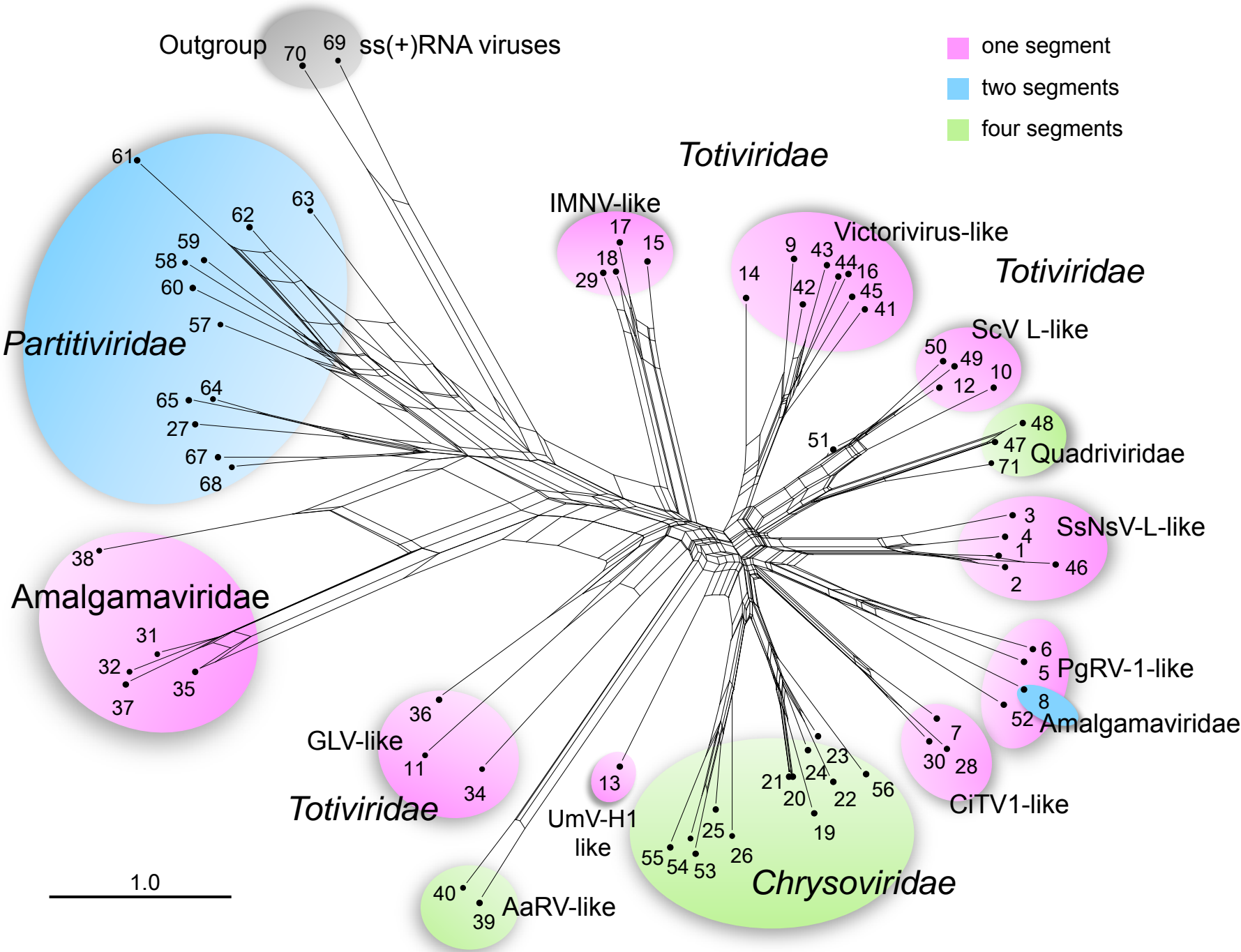
Figure S3 ML phylogenetic trees of the RdRps (A) and CPs (B) of viruses in the family *Partitiviridae*.

The GenBank accession numbers of viral proteins are included in taxon names. Viral lineages are colour-coded to reflect their host range. The trees were rooted with STV-like lineages. Only p-values of the SH-like approximate likelihood ratios (SH-aLRT) >0.5 (50%) are indicated. All scale bars correspond to 0.5 amino acid substitutions per site.

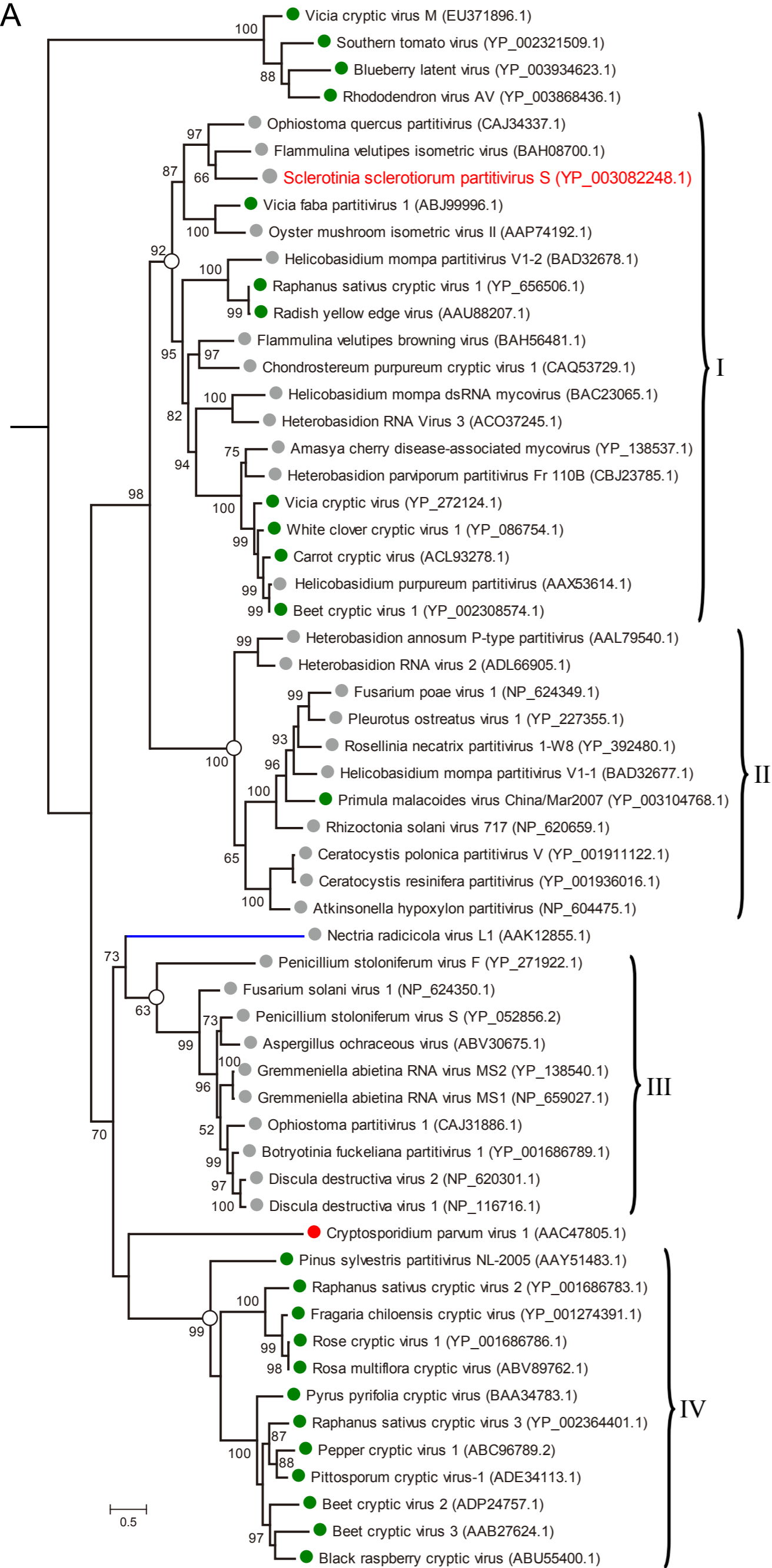
S-1 1 AGATTAAATTATCTTAGTCCACTTTCTAAGTTCAACGAAAAT TAAAATCAAAAAGC 54
S-2 1 AGATTAAATTATCTTAGTCTACTTTCTAAGTTCAACGAAAATCAA - TCAAAAAGC 53

S-1 55 TC TTAACCAACAGATCTTTTAAAACTAACAA - - - - - ATG 88
S-2 54 TT TTAACCAACA AATCTTTTAAAACTAAC TCTCTACTCAAG ATG 98

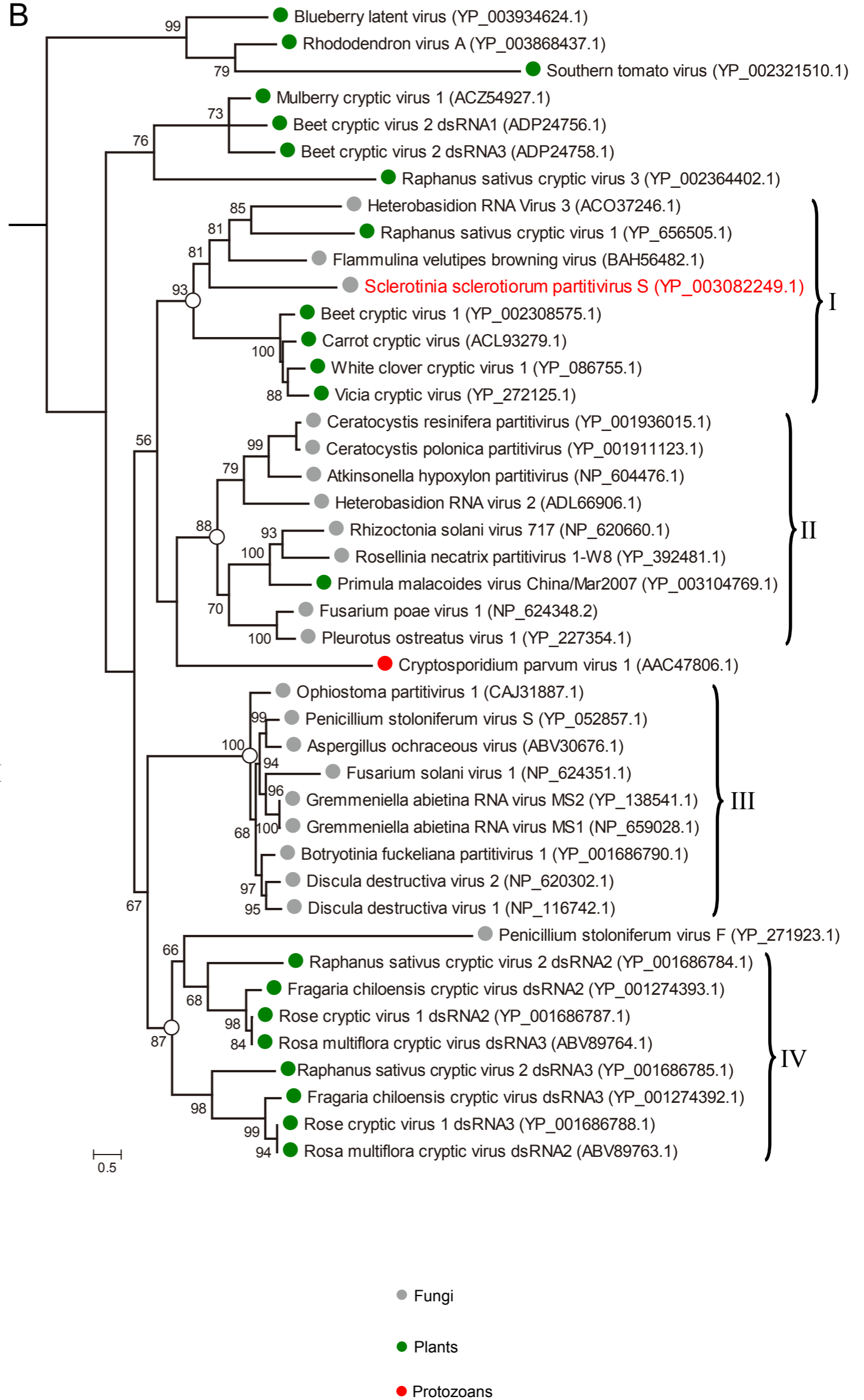
start codon



A



B



● Fungi

● Plants

● Protozoans