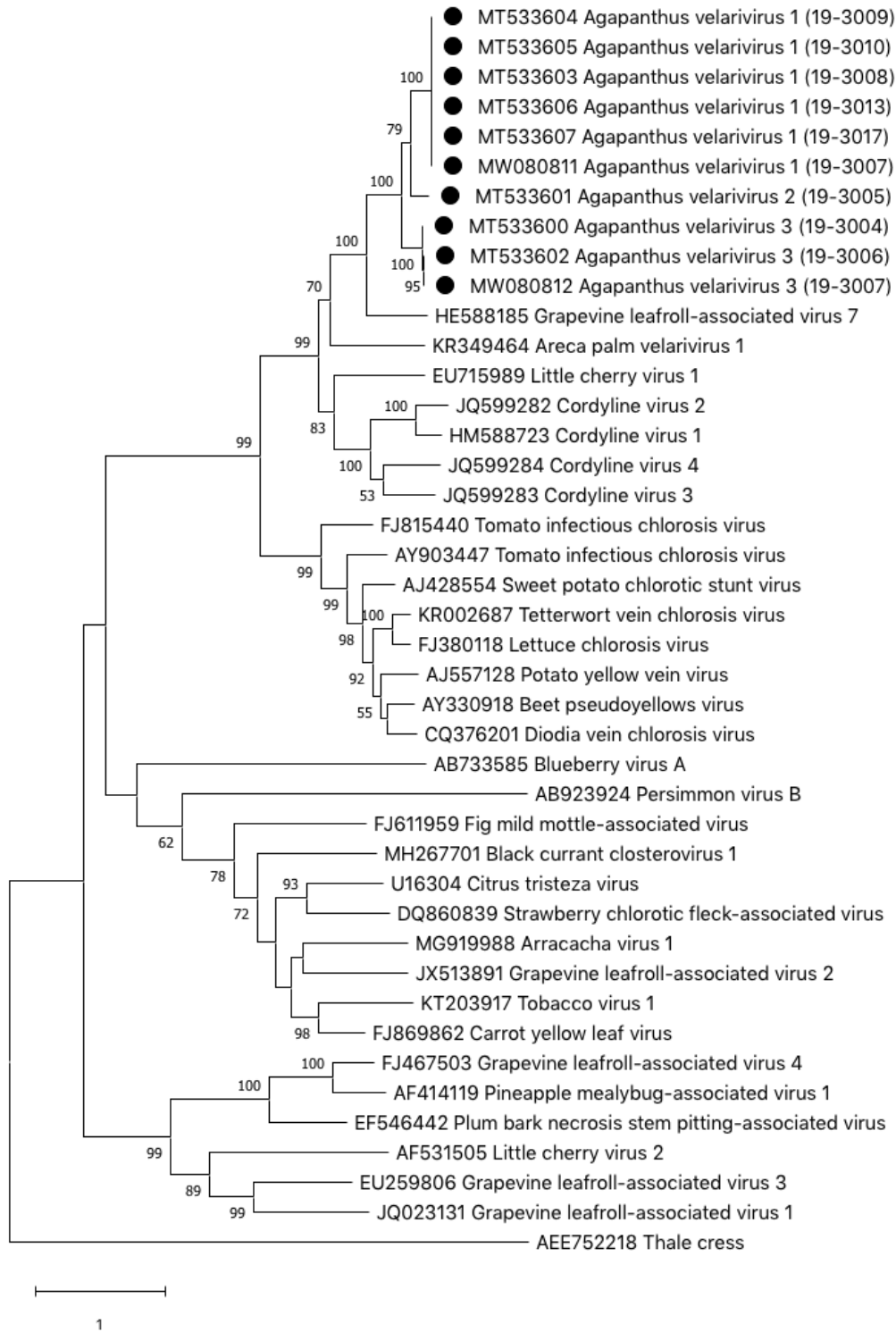
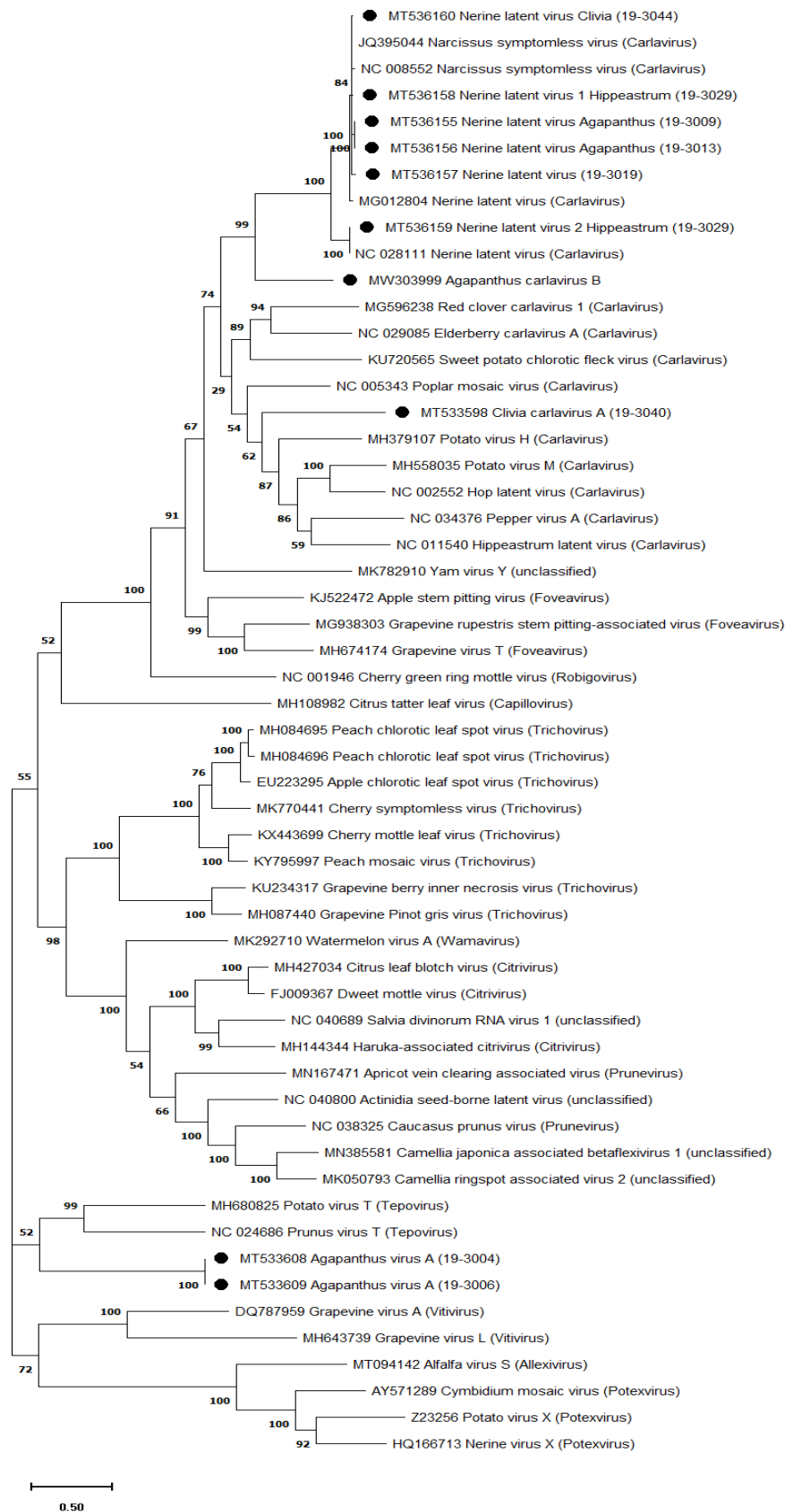


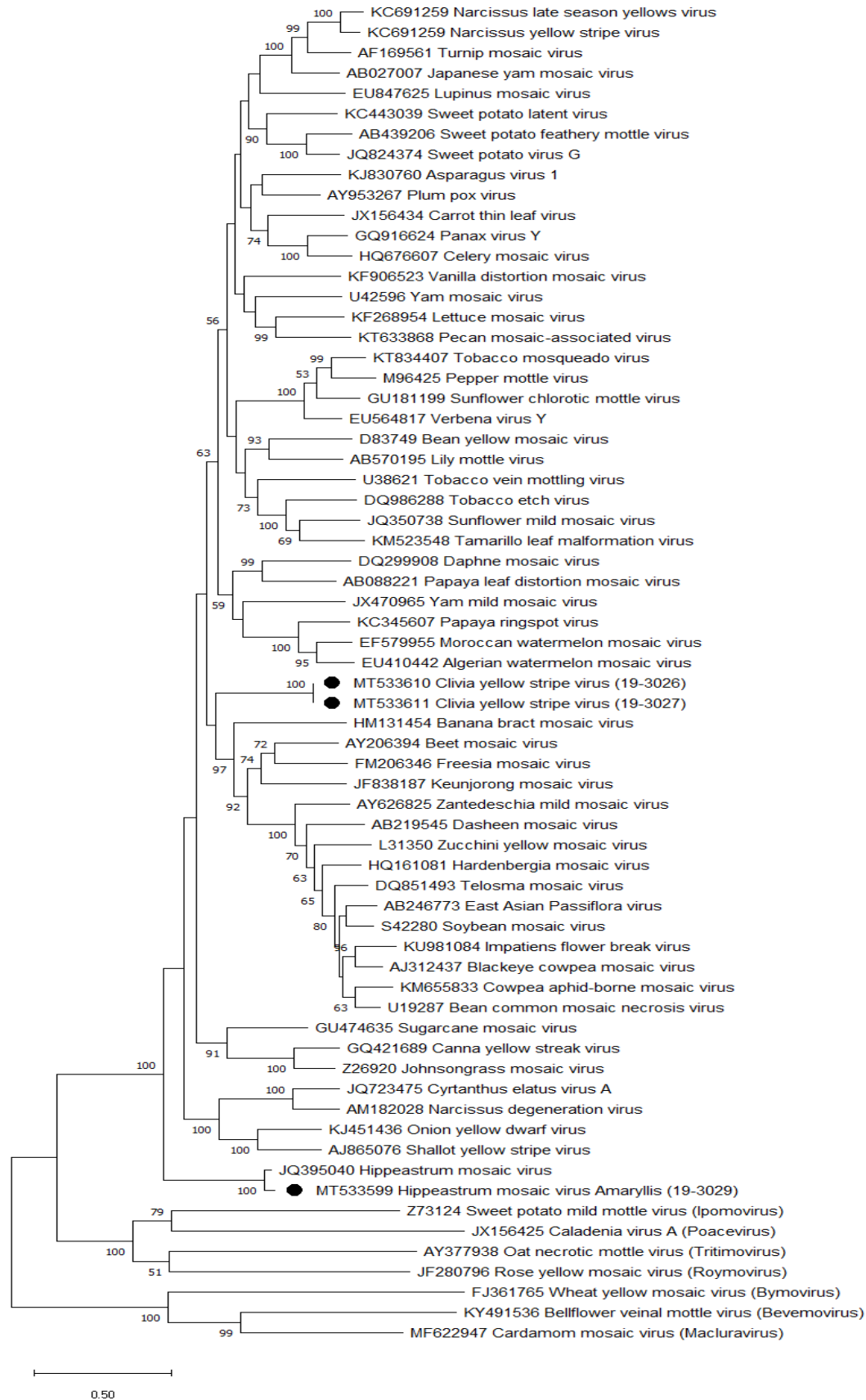
Supplementary Figure 3.1: Maximum likelihood phylogeny based on the complete nucleotide sequences of *Agapanthus tungro* virus variants (sources from this study indicated by a solid circle marker) and selected members of the *Caulimoviridae* family. The phylogeny represents the tree with the highest log likelihood and was generated in *MEGA X* using the General Time Reversible 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 viral genus corresponding to each reference is shown in brackets, while the sample number is indicated for samples related to this study.



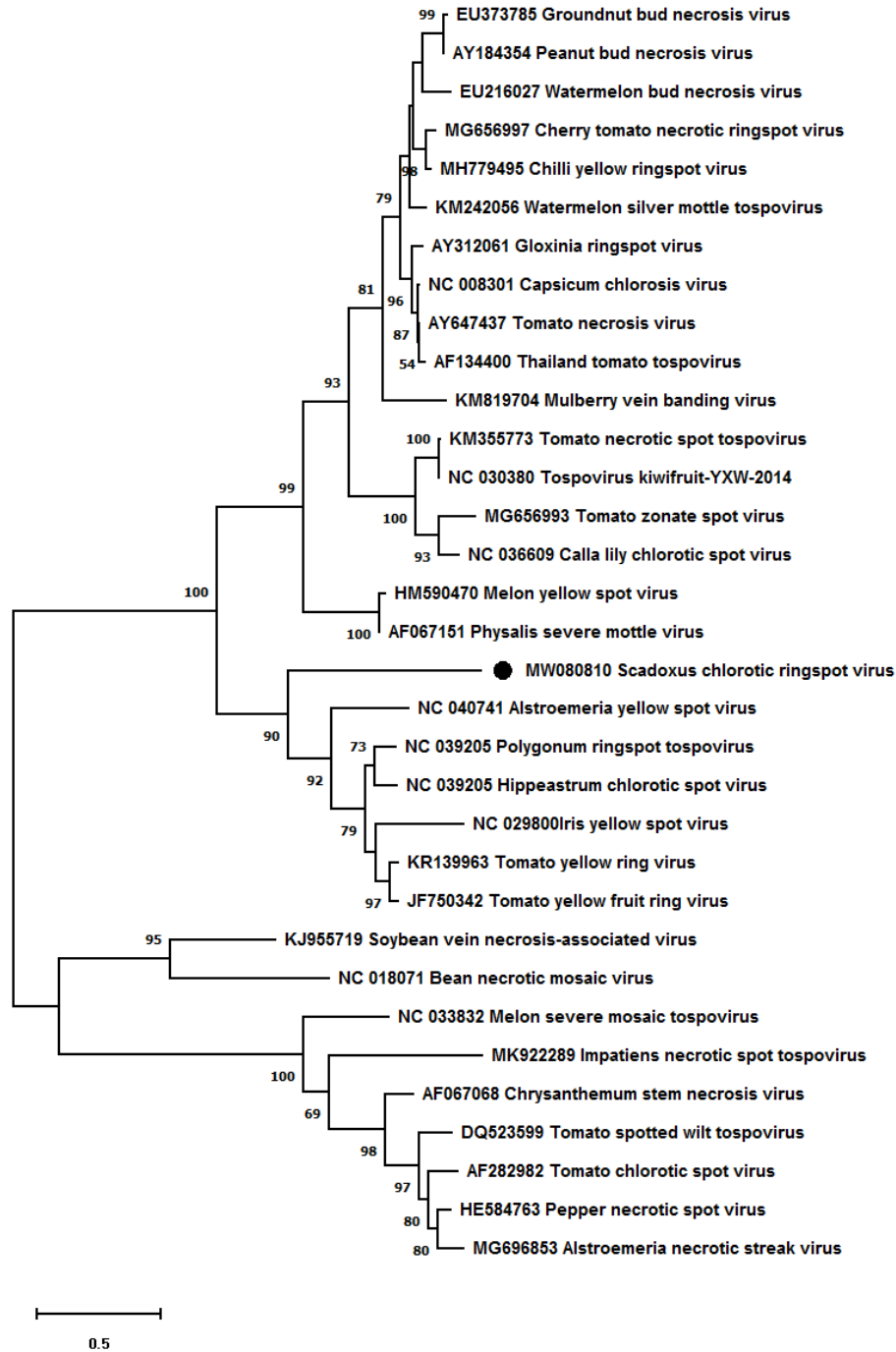
Supplementary Figure 3.2: Maximum likelihood phylogeny based on the amino acid sequences of the heat shock protein homolog of *Agapanthus velarivirus* variants (sources from this study indicated by solid circle markers) and selected members of the *Closteroviridae* family. The phylogeny represents the 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 viral genus corresponding to each reference is shown in brackets, while the sample number is indicated for samples related to this study. A heat shock protein 70 amino acid sequence of *Arabidopsis thaliana* was used as an outgroup.



Supplementary Figure 3.3: Maximum likelihood phylogeny based on the amino acid sequences of the replicase gene of members of the *Betaflexiviridae* family found in this study (sources from this study indicated by solid circle markers) and selected members of the same family. These include the nerine latent virus, well as novel viruses, clivia carlavirus A and agapanthus virus A, as well as. The phylogeny represents the tree with the highest log likelihood and was generated in *MEGA X* using the Le Gascuel model with gamma distribution ($n=5$). All positions containing gaps and missing data were eliminated (complete deletion option). 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 viral genus corresponding to each reference is shown in brackets, while the sample number is indicated for samples related to this study.



Supplementary figure 3.4: Maximum likelihood phylogeny based on the amino acid sequences of the polyprotein of the *Hippeastrum mosaic virus* and the novel clivia yellow stripe virus strains (sources from this study indicated by solid circle markers) and selected members of the Potyvirus genus. The phylogeny represents the tree with the highest log likelihood and was generated in *MEGA X* using the Le Gascuel model. All positions containing gaps and missing data were eliminated (complete deletion option). 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. Representatives from other genera of the *Potyviridae* family form the outgroup, with the genus name corresponding to each genus shown in brackets.



Supplementary figure 3.5: Maximum likelihood phylogeny based on the amino acid sequences of the product of the N gene of scadoxus chlorotic ringspot virus (sources from this study indicated by a solid circle marker) and selected members of the *Orthotospovirus* genus. The phylogeny represents the tree with the highest log likelihood and was generated in *MEGA X* using the Le Gascuel model with gamma distribution ($n=5$). All positions were used in the analysis. 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.