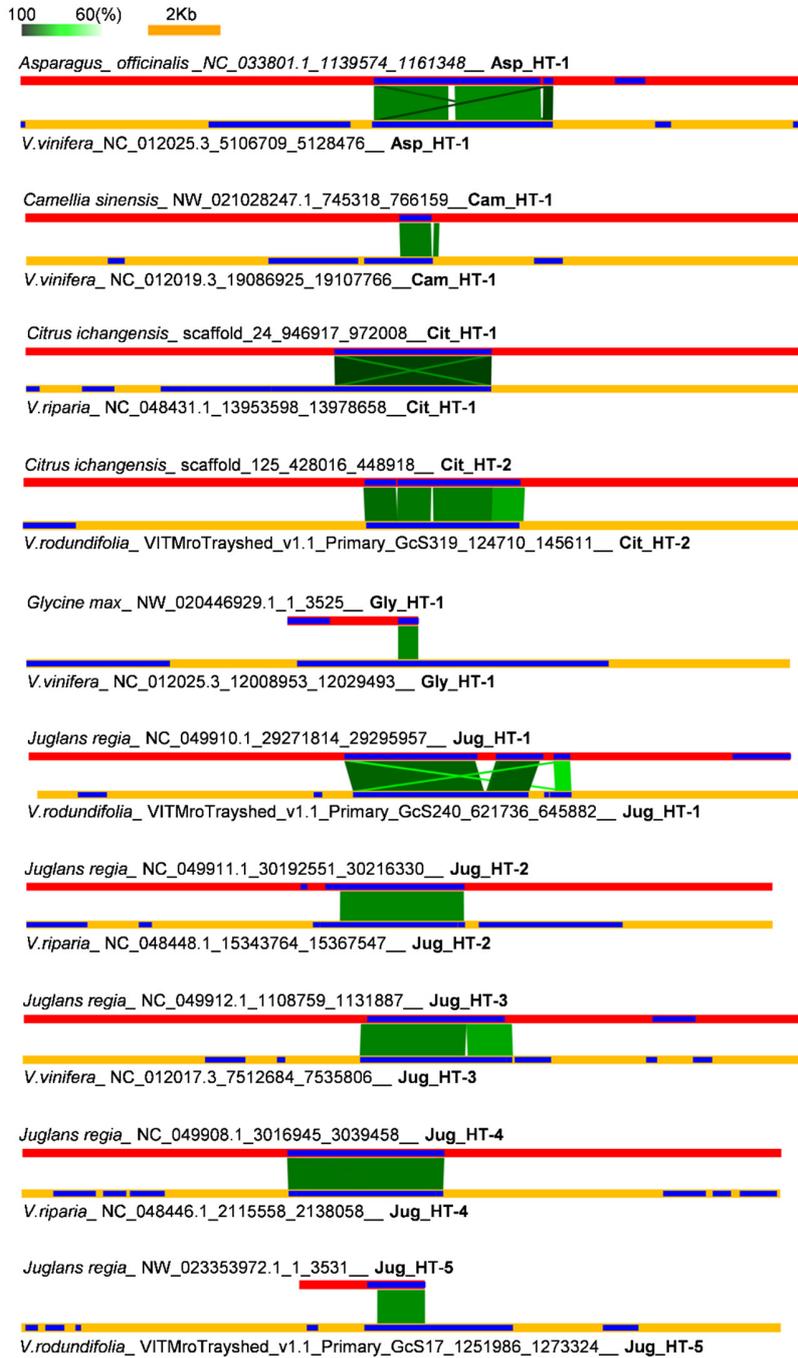


Supplementary Figure S1

	<i>Malus baccata</i>	<i>Pyrus ussuriensis</i>	<i>Prunus avium</i>	<i>Rubus occidentalis</i>	<i>Juglans regia</i>	<i>Quercus suber</i>	<i>Quercus lobata</i>	<i>Ziziphus jujuba</i>	<i>Morus notabilis</i>	<i>Camellia sinensis</i>	<i>Populus trichocarpa</i>	<i>Salix viminalis</i>	<i>Pistacia vera</i>	<i>Atalantia buxifolia</i>	<i>Citrus ichangensis</i>	<i>Nelumbo nucifera</i>	<i>Glycine max</i>	<i>Phaseolus vulgaris</i>	<i>Olea europaea</i>	<i>Phoenix dactylifera</i>	<i>Asparagus officinalis</i>	<i>Vitis rotundifolia</i>	<i>Vitis vinifera</i>	<i>Vitis riparia</i>	<i>Vitis arizonica</i>						
Mal_HT-1	1	0.974																							0.919						
Pru_HT-1			1		0.92	0.938	0.931			0.92											0.916	0.912	0.922								
Rub_HT-1				1																		0.906	0.910	0.909	0.913						
Jug_HT-1					1																		0.931	0.925	0.923	0.930					
Jug_HT-2						1																	0.907	0.910	0.910	0.909					
Jug_HT-3							1																0.902	0.909	0.905	0.904					
Jug_HT-4								1																0.912	0.917	0.916					
Jug_HT-5											0.913	0.904											0.912	0.903	0.909						
Que_HT-1						0.926	1																	0.977	0.973	0.977					
Que_HT-2						0.937	1																	0.919	0.919	0.922	0.932				
Que_HT-3							1	0.944																0.918	0.916	0.920					
Que_HT-4										0.91			0.912											0.904	0.904	0.901	0.903				
Que_HT-5						0.920	1	0.947		0.92														0.906	0.900		0.906				
Que_HT-6							0.930	1																0.952	0.955	0.956	0.956				
Que_HT-7								1																0.922	0.920	0.920	0.924				
Que_HT-8									1	0.915														0.911	0.906	0.909					
Que_HT-9							0.93	0.952	1				0.910											0.923	0.921	0.922	0.924				
Ziz_HT-1									1															0.951	0.953	0.947	0.954				
Cam_HT-1										1														0.910	0.914	0.909	0.906				
Pop_HT-1											1	0.950													0.963	0.969					
Pop_HT-2							0.91					1													0.911	0.913	0.913				
Sal_HT-1													1												0.909		0.901	0.900			
Pis_HT-1														1											0.907		0.905	0.906			
Pis_HT-2															1																
Pis_HT-3																0.930						0.93				0.931					
Pis_HT-4																										0.930					
Pis_HT-5																										0.904	0.903	0.905	0.908		
Pis_HT-6							0.93	0.923	0.925																	0.926	0.925	0.922	0.922		
Cit_HT-1																1										0.952	0.947	0.955	0.953		
Cit_HT-2				0.909		0.91	0.919			0.92	0.91		0.907	0.91	1	0.922									0.916	0.903	0.903				
Gly_HT-1																	1									0.904					
Pha_HT-1				0.901		0.93	0.922	0.913		0.92			0.918					1		0.914						0.913	0.917	0.924	0.913		
Ole_HT-1													0.905						1							0.911	0.910	0.906	0.916		
Pho_HT-1						0.92																				0.900					
Asp_HT-1												0.904														1	1	0.904	0.907	0.903	0.905

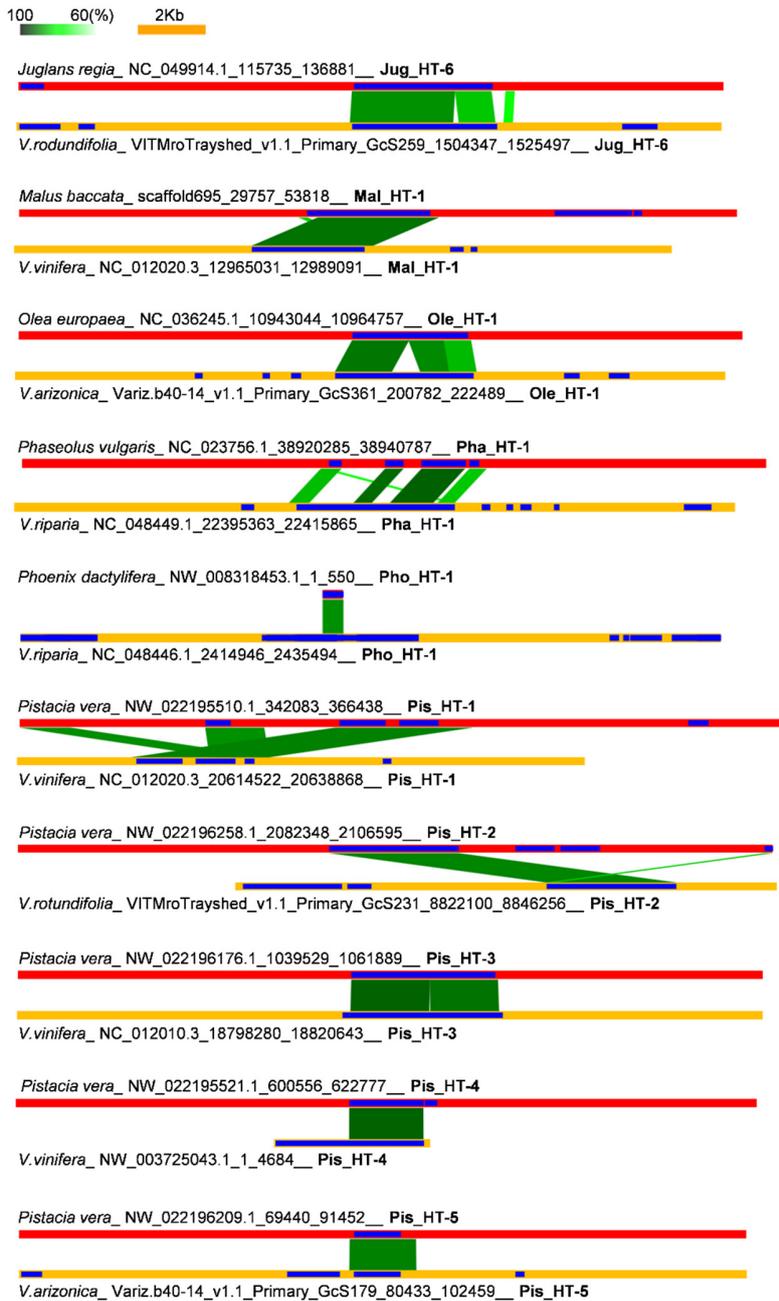
Supplementary Figure S1. Sequence identity of the horizontally transferred TEs. Columns and rows represent species and each of the TE events, respectively. The intensity of the red color in each box reveals identity. The boxes with 1.0 identity appear when the used sequence matches itself.

Supplementary Figure S2



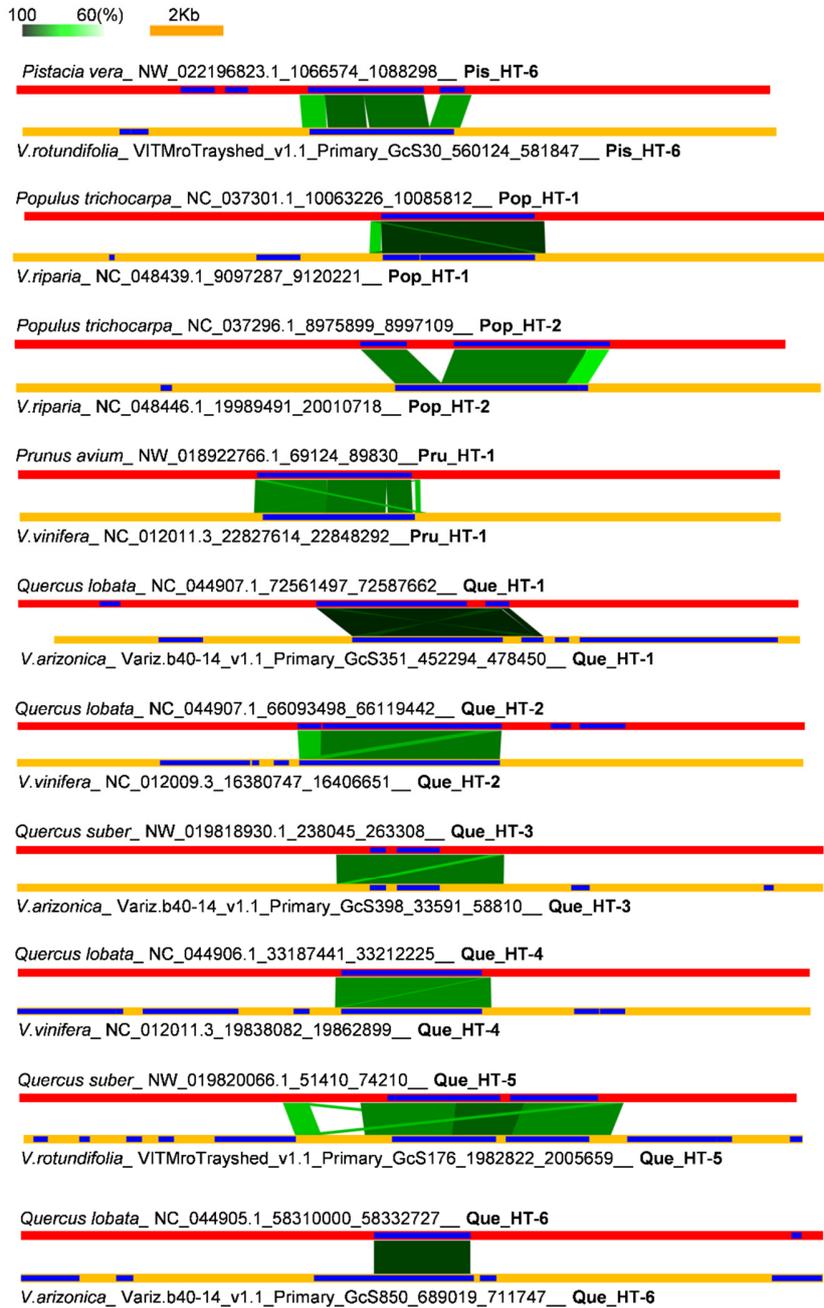
Supplementary Figure S2. *Cont.*

Supplementary Figure S2



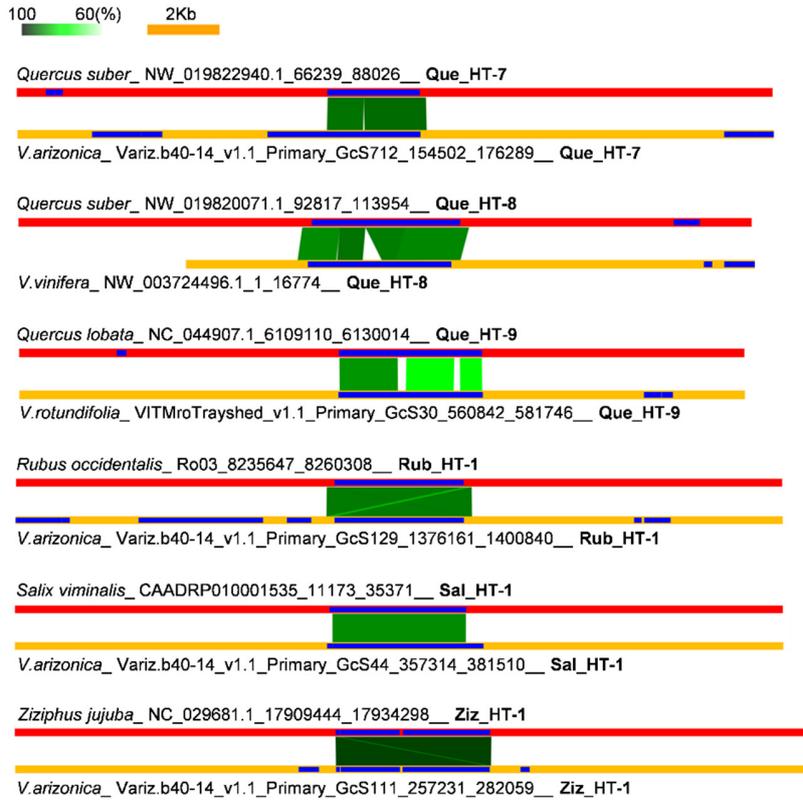
Supplementary Figure S2. *Cont.*

Supplementary Figure S2



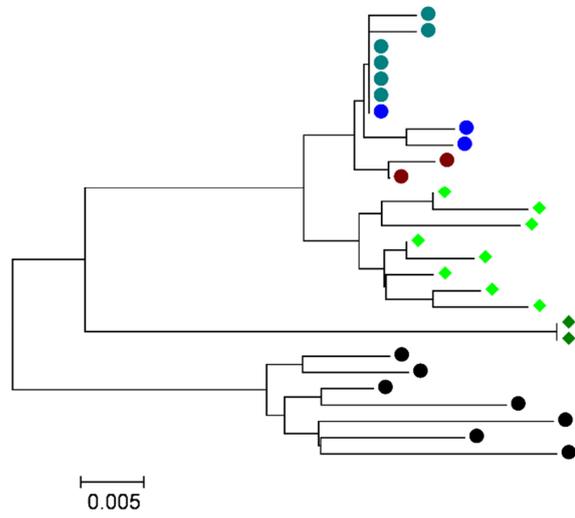
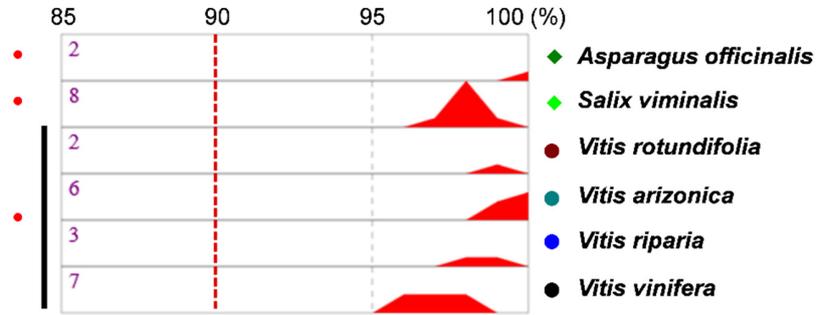
Supplementary Figure S2. *Cont.*

Supplementary Figure S2



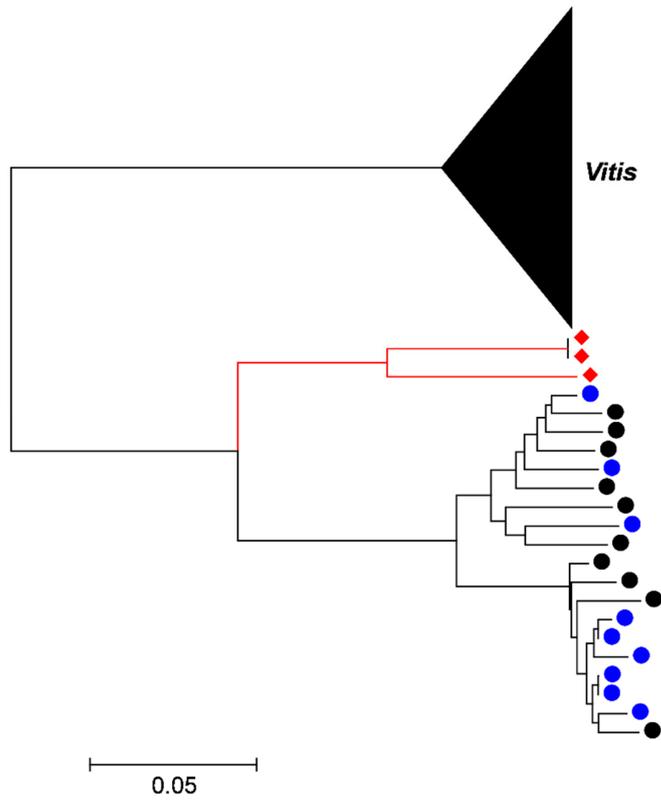
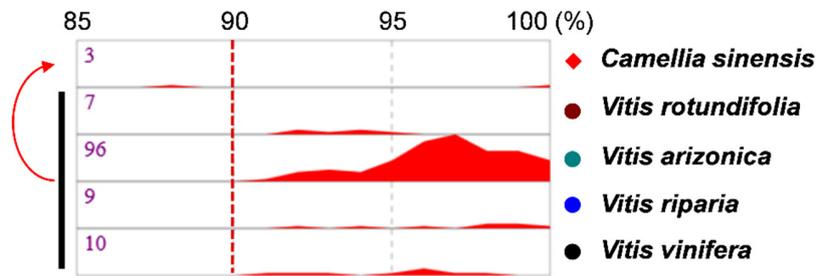
Supplementary Figure S2. Comparative sequence analysis of the 35 HT events. The sequence contigs containing the horizontally transferred TEs are compared to the *Vitis* collinear regions. The horizontal red and yellow bars represent non-*Vitis* and *Vitis* sequence contigs, respectively. The blue bars indicate annotated TEs. The matched sequence regions are linked with green boxes and the color intensity is proportional to the identity.

Asp_HT-1



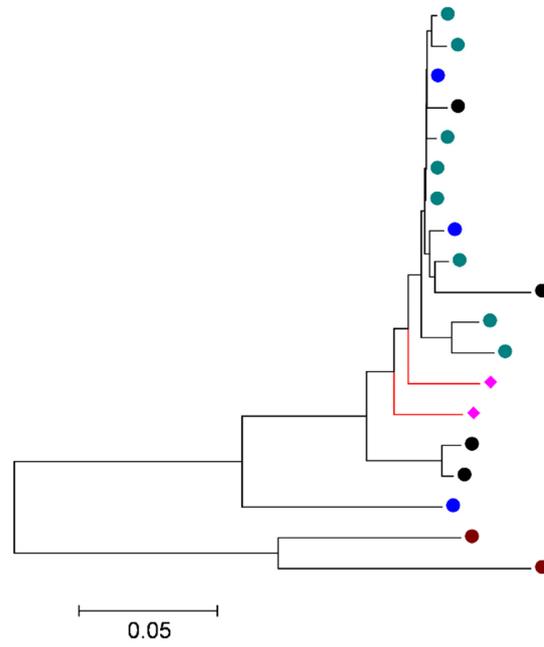
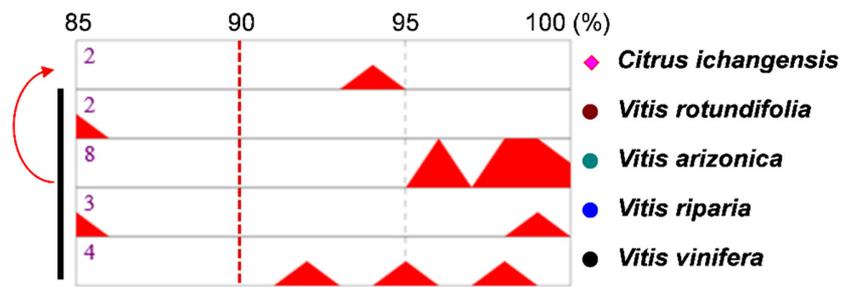
Supplementary Figure S4. *Cont.*

Cam_HT-1



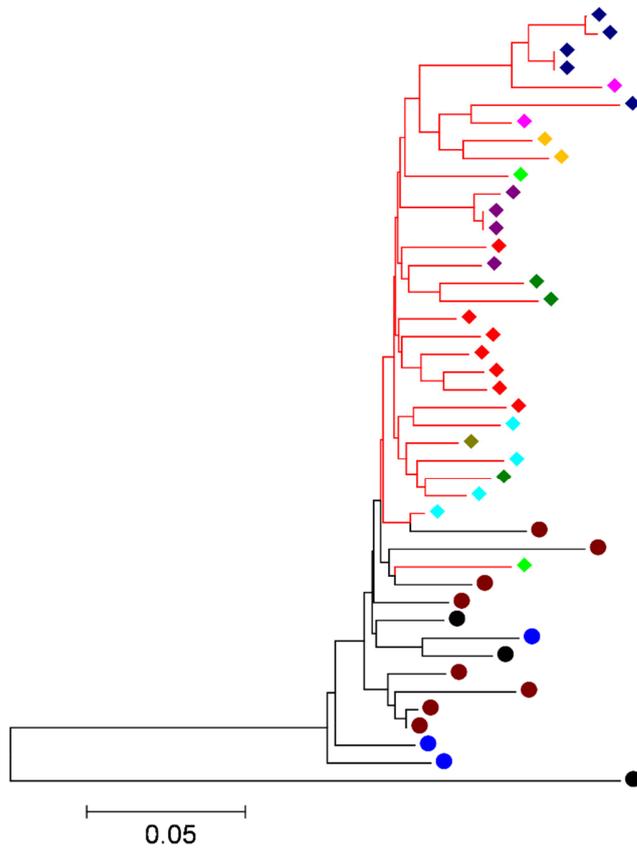
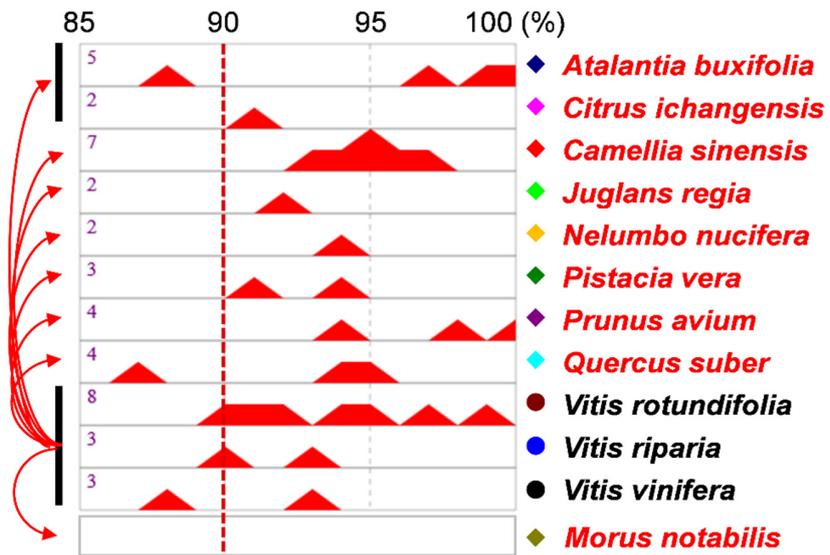
Supplementary Figure S4. *Cont.*

Cit_HT-1



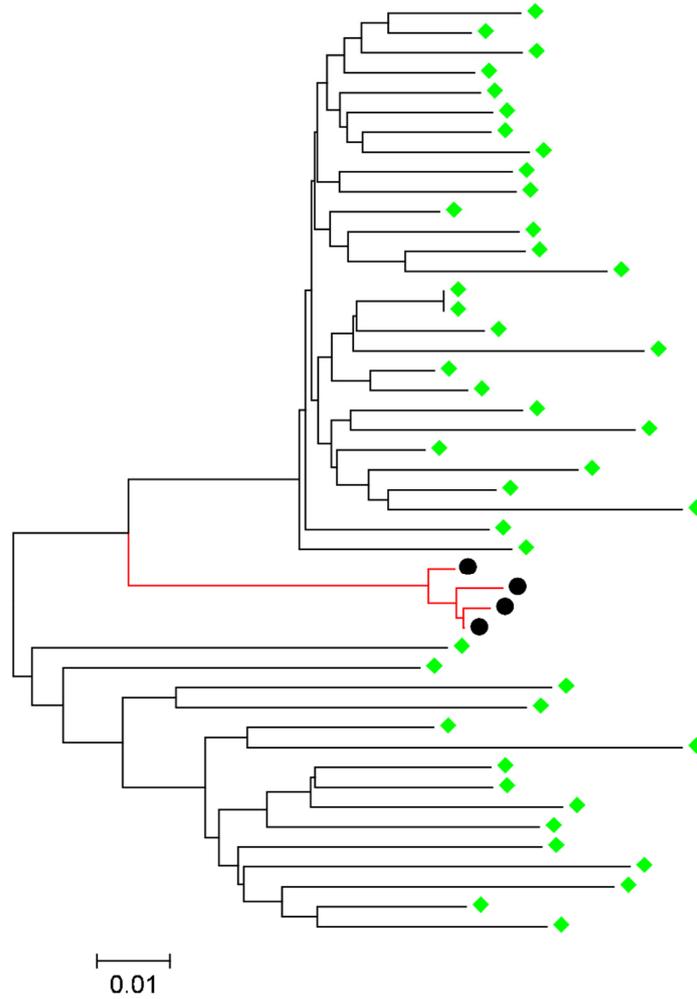
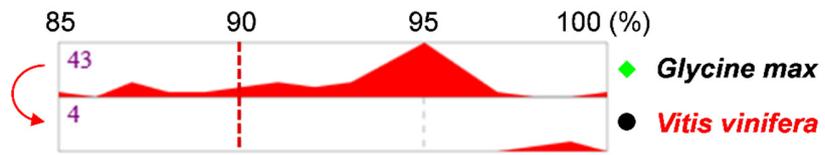
Supplementary Figure S4. *Cont.*

Cit_HT-2



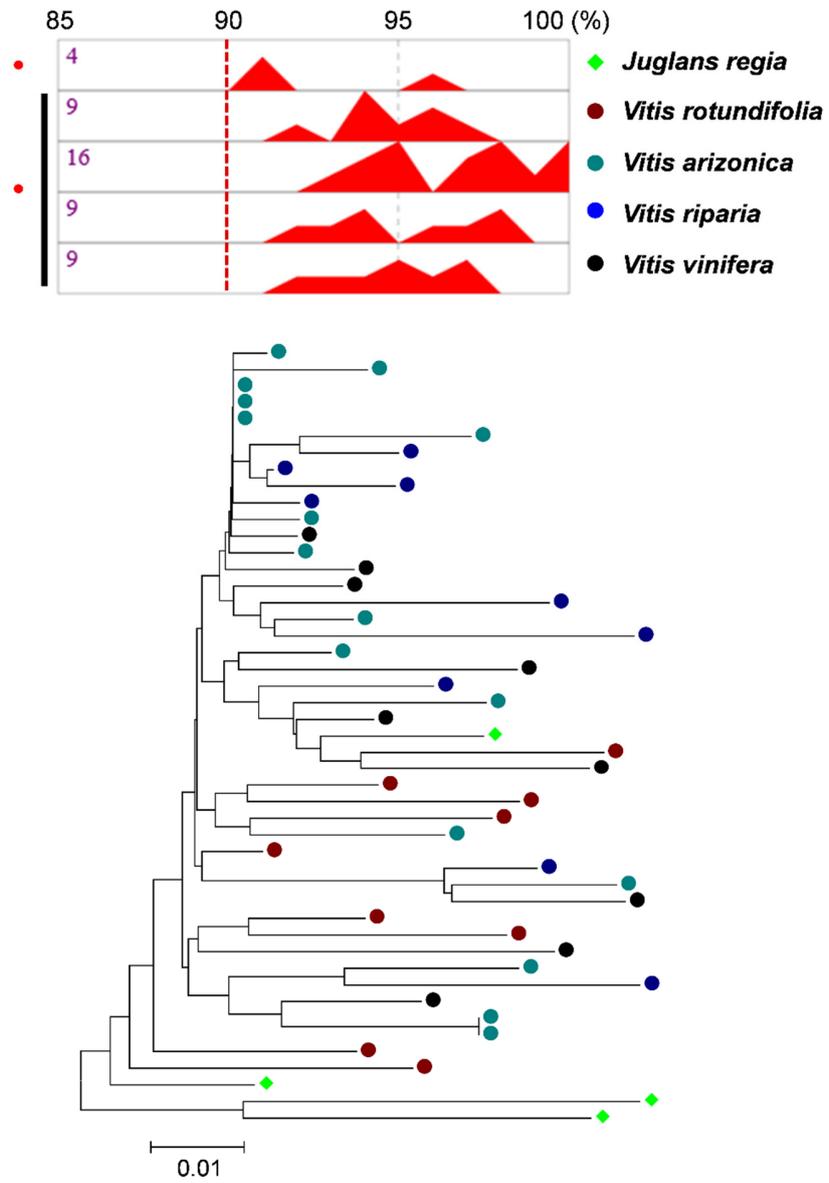
Supplementary Figure S4. *Cont.*

Gly_HT-1



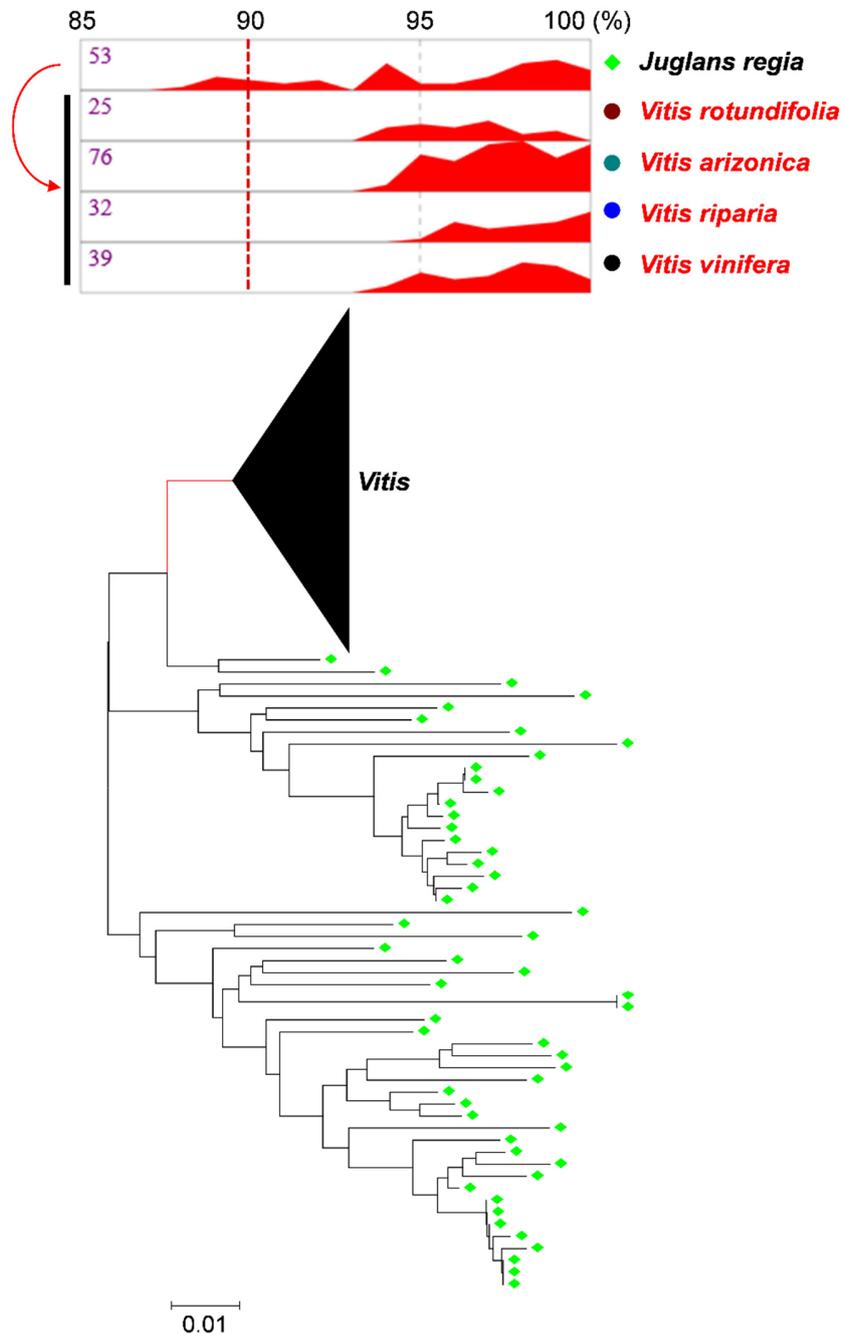
Supplementary Figure S4. *Cont.*

Jug_HT-1



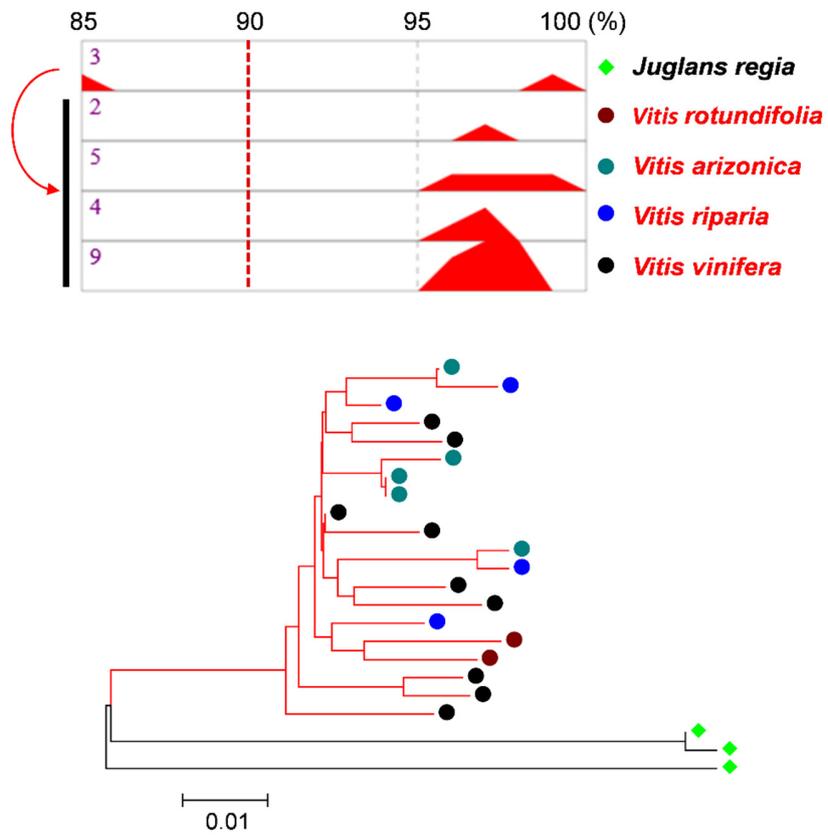
Supplementary Figure S4. *Cont.*

Jug_HT-2



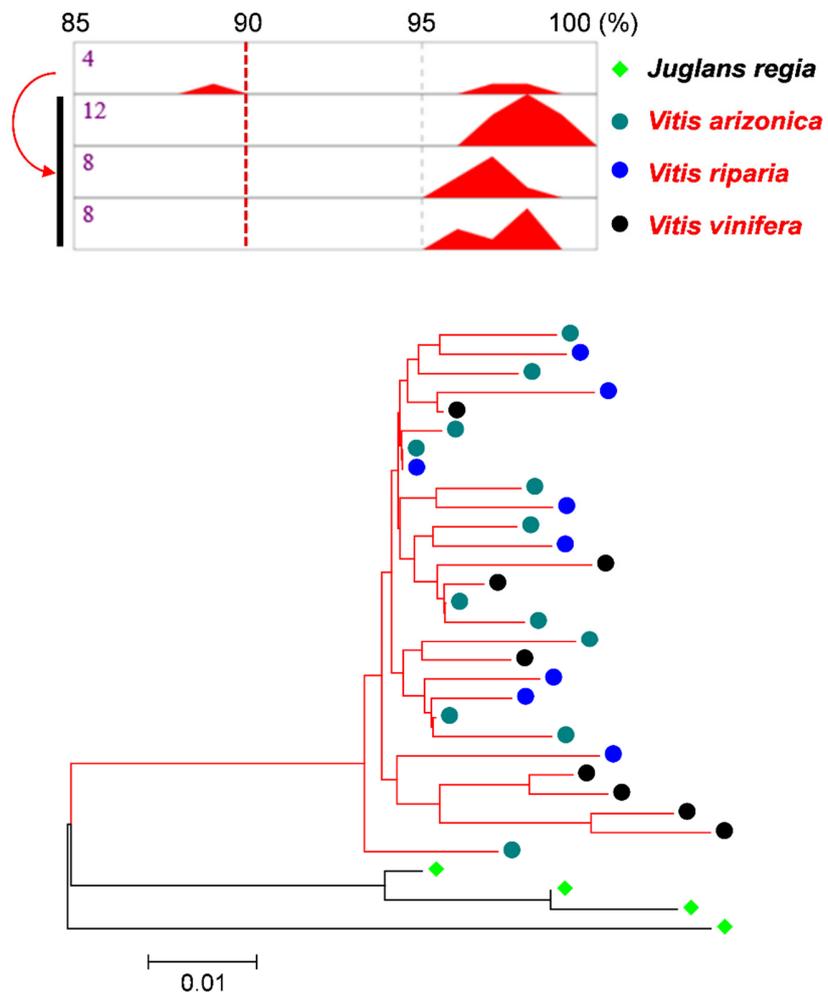
Supplementary Figure S4. *Cont.*

Jug_HT-3



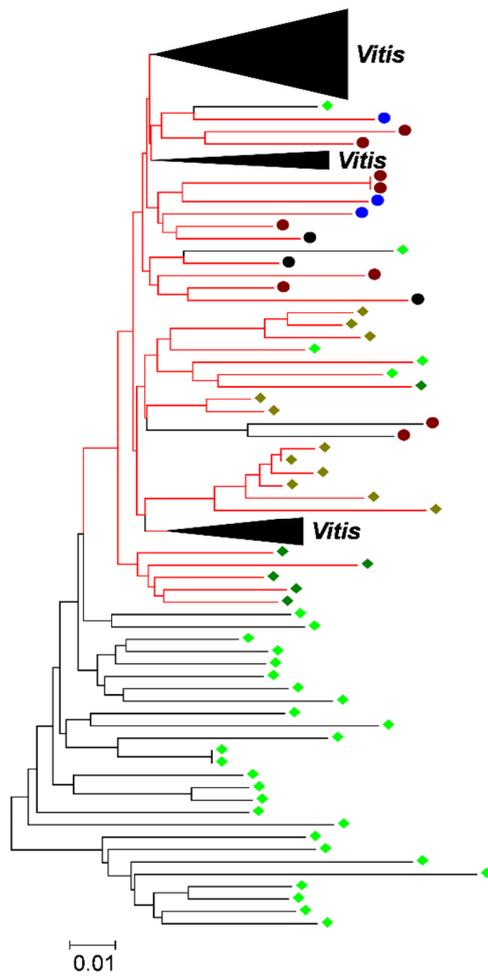
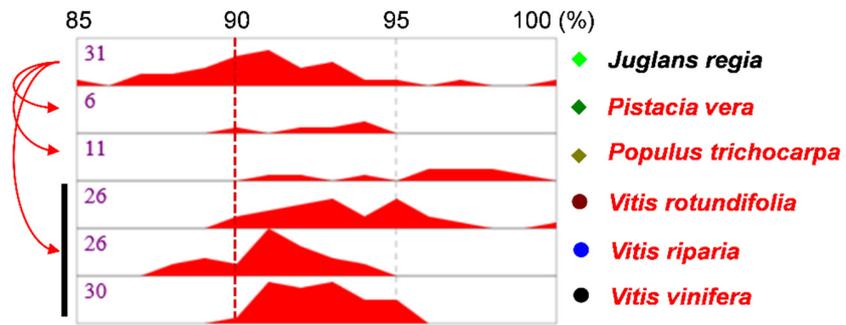
Supplementary Figure S4. *Cont.*

Jug_HT-4



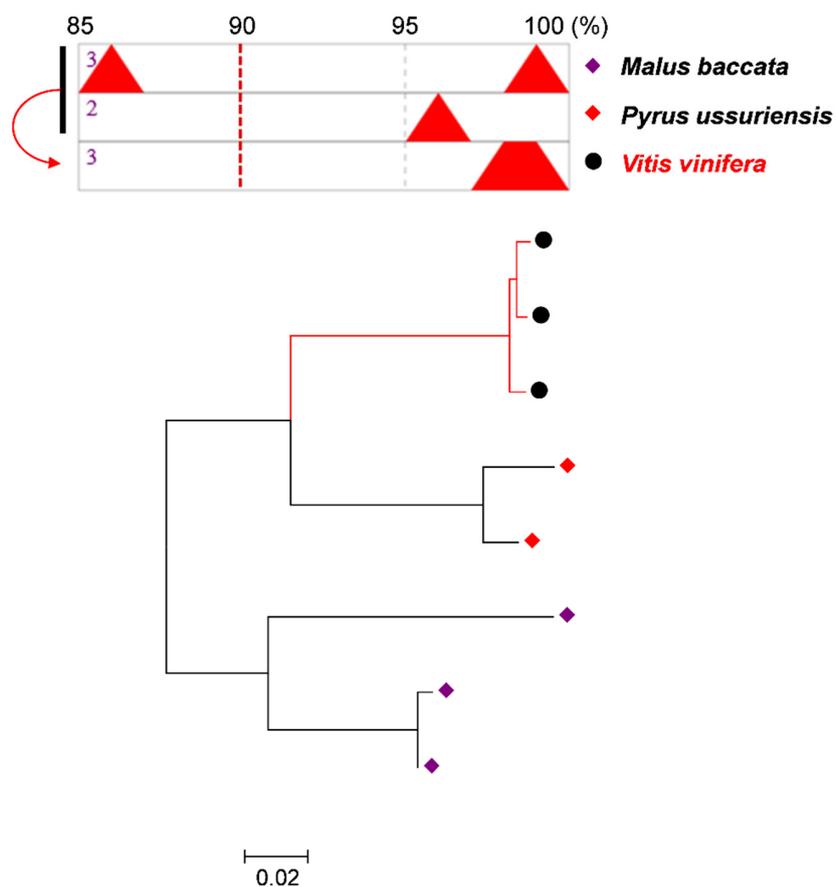
Supplementary Figure S4. *Cont.*

Jug_HT-5



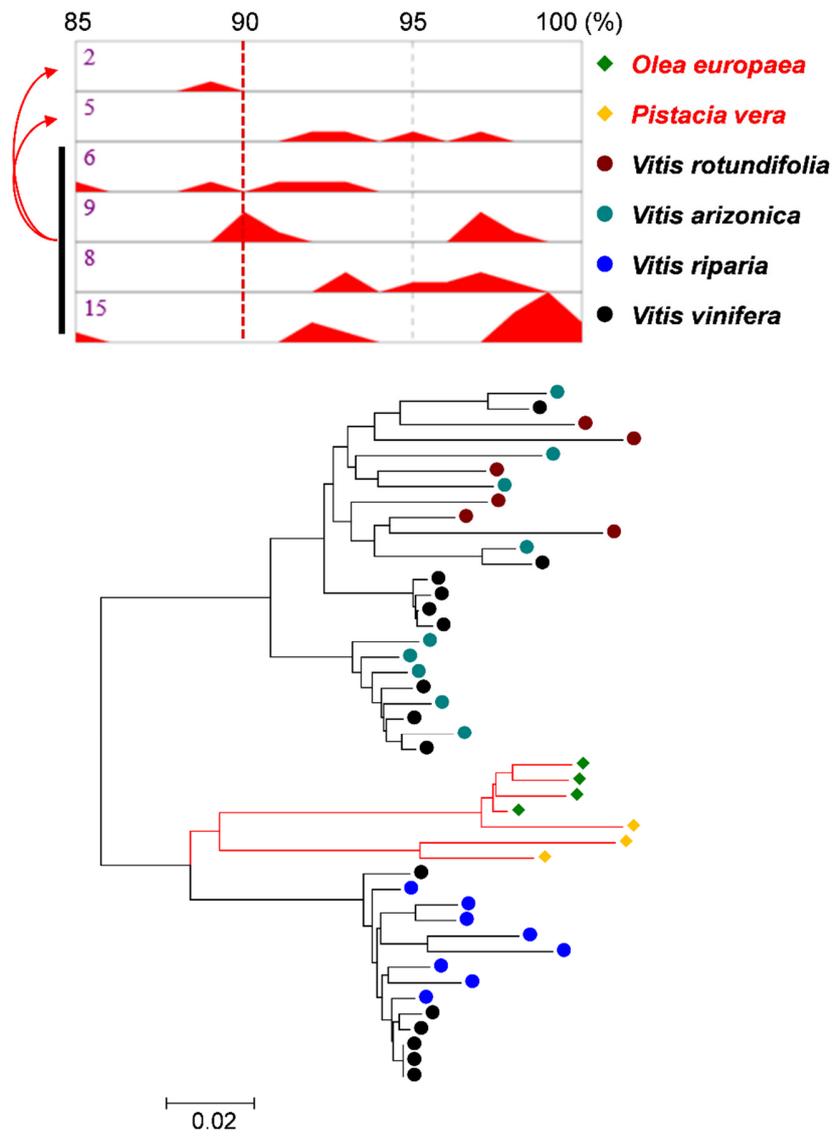
Supplementary Figure S4. *Cont.*

Mal_HT-1



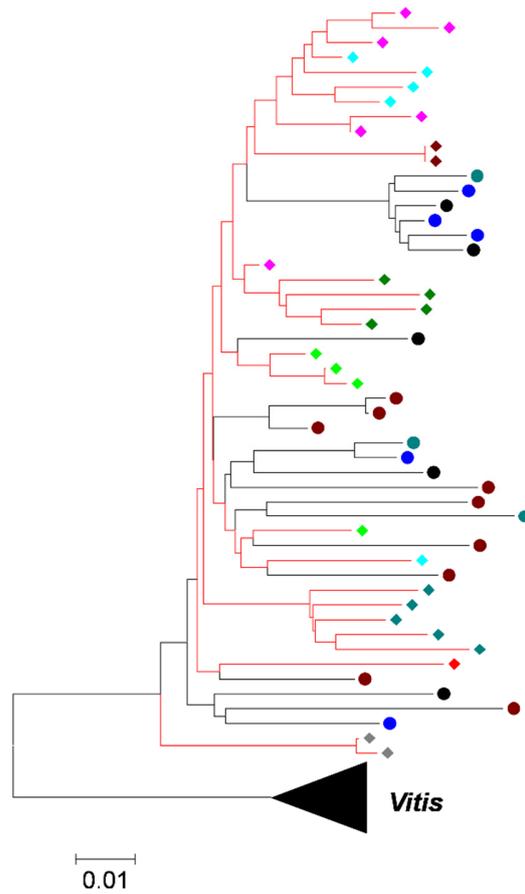
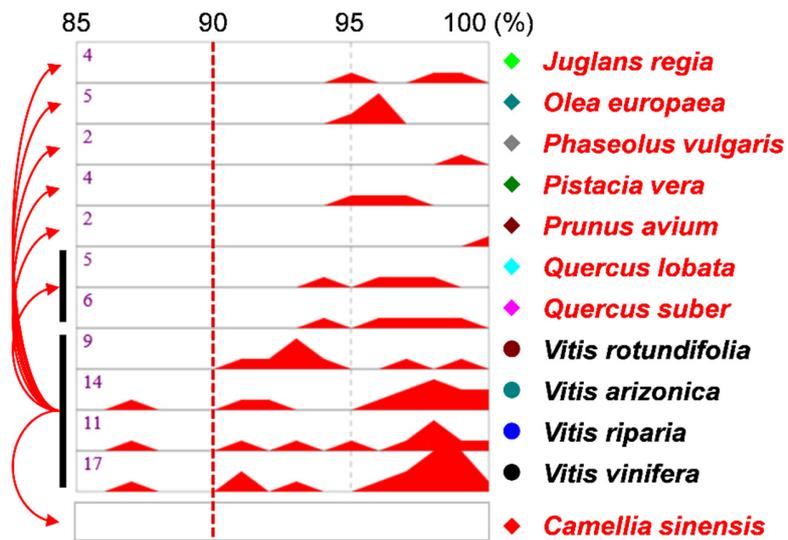
Supplementary Figure S4. *Cont.*

Ole_HT-1



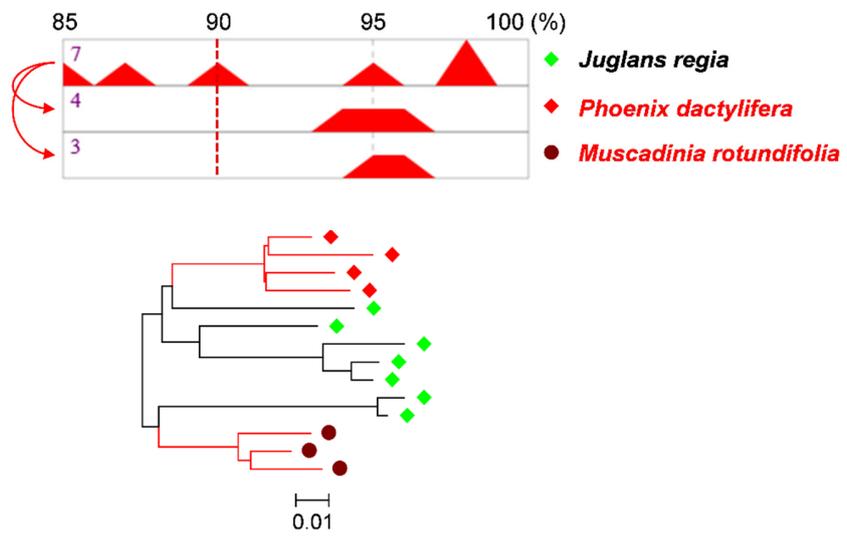
Supplementary Figure S4. *Cont.*

Pha_HT-1



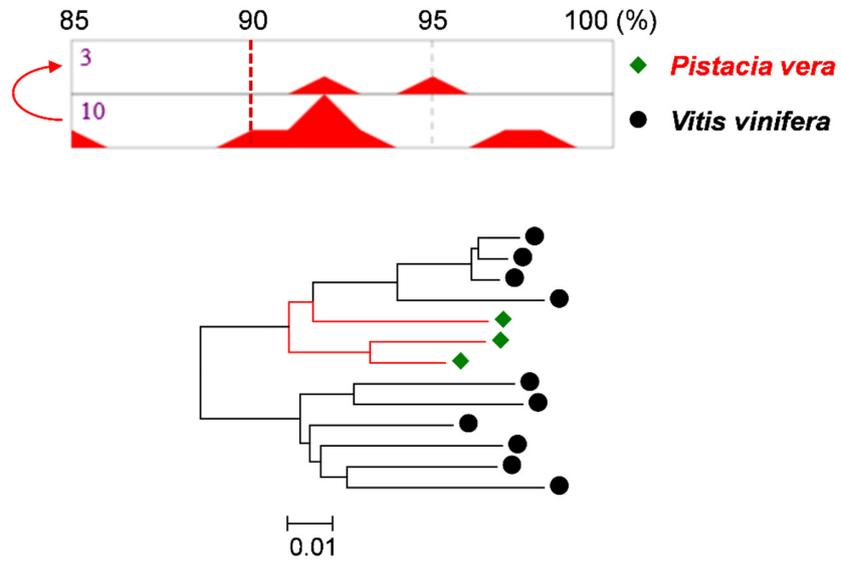
Supplementary Figure S4. *Cont.*

Pho_HT-1



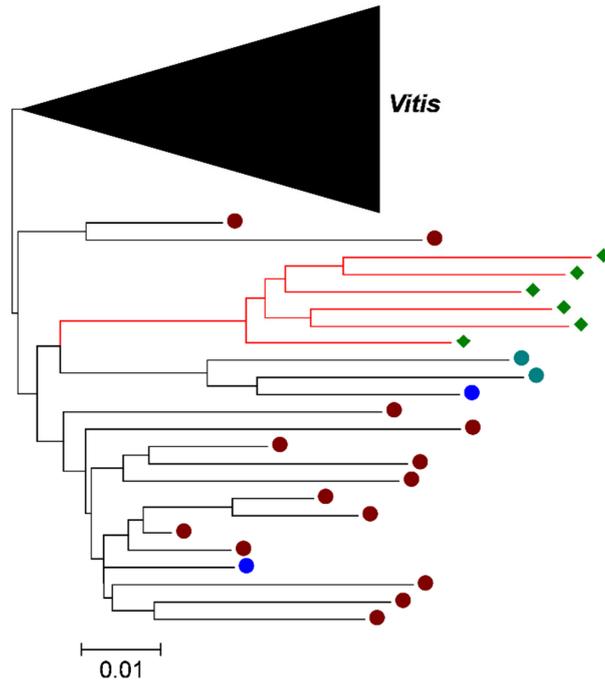
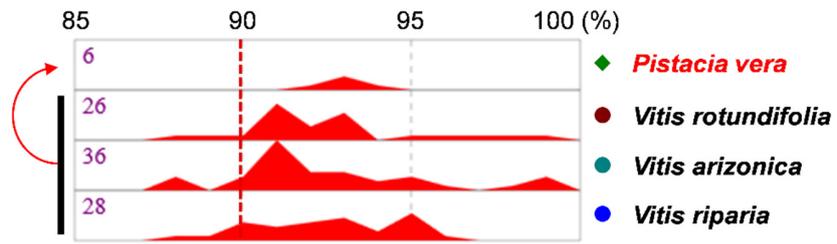
Supplementary Figure S4. *Cont.*

Pis_HT-1



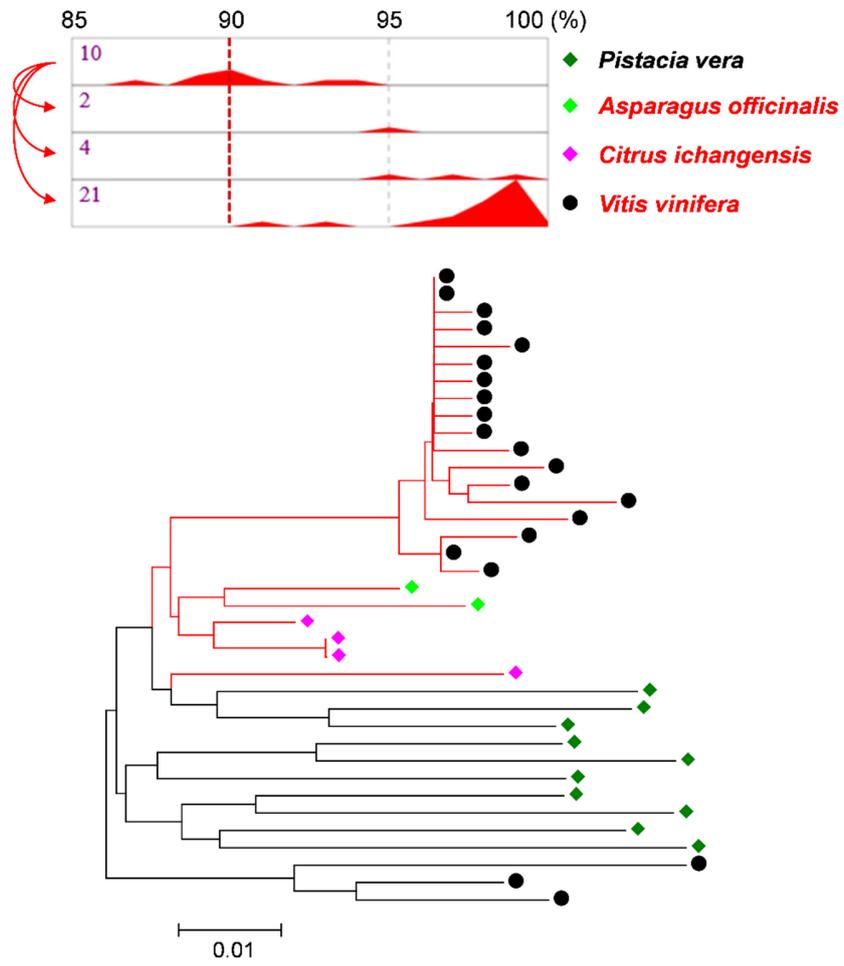
Supplementary Figure S4. *Cont.*

Pis_HT-2



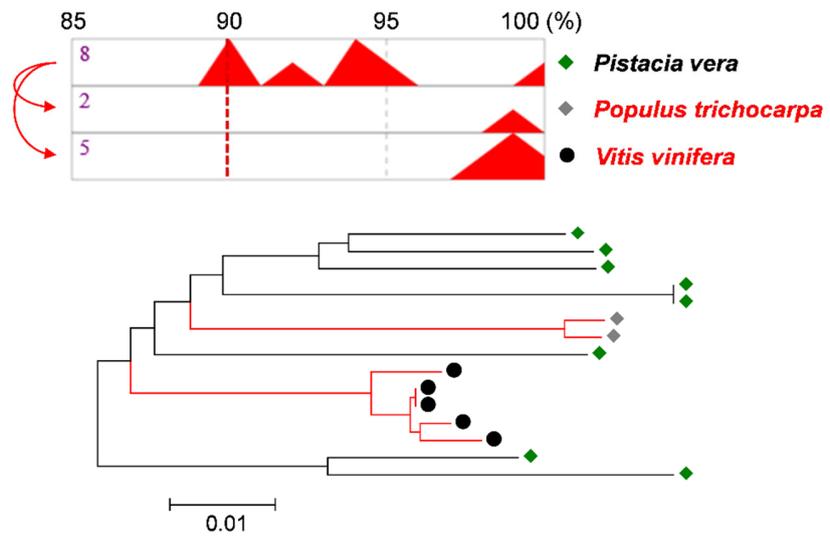
Supplementary Figure S4. *Cont.*

Pis_HT-3



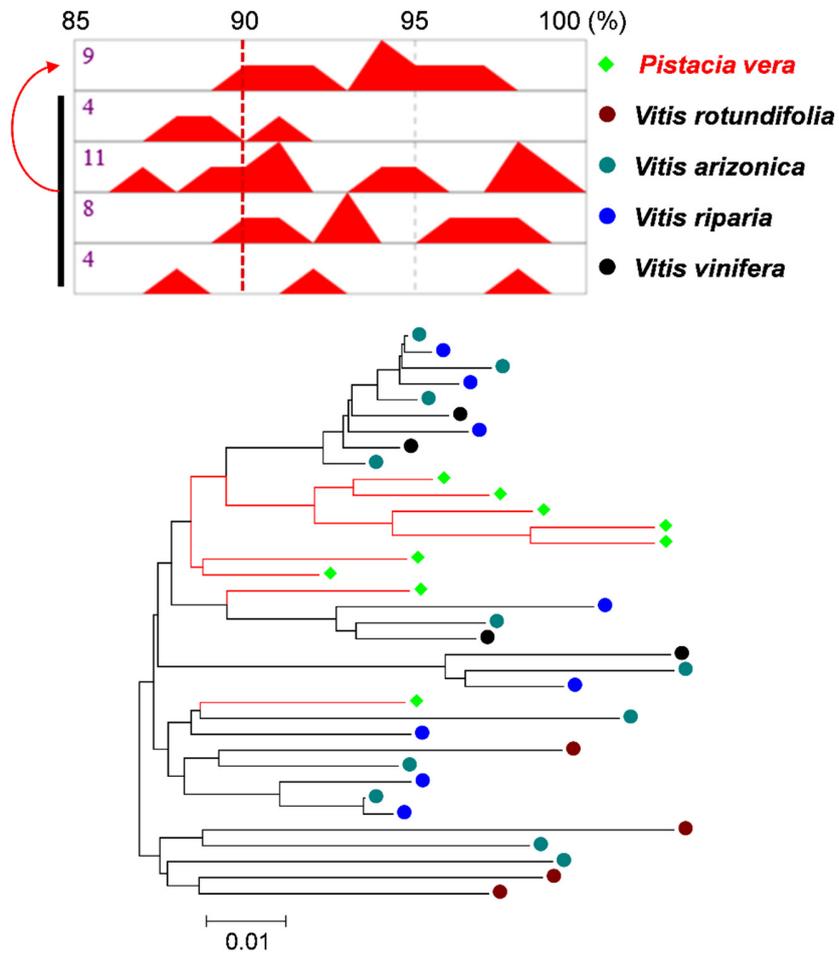
Supplementary Figure S4. *Cont.*

Pis_HT-4



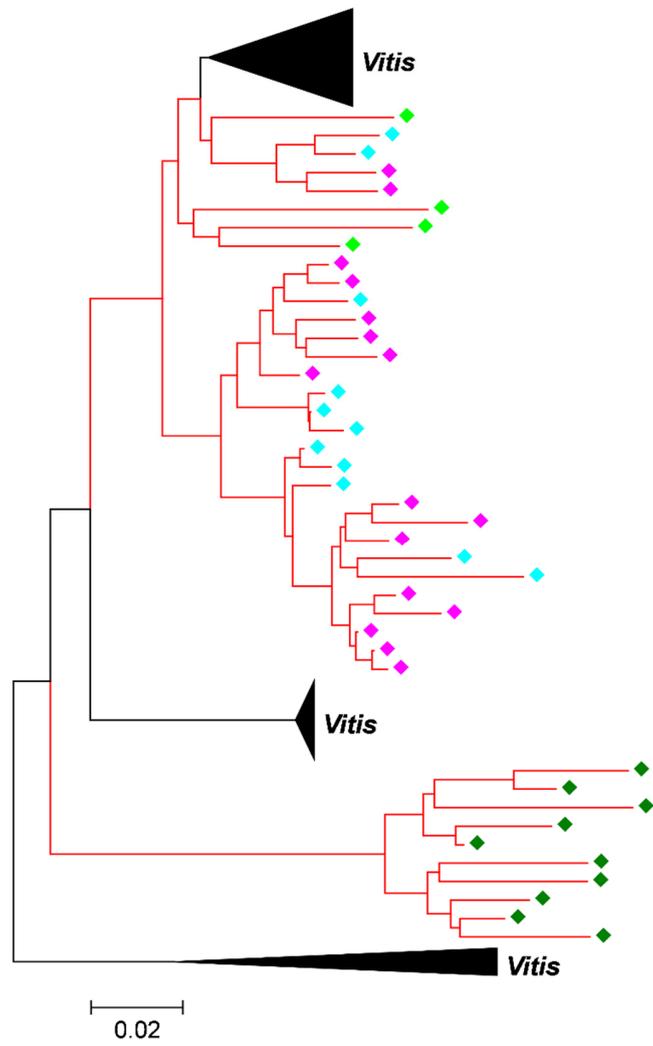
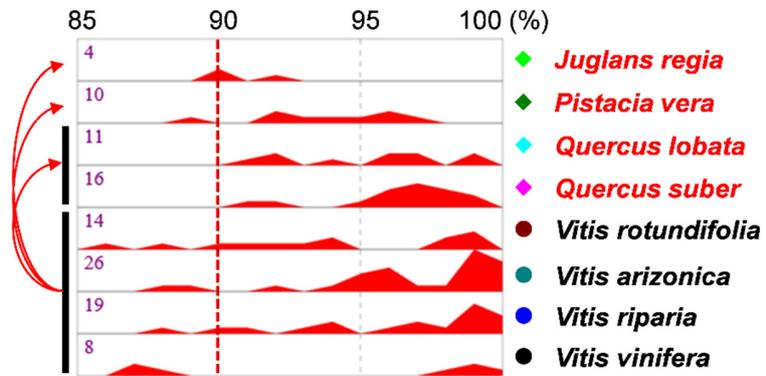
Supplementary Figure S4. *Cont.*

Pis_HT-5



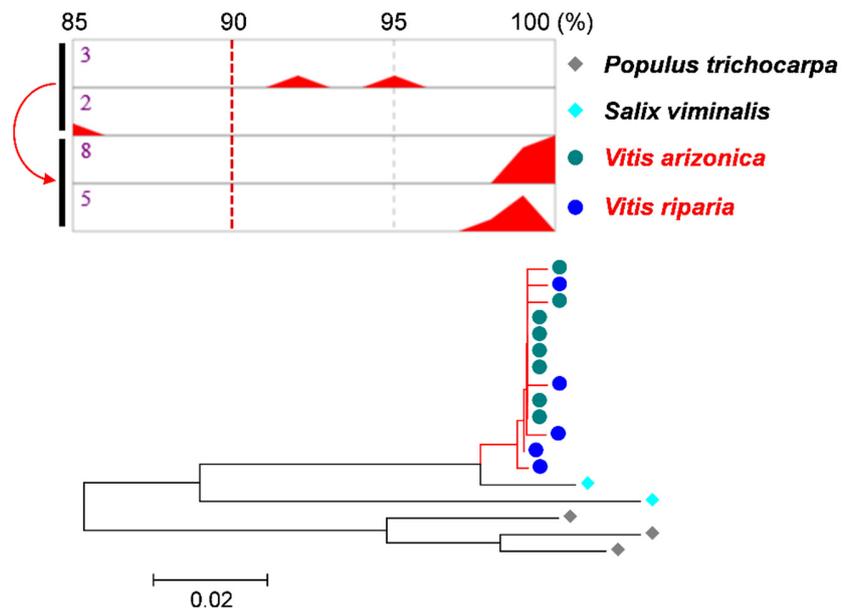
Supplementary Figure S4. *Cont.*

Pis_HT-6



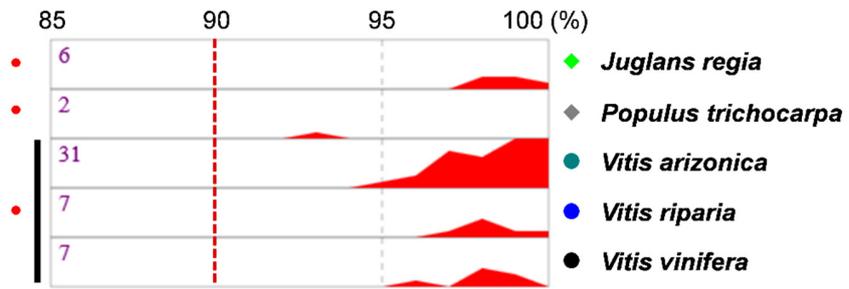
Supplementary Figure S4. *Cont.*

Pop_HT-1



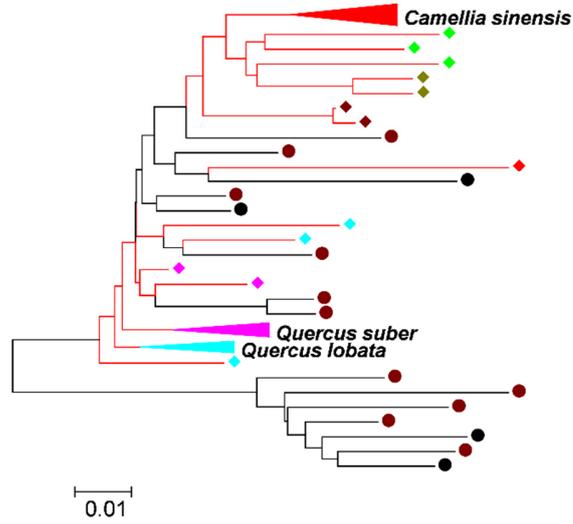
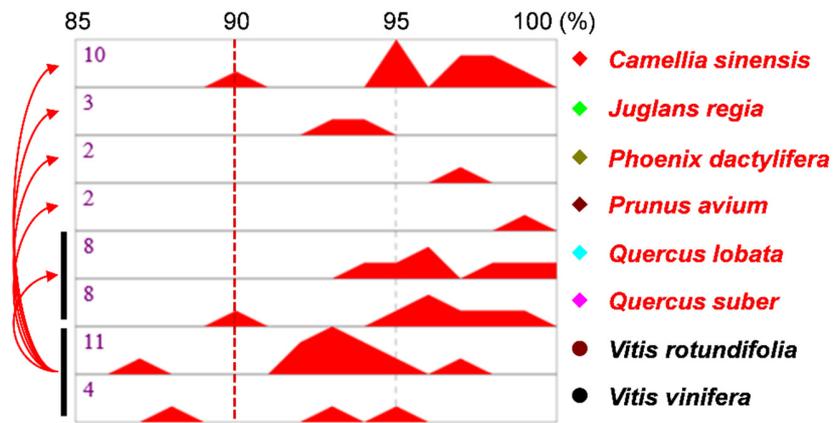
Supplementary Figure S4. *Cont.*

Pop_HT-2



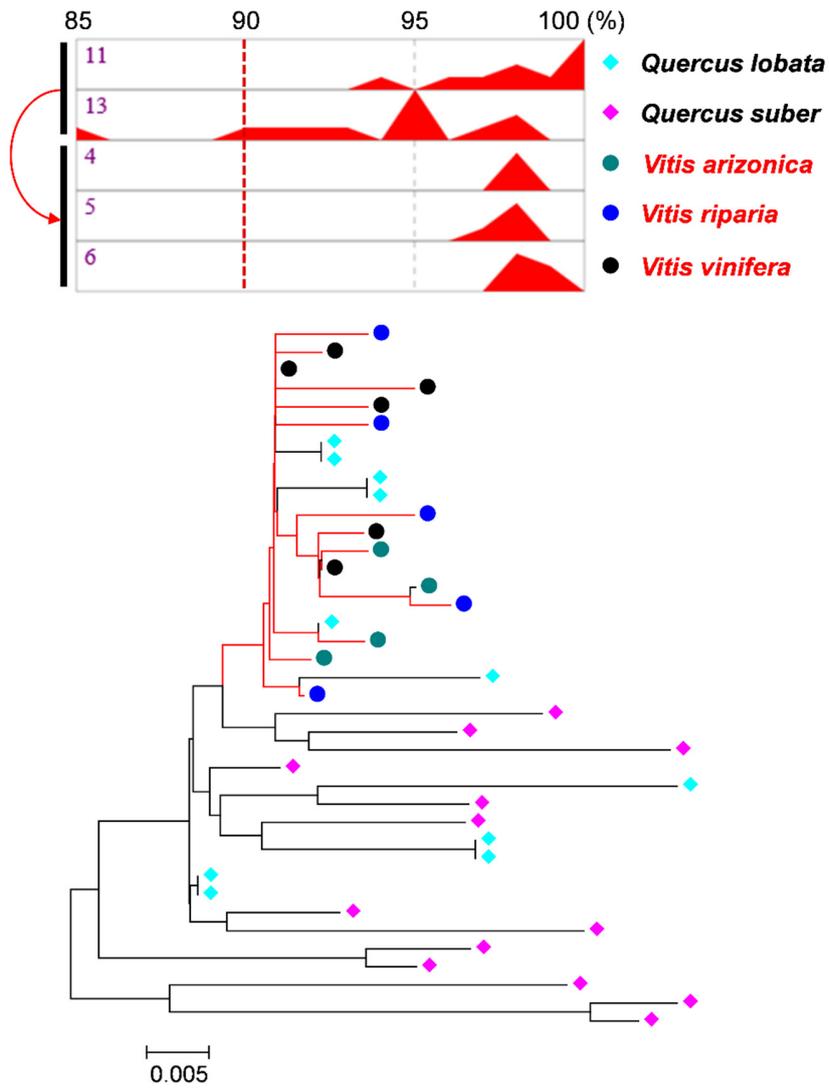
Supplementary Figure S4. *Cont.*

Pru_HT-1



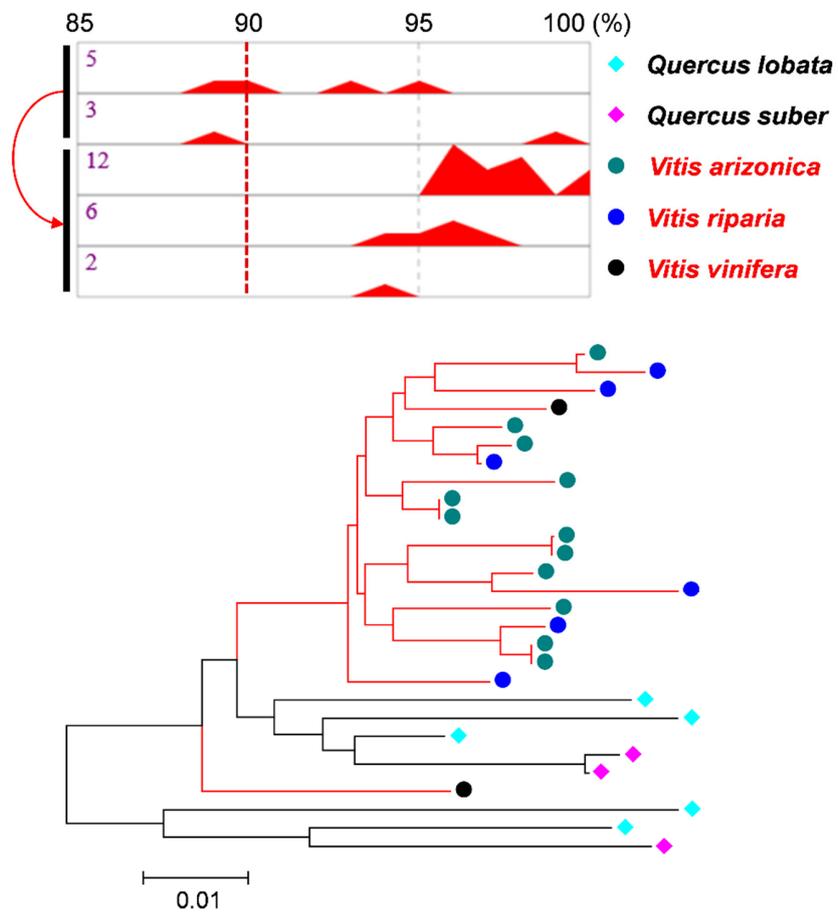
Supplementary Figure S4. *Cont.*

Que_HT-1



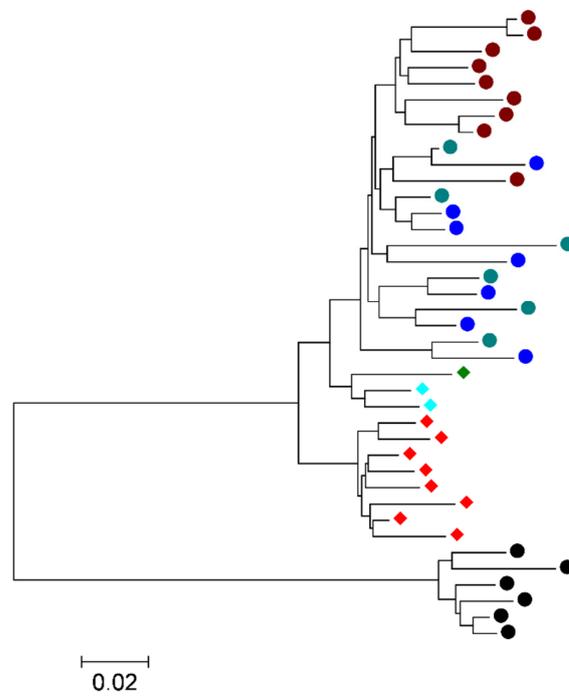
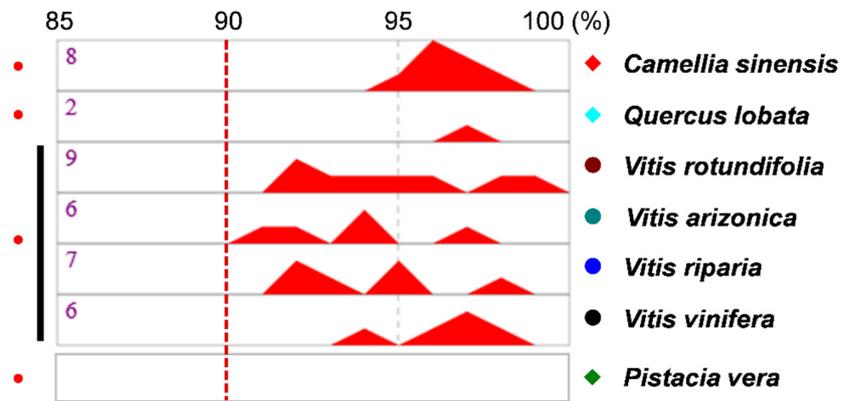
Supplementary Figure S4. *Cont.*

Que_HT-3



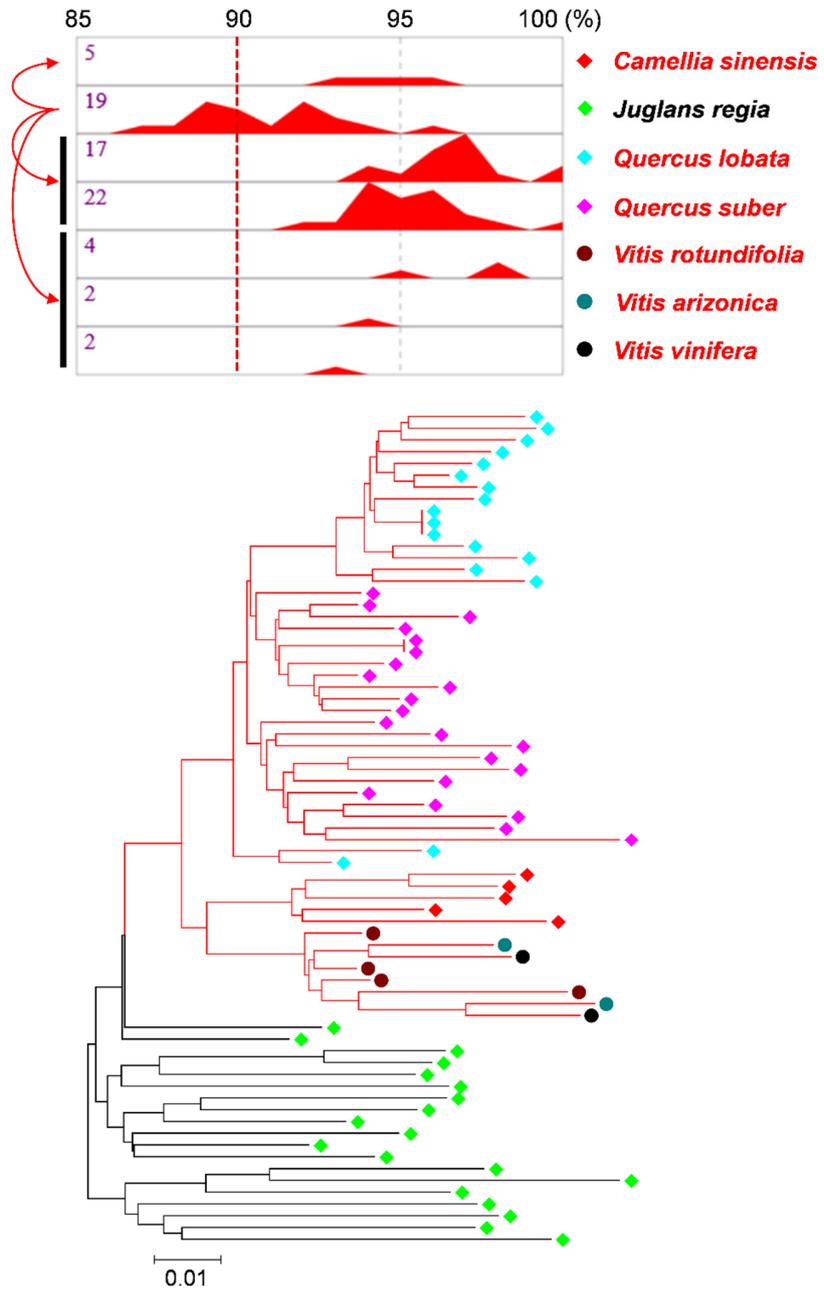
Supplementary Figure S4. *Cont.*

Que_HT-4



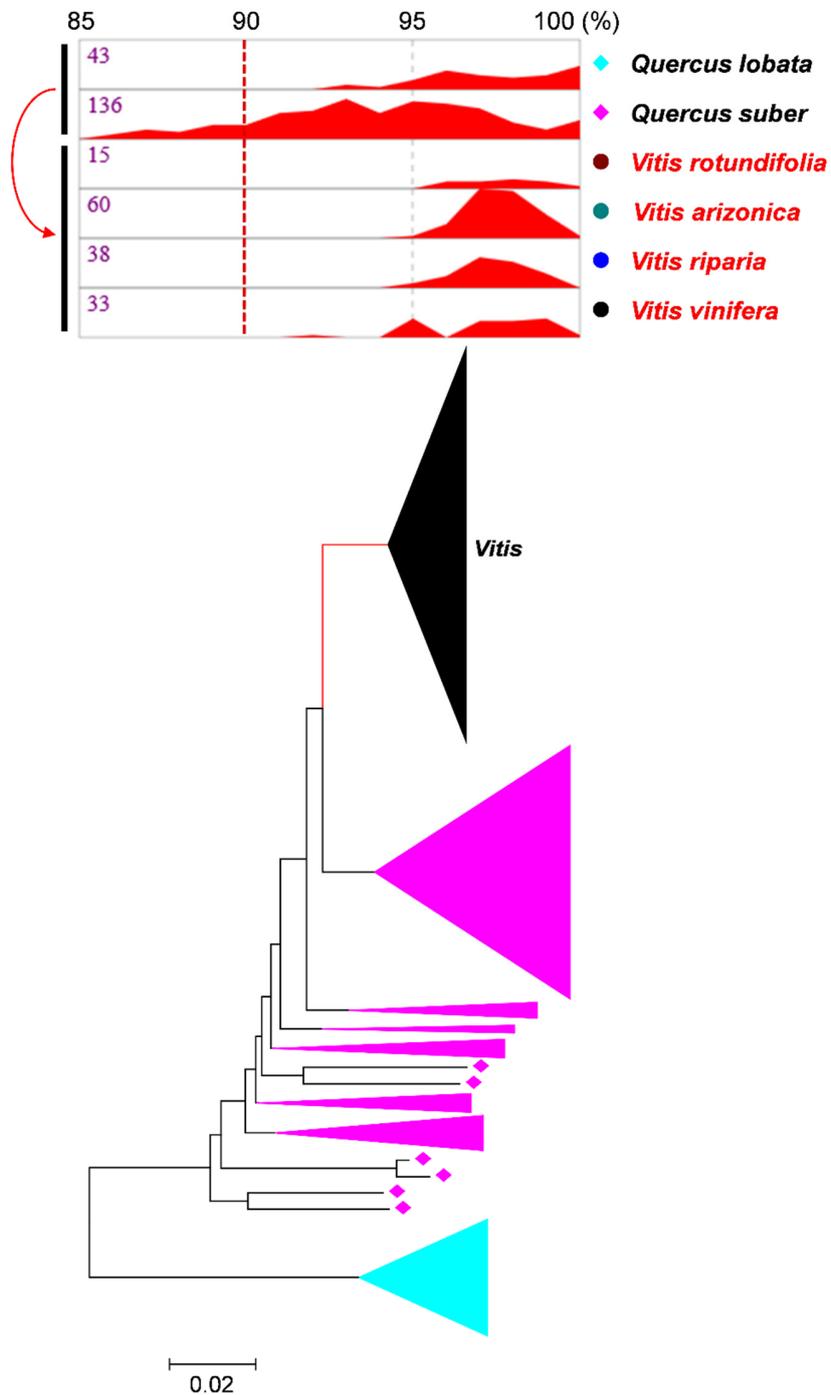
Supplementary Figure S4. *Cont.*

Que_HT-5



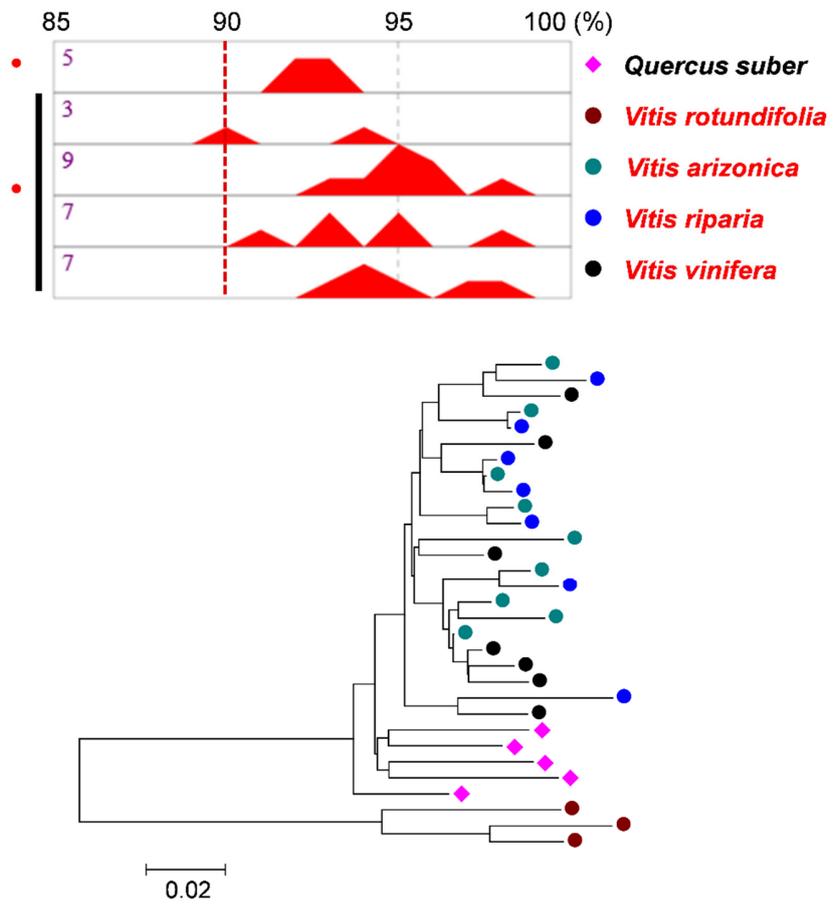
Supplementary Figure S4. *Cont.*

Que_HT-6



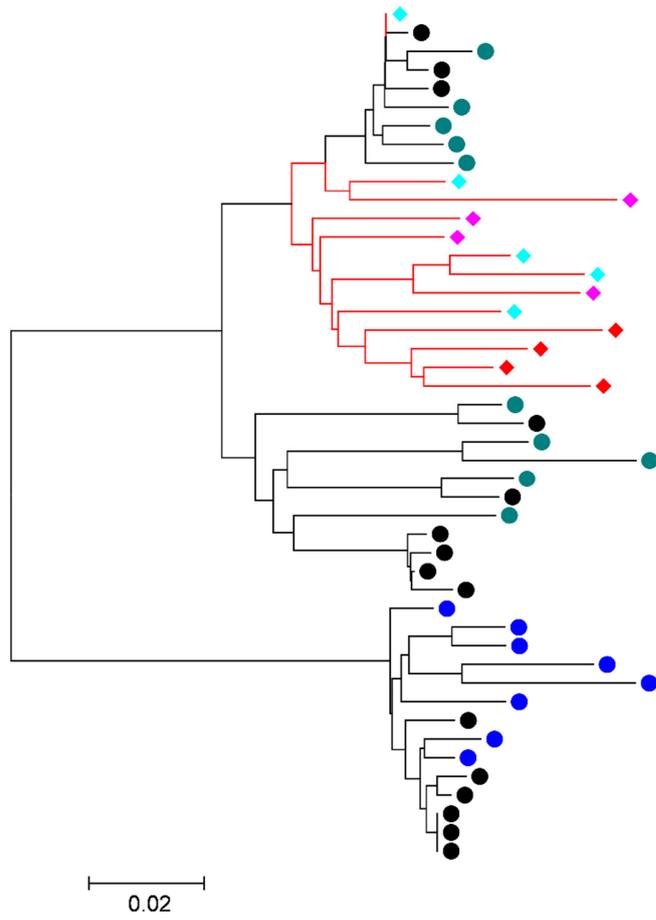
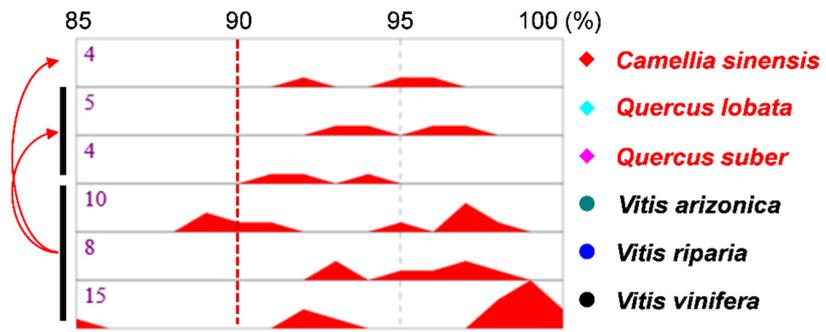
Supplementary Figure S4. *Cont.*

Que_HT-7



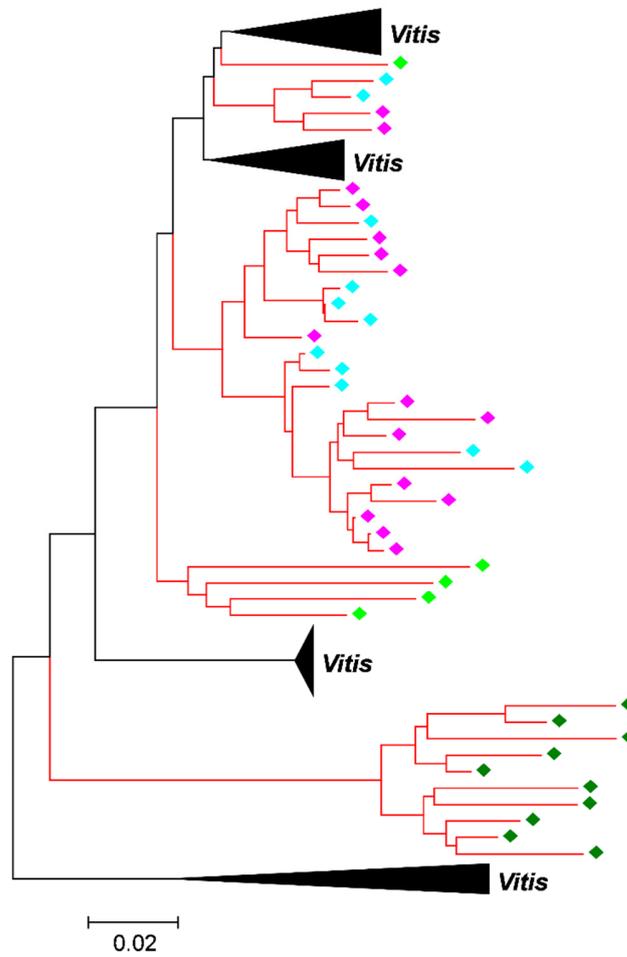
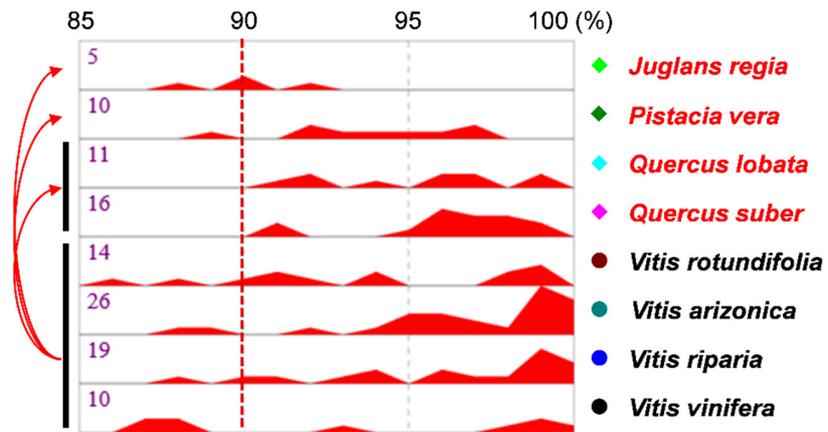
Supplementary Figure S4. *Cont.*

Que_HT-8



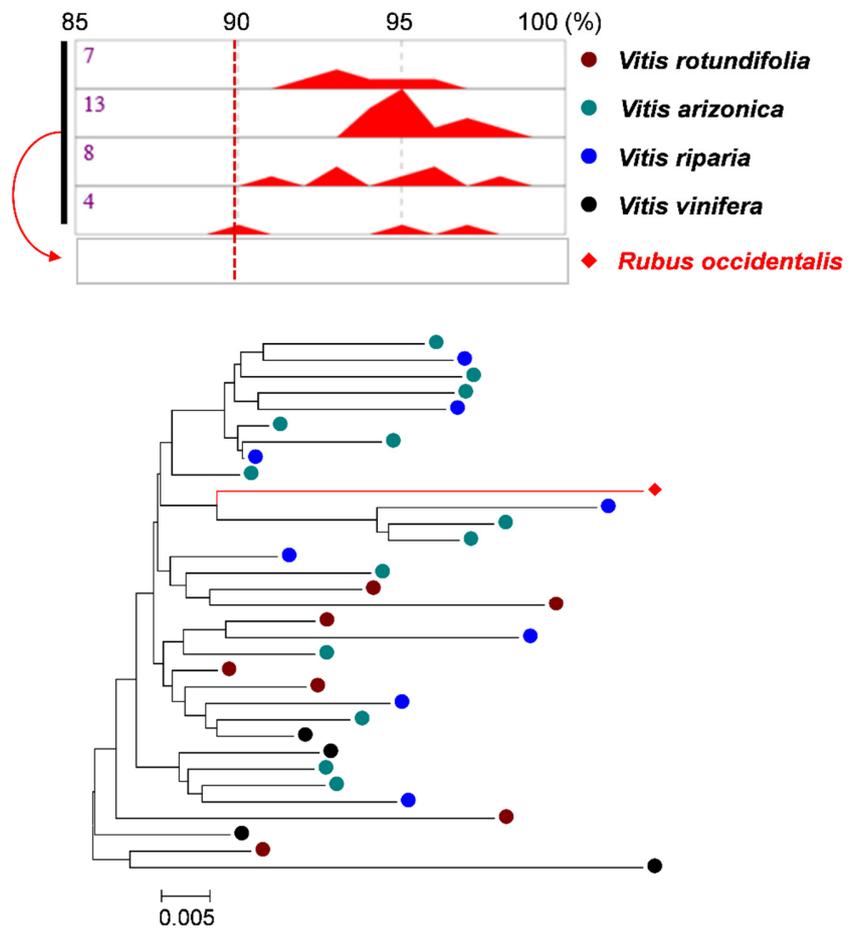
Supplementary Figure S4. *Cont.*

Que_HT-9



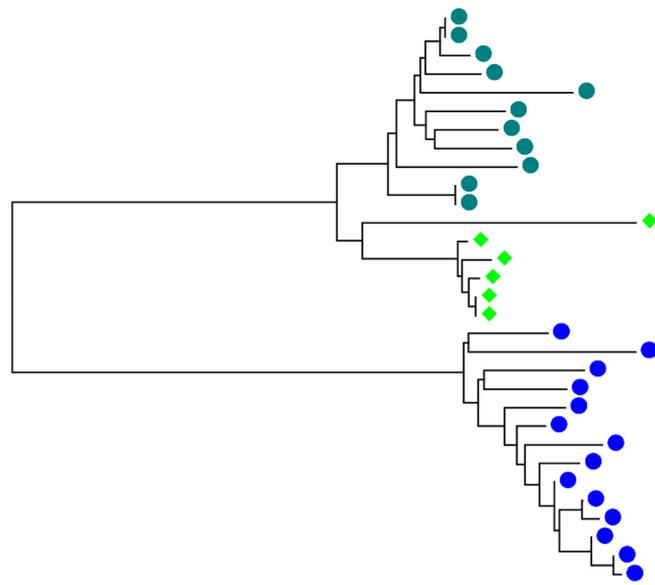
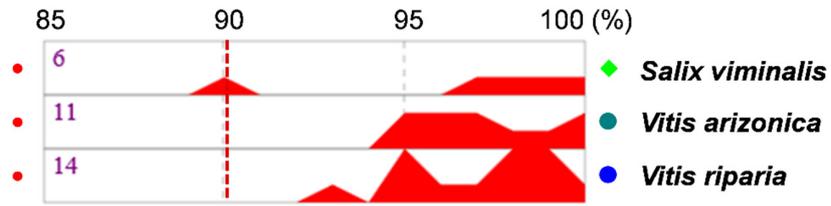
Supplementary Figure S4. *Cont.*

Rub_HT-1



Supplementary Figure S4. *Cont.*

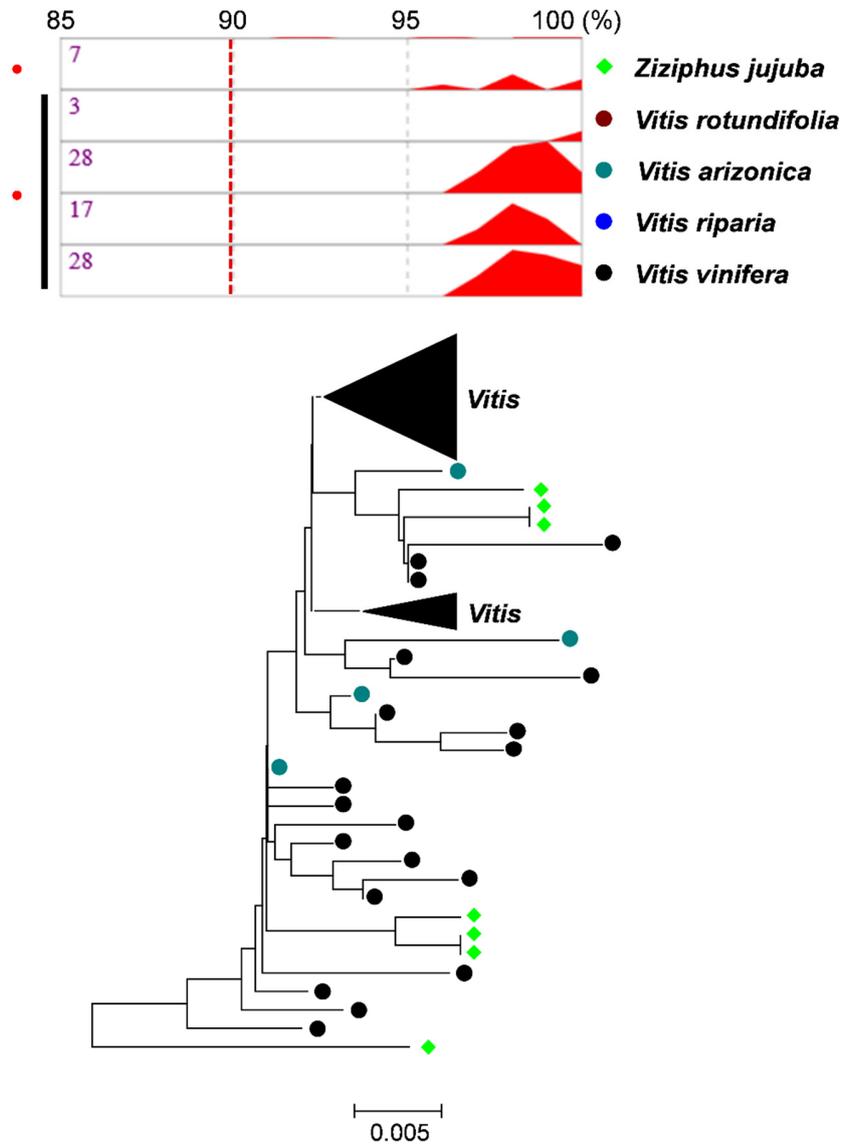
Sal_HT-1



0.02

Supplementary Figure S4. *Cont.*

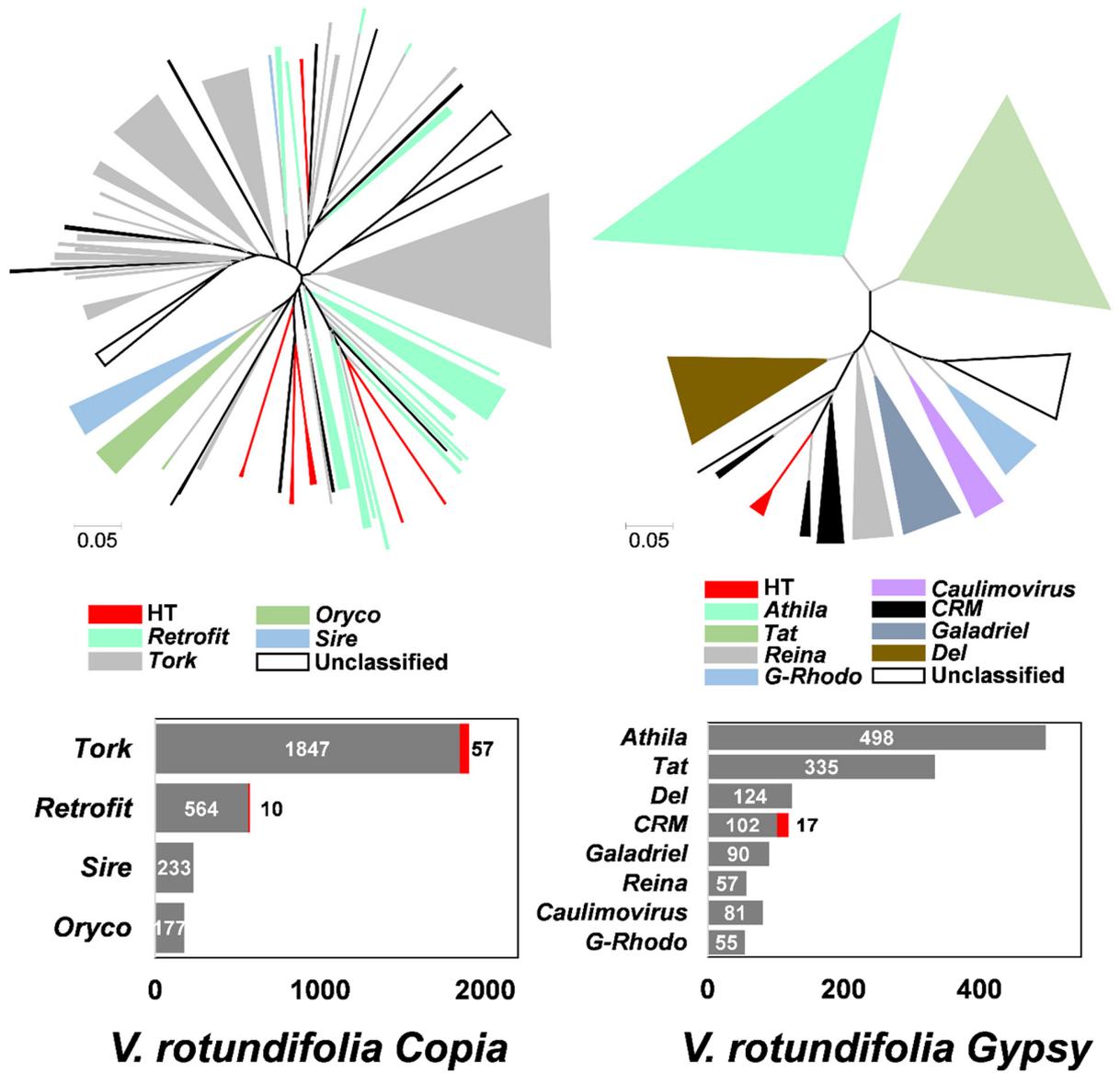
Ziz_HT-1



Supplementary Figure S4. Activity history and phylogenetic tree analyses of the horizontally transferred TEs and their homologs. The activity history is shown in the upper panel. The name of the genus or species is shown on the right side of the panel. Each of the *Vitis* species is marked with a colored circle and other non-*Vitis* genera are with colored rhombuses. The percent identity is shown at the top of the panel. The red graph in each square represents the relative activity history of the paralogs of the horizontally transferred TE. The numbers in the panel indicate the number of the used paralogs in each species. The species of the same genus are marked with black bars on the left side of the panel. The red dots indicate the species or genera for which the donor or recipient was undetermined. The red dotted lines present the 90% identity threshold used in the identification of HTs. The lower panel presents the phylogenetic tree of the homologs of the horizontally transferred TE. The species or genus of each element is marked with the same colored circle or rhombus used in the activity history panel. The

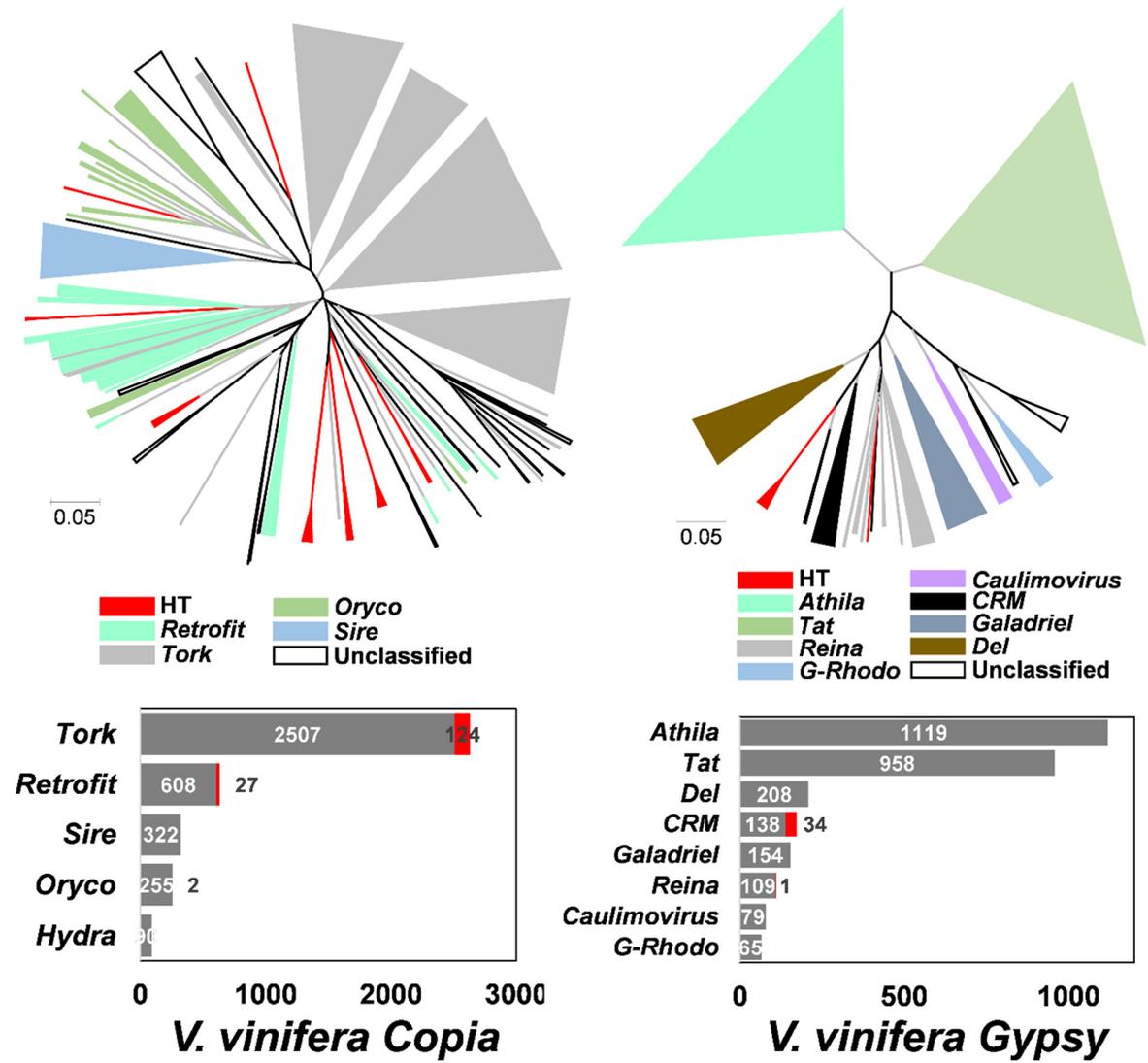
branches of recipients are marked with red lines. The triangles represent the merged clusters of the same genus or species. The triangles of the species or genera, except for *Vitis*, are presented in the same color used in the activity history panel. The *Vitis* genus is presented with a black triangle.

Supplementary Figure S5



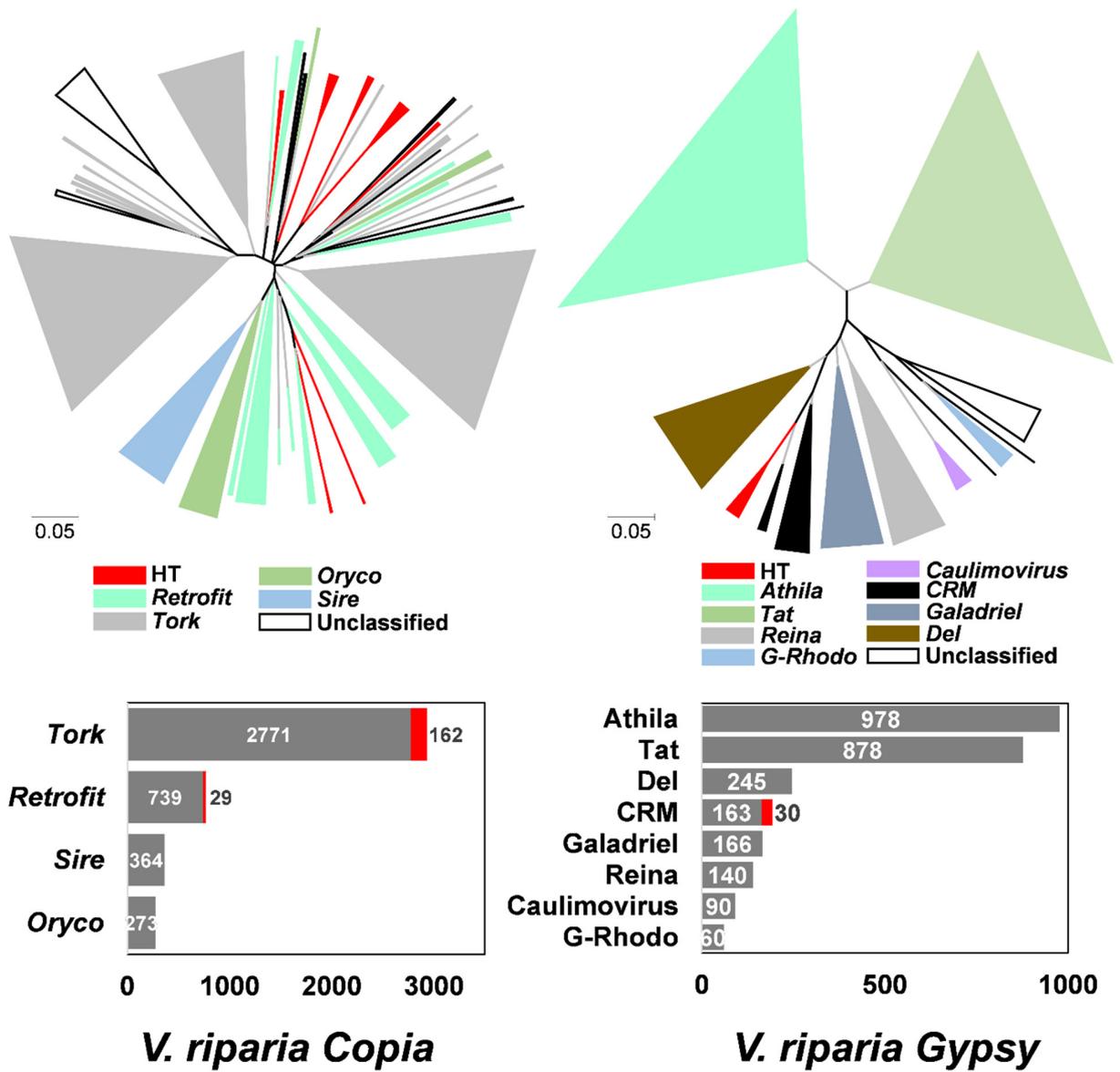
Supplementary Figure S5. Cont.

Supplementary Figure S5



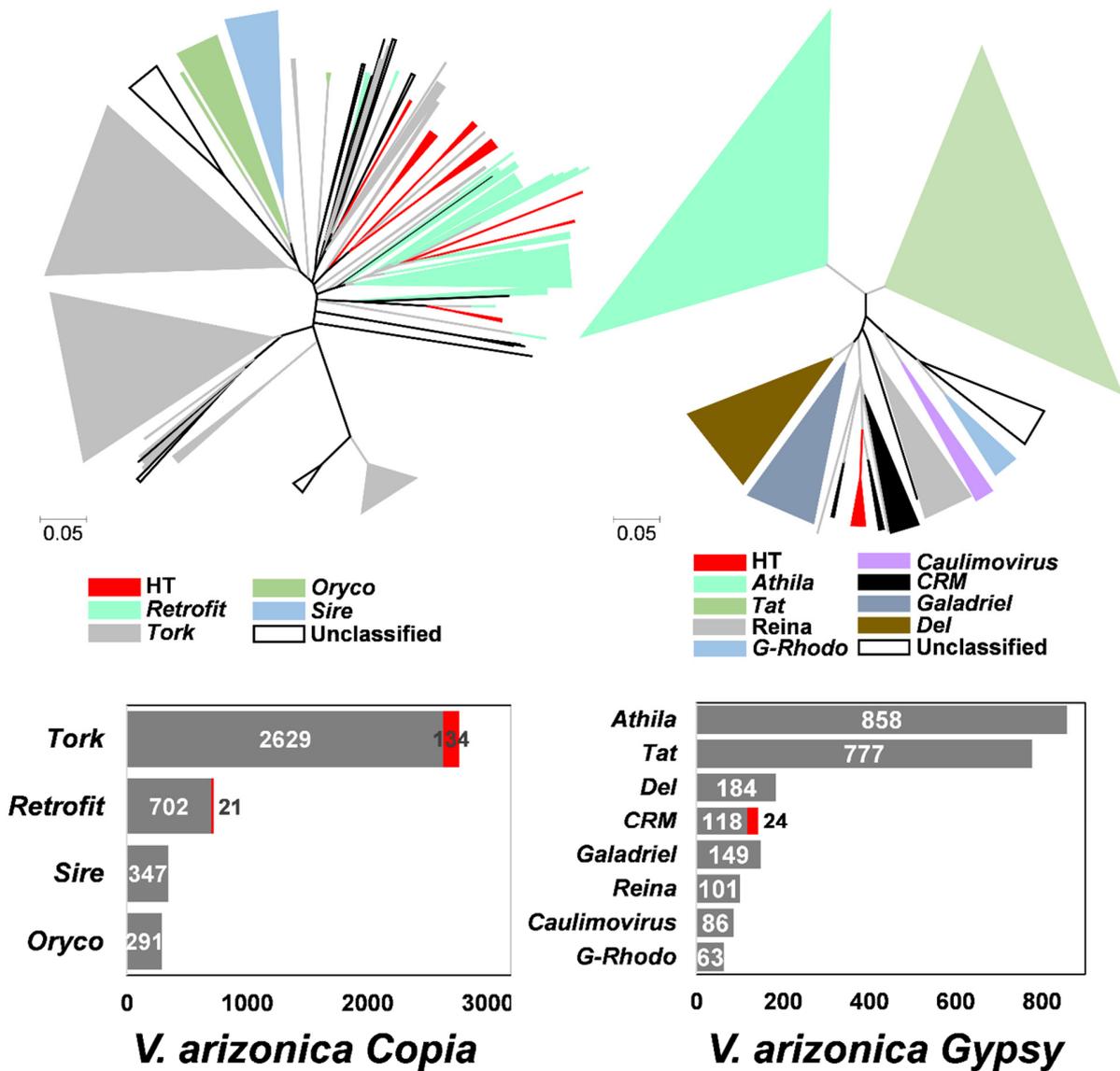
Supplementary Figure S5. Cont.

Supplementary Figure S5



Supplementary Figure S5. Cont.

Supplementary Figure S5



Supplementary Figure S5. Composition of the horizontally transferred LTR retrotransposons in the four *Vitis* genomes. The phylogenetic trees and composition of the horizontally transferred elements among native *Copia* and *Gypsy* elements in the four *Vitis* species are presented. In the phylogenetic trees, the clusters are represented with triangles and the classified families are presented with different colors. The unclassified clusters are presented with empty triangles. The clusters for the horizontally transferred LTR retrotransposons are marked with red triangles. The composition of the horizontally transferred LTR retrotransposons is shown in the lower panel. The size of LTR retrotransposons (excluding horizontally transferred elements) in each family and the part of horizontally transferred elements are shown with gray and red bar graphs, respectively, and the values are shown with the numbers. The species names and the names of the LTR retrotransposon families are presented on the left side of the panel.

Supplementary Figure S6

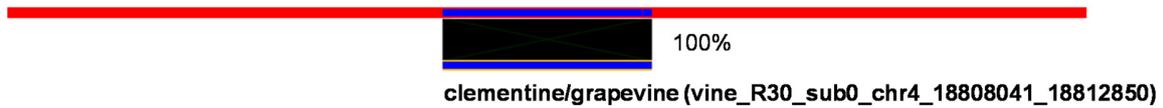
100 60(%) 2 Kb



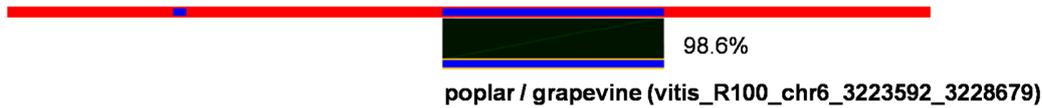
Cit_HT-1 (*V. riparia* NC_048431.1_13953598-13978658)



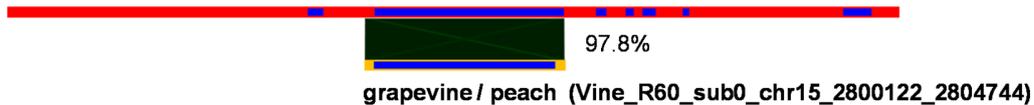
Cit_HT-2 (*V. riparia* NC_012010.3_18798039-18822853)



Pop_HT-2 (*V. riparia* NC_048446.1_19989491-20010718)

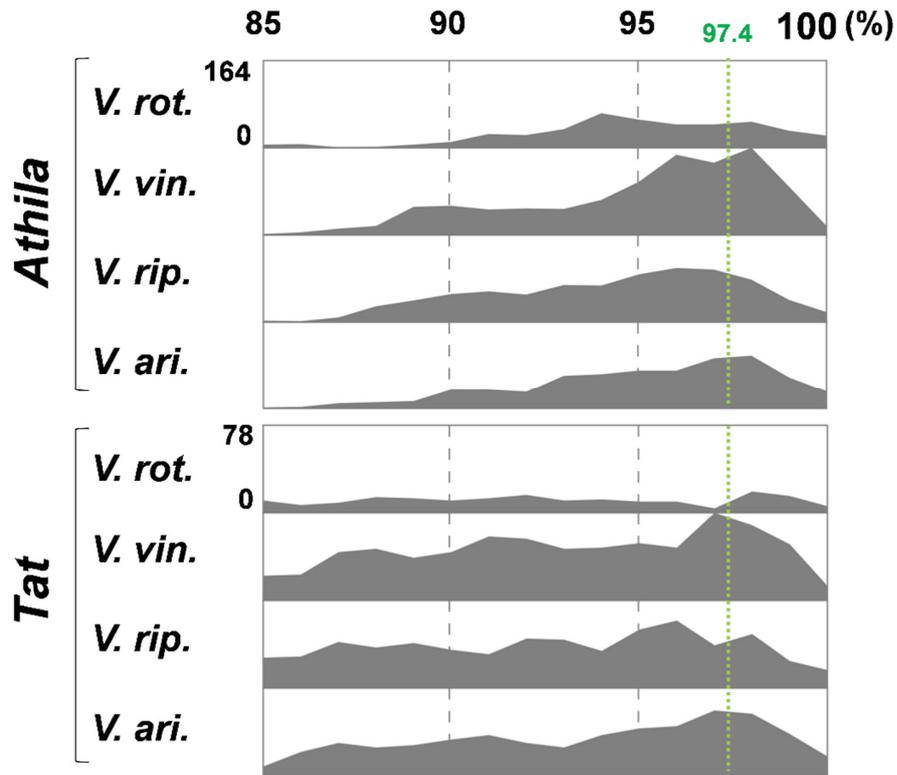


Pha_HT-1 (*V. riparia* NC_048449.1_22395363-22415865) (The same event with *Prunus avium*.)



Supplementary Figure S6. Comparative sequence analysis of the four HT events with the previously identified HT events. The *Vitis* sequence contigs containing the horizontally transferred LTR retrotransposons (red bars) are compared to the sequences of the horizontally transferred LTR retrotransposons (yellow bars) identified in the previous study by El Baidouri et al.. The blue bars indicate annotated TEs. The matched sequence regions are linked with green boxes, and the color intensity is proportional to the identity.

Supplementary Figure S7



Supplementary Figure S7. Activity history of the two major *Gypsy* families. The relative activity history of the two *Gypsy* families, *Athila* and *Tat*, is presented. The activity history for the two families is shown with gray graphs. The range of the X-axis is shown at the top of the panel. The estimated speciation point of *V. rotundifolia* is indicated with green dotted lines and its identity value is shown at the top of the line. The range of the Y-axis is shown on the left side of each panel and the range is the same as in the other three *Vitis* species. The abbreviations are the same as in Figure 5.