

Fig. S1: Diagram showing the flow of analyses for this manuscript.

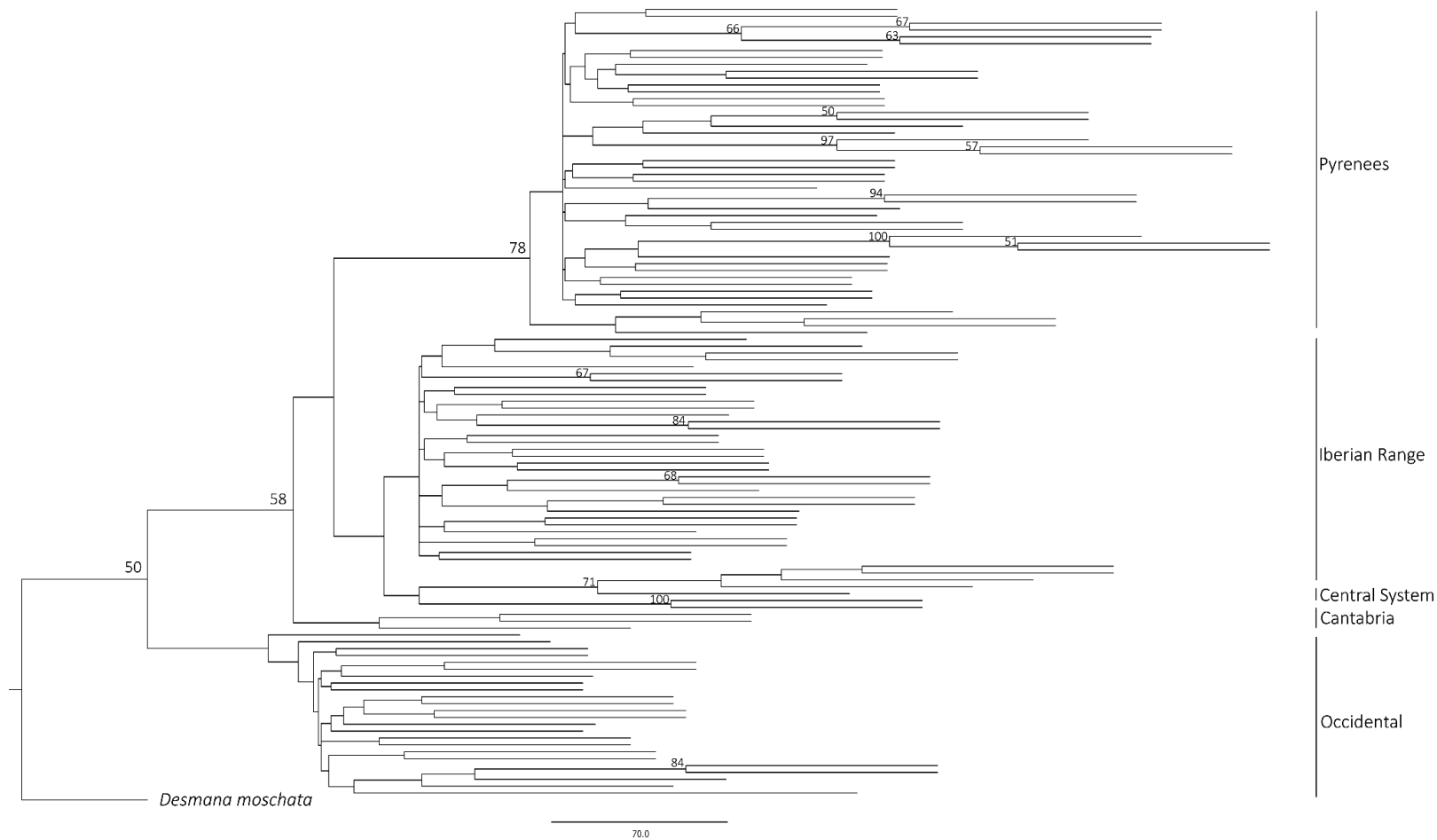


Fig. S2: Neighbour-joining tree based on the 115 samples and 110 SNPs using PHYLIP with 100 bootstraps and the Russian desman (*Desmana moschata*) as outgroup. Bootstrap values from 100 replicates are displayed for nodes with support $\geq 50\%$. The five phylogeographic units are highlighted.

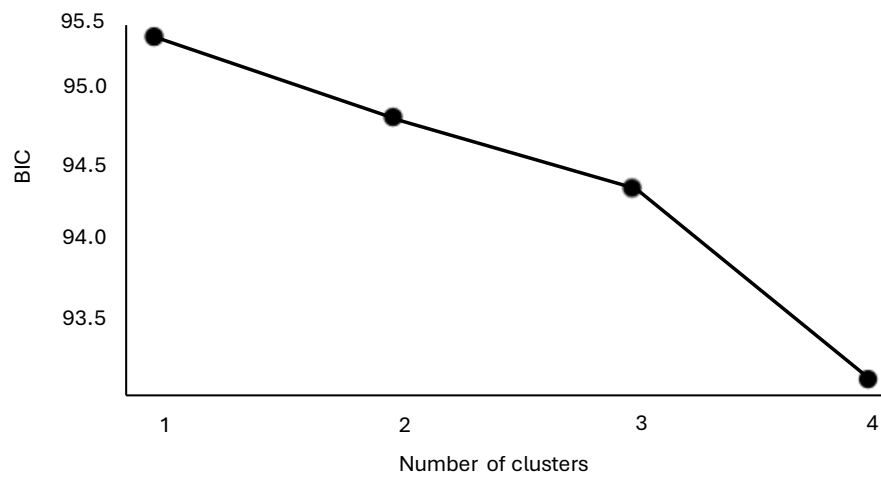


Fig. S3: Bayesian Information Criterion (BIC) values for each number of clusters for the Discriminant Analysis of Principal Components analysis taking 6 principal components into account for the samples from the Occidental population, based on 7,604 SNPs.

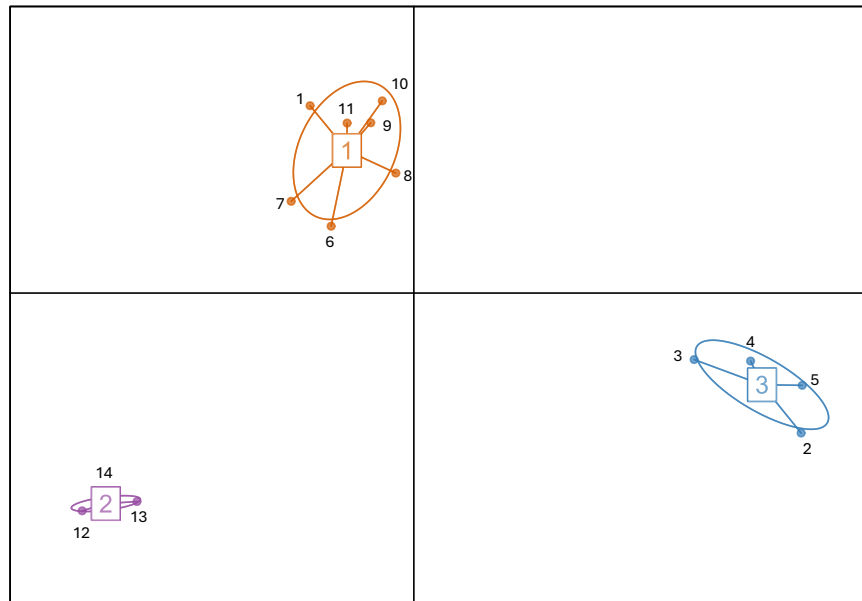


Fig. S4: Discriminant Analysis of Principal Components for the Occidental phylogeographic unit, with 6 principal components and based on 7,604 SNPs, showing 3 clusters.

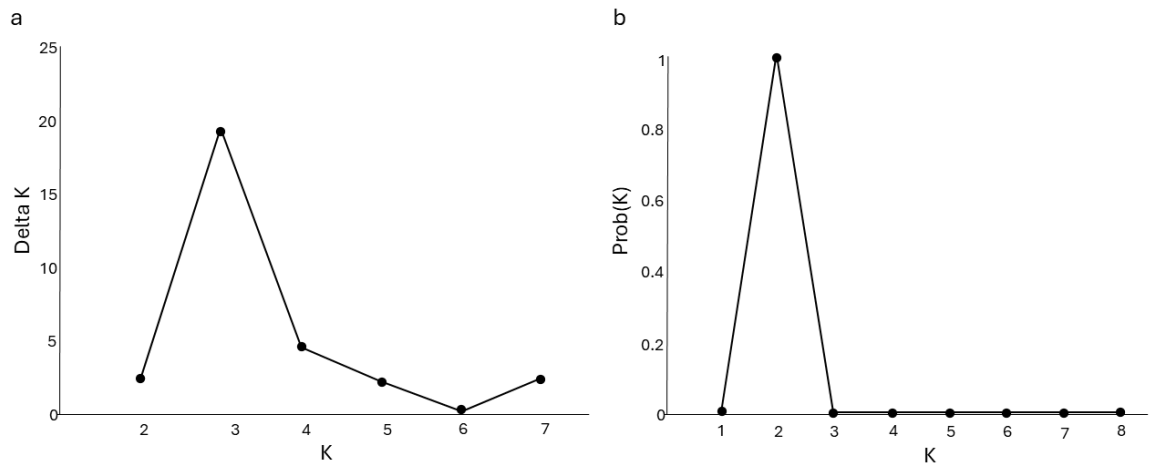


Fig. S5: STRUCTURE analyses for the Occidental phylogeographic unit, based on 7,604 SNPs: **a.** the rate of change in the likelihood of the data as K increases (Delta K) by Evanno et al. [1]; **b.** the probability or likelihood of the data for each K (Prob(K)) based on the Bayesian clustering algorithm by Pritchard et al. [2].

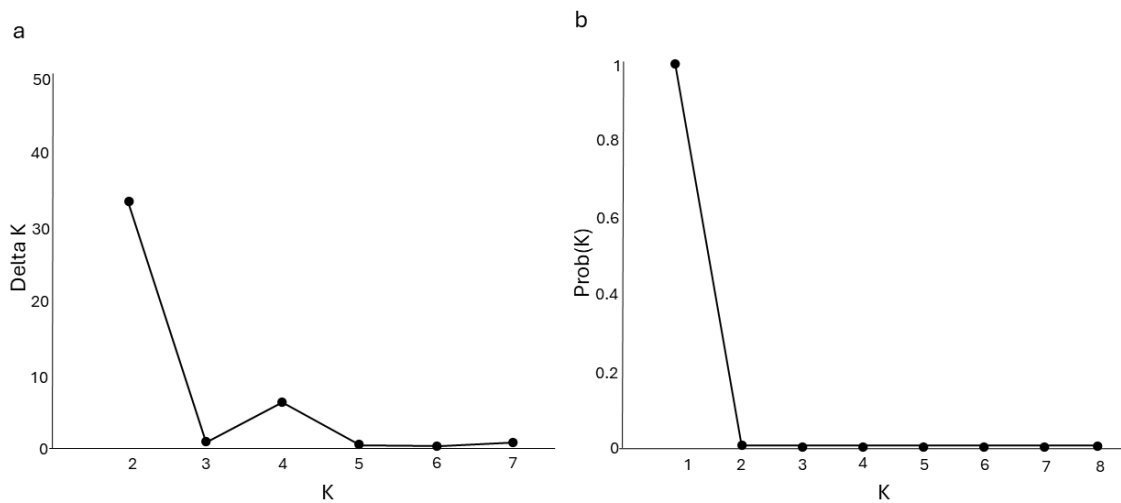


Fig. S6: STRUCTURE analyses for the Douro river system, based on 8,771 SNPs: **a.** the rate of change in the likelihood of the data as K increases (Delta K) by Evanno et al. [1]; **b.** the probability or likelihood of the data for each K (Prob(K)) based on the Bayesian clustering algorithm by Pritchard et al. [2].

References

1. Evanno G, Regnaut S, Goudet J. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol Ecol*. 2005;14:2611-20.
2. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. *Genetics*. 2000;155:945–59.