



**Supplementary Figure 1.** Maximum likelihood phylogeny based on the amino acid sequences derived from ORF 1 of grapevine virus L (GVL) from this study and references derived from extant GVL genomes (references indicated by a solid circle marker). The cognate sequence from grapevine virus E (GVE) was used as an outgroup. The phylogeny represents the tree with the highest log likelihood and was generated in MEGA X using the Le Gascuel model with gamma distribution (n=5). Bootstrapping was applied (1000 replicates) and the percentage of trees in which the associated taxa clustered together is shown next to the branches. Bootstrap percentages lower than 50 are not shown. The identity of each phylogroup is shown alongside the phylogeny.