



Appendix D. Nomenclature based on phylogenetic analysis of grapevine and Arabidopsis.

Via the ML (Maximum likelihood) method and JTT model, MEGA 7.0 was used to construct phylogenetic trees of grapevine (40) and Arabidopsis (38) with DEAD-box proteins. The number of bootstrap repeats was $n = 1000$. Branches corresponding to partitions reproduced in less than 70% of bootstrap replicates were collapsed.