Figure S5. ITS2 variants representing molecular fossils in the genus *Armeniaca* (Rosaceae) **(A)** The variants are linked using red and blue lines at 100% and 95% identities, respectively. Each open box represents a single variant with RVA over 1%, and each solid box represents the variants with RVA less than 1%. The ruler shows the RVA in percentage. **(B,C)** The Neighbor-Joining (NJ) and Maximum Parsimony (MP) trees of ITS2 variants indicated that genetic information from the common ancestor was maintained in the genomes of two species derived from *Armeniaca* (Rosaceae). The same colors represent the same species. The same shade and color of symbols show the variants with 100% identity. The Latin names of species are followed by the rank and RVA of the variants. **(D)** The ITS2 variants in *A. vulgaris* were confirmed by direct sequencing of PCR products. The sequencing trace from *A. vulgaris* shows double peaks at some bases, and these double peaks correspond to the different ITS2 variants in *A. vulgaris*. The bases with double peaks are boxed in red. **(E-H)** The variants as molecular fossils of *A. sibirica* were confirmed by cloning of PCR products.

Figure S5A.

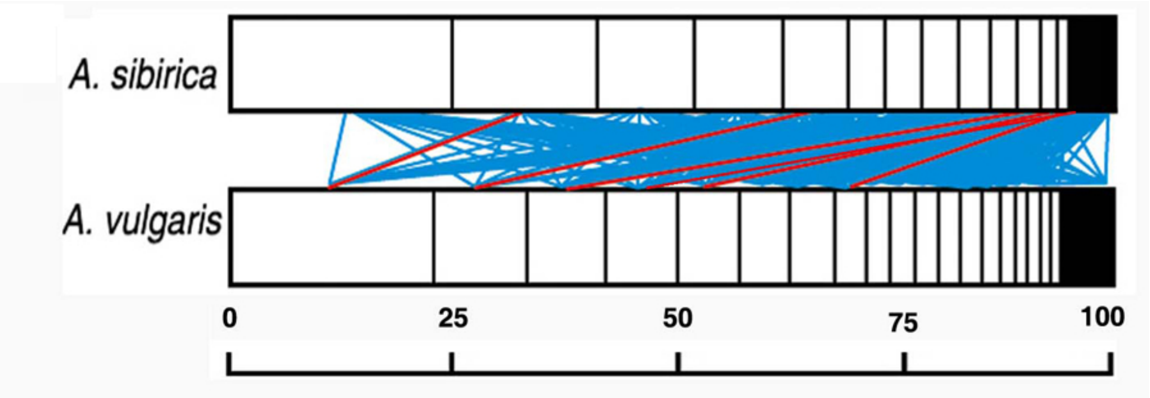

Figure S5B.

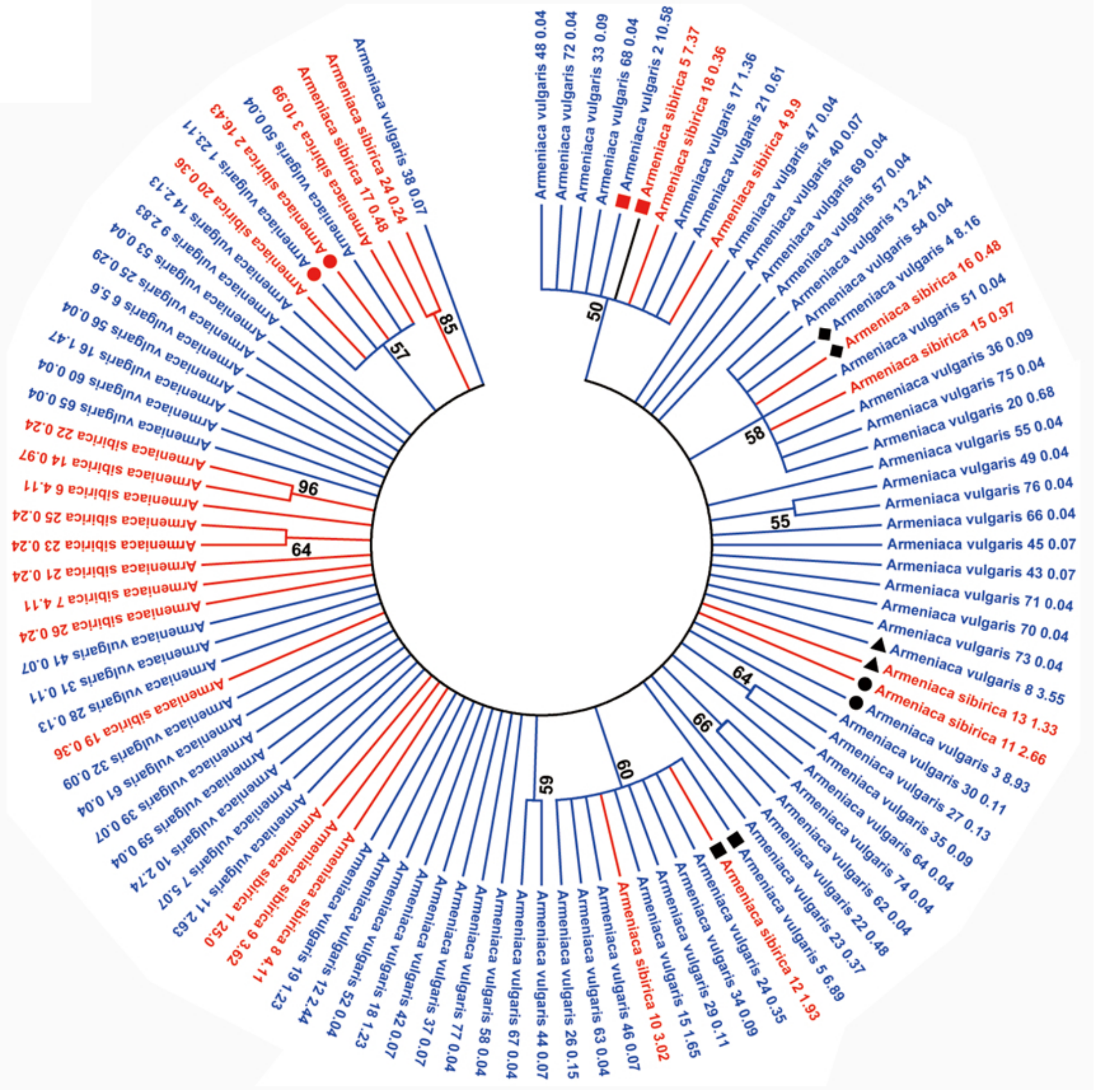

Figure S5C.

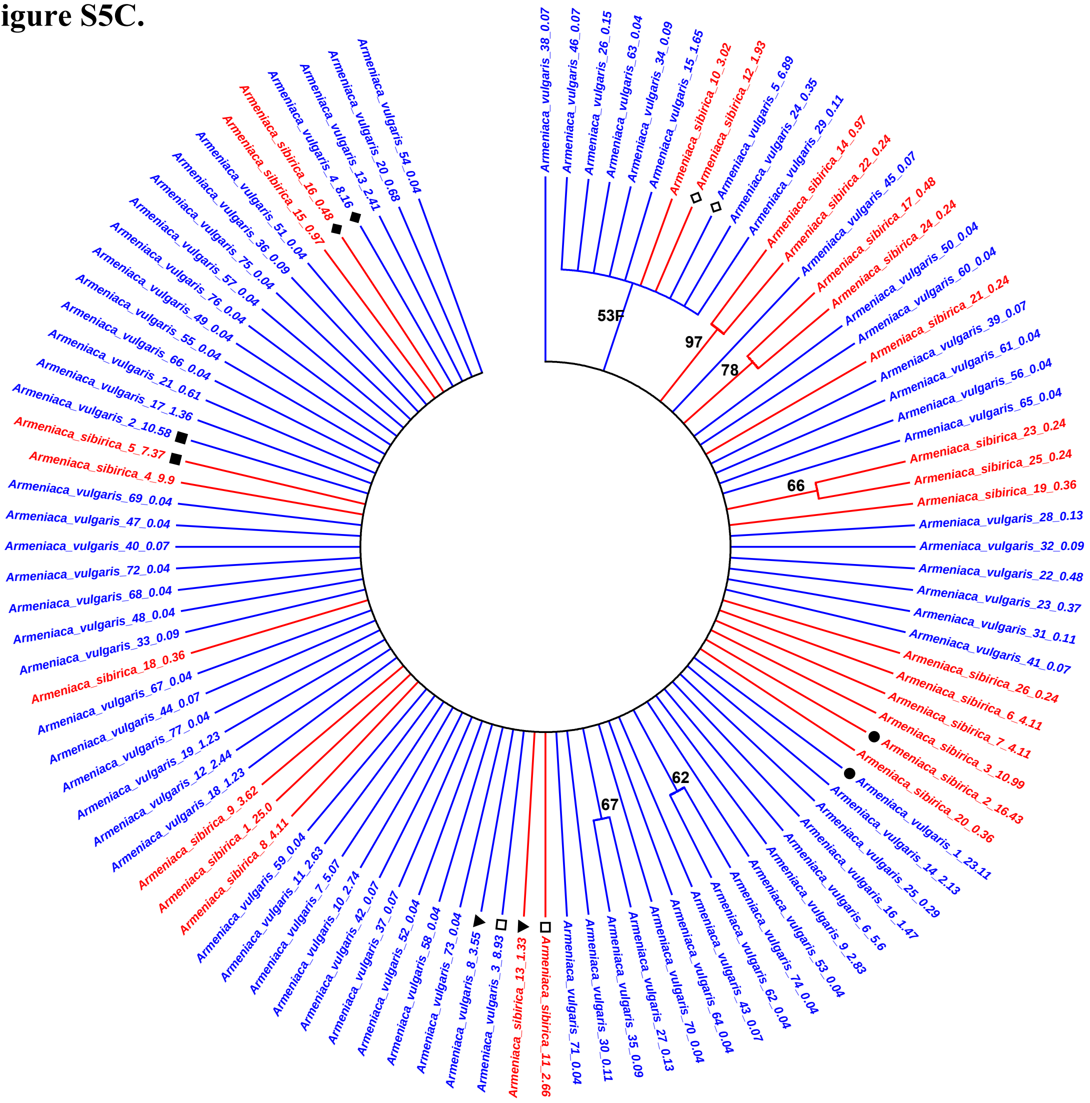
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Figure S5D.

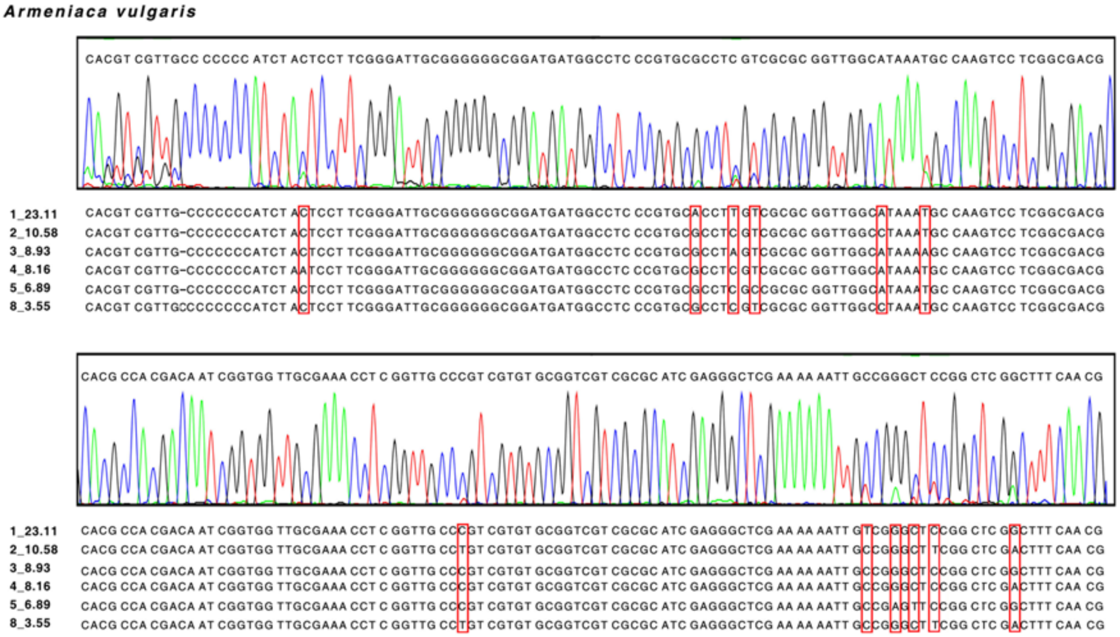


Figure S5E.

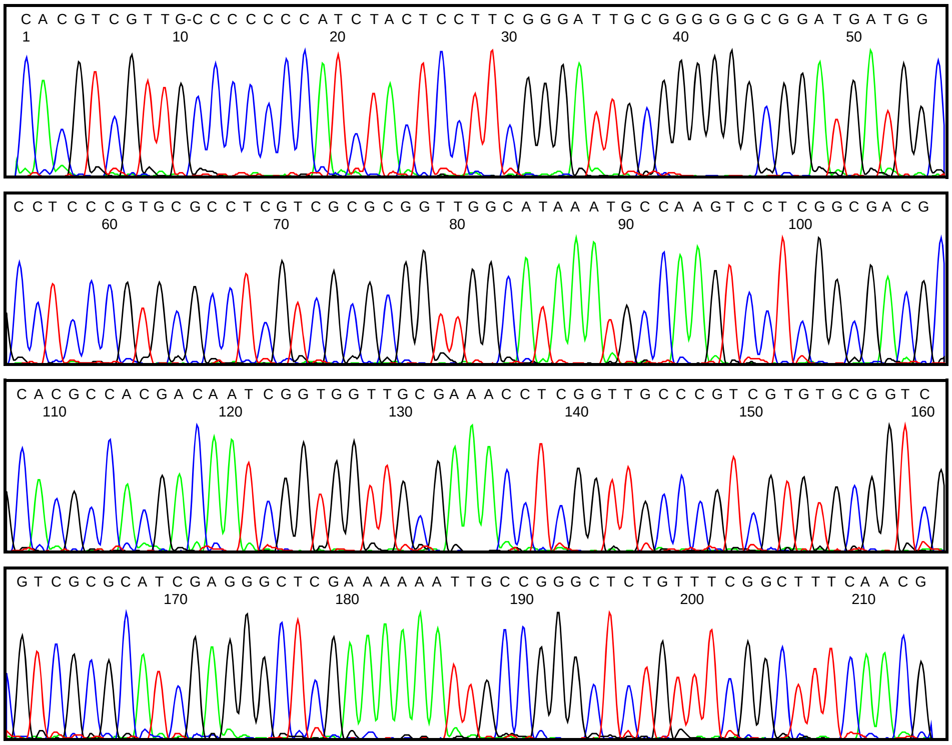


Figure S5F.

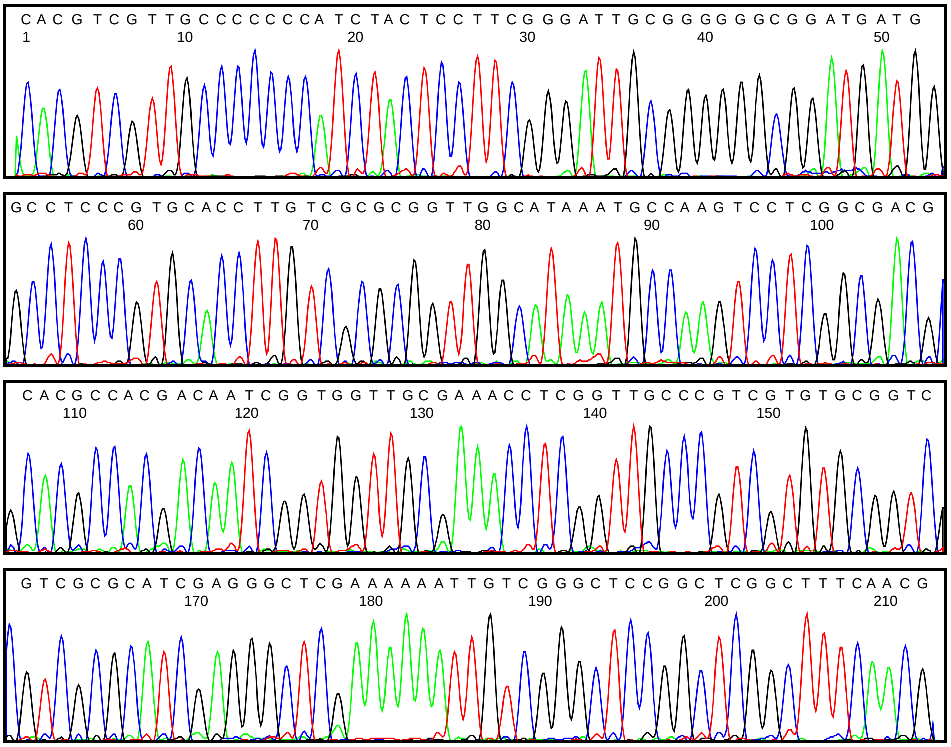


Figure S5G.

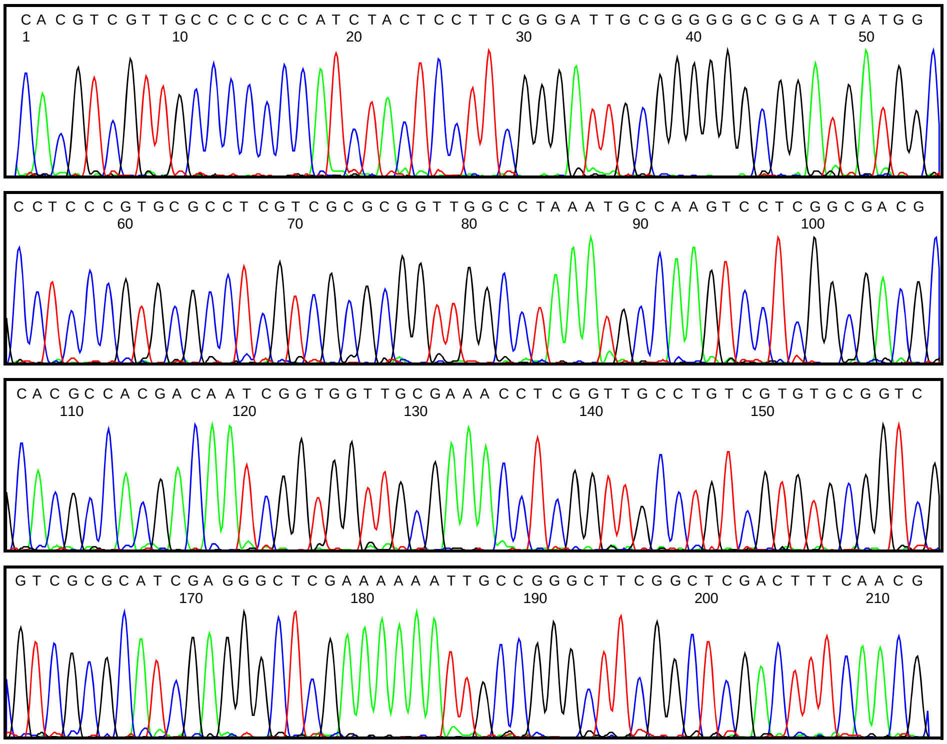
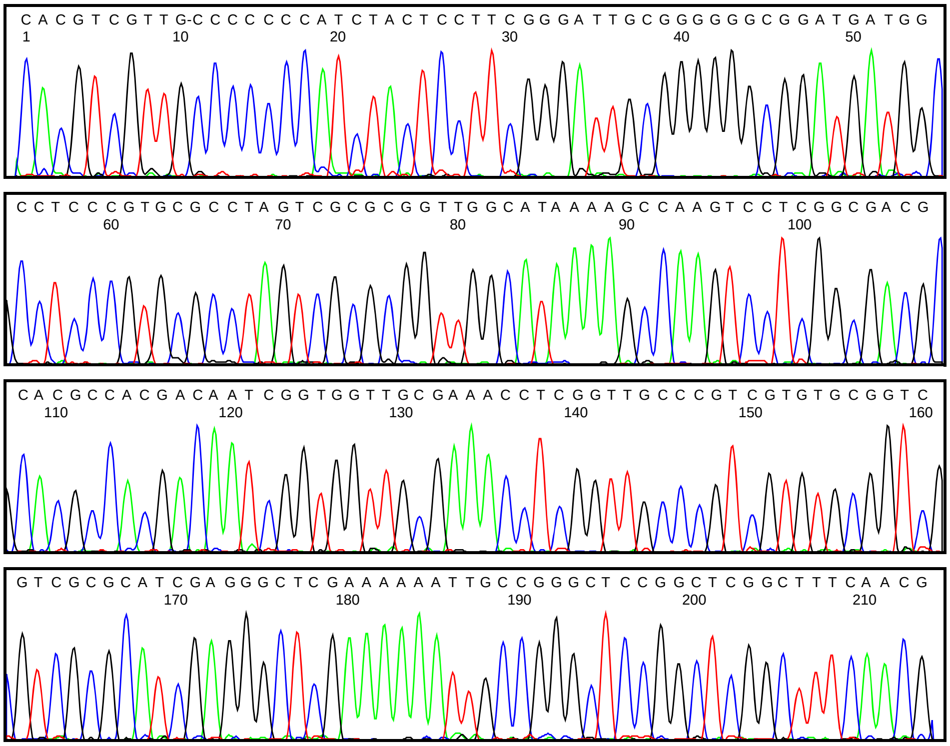


Figure S5H.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