

Descriptions of Additional Supplementary Files

Supplementary Data 1. List of ancient samples included in this study

Supplementary Data 2. Sequencing statistics of ancient samples included in this study

Supplementary Data 3. Occurrences for each type of mutations and relative positions from the reads ends for each ancient library

Supplementary Data 4. Read length distributions per strand

Supplementary Data 5. MCMC output of the five model parameters and log likelihood from MapDamage2 v2.0.9-2-gd251da0 for each ancient library

Supplementary Data 6. List of modern samples included in this study

Supplementary Data 7. Sequencing statistics of modern samples included in this study

Supplementary Data 8. Number of samples from each group for whole, population and subpopulation datasets

Supplementary Data 9. Number SNPs in the different datasets

Supplementary Data 10. Optimal number of substructure depending the input datasets according to the consensus-based algorithm from NbClust R package (v3.0.1)

Supplementary Data 11. Kmean clustering output for the definition of subpopulation groups

Supplementary Data 12. f3-outgroup statistic

Supplementary Data 13. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis with all modern accessions of the core dataset (N = 991)."

Supplementary Data 14. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis at the population level

Supplementary Data 15. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis all modern accessions of the core dataset at the subpopulation level (N = 559)

Supplementary Data 16. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis all modern grapevine accessions of the core dataset (N = 908).

Supplementary Data 17. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis at the population level without outgroup

Supplementary Data 18. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis all modern grapevine accessions of the core dataset at the sub-population level (N = 506).

Supplementary Data 19. PCA coefficients for the first 50 Principal Components with highest eigenvalue from SMARTPCA analysis at the population level using genomic positions from Ramos-Madrigal et al found in the core dataset (N = 4,363)

Supplementary Data 20. Ancestry coefficients from unsupervised ADMIXTURE analysis for the whole dataset

Supplementary Data 21. Ancestry coefficients from unsupervised ADMIXTURE analysis at the population level

Supplementary Data 22. Ancestry coefficients from unsupervised ADMIXTURE analysis at the subpopulation level

Supplementary Data 23. Ancestry coefficients from supervised ADMIXTURE at the population level

Supplementary Data 24. Ancestry coefficients from supervised ADMIXTURE at the subpopulation level

Supplementary Data 25. Two, three and four-way qpAdm models (pvalue > 0.01) explaining ancient sample ancestry as a mixture of modern populations

Supplementary Data 26. Proportion of *V. vinifera* pairs assigned to each relatedness levels depending to their true genetic relatedness and the normalisation value

Supplementary Data 27. Proportion of *V. sylvestris* identical pairs assigned to each relatedness levels depending to the normalisation value

Supplementary Data 28. Proportion of *V. vinifera* pairs assigned to each relatedness levels depending to their true genetic relatedness and the normalisation value using genomic positions from Ramos-Madrigal et al found in the core dataset (N = 4,363)

Supplementary Data 29. ReadV2 output for genetic relatedness analysis