

	OR031866 05-11 Beauty seedless GVH
93	OR031862 04-08 Anglianico GVH
89	MW309674 05-09 Barrocal GVH
	MW309673 05-08 Baroque GVH
	OR031870 06-08 Blauer Limberger GVH
	○ NC 040545 TT2016-3 Portugal
99	MW309683 23-15 Muscat St Laurent GVH
	OR031876 09-04 Cinsault Noir GVH
	OR031872 07-02 Bukettraube GVH
	OR031875 08-09 Chardonnay GVH
91	OR031864 05-02 Azal branco GVH
76	OR031860 04-01 Assyrtiko GVH
	MW309697 35-15 Weisser Vernatsch GVH
	MW309690 30-05 Schonberger GVH
85	OR031902 20-12 Mansenc Blanc GVH
	OR031907 23-12 Muscat Ottonel GVH
	OR031905 21-14 Moscatel Negro GVH
	OR031879 09-11 Colombard GVH
97	OR031865 05-03 Azal tinto GVH
86	MW309682 22-12 Muller Thurgau GVH
	OR031904 21-13 Morio Muscat GVH
	OR031899 19-09 Madeleine Royale GVH
	OR031857 03-03 Affenthaler GVH
	○ MN716768 TN1 USA
	OR031893 15-07 Grillo GVH
	OR031916 46-13 St Laurent GVH
95	OR031912 34-11 Tinta Francisca GVH
	MW309687 29-01 Savagnin GVH
	OR031882 10-13 Zante Corinthe GVH
	OR031904 21-13 Morio Muscat GVH
	MW309702 38-10 Kuhlmann 188-2 Marechal Foch GVH
	OR031914 35-09 Viura GVH
	OR031911 33-05 Tempranillo GVH
65	MW309695 35-08 Vital GVH
	MW309708 54-13 Merzling GVH
	MW309692 33-06 Teoulier GVH
	OR031913 35-05 Verdelho GVH
86	MW309676 07-15 Cataratto GVH
	OR031883 10-15 Cape Corinth GVH
	MW309672 04-15 Aligote GVH
	OR031909 27-03 Reichensteiner GVH
84	MW309680 18-02 Limberger GVH
	OR031856 02-09 V shutteworthii GVH
	OR031869 06-04 Bourboulenc GVH
71	OR031858 03-12 Albanello GVH
	OR031874 07-14 Carignan-noir GVH
	OR031859 03-15 Alicante bouchet GVH
	OR031863 04-13 Alphonse Lavallee GVH
	OR031871 06-13 Black Prince GVH
	OR031855 02-08 V riparia GVH
	OR031867 05-14 Black Hamburg GVH
	OR031861 04-05 Aramon blanc GVH
	MW309699 36-06 Zinfandel GVH
	OR031888 12-10 Emerald Riesling GVH
	OR031892 15-05 Grenache Noir GVH
	OR031884 11-02 Dauphine GVH
65	OR031886 12-02 Fernao Pires GVH

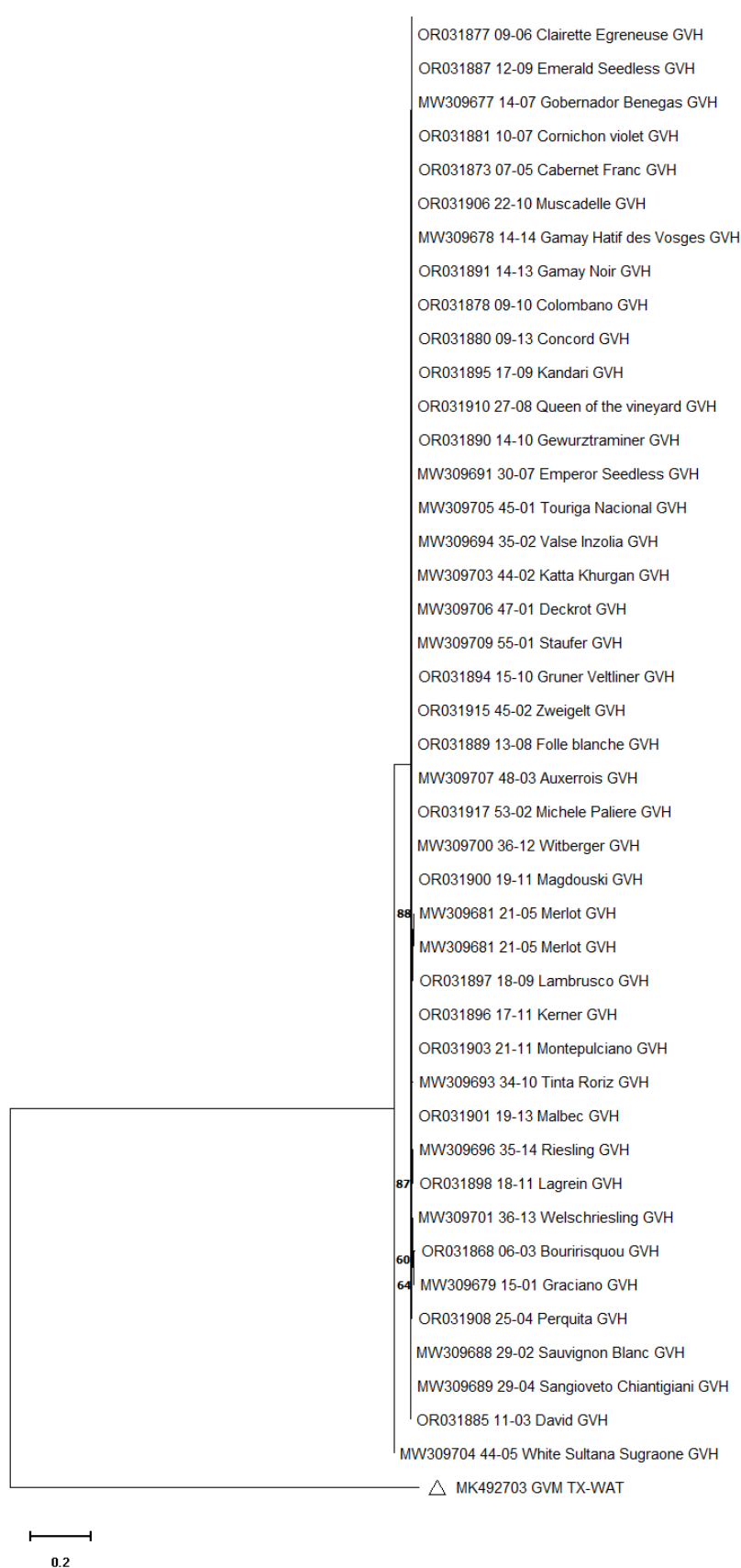


Figure S11: Maximum likelihood phylogeny based on the amino acid sequences of the RNA-dependant RNA polymerase (RdRp) gene of grapevine virus H (GVH) from this study together the cognate sequences from selected variants of GVH from GenBank (indicated by open circles). The cognate RdRp sequence from grapevine virus M was used as an outgroup (indicated by an open triangle). The phylogeny represents the tree with the highest log likelihood and was generated in MEGA X (Stecher et al. 2020) using the Jones-Taylor-Thornton (JTT) (Jones, W. R. Taylor, and J. M. Thornton. (1992) with gamma distribution (n=5) and invariant sites. 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.