

Grapevine Virome of the Don Ampelographic Collection in Russia Has Concealed Five Novel Viruses

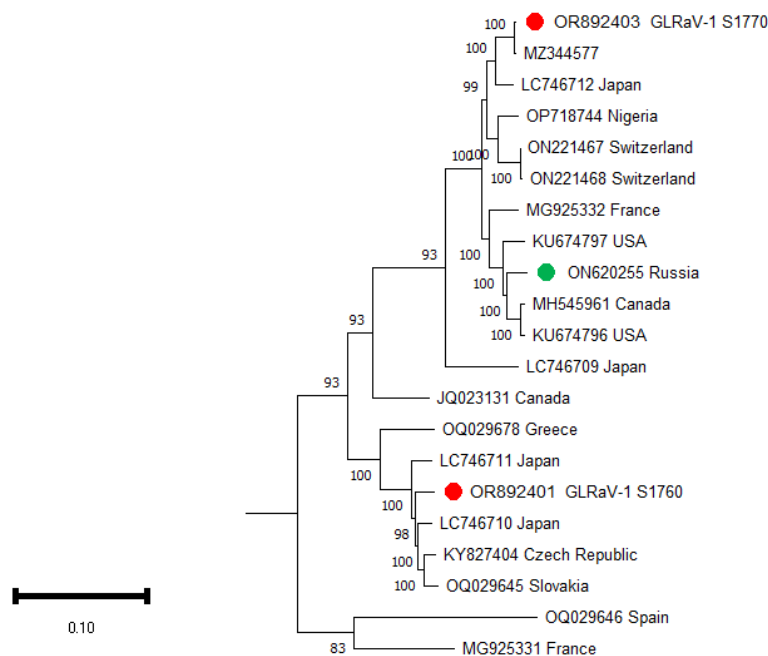
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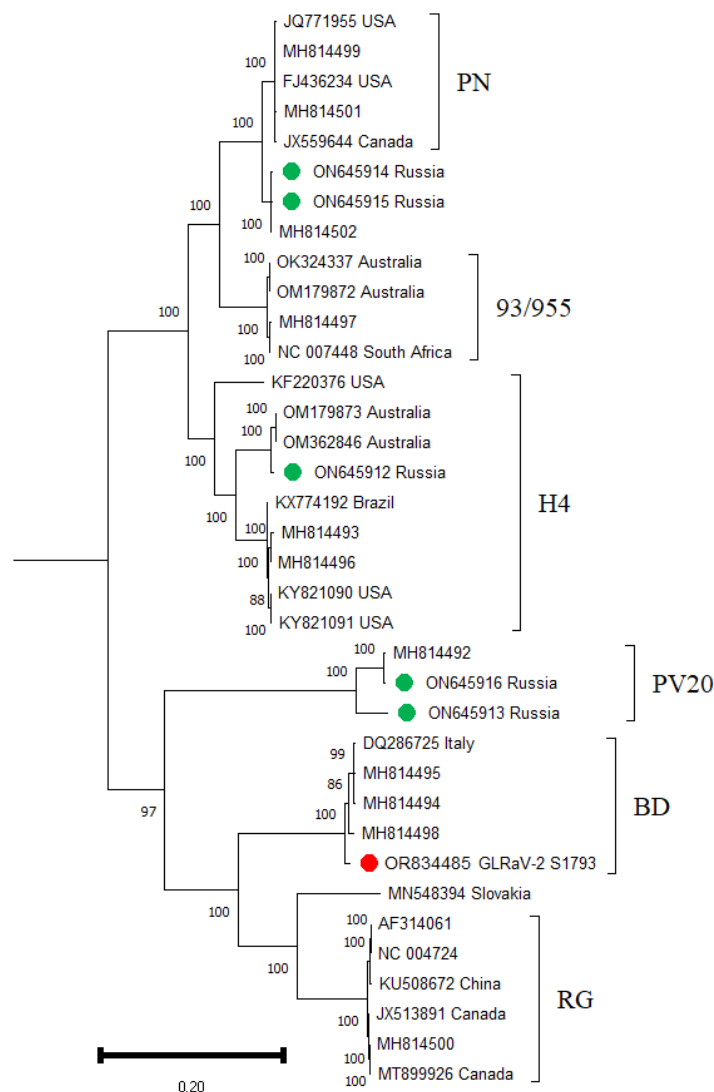
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Supplementary Materials



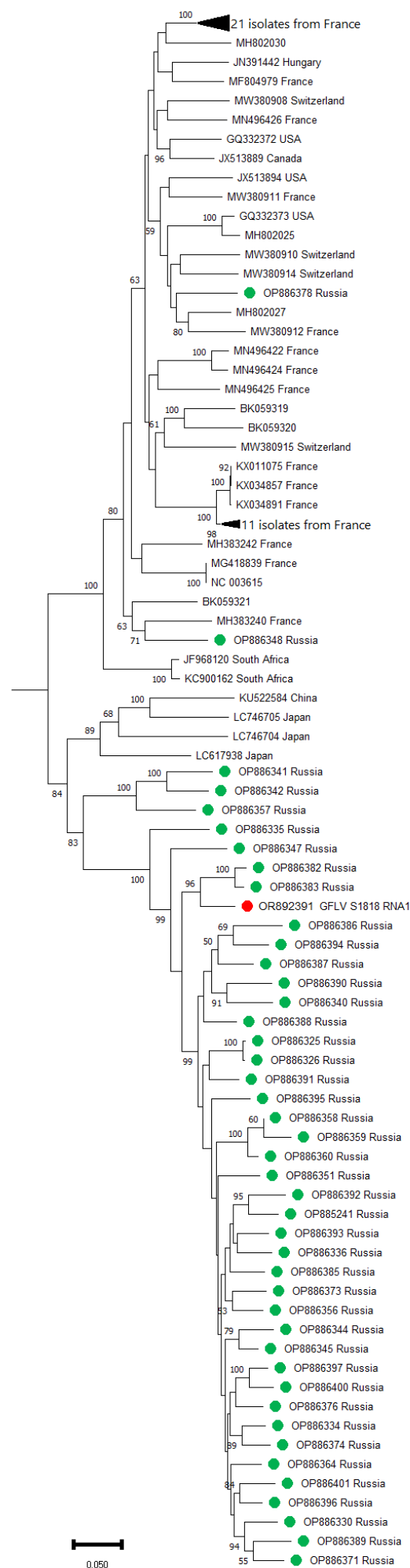
Supplementary Figure S1. Phylogenetic tree based on complete genome sequences of grapevine leafroll-associated virus 1 (GLRaV-1) isolates obtained in this study (red dots), other Russian isolate (green dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates.



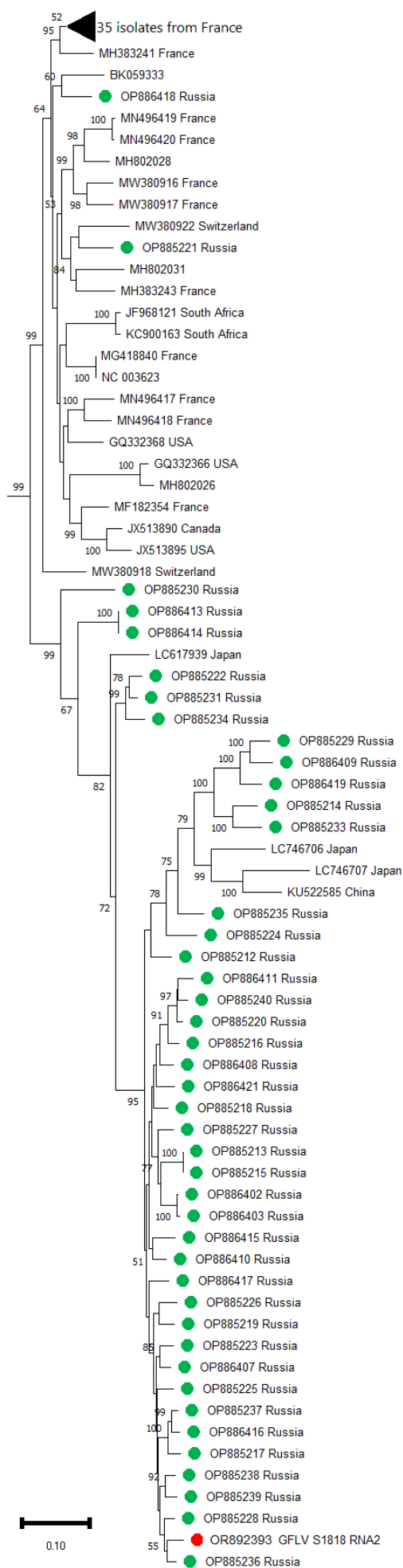
Supplementary Figure S2. Phylogenetic tree based on complete genome sequences of grapevine leafroll-associated virus 2 (GLRaV-2) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates.



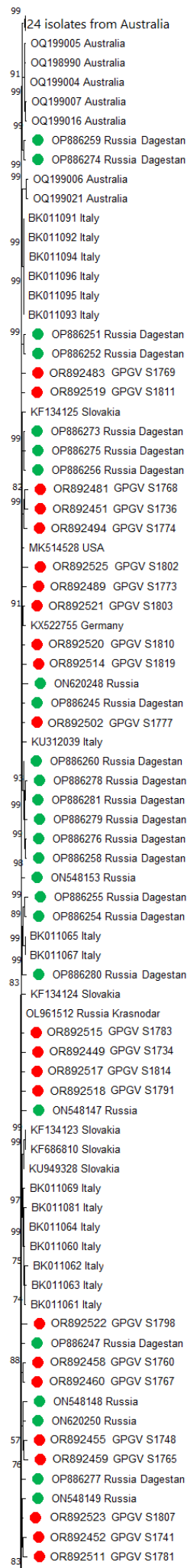
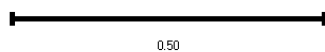
Supplementary Figure S3. Phylogenetic tree based on complete genome sequences of grapevine leafroll -associated virus 3 (GLRaV-3) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates.



Supplementary Figure S4. Phylogenetic tree based on complete nucleotide sequences of RNA1 of grapevine fanleaf virus (GFLV) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



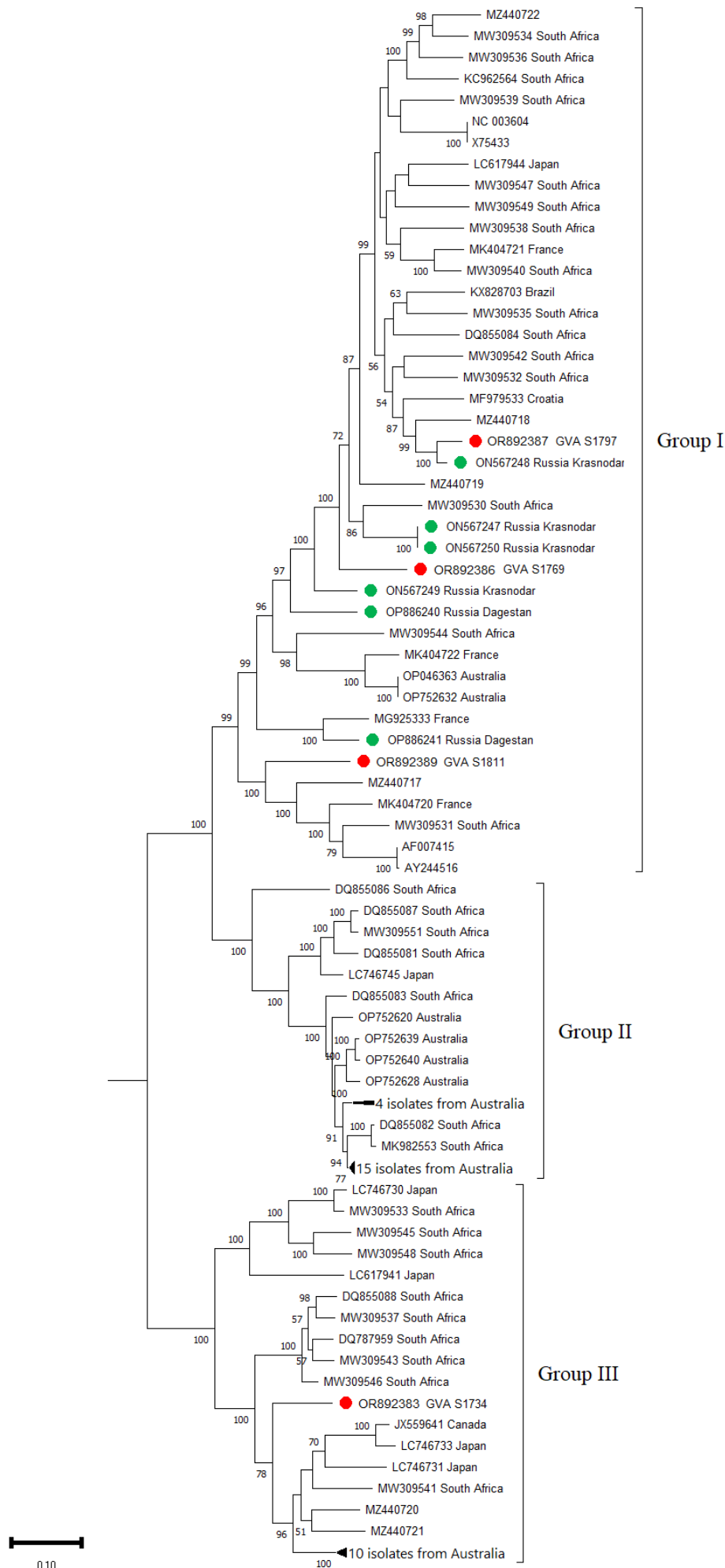
Supplementary Figure S5. Phylogenetic tree based on complete nucleotide sequences of RNA2 of grapevine fanleaf virus (GFLV) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



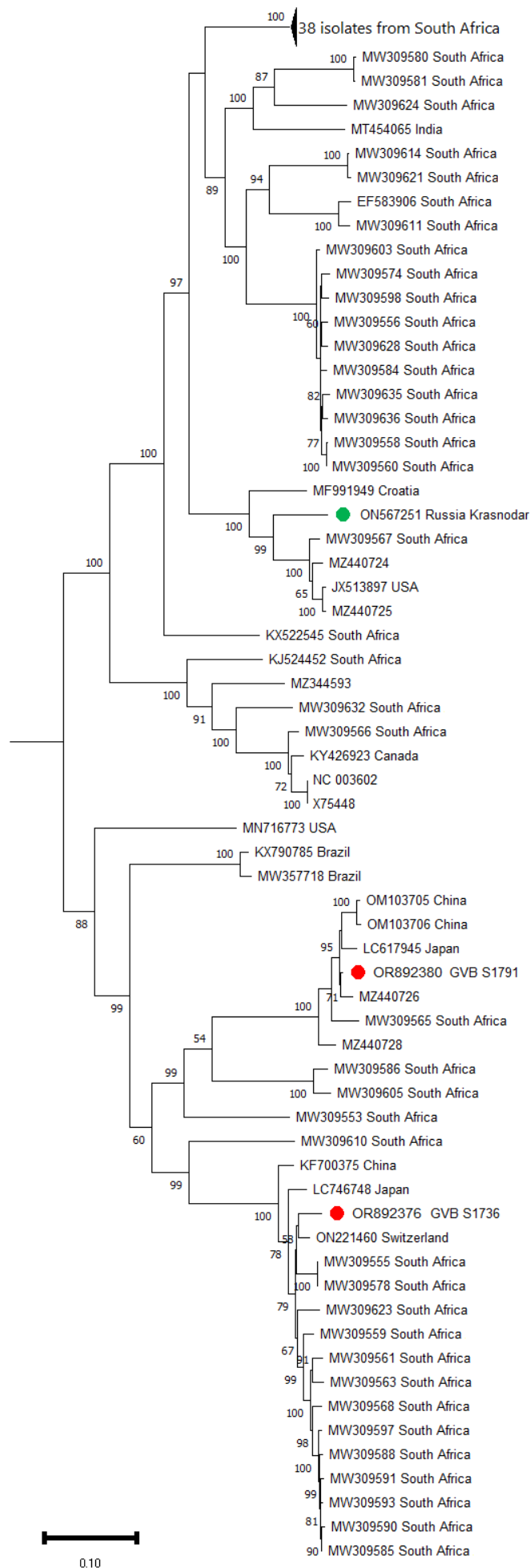
(a)



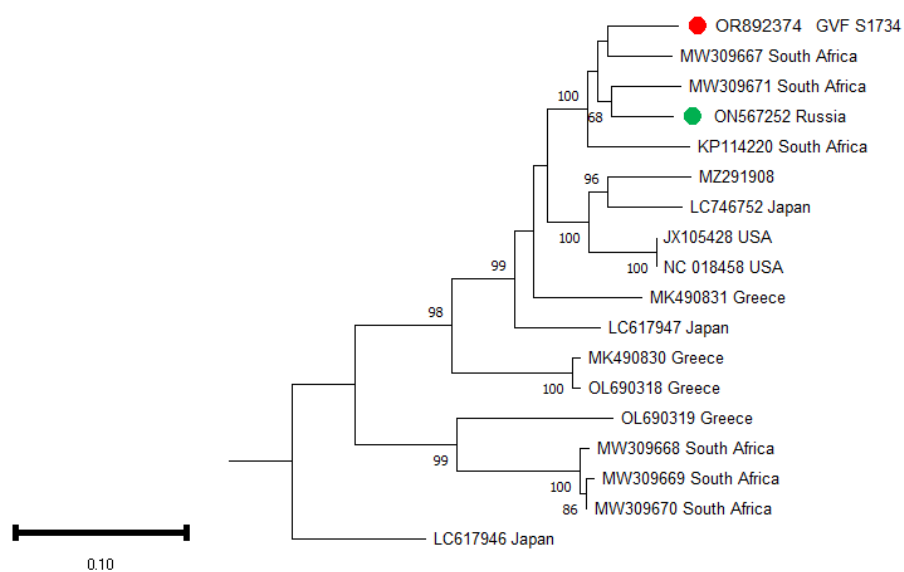
Supplementary Figure S6 (a-b). Phylogenetic tree based on complete genome sequences of grapevine Pinot gris virus (GPGV) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



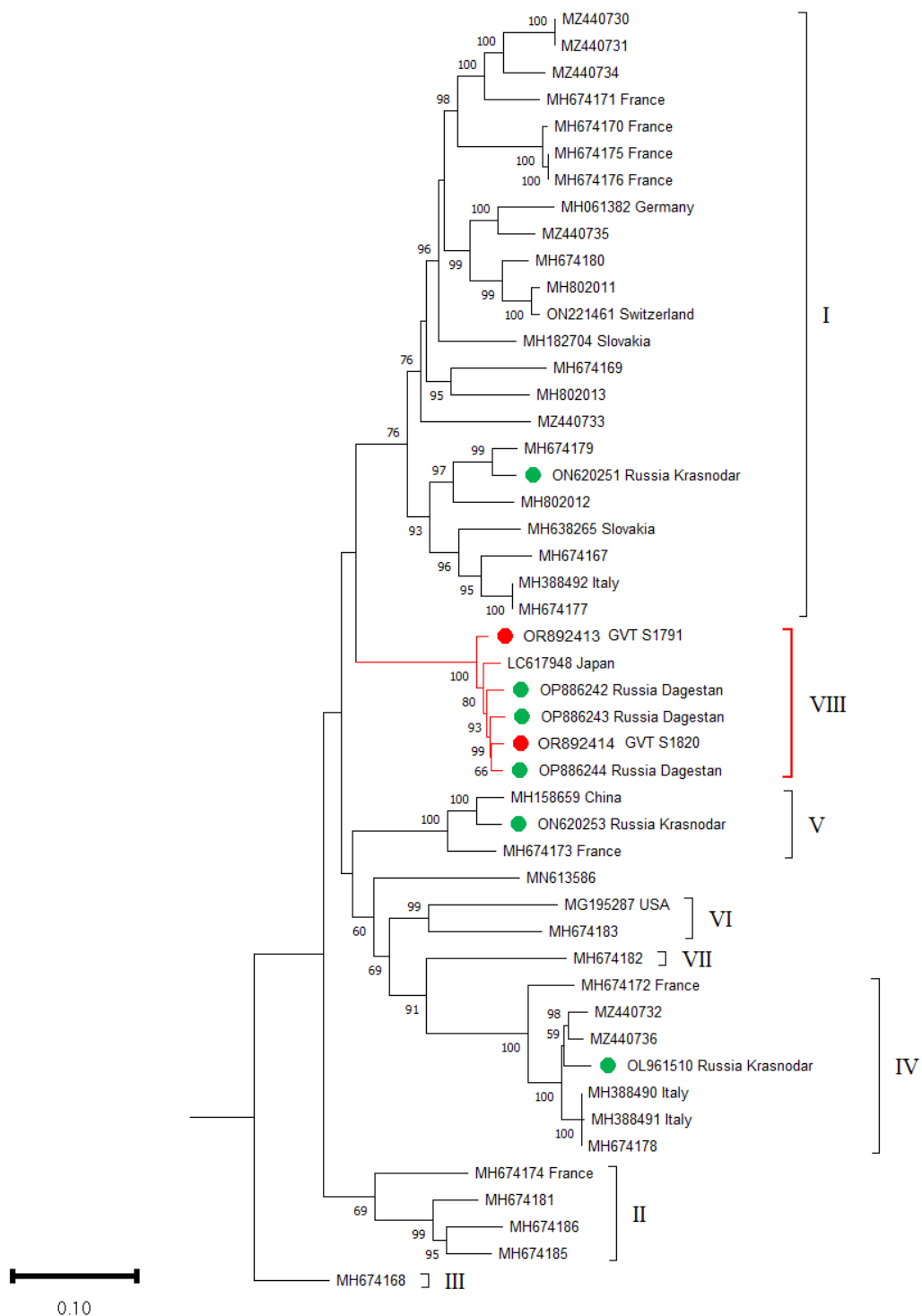
Supplementary Figure S7. Phylogenetic tree based on complete genome sequences of grapevine virus A (GVA) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



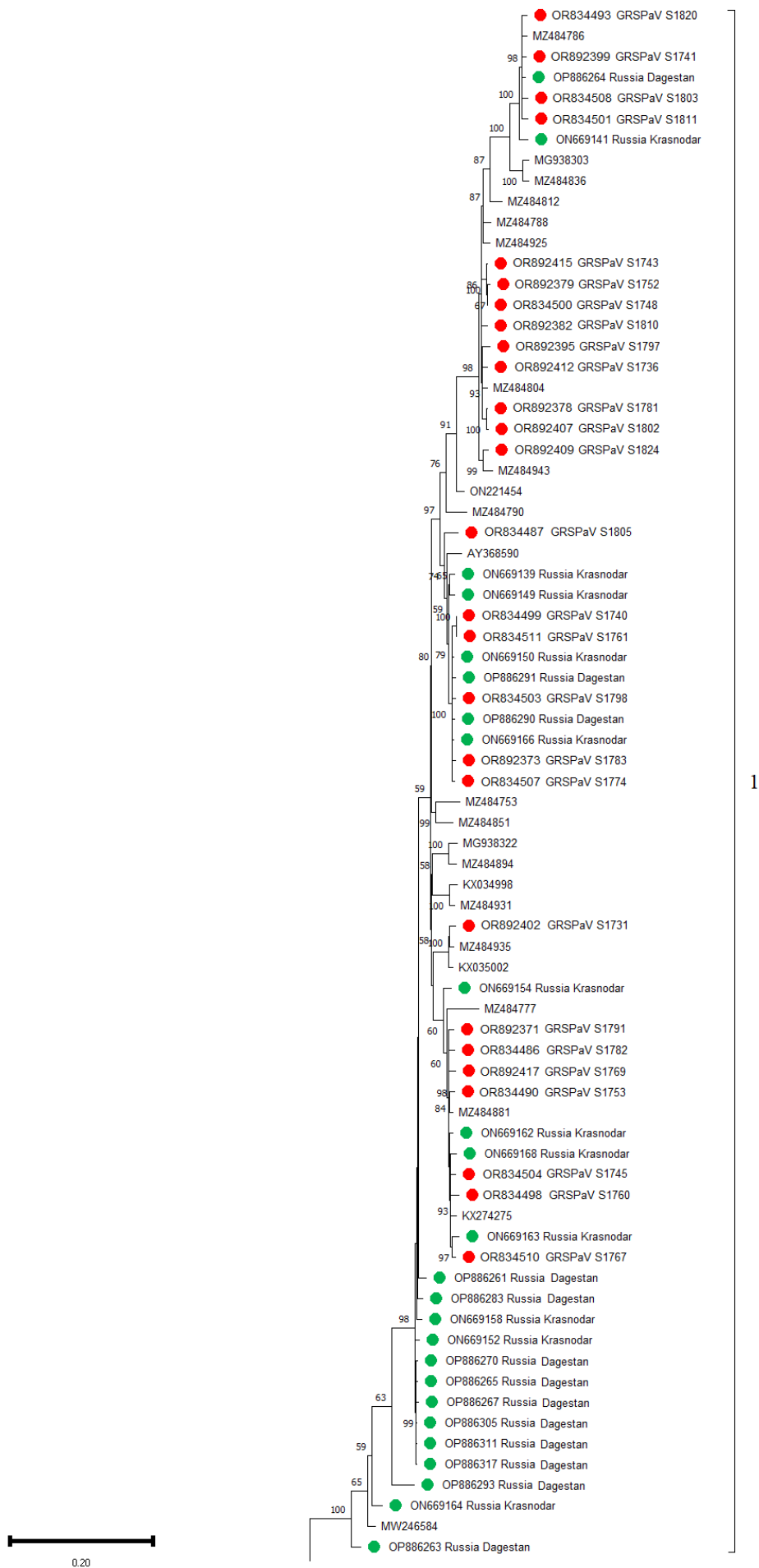
Supplementary Figure S8. Phylogenetic tree based on complete genome sequences of grapevine virus B (GVB) isolates obtained in this study (red dots), other Russian isolate (green dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



Supplementary Figure S9. Phylogenetic tree based on complete genome sequences of grapevine virus F (GVF) isolates obtained in this study (red dot), other Russian isolate (green dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 boot-strap replicates. Bootstrap values below 50 are not shown.



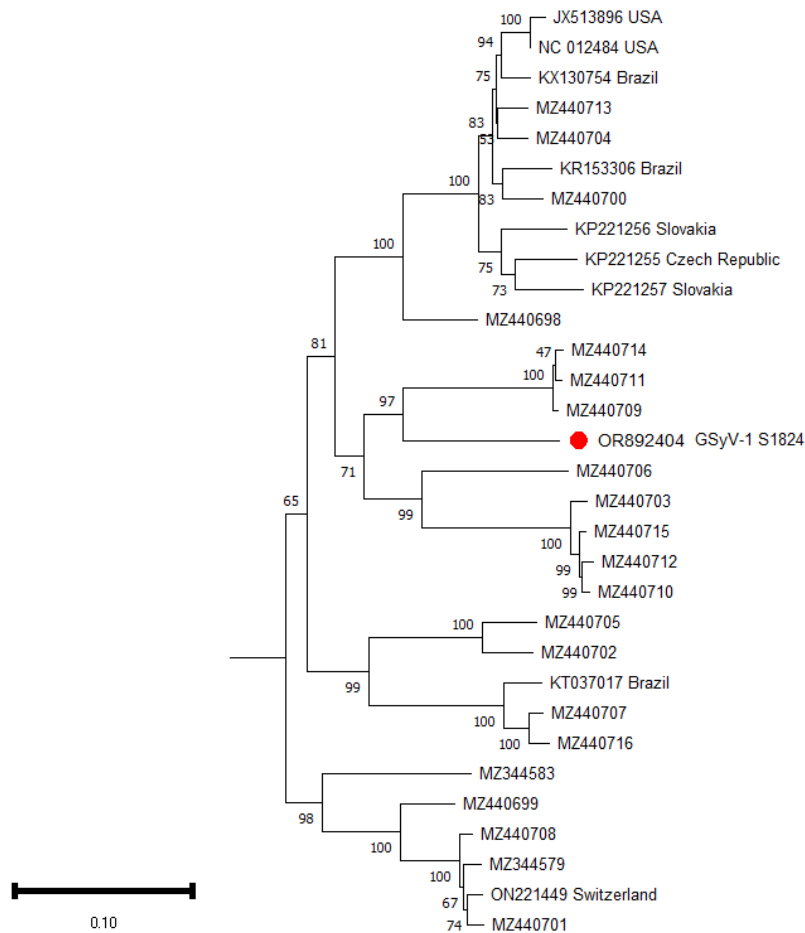
Supplementary Figure S10. Phylogenetic tree based on complete genome sequences of grapevine virus T (GVT) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



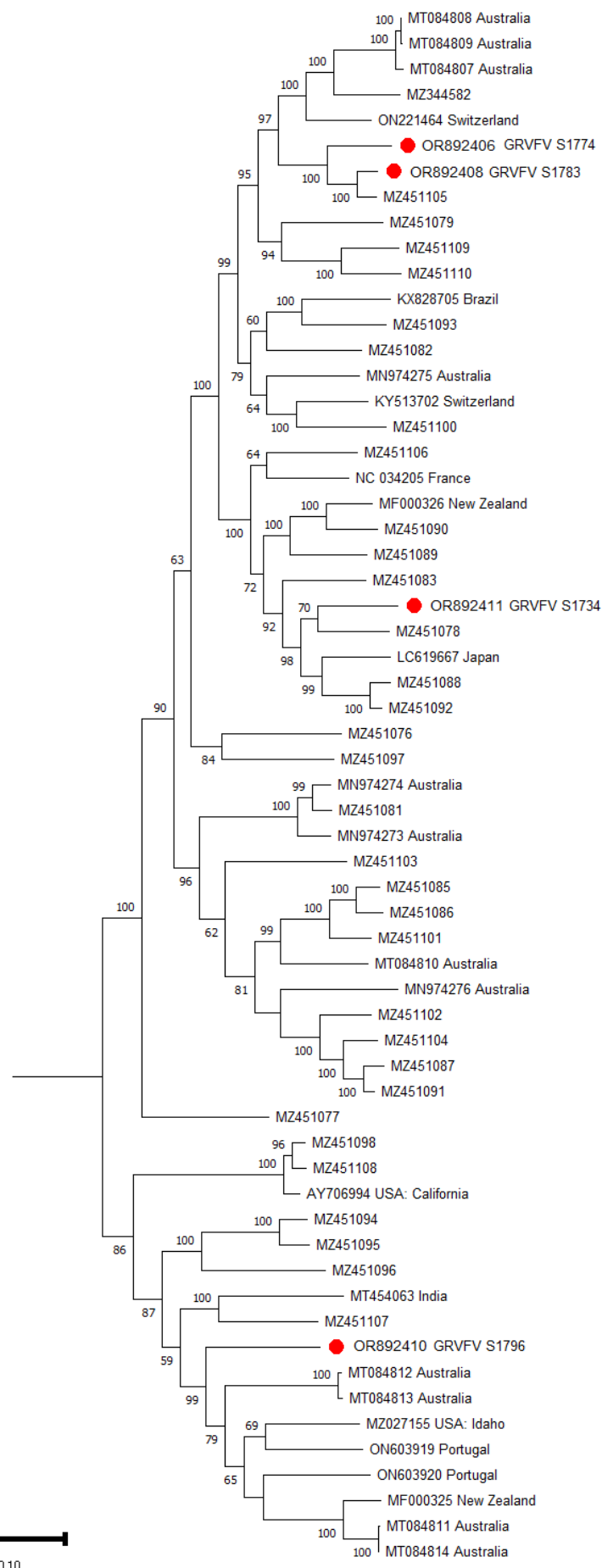
(a)



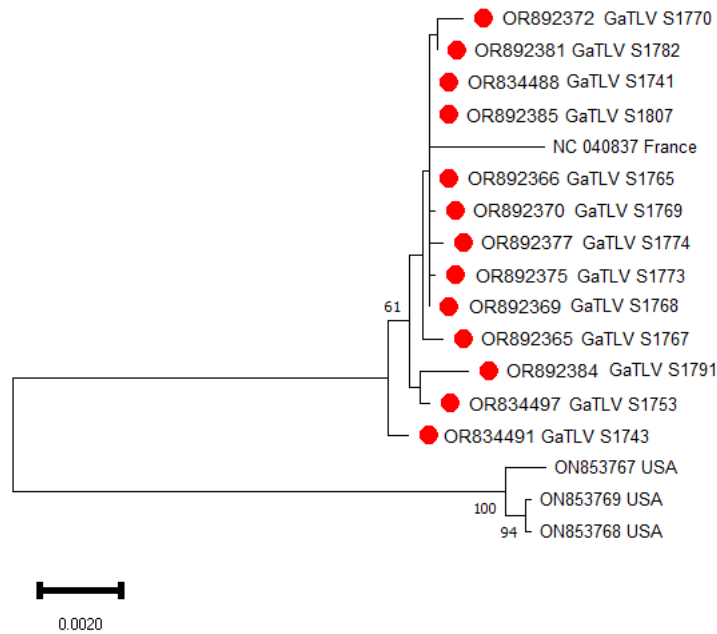
Supplementary Figure S11 (a-b). Phylogenetic tree based on complete genome sequences of grapevine rupestris stem pitting-associated virus (GRSPaV) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



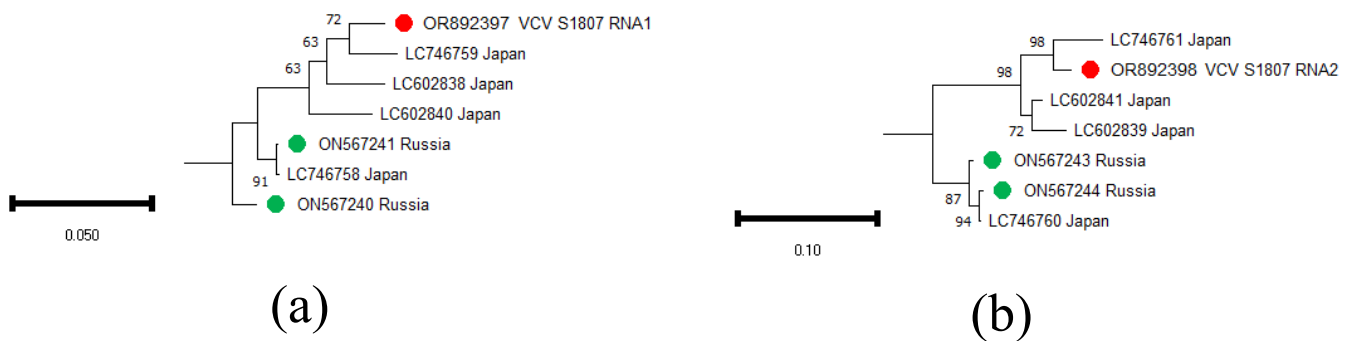
Supplementary Figure S12. Phylogenetic tree based on complete and nearly complete genome sequences of grapevine Syrah virus 1 (GSyV-1) isolates obtained in this study (red dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 boot-strap replicates. Bootstrap values below 50 are not shown.



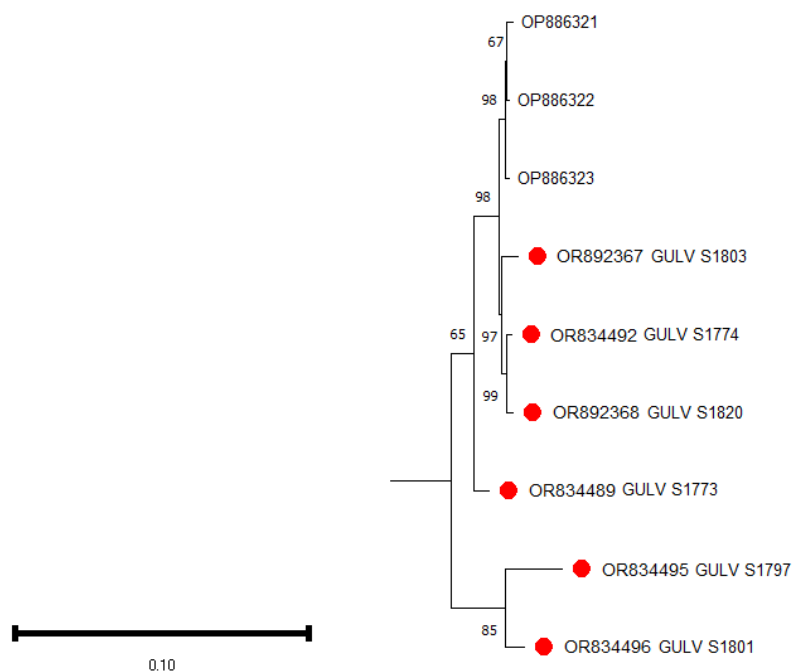
Supplementary Figure S13. Phylogenetic tree based on complete genome sequences of grapevine rupestris vein feathering virus (GRV) isolates obtained in this study (red dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



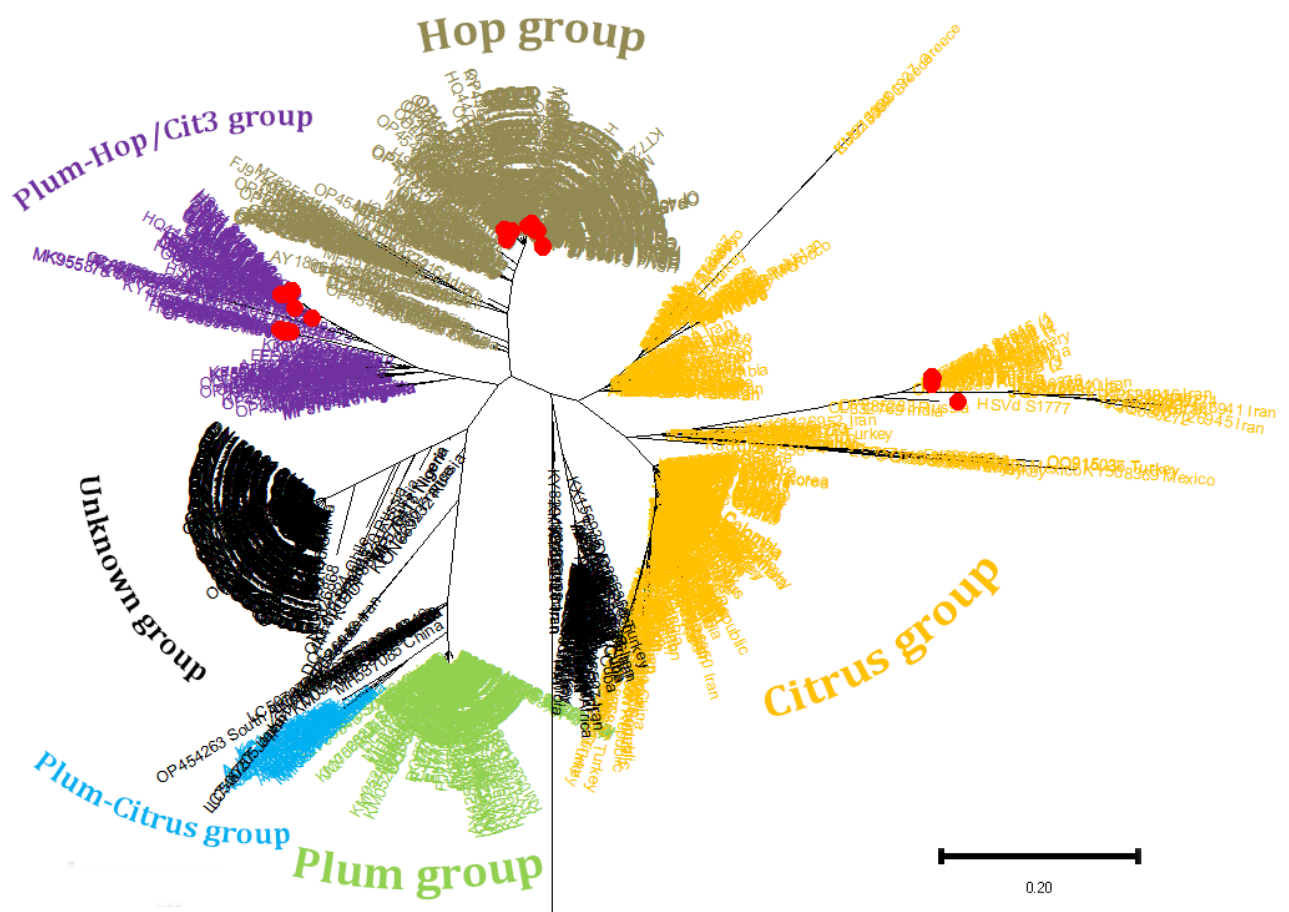
Supplementary Figure S14. Phylogenetic tree based on complete genome sequences of grapevine-associated tymo-like virus (GaTLV) isolates obtained in this study (red dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 boot-strap replicates. Bootstrap values below 50 are not shown.



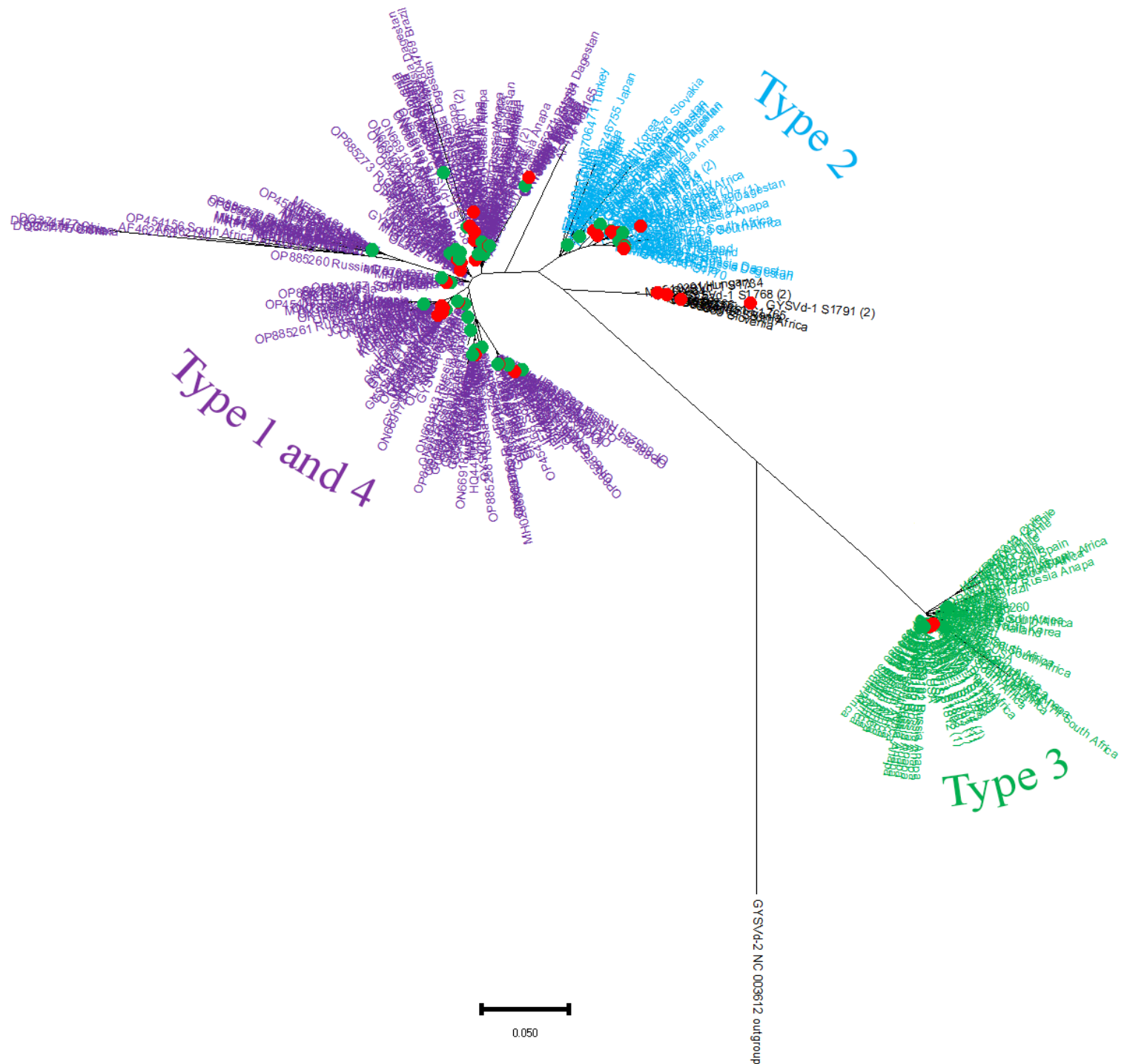
Supplementary Figure S15 (a-b). Phylogenetic tree based on complete nucleotide sequences of RNA1 (a) and RNA2 (b) of Vitis cryptic virus (VCV) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



Supplementary Figure S16. Phylogenetic tree based on complete genome sequences of grapevine umbra-like virus (GULV) isolates obtained in this study (red dots) and other Russian isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and Tamura-Nei model with 1000 boot-strap replicates. Bootstrap values below 50 are not shown.



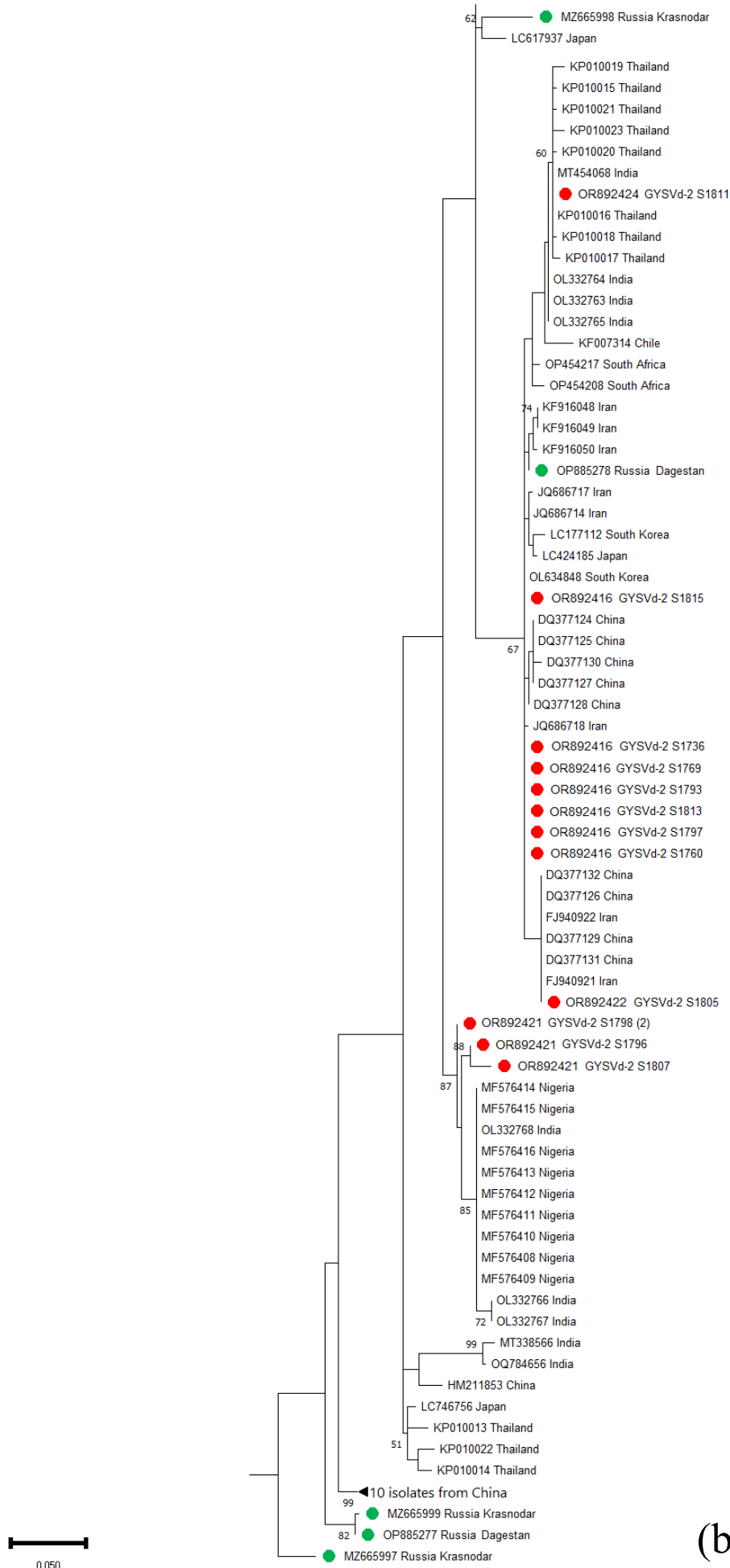
Supplementary Figure S17. Phylogenetic tree based on complete genome sequences of hop stunt viroid (HSVd) isolates obtained in this study (red dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and Tamura 3-parameter model with 1000 bootstrap replicates.



Supplementary Figure S18. Phylogenetic tree based on complete genome sequences of grapevine yellow speckle viroid 1 (GYSD-1) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates.



(a)



(b)

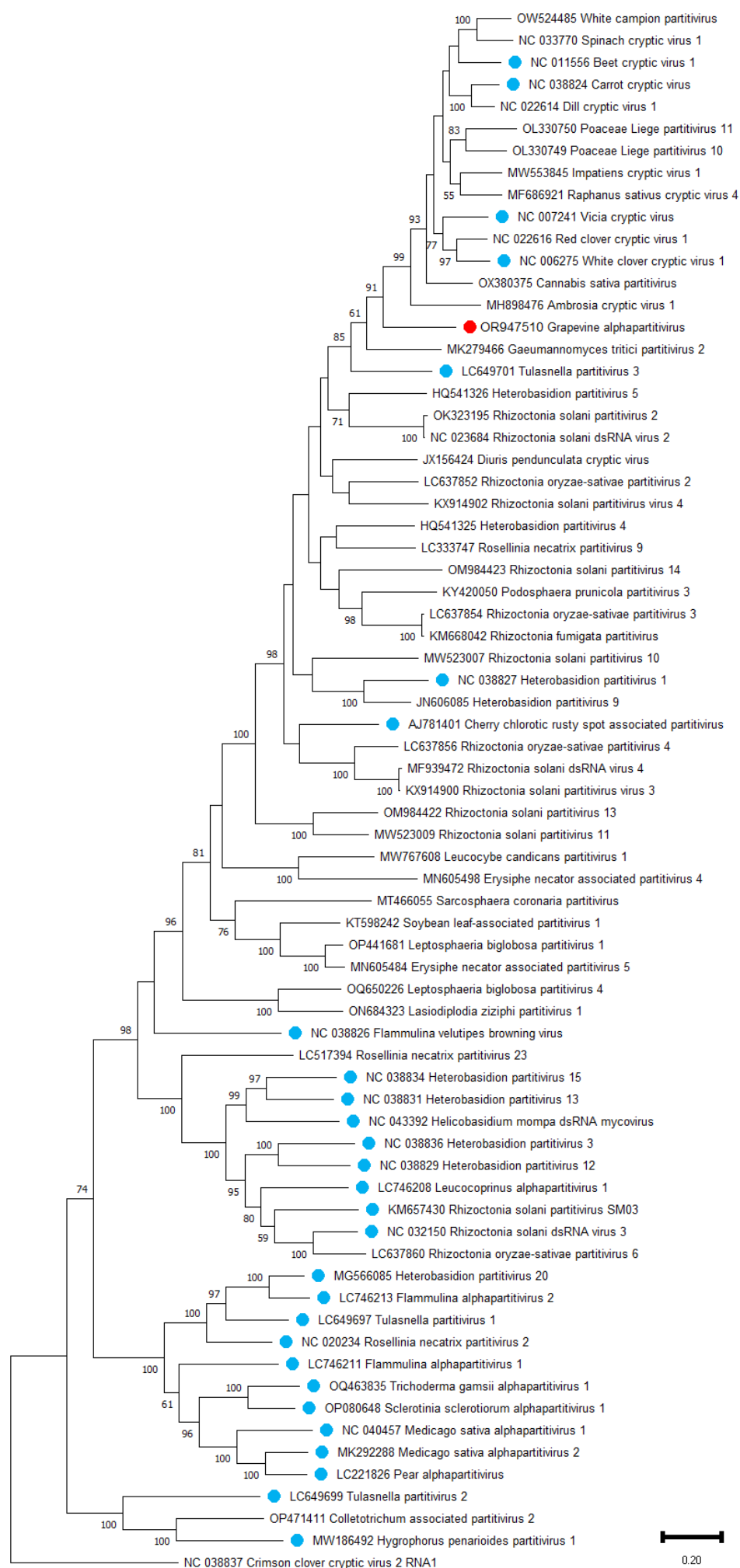
Supplementary Figure S19 (a-b). Phylogenetic tree based on complete genome sequences of grapevine yellow speckle viroid 2 (GYSVd-2) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



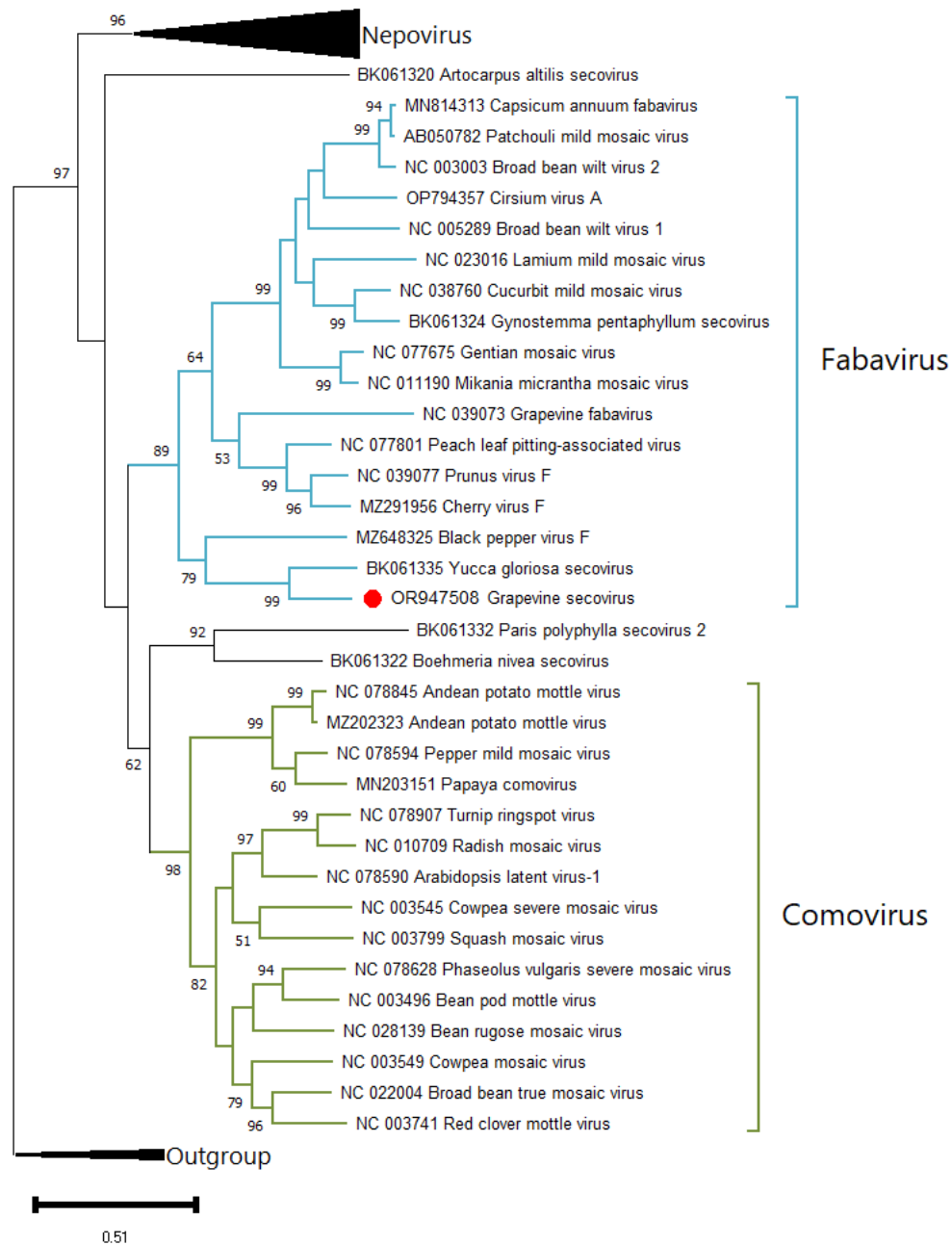
(a)



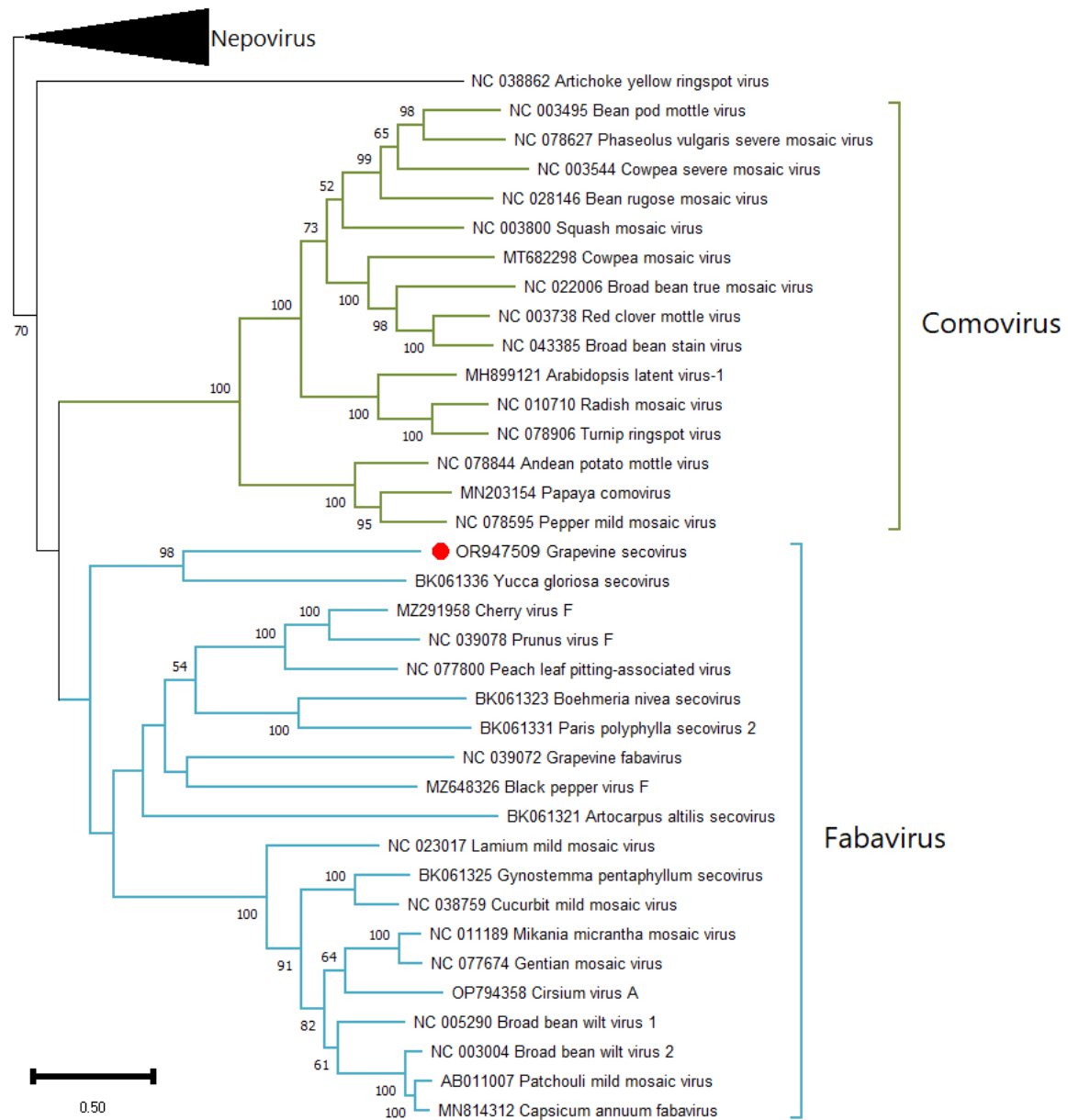
Supplementary Figure S20 (a-b). Phylogenetic tree based on complete genome sequences of australian grapevine viroid (AGVd) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and Tamura 3-parameter model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



Supplementary Figure S21. Phylogenetic tree based on complete nucleotide sequences of RNA1 of GAPV (red dot), alphapartitiviruses (blue dots) and unclassified partitiviruses. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Boot-strap values below 50 are not shown.



Supplementary Figure S22. Phylogenetic tree based on amino acid sequences of the Pro-Pol region of GSV (red dot) and members of the genera *Nepovirus*, *Fabavirus*, *Comovirus*. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Boot-strap values below 50 are not shown.



Supplementary Figure S23. Phylogenetic tree based on CP amino acid sequences of GSV (red dot) and members of the genera *Nepovirus*, *Fabavirus*, *Comovirus*. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates. Bootstrap values below 50 are not shown.



Supplementary Figure S24. Map of the southern regions of Russia, where metaviromic studies of ampe-lographic collections were conducted.