

Supplementary Materials for

**Through 40.000 years of human presence
in Southern Europe: the Italian case study**

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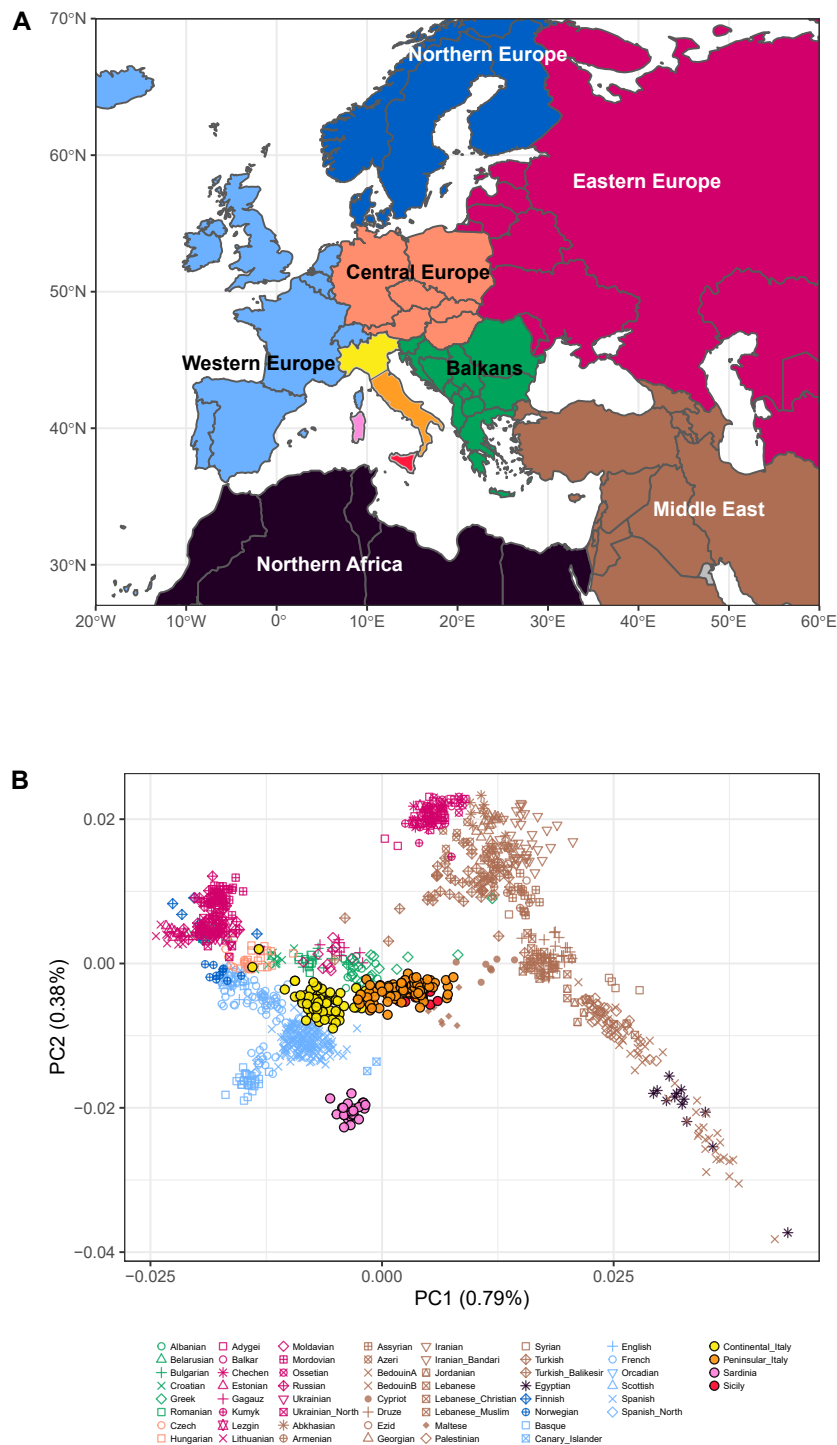
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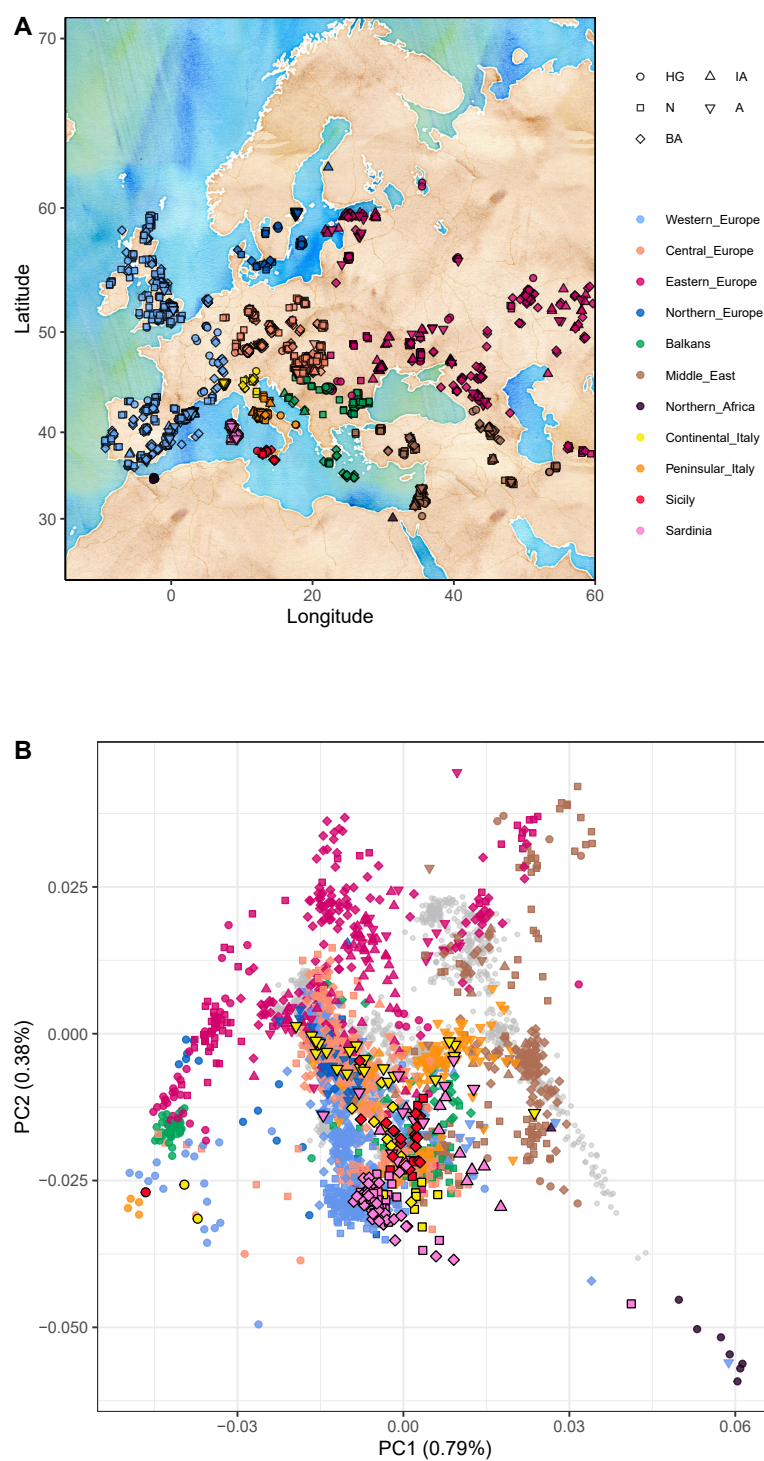
- Supplementary Figures 1 to 5.

Other Supplementary Materials for this manuscript include the following:

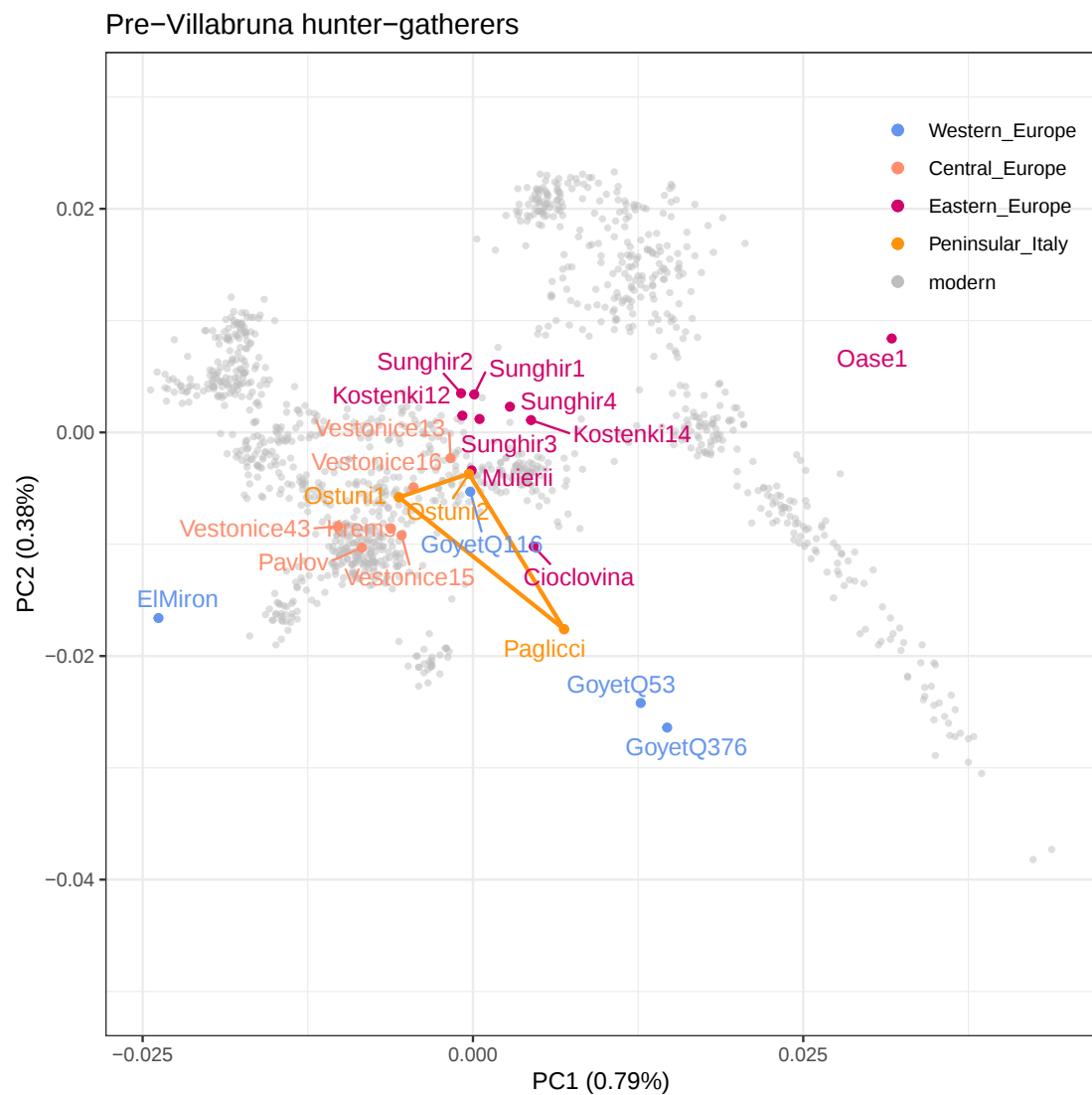
- **Supplementary Table 1.** List and available information for 2,146 ancient samples used in this work.
- **Supplementary Table 2.** List of modern samples used in the Principal Component Analysis.
- **Supplementary Table 3.** List of modern samples from the 1240K dataset and from Raveane et al. used for allele frequencies computation for twelve genetic variants under selection.
- **Supplementary Table 4.** f_3 outgroup results.



Supplementary Figure 1. Geographical location of modern samples and their genetic variability. A) Map of West Eurasia with the indication of the macro-areas subdivisions used in the review. B) PCA of modern samples with colors and shapes corresponding to the macro-areas and the population groups, respectively.

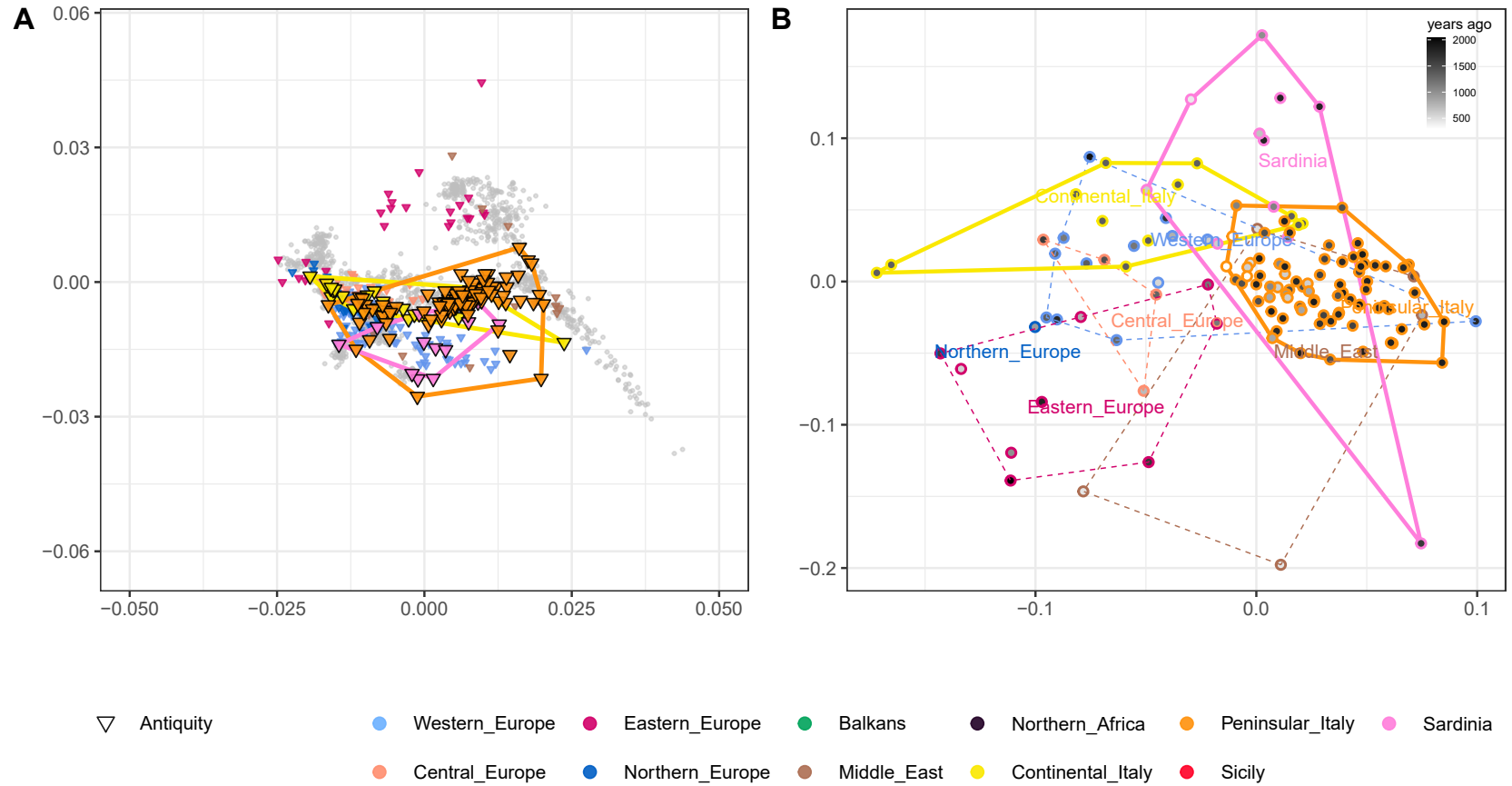


Supplementary Figure 2. Geographical location of ancient samples and their genetic variability. A) Map of West Eurasia and geographical location of ancient samples analysed in this review. B) PCA projecting the ancient samples onto the components inferred from moderns (in grey). Colors and shapes corresponding to the macro-areas and time layers, respectively. HG: hunter-gatherers; N: Neolithic; BA: Bronze Age; IA: Iron Age; A: Antiquity.

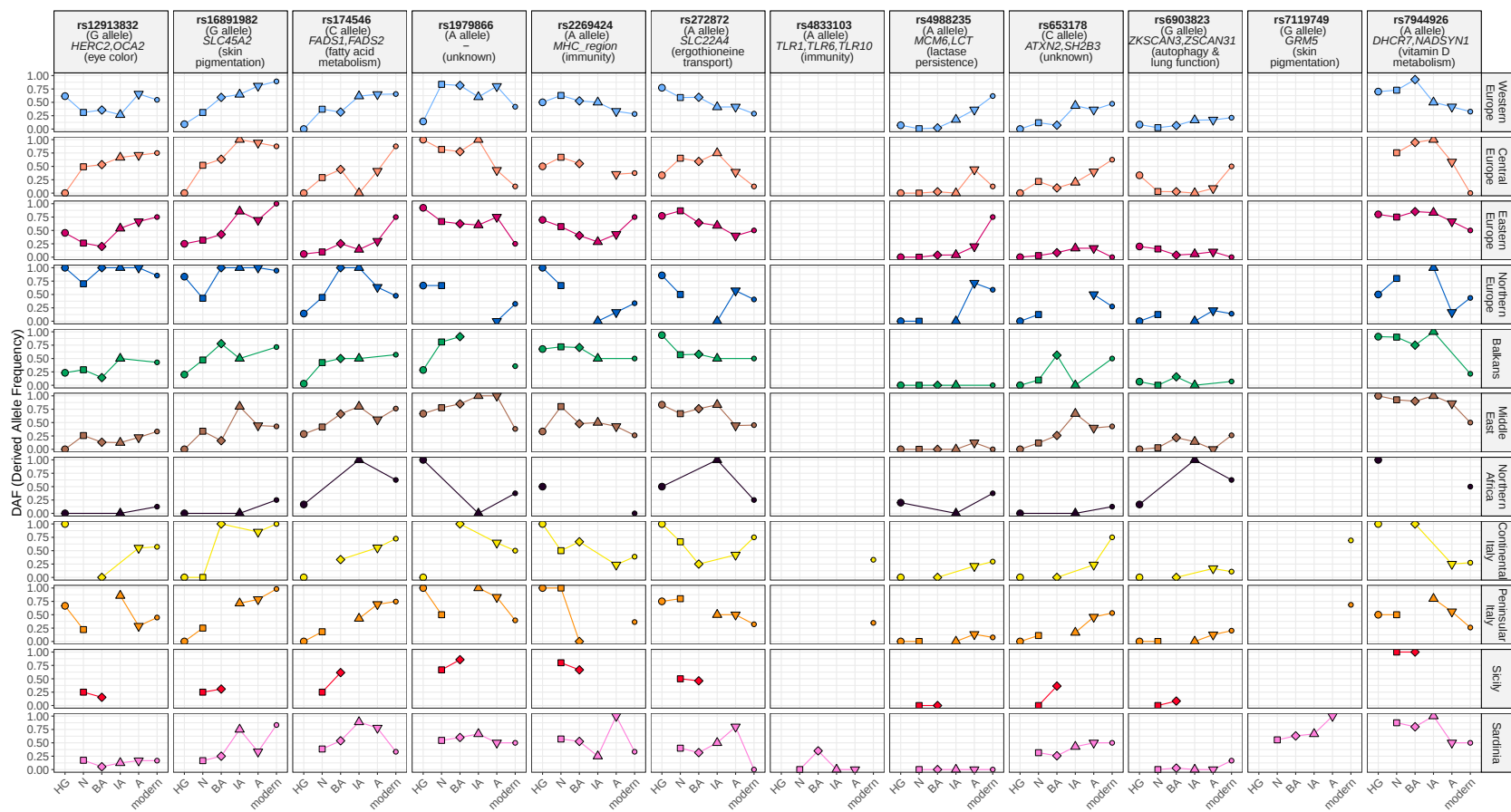


Supplementary Figure 3. PCA of Pre-Villabruna hunter-gatherers. PCA of pre-Villabruna hunter-gatherers projected onto the components inferred from moderns (in grey). Colors correspond to the geographical area where the ancient samples had been recovered.

Antiquity



Supplementary Figure 4. Genetic analysis of individuals dated to the Antiquity period. PCA (A) and outgroup-f3 MDS (B) for the “Antiquity” time layer. Colors correspond to the geographical macro-areas assigned to the samples.



Supplementary Figure 5. Derived allele frequencies of twelve variants, reported to be significant signals of selection in literature (see Materials and Methods), across all the macro areas and the time layers. Name of the variant (in bold), the allele for which the genetic frequencies are computed (the derived one), the gene where it falls, and the associated function are shown above each plot.