Supplementary Tables

Table S1: summary table reporting sample coordinates, normalized bioclimatic variables, elevation, Shannon Index (computed on land use data), and sample coordinates on the first three axes of PCA for dimensionality reduction on the bioclimatic variables.

Table S2: list of candidate SNPs implied in local adaptation. The position in the genome (Sscrofa11.1) is reported together with the result of annotation. The two SNPs in common among all methods are shown in bold. The SNPs showing a north−south pattern of variation in allele frequencies are highlighted in yellow and the ones showing a west−east pattern in red.

Table S3: Candidate genes are reported if a known transcript according to the UCSC Sscrofa11.1 dataset was found within a 100,000 kb window around the candidate SNP. One candidate SNP (CASI0009814) on chromosome 4 was lost during the conversion of SNP coordinates from Sscrofa10.2 to Sscrofa11.1 so this was manually annotated with resources from Sscrofa10.2 genome assembly.

Table S4: Gene Ontology (GO) enrichment analysis of the list of candidate genes from g:Profiler.

Supplementary Figures

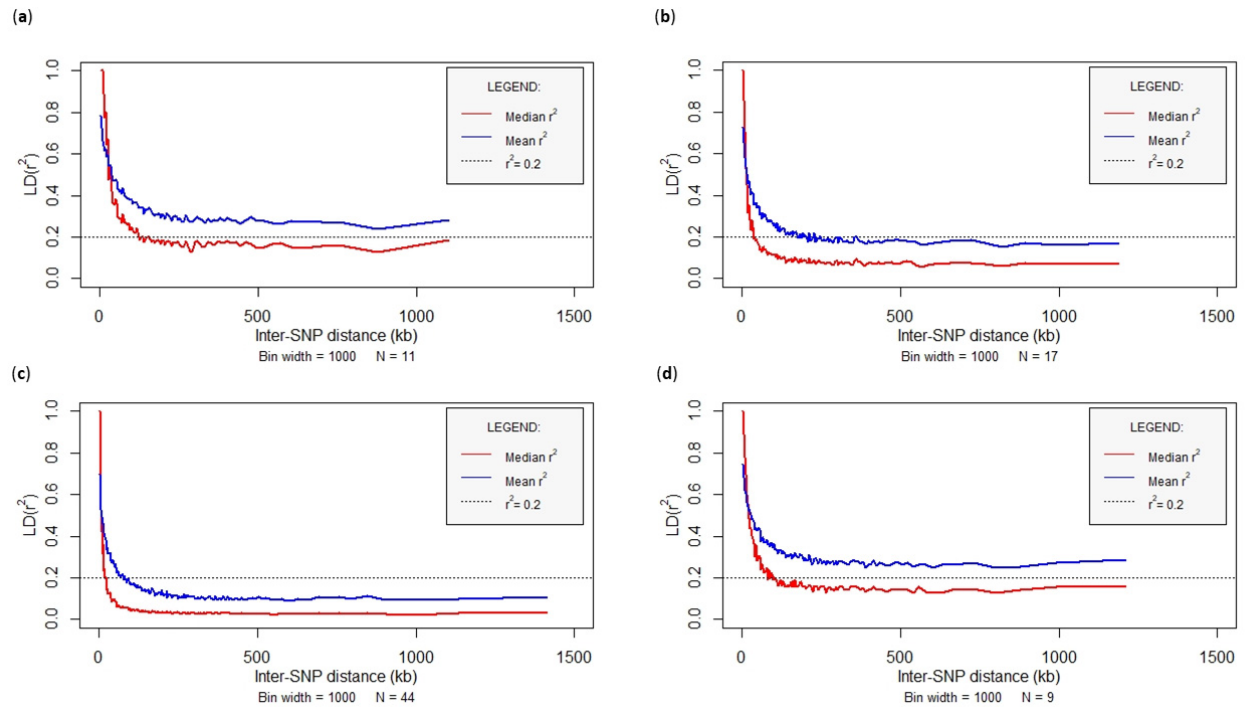

Figure S1: LD decay plot computed with PLINK on 81 Sardinian wild boar and 46634 SNPs. All pairwise comparisons within 50 Mb windows are shown. Wild boars were divided into the 4 clusters identified with snmf: (**a**) CSE or central and south-eastern population, (**b**) SW or south-western population, (**c**) NE or north-eastern population, (**d**) NW or north-western population. Plots were drawn with the functions included in Zecca et al. [1].

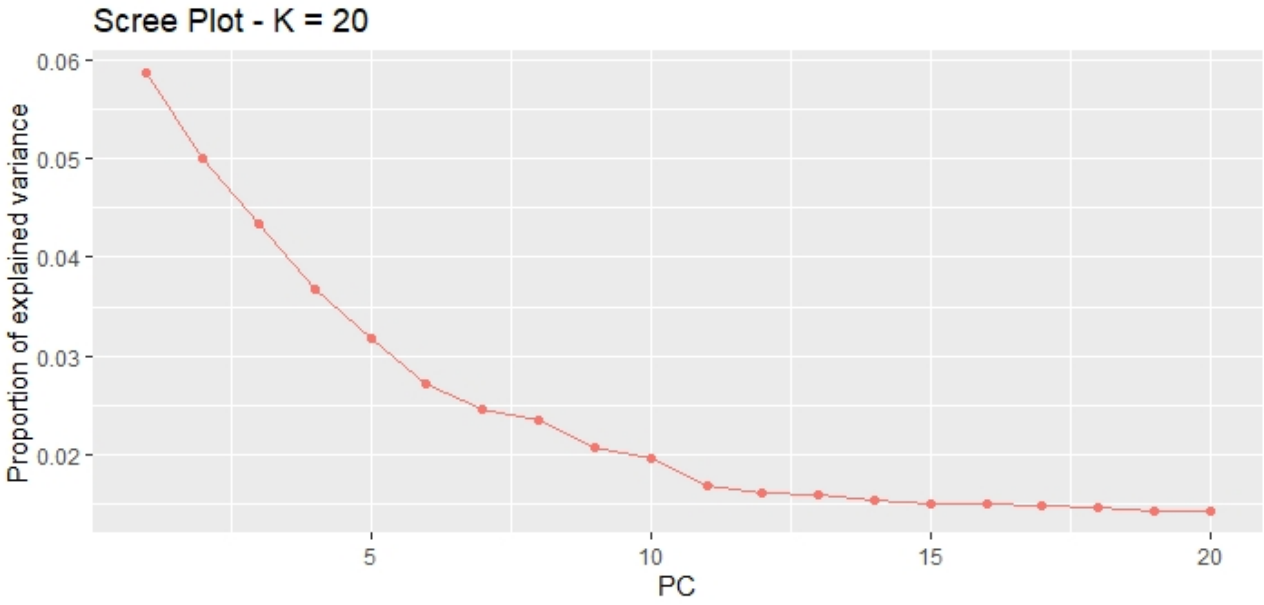

Figure S2: Proportion of variance explained by the first 20 PCs for 83 Sardinian wild boar. 13,290 autosomal SNPs were included in the analysis.

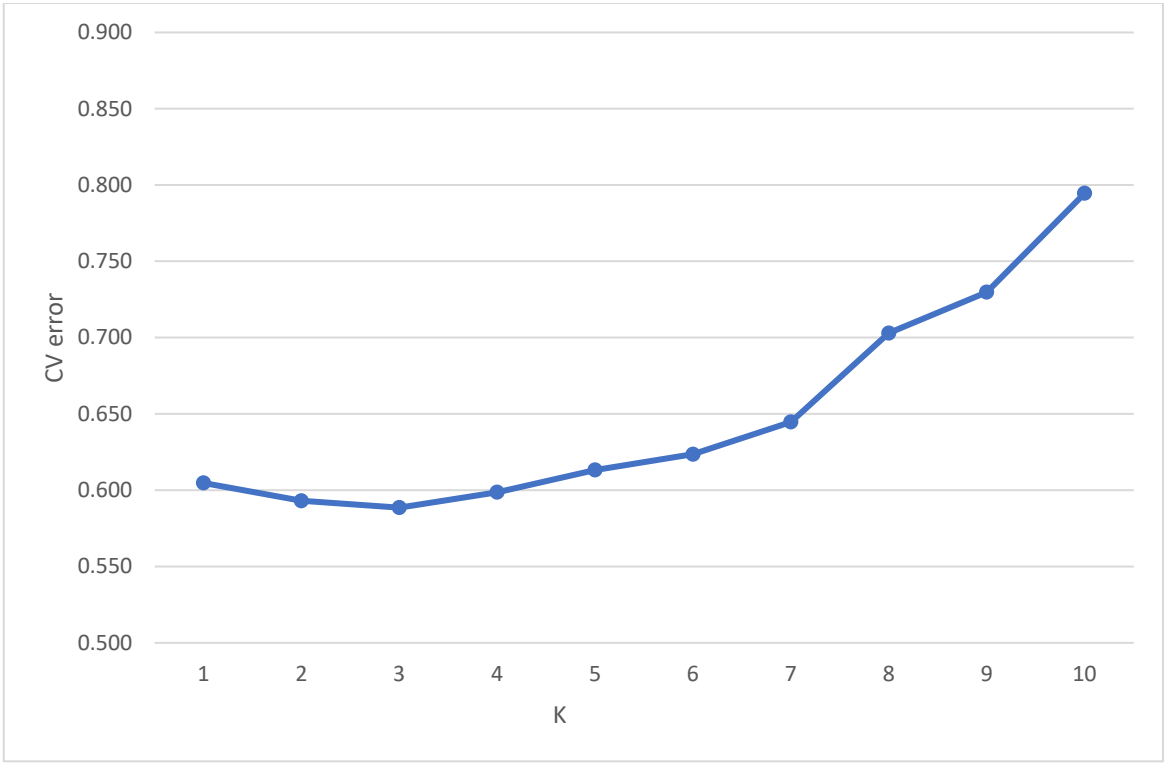

Figure S3: Cross-validation error from ADMIXTURE for 83 Sardinian wild boar. 13,290 autosomal SNPs were included in the analysis.

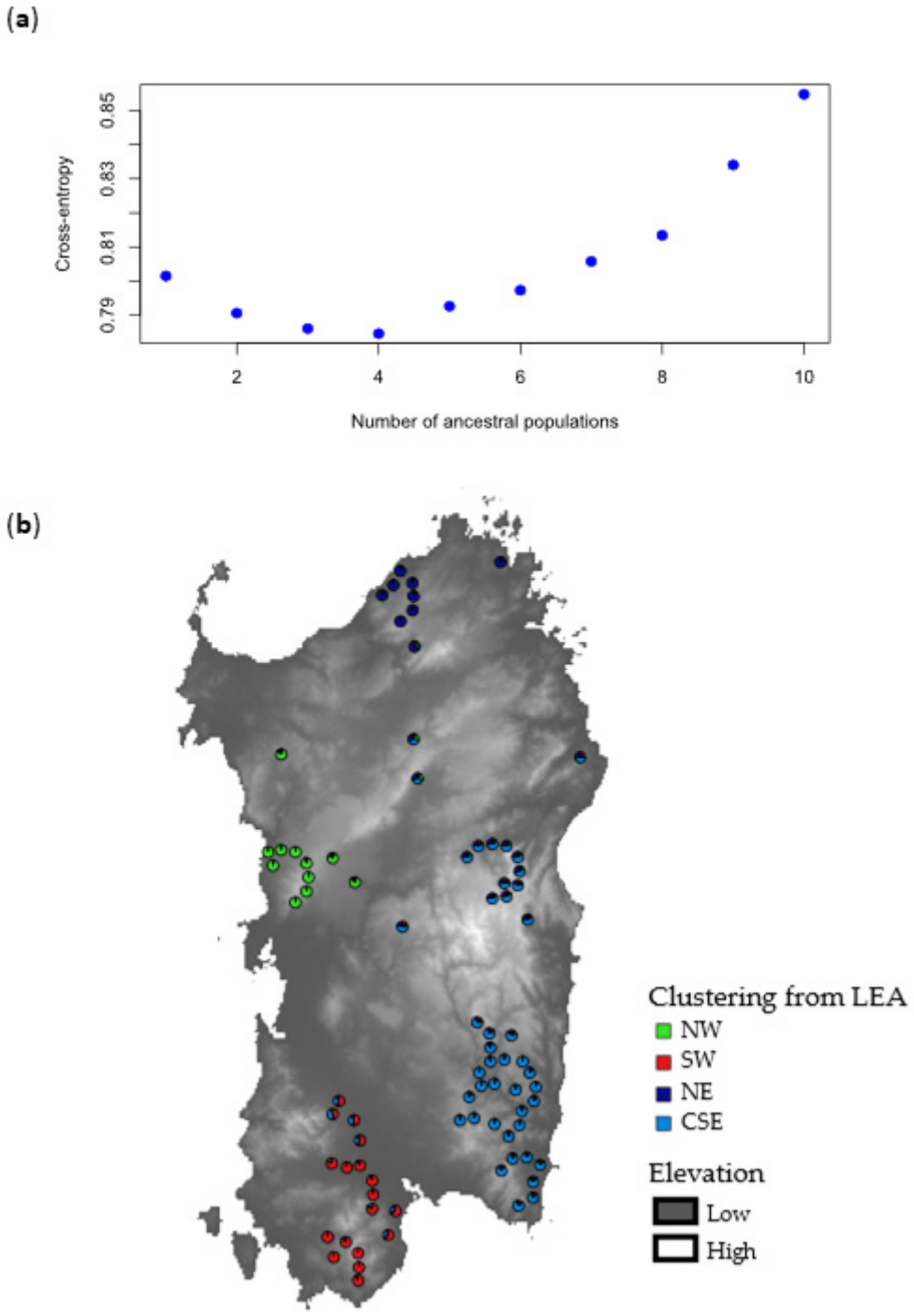

Figure S4: Genetic structure identified with the analysis snmf from the R package LEA. (**a**) Cross-entropy plot obtained for K = 1–10. (**b**) Map displaying the genetic structure at K = 4 in the best run out of 10 replicates. Blue = north-east (NE), light blue = central and south-east (CSE), green = north-west (NW), red = south-west (SW).

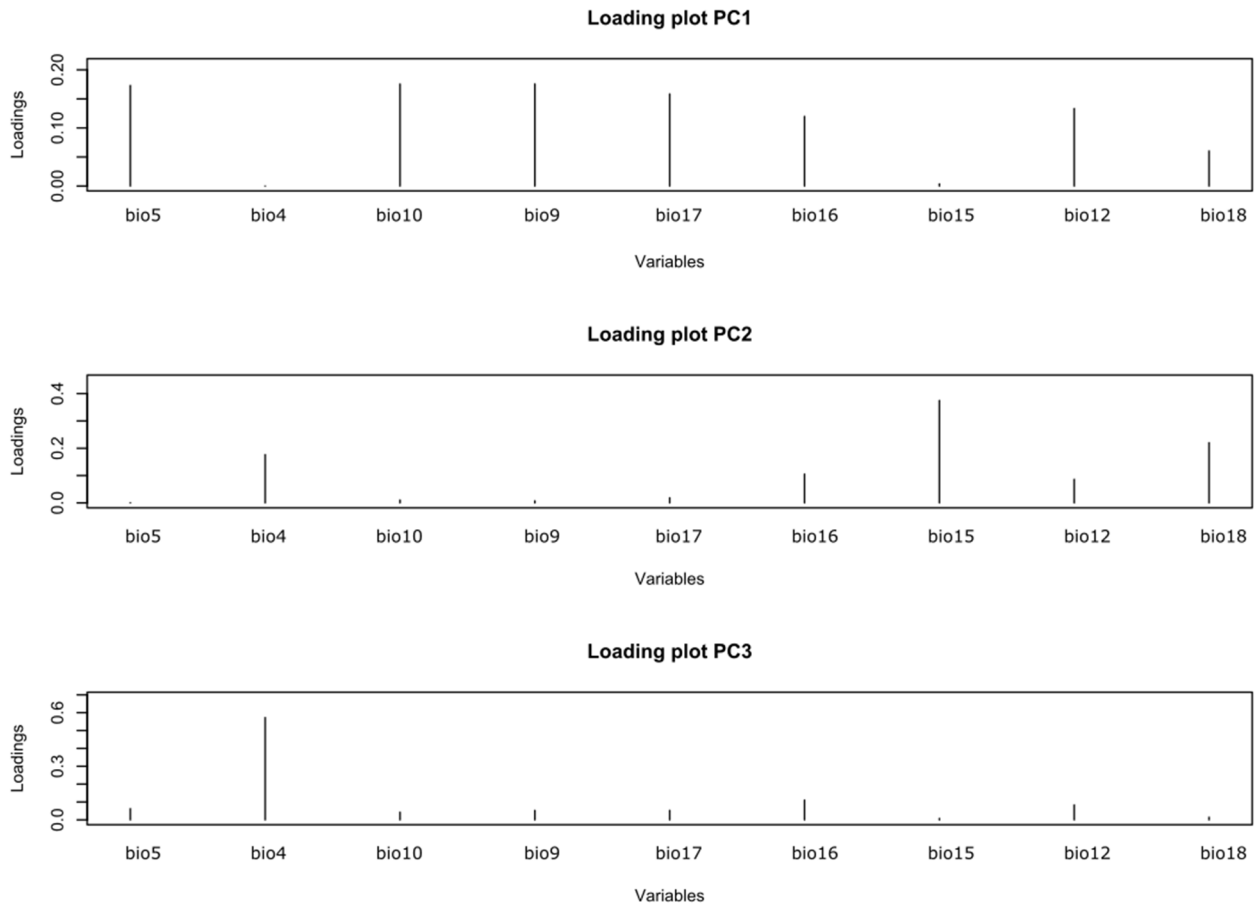

Figure S5: Loading plots of the first 3 PCs resulting from the principal component analysis (PCA) in "adegenet", summarizing the variation in the environmental conditions considered in this study. See Tab. 1 for a detailed description of the environmental variables.

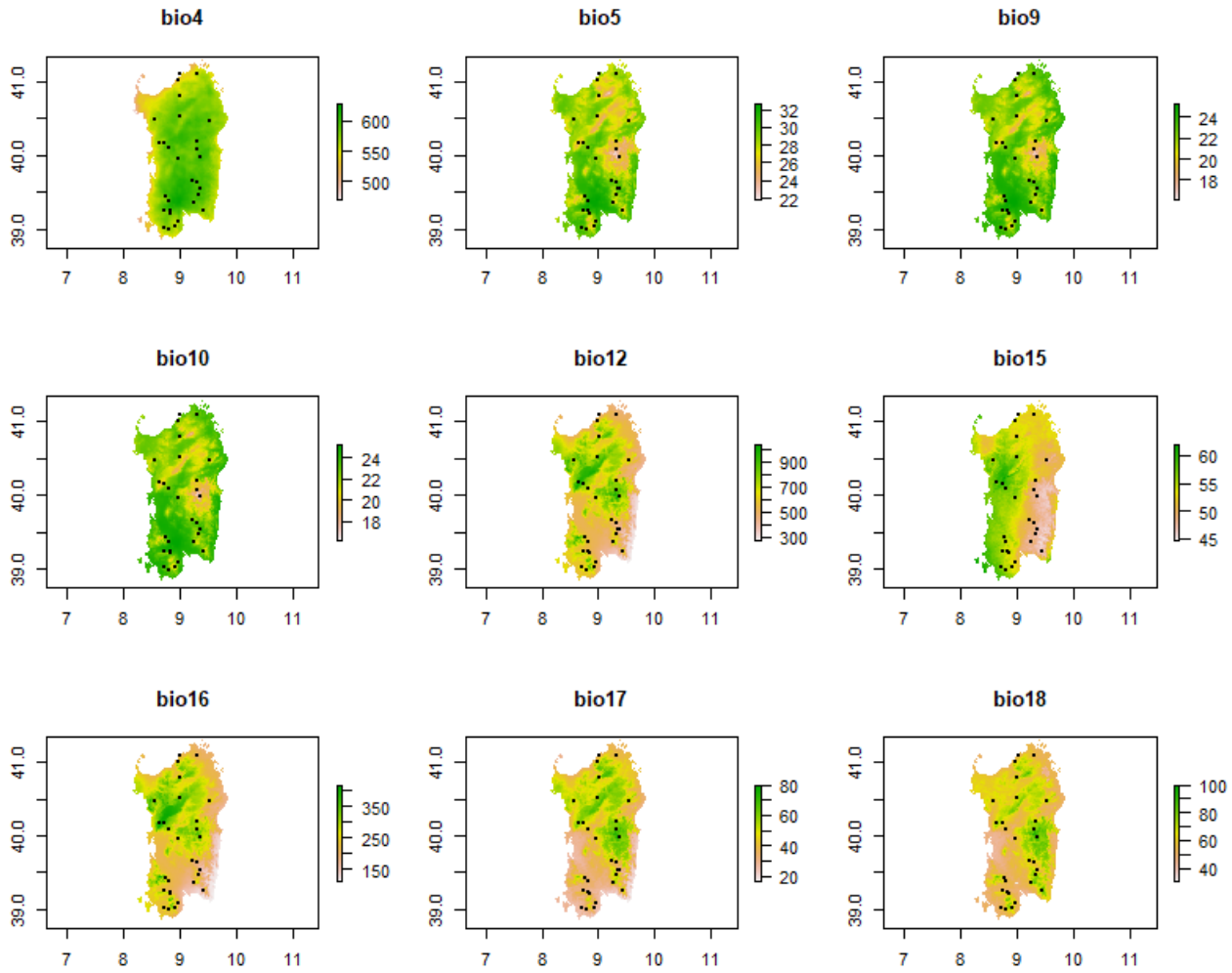

Figure S6: Bioclimatic variables from Worldclim2 considered in this study.

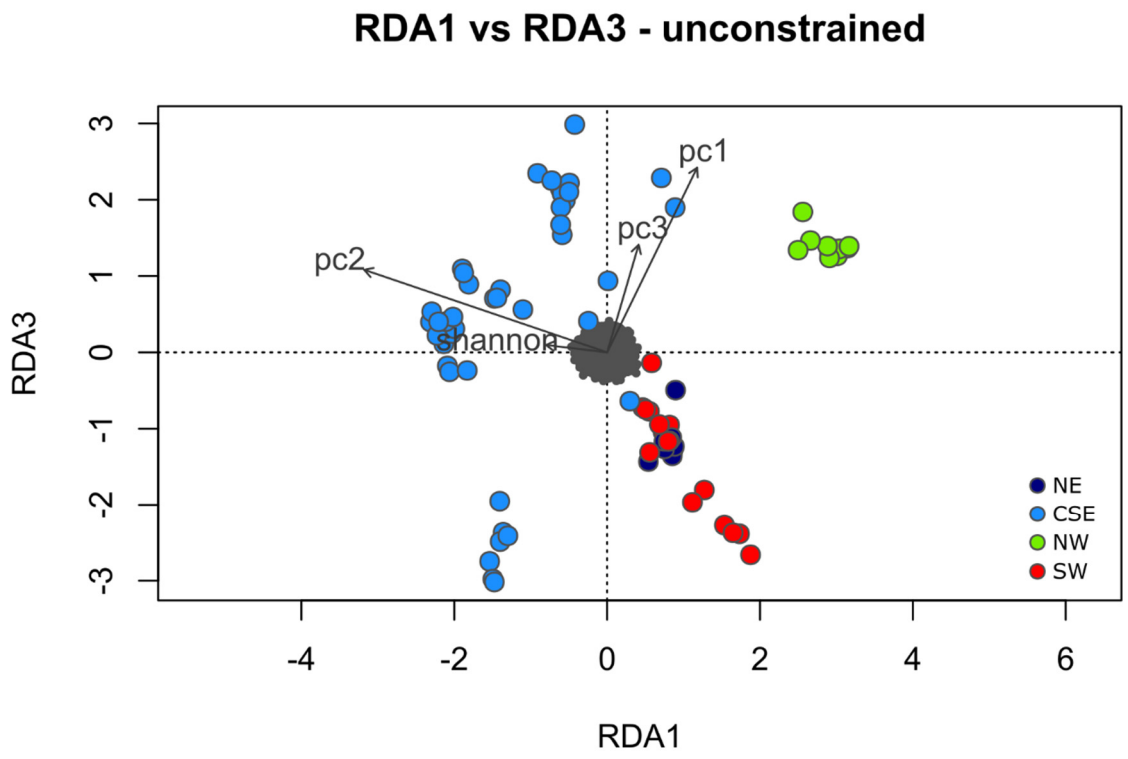

Figure S7: Triplot showing the first (RDA1) versus third (RDA3) axes from the simple RDA. Colour code: blue = north-east (NE), light blue = central and south-east (CSE), green = north-west (NW), red = south-west (SW).

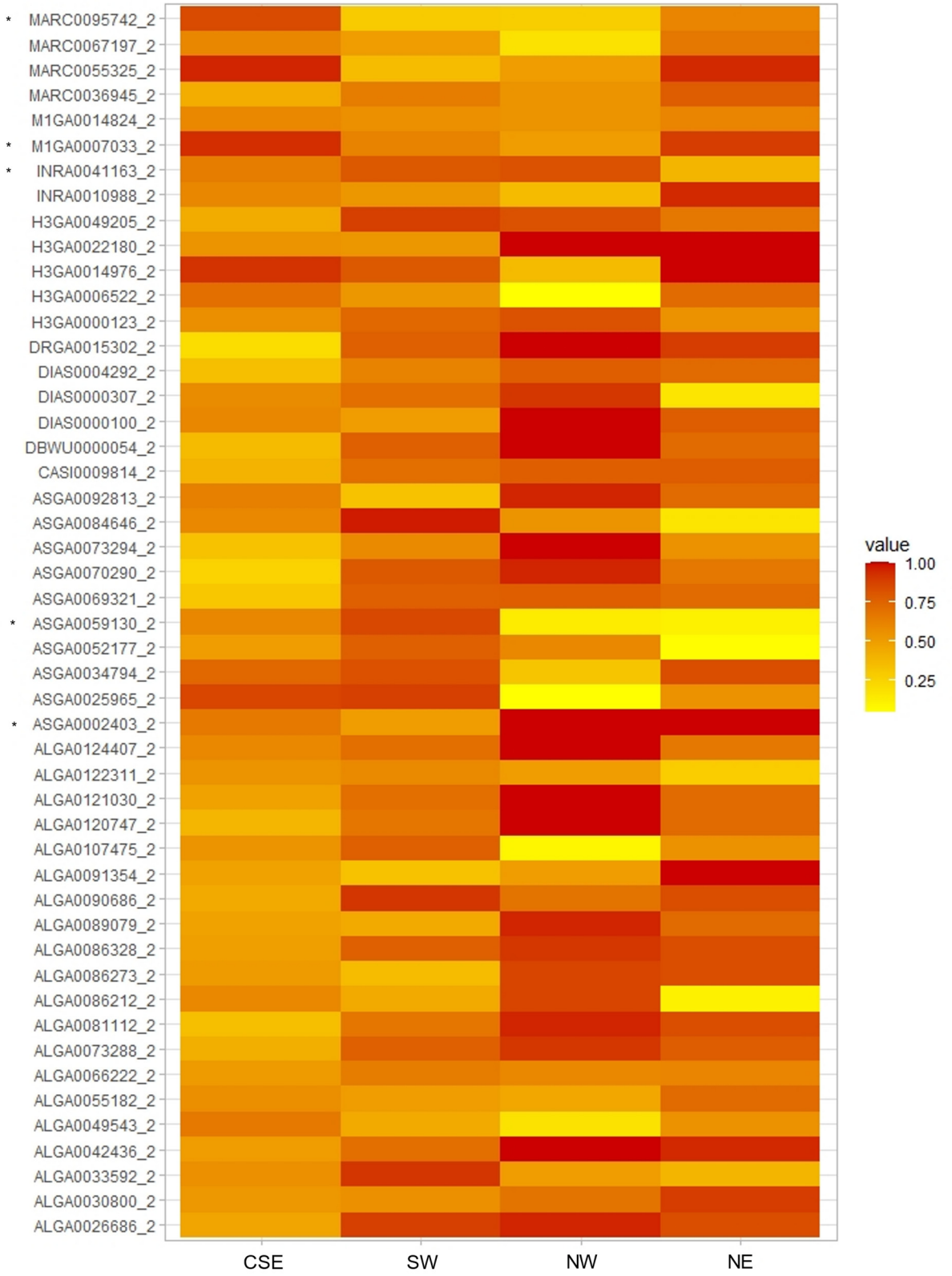

Figure S8: Heatmap of the allele frequencies by cluster for the 49 candidate loci. The SNPs with a north-to-south or west-to-east pattern are marked by an asterisk.

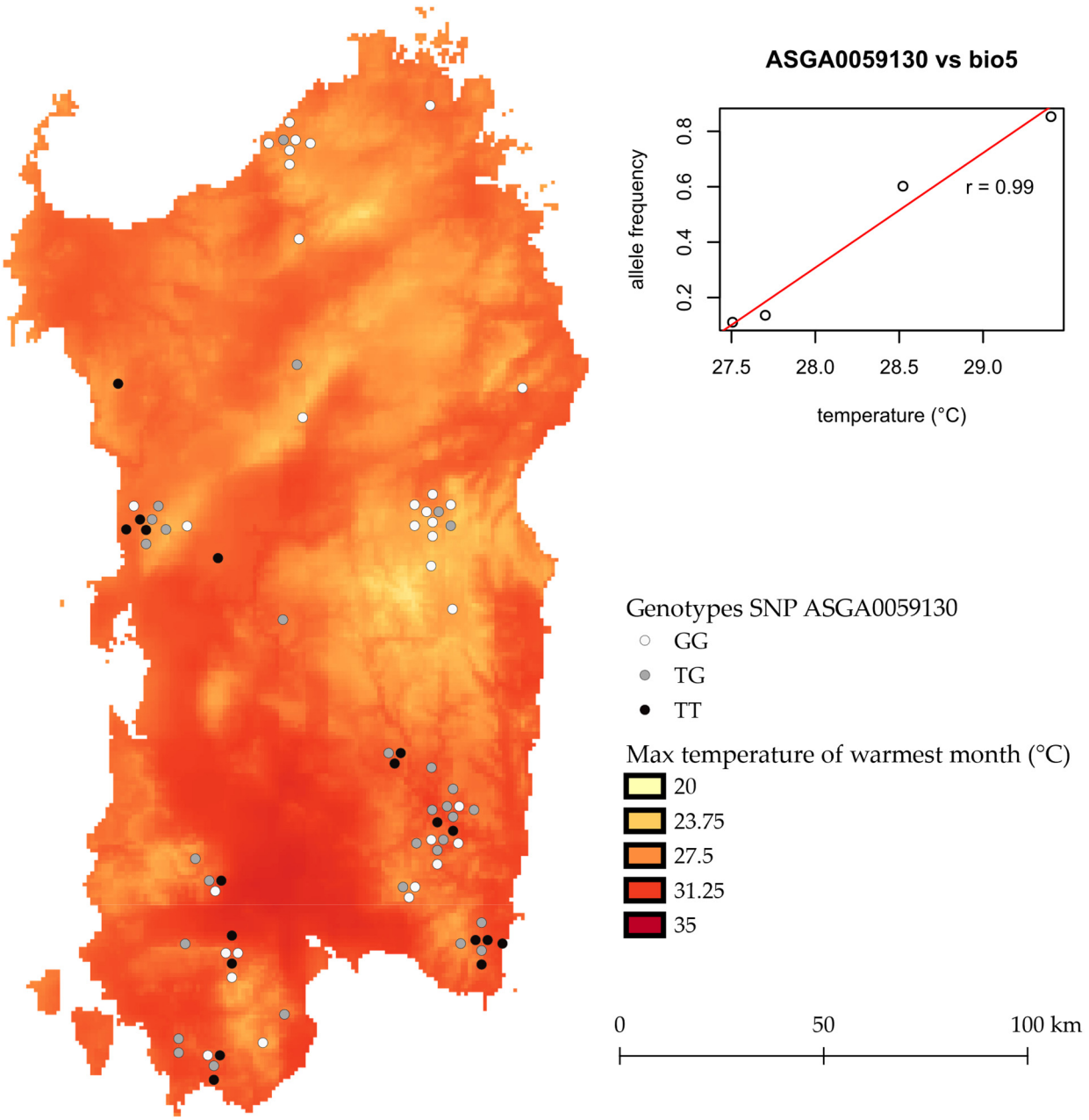

Figure S9: Spatial distribution of the two alleles at SNP ASGA0059130 over bio5 (maximum temperature of the warmest month) and correlation plot. Trend line is shown in red in the scatterplot and Pearson's correlation coefficient is reported.

References

1. Zecca, G.; Labra, M.; Grassi, F. Untangling the Evolution of American Wild Grapes: Admixed Species and How to Find Them. *Front. Plant Sci.* **2020**, *10*, 1–17, doi:10.3389/fpls.2019.01814.