

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

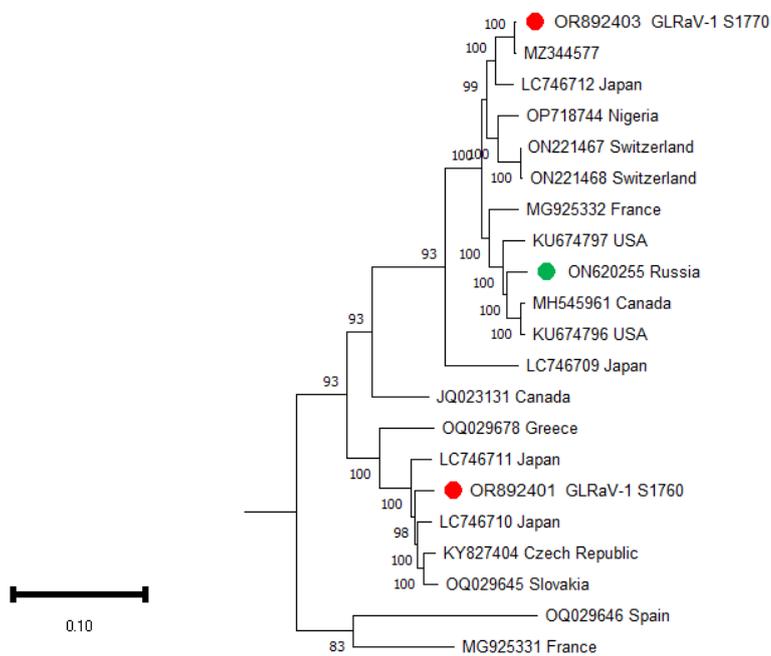
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and Svetlana Vinogradova^{1,2*}**

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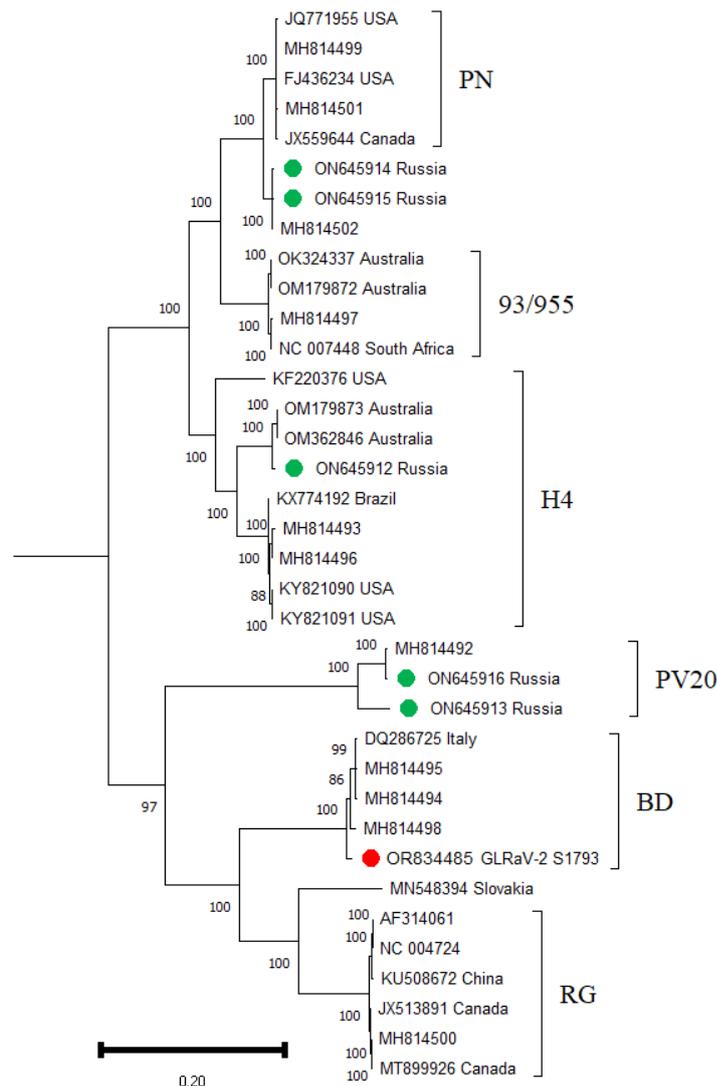
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Supplementary Materials



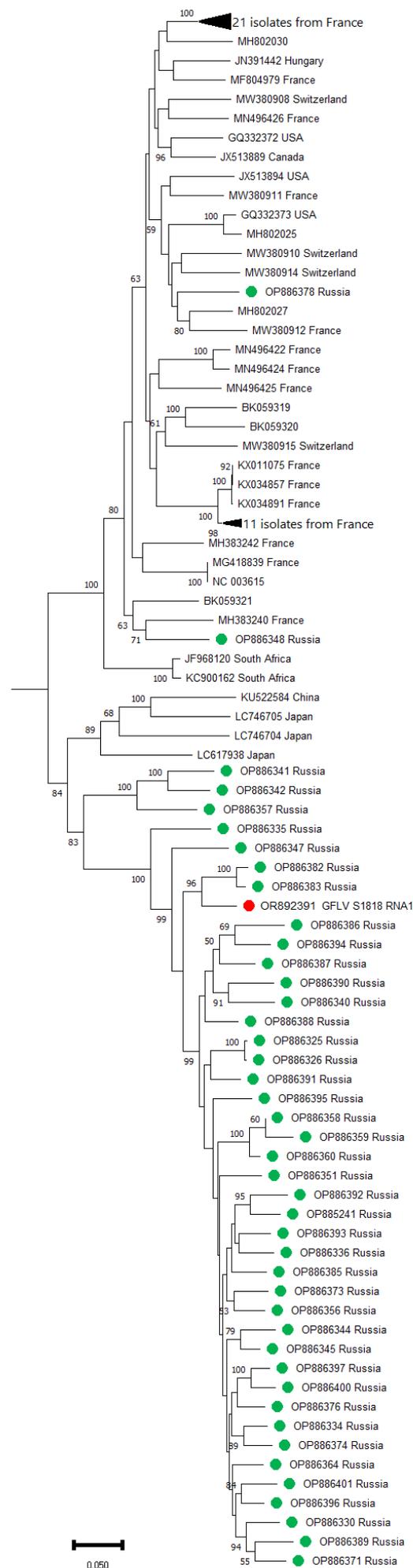
Supplementary Figure S1. Phylogenetic tree based on complete genome sequences of grapevine leafroll-associated virus 1 (GLRaV-1) isolates obtained in this study (red dots), other Russian isolate (green dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR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



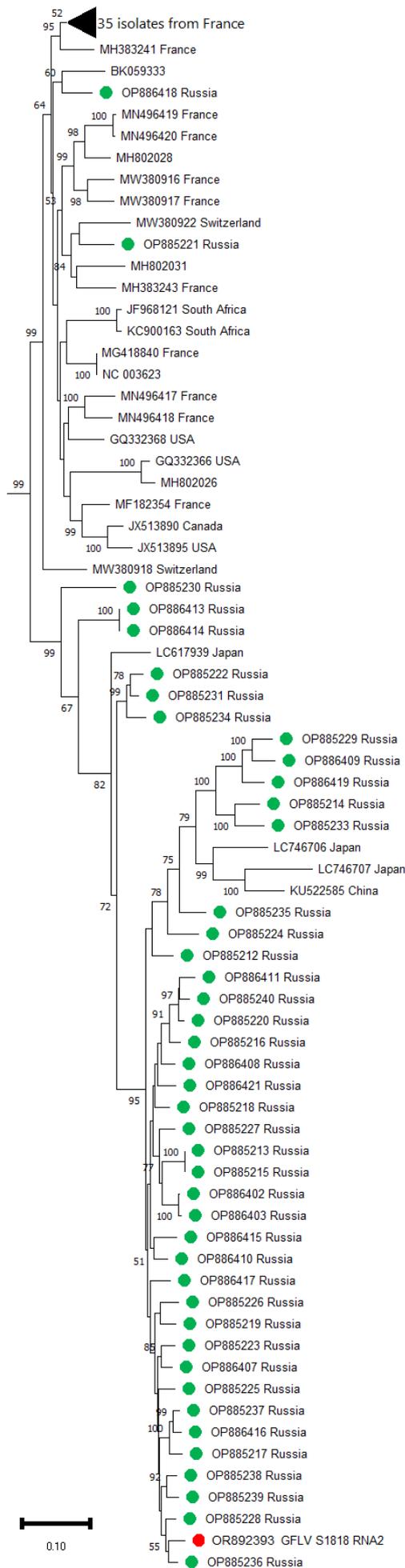
Supplementary Figure S2. Phylogenetic tree based on complete genome sequences of grapevine leafroll-associated virus 2 (GLRaV-2) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR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

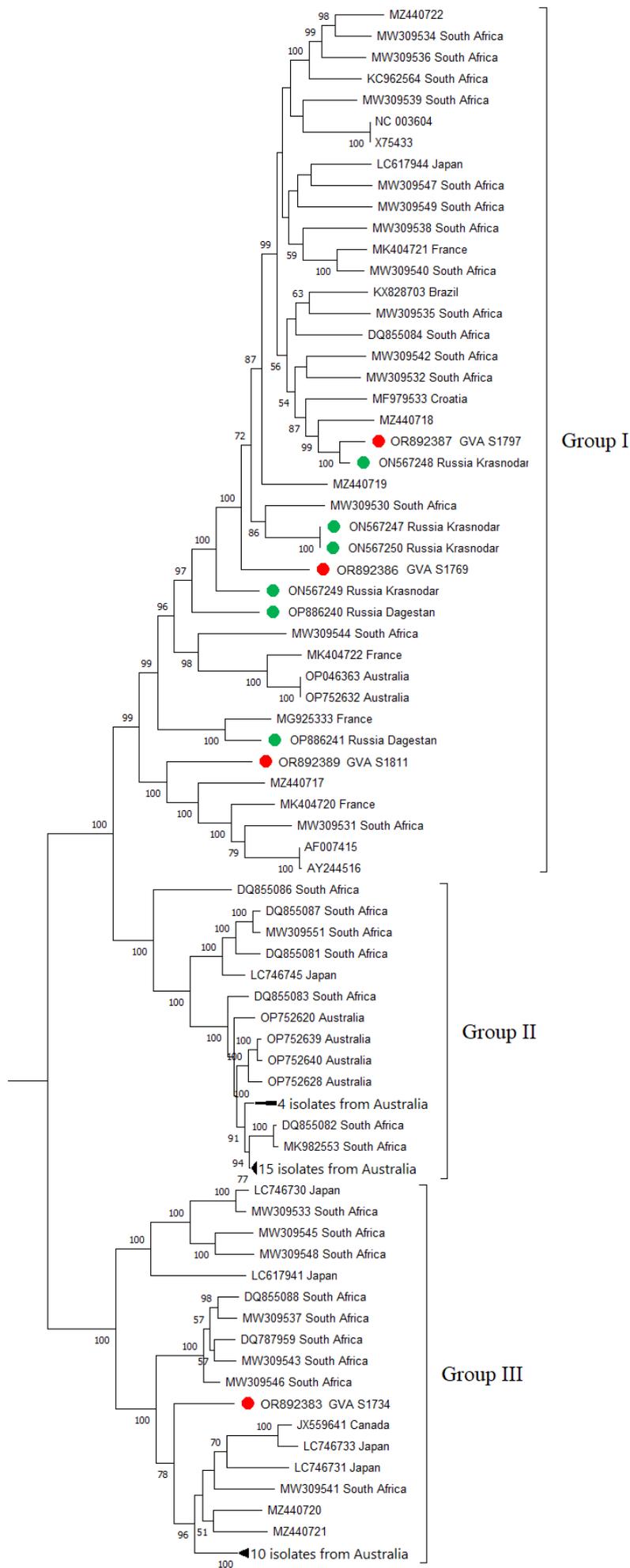
24 isolates from Australia
 OQ199005 Australia
 OQ198990 Australia
 OQ199004 Australia
 OQ199007 Australia
 OQ199016 Australia
 ● OP886259 Russia Dagestan
 ● OP886274 Russia Dagestan
 OQ199006 Australia
 OQ199021 Australia
 BK011091 Italy
 BK011092 Italy
 BK011094 Italy
 BK011096 Italy
 BK011095 Italy
 BK011093 Italy
 ● OP886251 Russia Dagestan
 ● OP886252 Russia Dagestan
 ● OR892483 GPGV S1769
 ● OR892519 GPGV S1811
 KF134125 Slovakia
 ● OP886273 Russia Dagestan
 ● OP886275 Russia Dagestan
 ● OP886256 Russia Dagestan
 ● OR892481 GPGV S1768
 ● OR892451 GPGV S1736
 ● OR892494 GPGV S1774
 MK514528 USA
 ● OR892525 GPGV S1802
 ● OR892489 GPGV S1773
 ● OR892521 GPGV S1803
 KX522755 Germany
 ● OR892520 GPGV S1810
 ● OR892514 GPGV S1819
 ● ON620248 Russia
 ● OP886245 Russia Dagestan
 ● OR892502 GPGV S1777
 KU312039 Italy
 ● OP886260 Russia Dagestan
 ● OP886278 Russia Dagestan
 ● OP886281 Russia Dagestan
 ● OP886279 Russia Dagestan
 ● OP886276 Russia Dagestan
 ● OP886258 Russia Dagestan
 ● ON548153 Russia
 ● OP886255 Russia Dagestan
 ● OP886254 Russia Dagestan
 BK011065 Italy
 BK011067 Italy
 ● OP886280 Russia Dagestan
 KF134124 Slovakia
 OL961512 Russia Krasnodar
 ● OR892515 GPGV S1783
 ● OR892449 GPGV S1734
 ● OR892517 GPGV S1814
 ● OR892518 GPGV S1791
 ● ON548147 Russia
 KF134123 Slovakia
 KF686810 Slovakia
 KU949328 Slovakia
 BK011069 Italy
 BK011081 Italy
 BK011064 Italy
 BK011060 Italy
 BK011062 Italy
 BK011063 Italy
 BK011061 Italy
 ● OR892522 GPGV S1798
 ● OP886247 Russia Dagestan
 ● OR892458 GPGV S1760
 ● OR892460 GPGV S1767
 ● ON548148 Russia
 ● ON620250 Russia
 ● OR892455 GPGV S1748
 ● OR892459 GPGV S1765
 ● OP886277 Russia Dagestan
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 ● OR892523 GPGV S1807
 ● OR892452 GPGV S1741
 ● OR892511 GPGV S1781



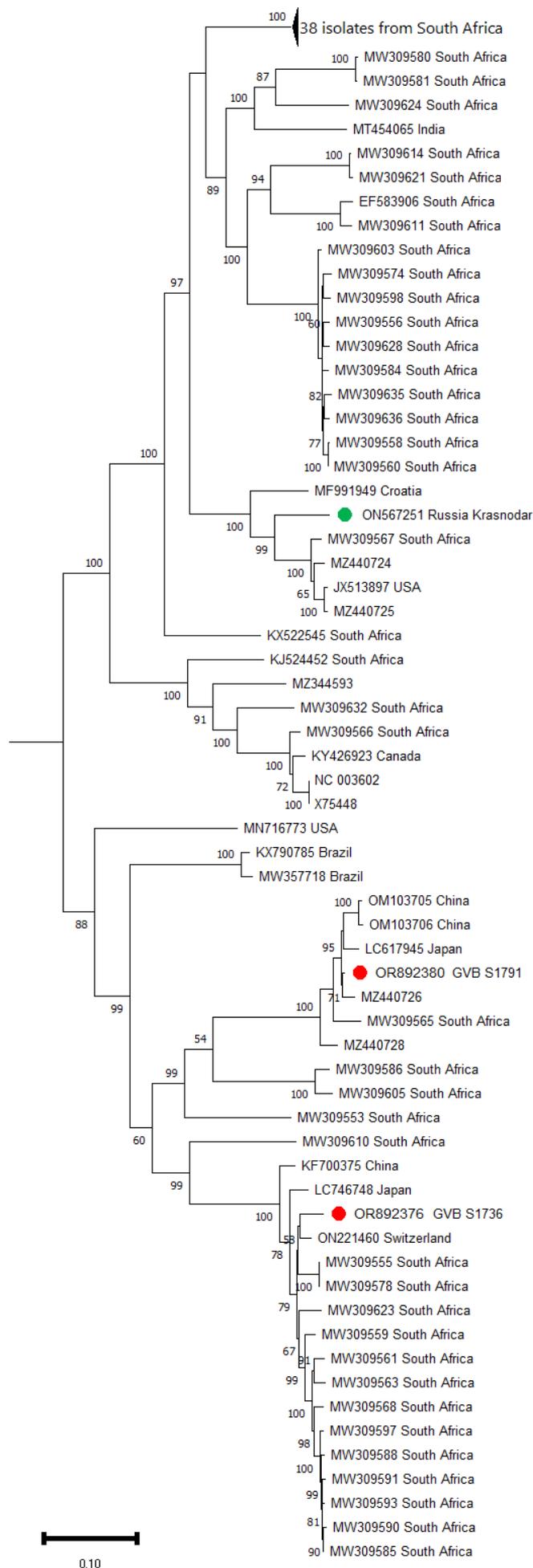
(a)



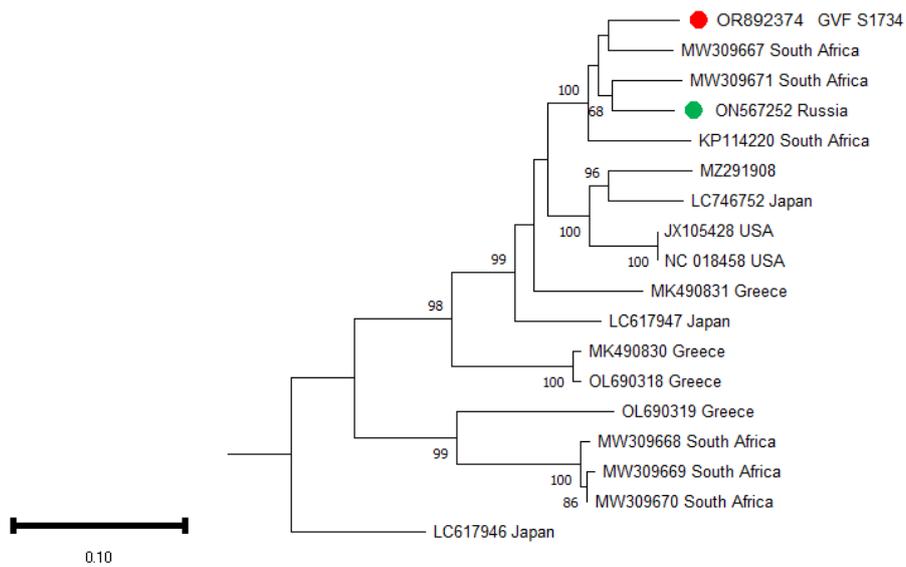
Supplementary Figure S6 (a-b). Phylogenetic tree based on complete genome sequences of grapevine Pinot gris virus (GPGV) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model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



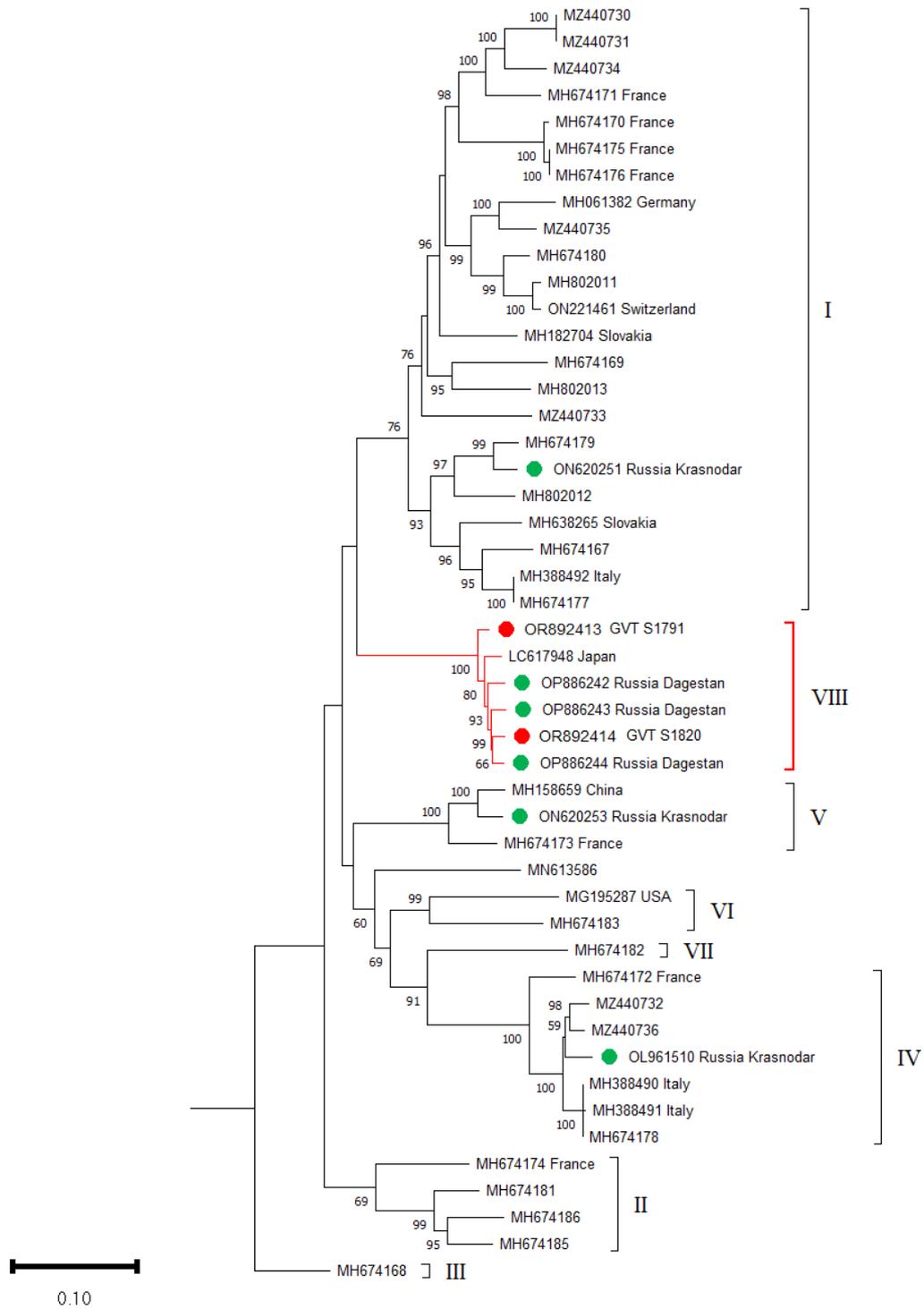
Supplementary Figure S7. Phylogenetic tree based on complete genome sequences of grapevine virus A (GVA) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap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



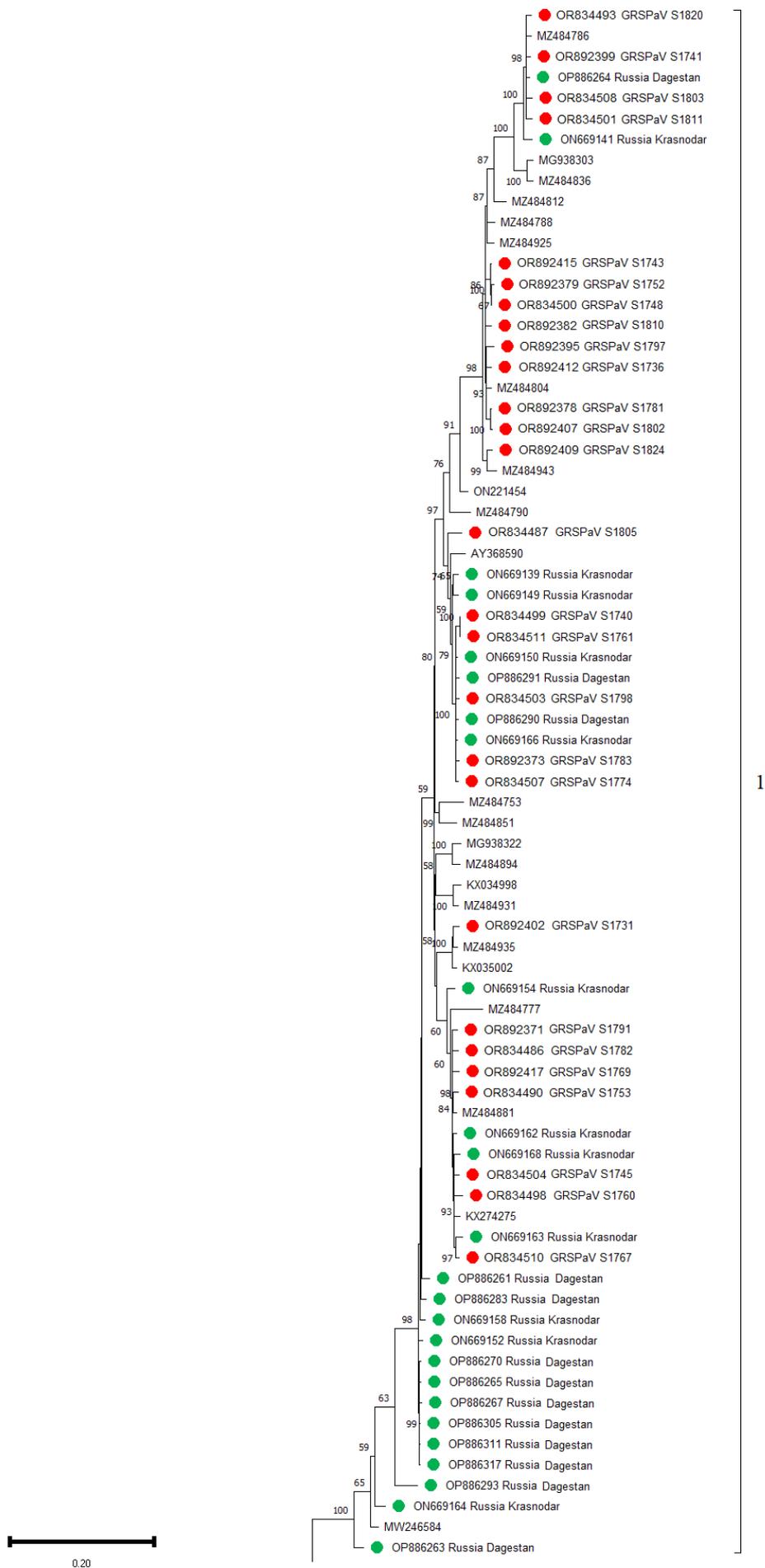
Supplementary Figure S8. Phylogenetic tree based on complete genome sequences of grapevine virus B (GVB) isolates obtained in this study (red dots), other Russian isolate (green dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap 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.

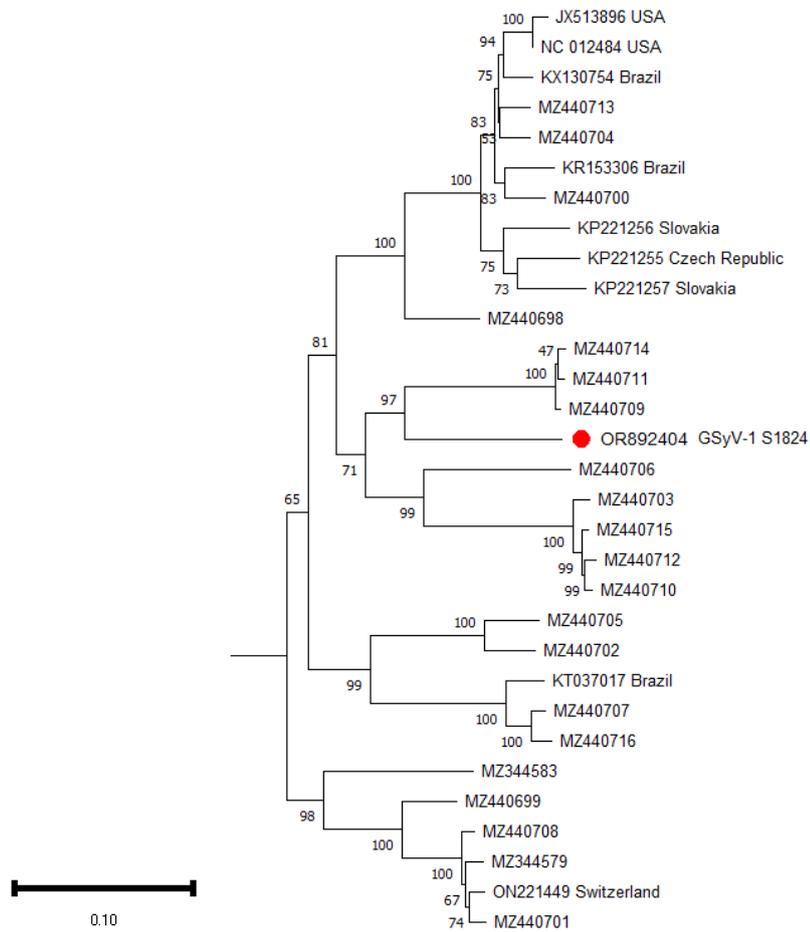


(a)

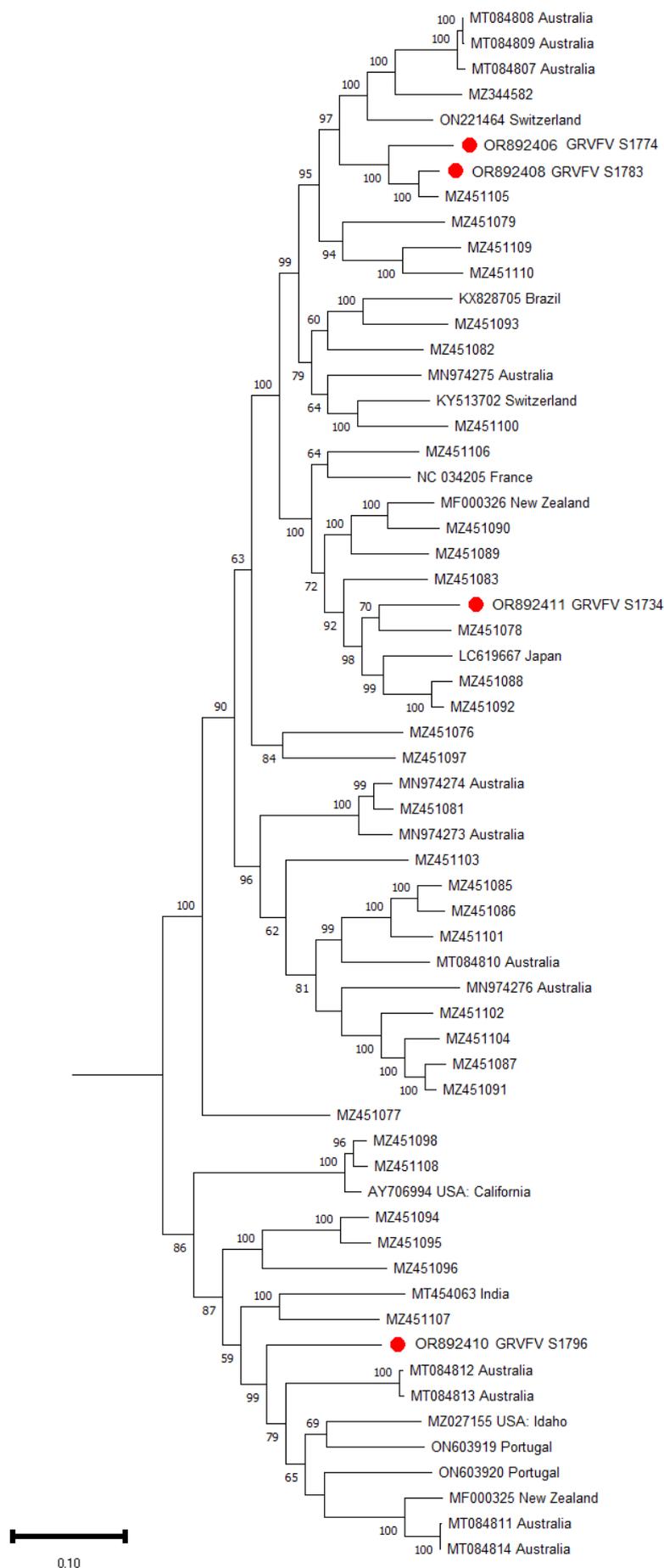


(b)

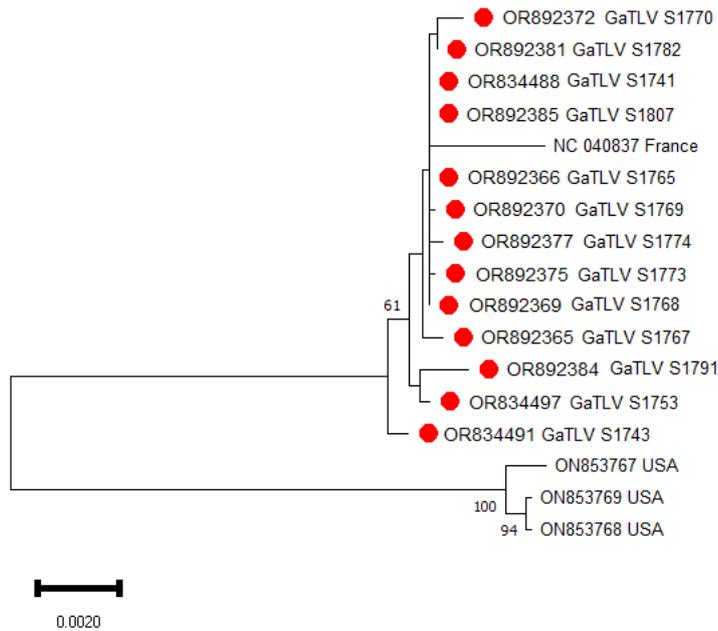
Supplementary Figure S11 (a-b). Phylogenetic tree based on complete genome sequences of grapevine rupestris stem pitting-associated virus (GRSPaV) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood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



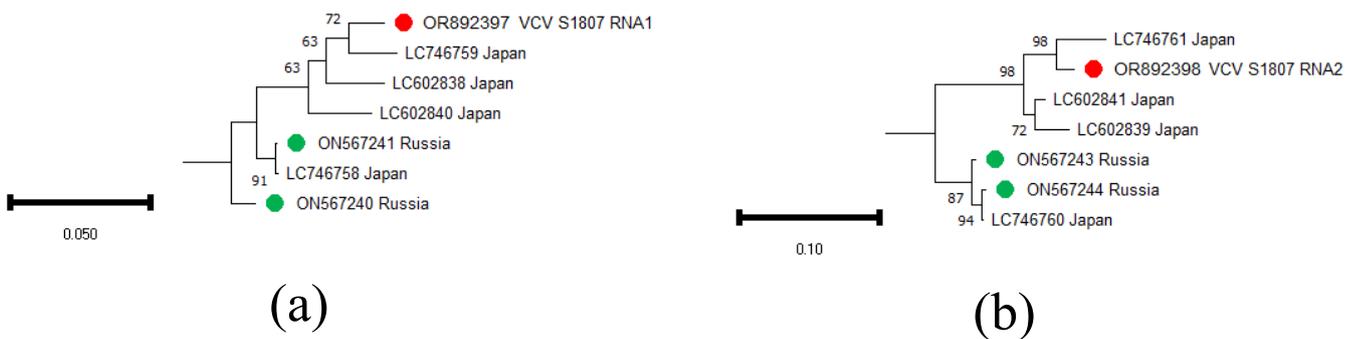
Supplementary Figure S12. Phylogenetic tree based on complete and nearly complete genome sequences of grapevine Syrah virus 1 (GSyV-1) isolates obtained in this study (red dot) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 boot-strap replicates.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



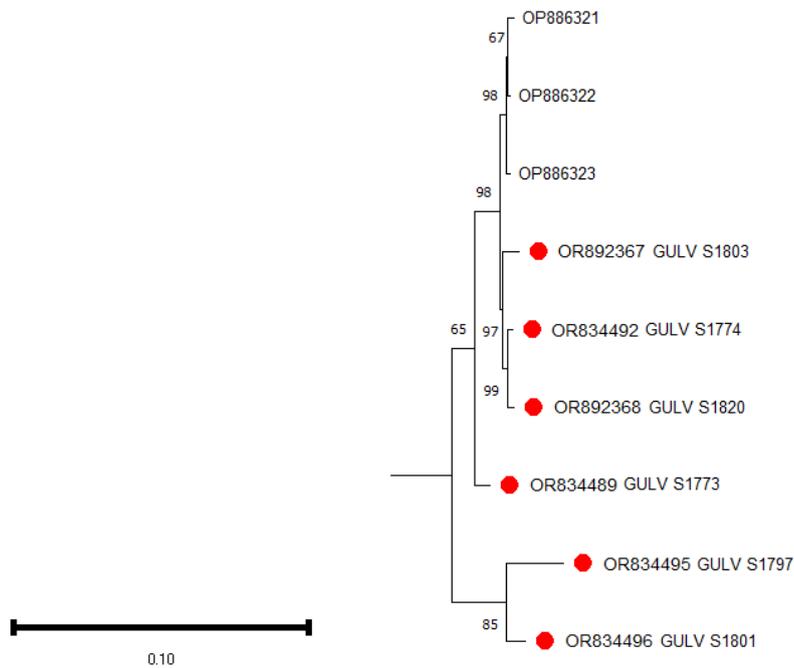
Supplementary Figure S13. Phylogenetic tree based on complete genome sequences of grapevine rupestris vein feathering virus (GRV) isolates obtained in this study (red dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 bootstrap replicates.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



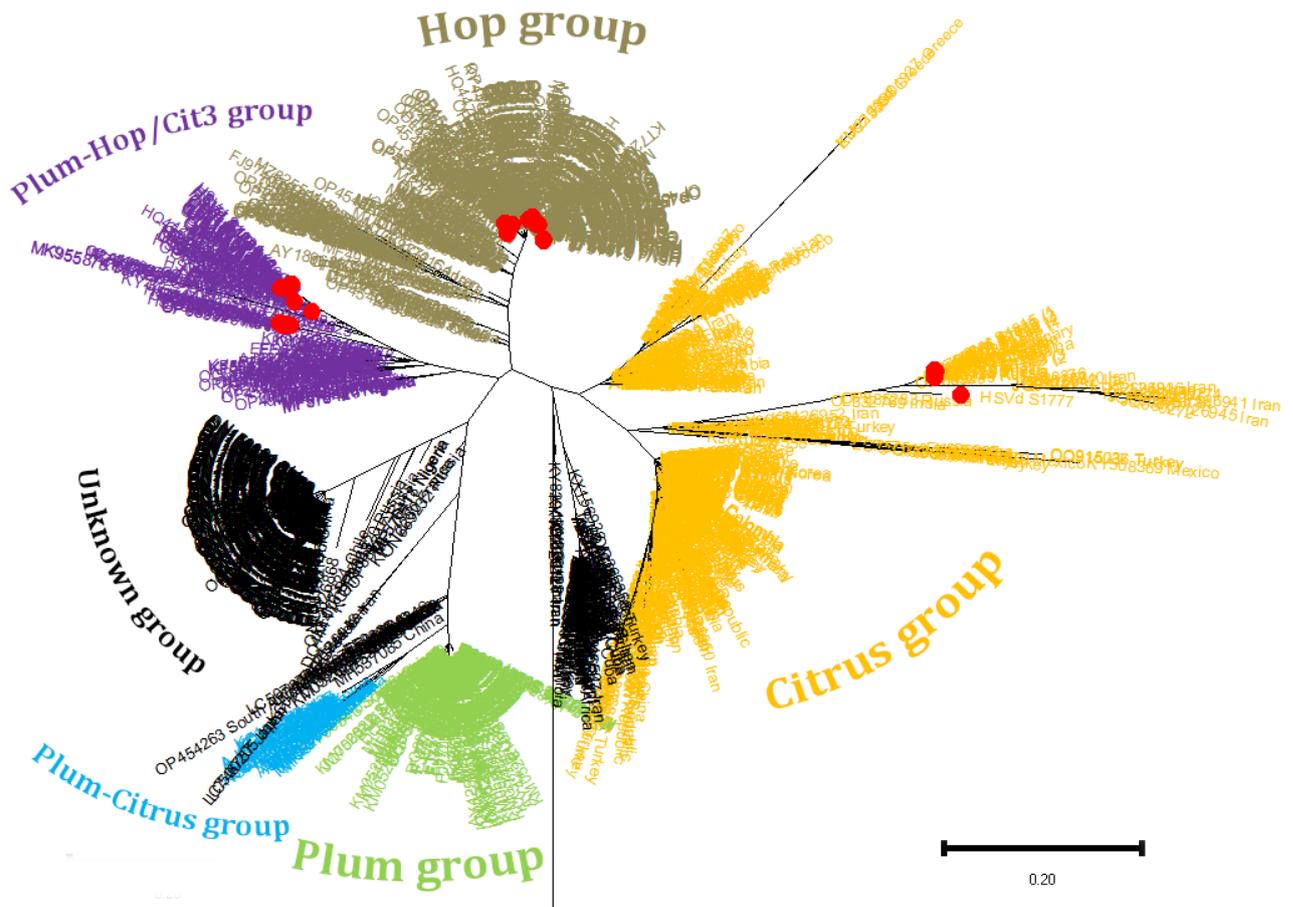
Supplementary Figure S14. Phylogenetic tree based on complete genome sequences of grapevine-associated tymo-like virus (GaTLV) isolates obtained in this study (red dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR model with 1000 boot-strap replicates.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



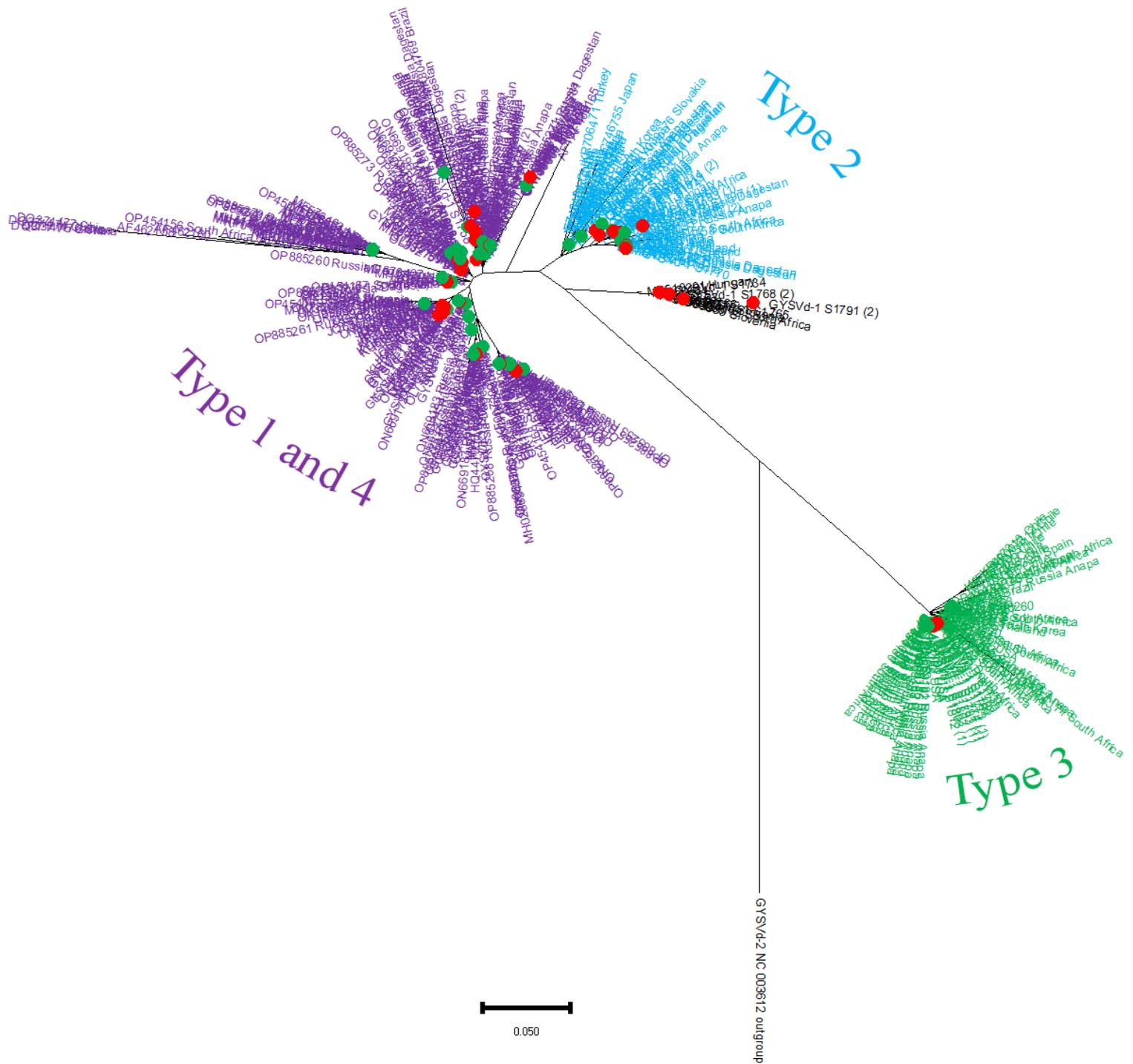
Supplementary Figure S15 (a-b). Phylogenetic tree based on complete nucleotide sequences of RNA1 (a) and RNA2 (b) of Vitis cryptic virus (VCV) isolates obtained in this study (red dot), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood 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.

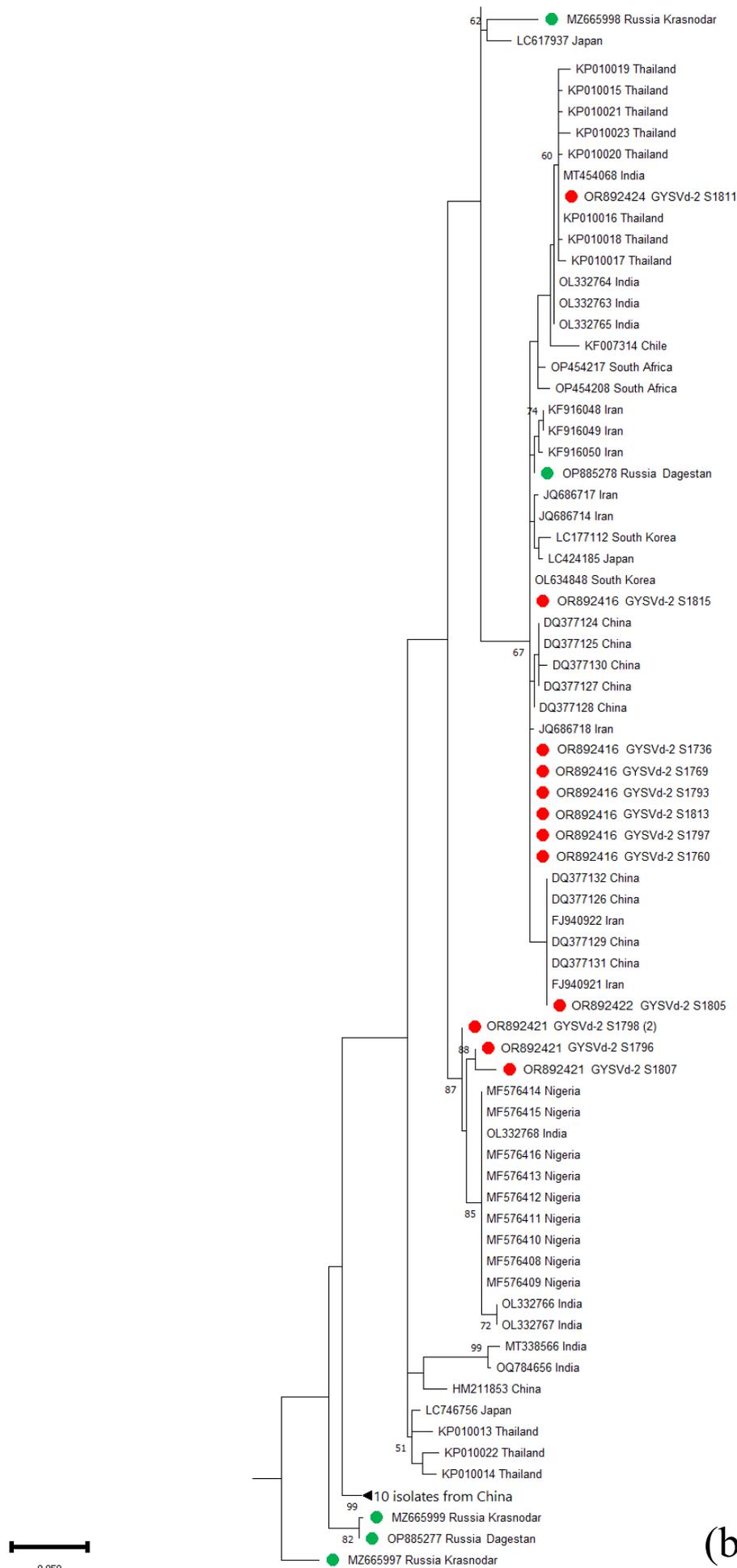


Supplementary Figure S18. Phylogenetic tree based on complete genome sequences of grapevine yellow speckle viroid 1 (GYSVd-1) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and GTR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



0.050

(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.

51 isolates from China

KF876035 Iran
KY404212 Iran
EU743601 China
FJ746843 China
KF876036 Iran
JQ686706 Iran
FJ746773 China
FJ746756 China
FJ746780 China
FJ746746 China
FJ746781 China
DQ362913 China
FJ746802 China
FJ746803 China
● OR892438 AGVd S1796
FJ746782 China
55 FJ746768 China
FJ746831 China
EU743609 China
FJ746819 China
FJ746770 China
FJ746824 China
FJ746841 China
FJ746759 China
FJ746779 China
FJ746811 China
FJ746795 China
FJ746835 China
FJ746833 China
FJ746796 China
DQ362910 China
DQ362912 China
FJ746789 China
FJ746787 China
FJ746792 China
FJ746785 China
FJ746799 China
FJ746801 China
FJ746798 China
FJ746791 China
FJ746805 China
FJ746793 China
DQ362914 China
DQ362908 China
● OR892436 AGVd S1793
66 JQ686704 Iran
KY404210 Iran
KF007271 Chile
KF007274 Chile
69 MT227864
OL332752 India
ON049350 South Korea
● OR892446 AGVd S1813
OP454152 South Africa
FJ746766 China
JQ686707 Iran
FJ746744 China
JQ686705 Iran
FJ746752 China
FJ746745 China
FJ746765 China

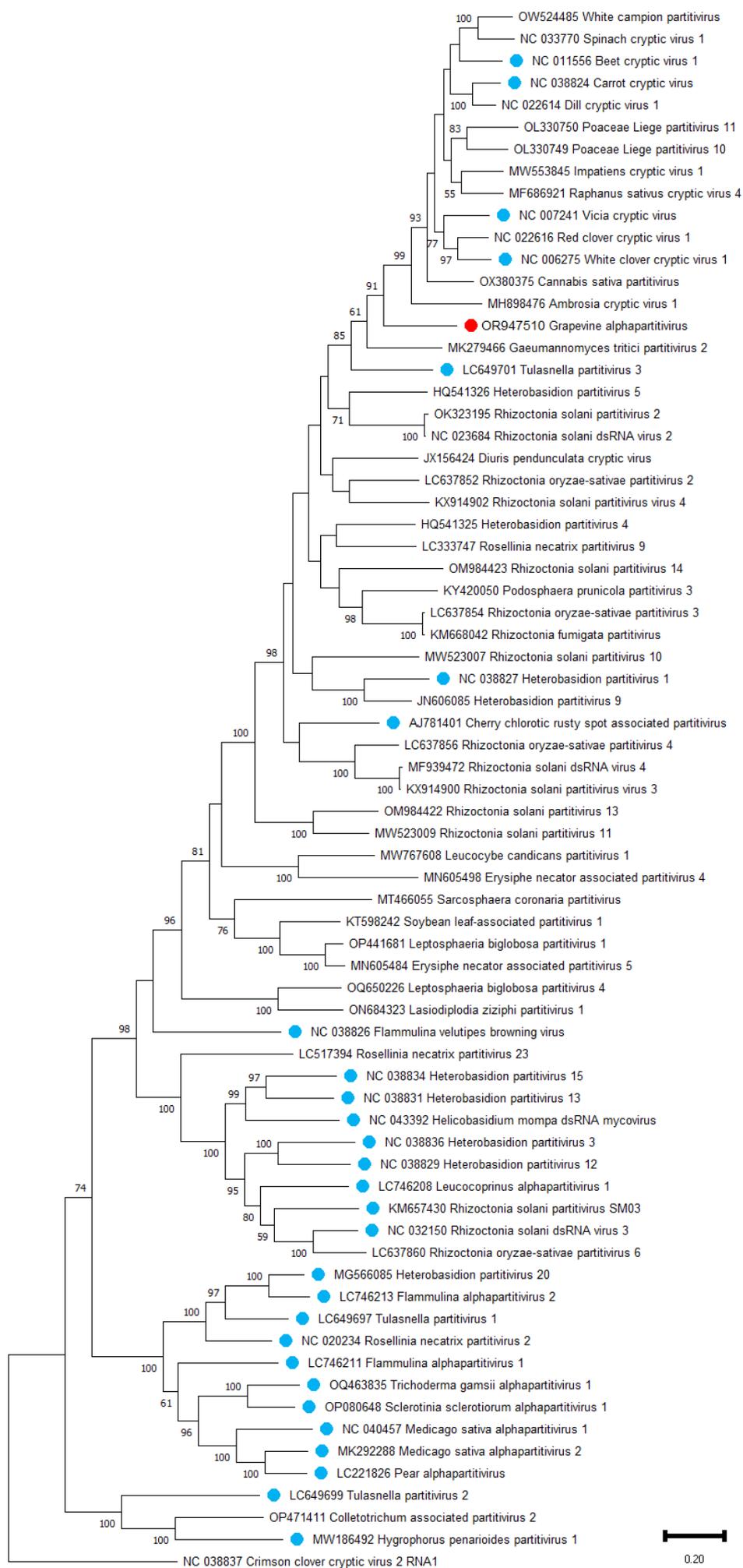


0.12

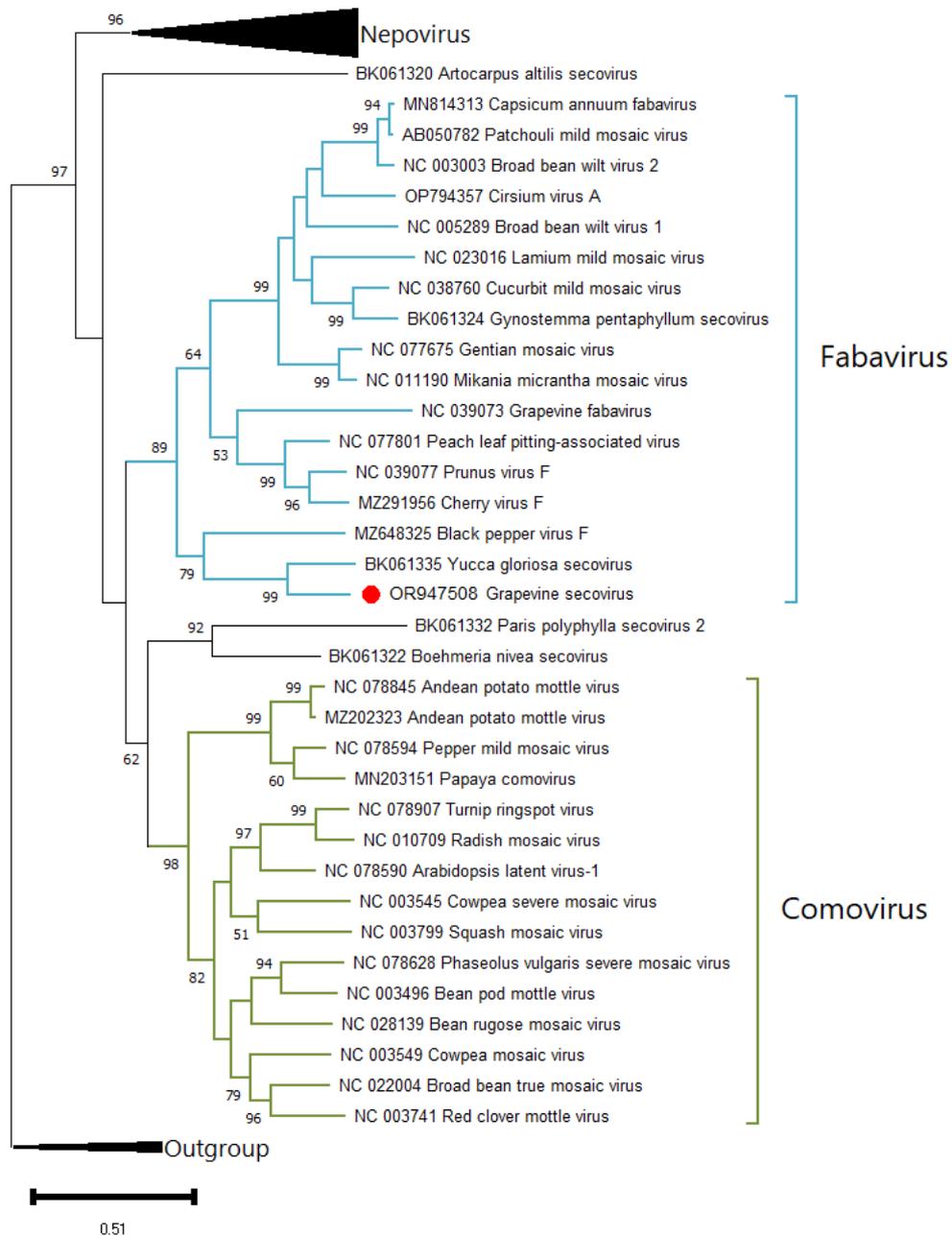
(a)



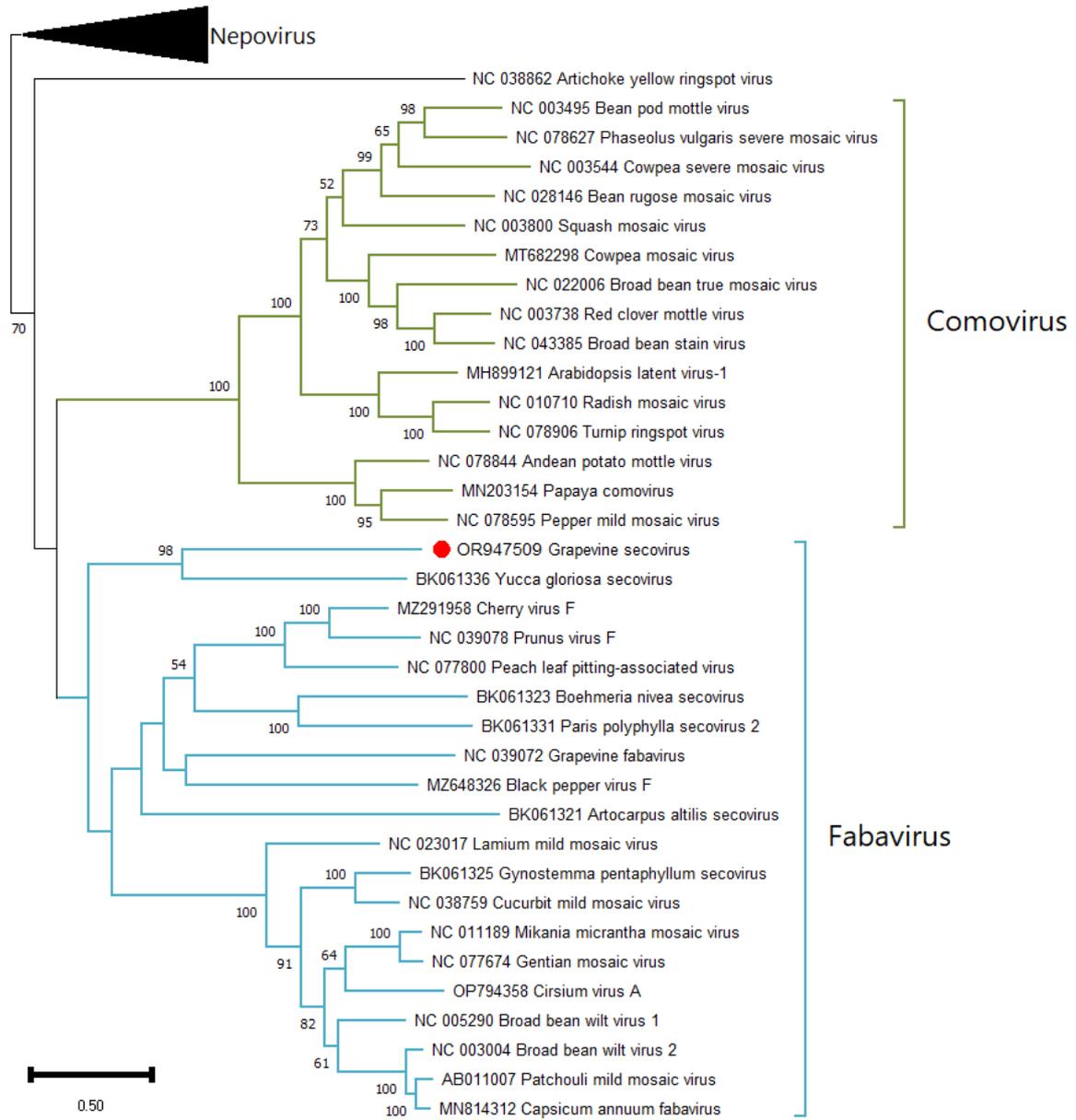
Supplementary Figure S20 (a-b). Phylogenetic tree based on complete genome sequences of Australian grapevine viroid (AGVd) isolates obtained in this study (red dots), other Russian isolates (green dots) and world isolates. Tree was constructed in MEGA11 using the maximum-likelihood method and Tamura 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.