

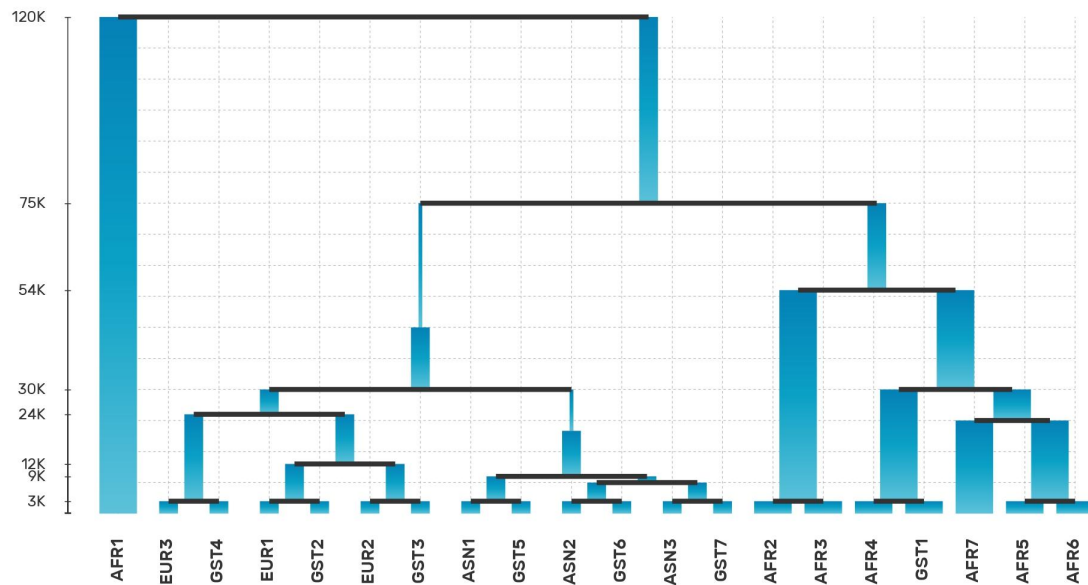


Fig. S1: Overview of the simulated scenario. We used a simulated genotype dataset composed by 13 simulated demes with different population sizes and split times ranging from 250 to 4,000 generations, to represent a simplified scenario for current European-like (EUR 1-3), East Asian-like (ASN 1-3) and African-like (AFR 1-7) groups and 7 sister groups characterized by a split time from their closest population of 100 generations (Molinaro et al., 2021)



Fig. S2: Effect of drift on PANE estimations, results showing the difference between the observed and expected major ancestry assignment by PANE (y-axis) across 10 admixture generations (x-axis), ranging from 50 to 500. For each admixture generation, the dots represent each simulated sample (50 per each group) and the boxplot shows the group distribution. The group average error increases with the number of admixture generations elapsed since the admixture event, indicating that substantial drift does have an impact on the ancestry assignment accuracy. Notably, in this scenario PANE carried a maximum 0.15 error in individual-based analyses, and a 0.12 error in the population average.

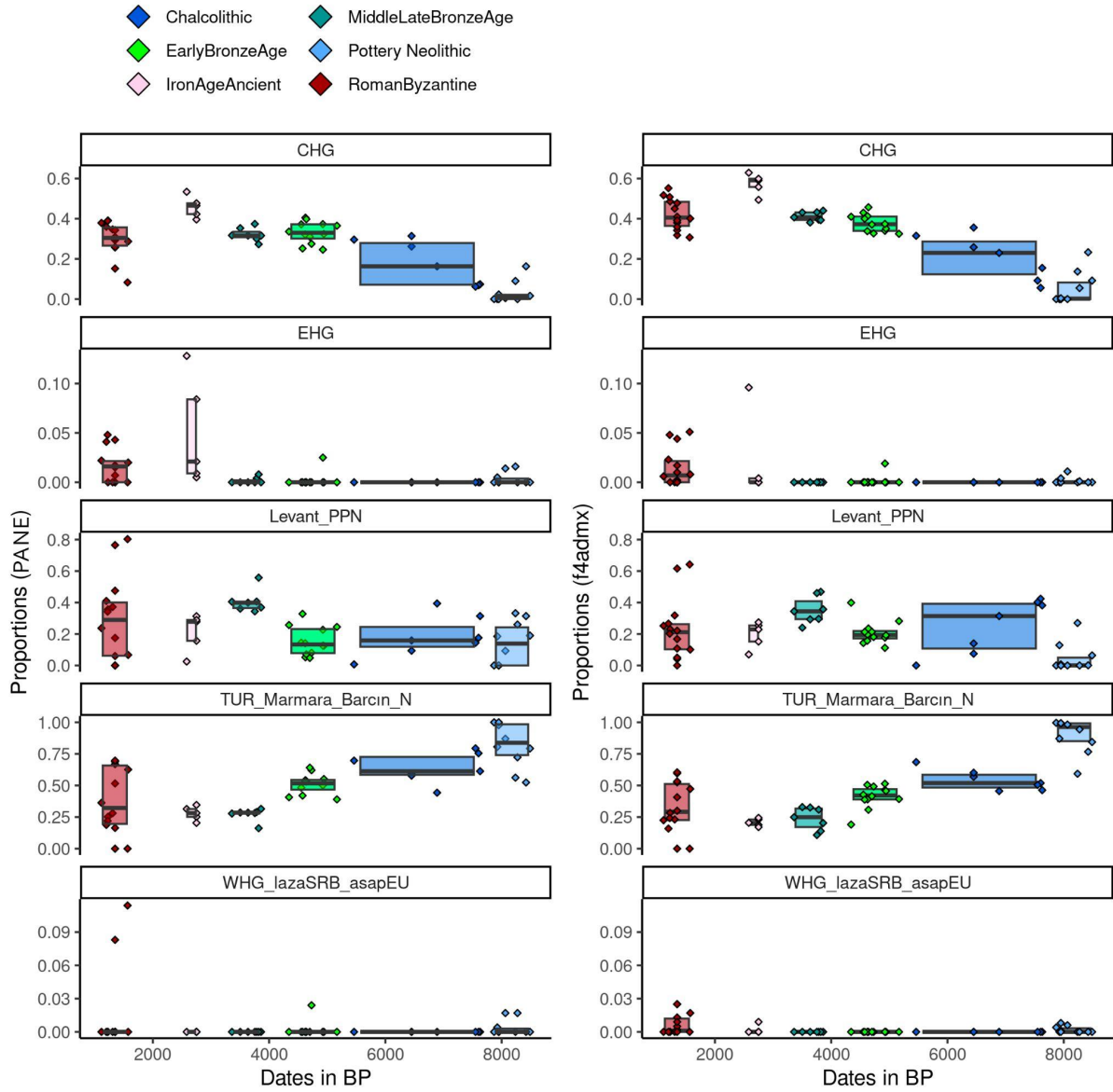


Fig. S3: Ancestry proportion patterns in Anatolia. Following Lazaridis et al. 2022, we estimated ancestry composition in different Eurasian broad regions. The left and right panel shows the ancestry composition using PANE and F4admix (as estimated by (Lazaridis et al., 2022)).

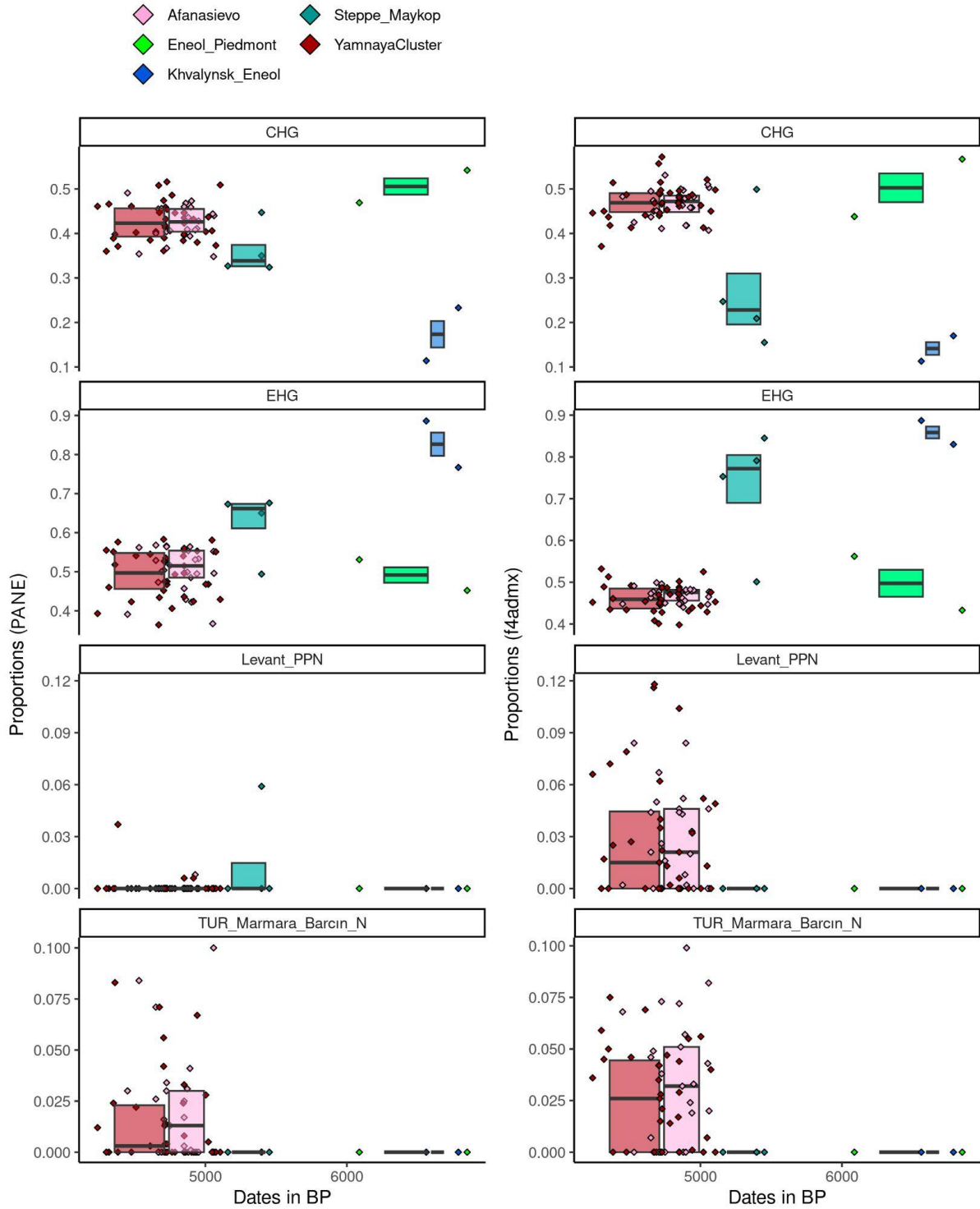


Fig. S4: Ancestry proportion patterns in the Steppe region. Following Lazaridis et al. 2022, we estimated ancestry composition in different Eurasian broad regions. The left and right panel shows the ancestry composition using PANE and F4admX (as estimated by (Lazaridis et al., 2022)).

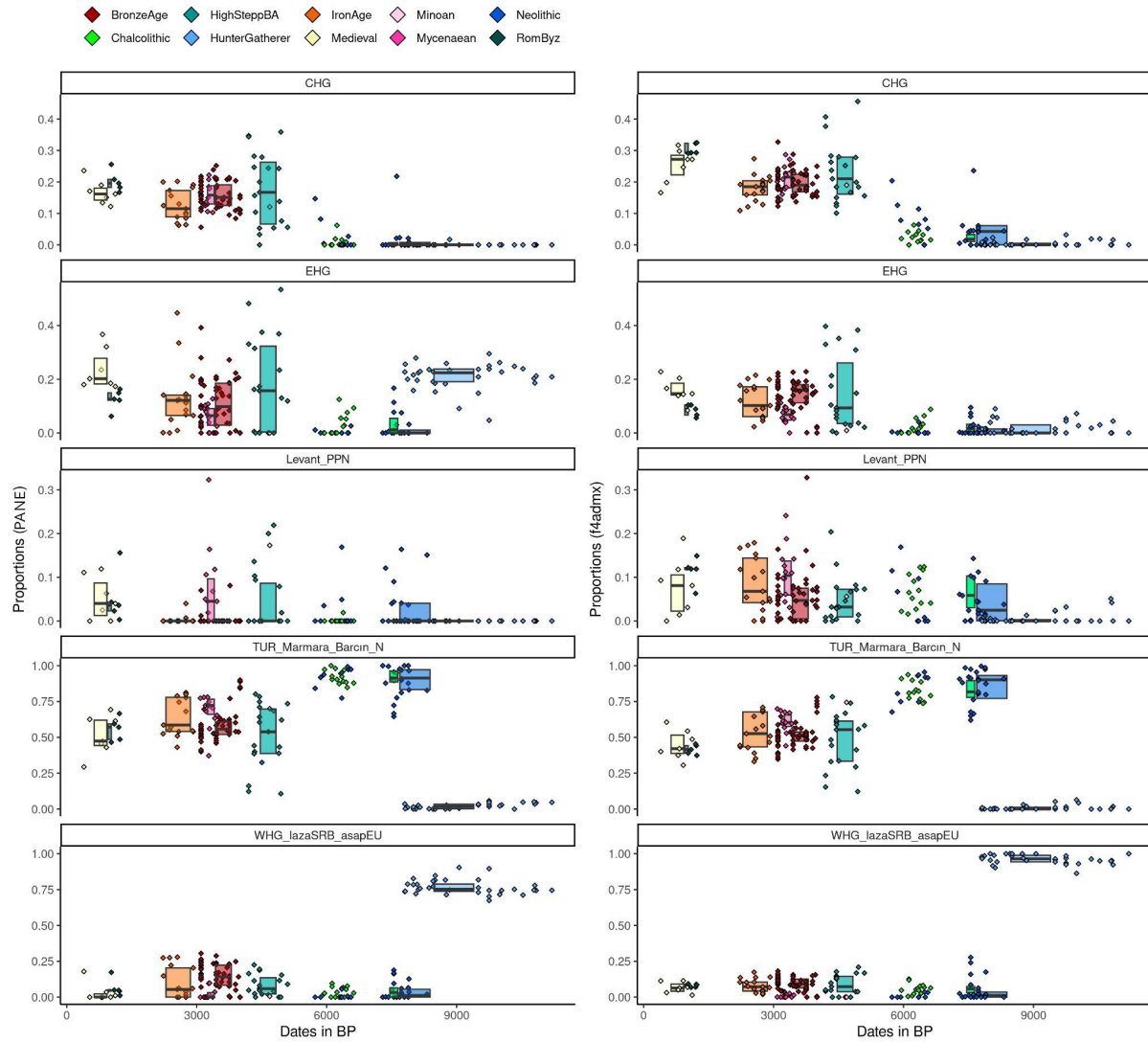


Fig. S5: Ancestry proportion patterns in Southern East Europe. Following Lazaridis et al. 2022, we estimated ancestry in different Eurasian broad regions. The left and right panel shows the ancestry composition using PANE and F4admix (as estimated by (Lazaridis et al., 2022)).

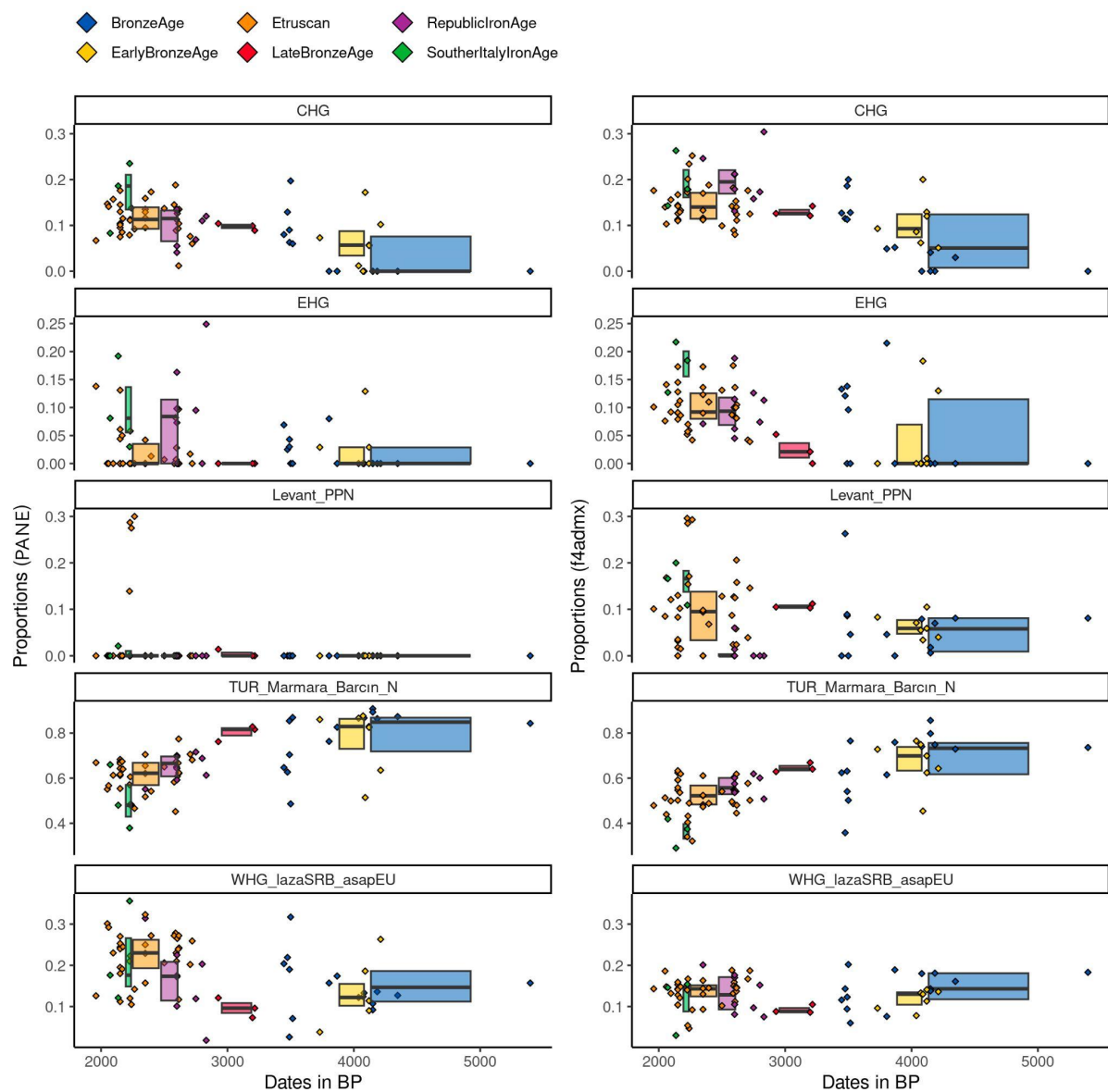


Fig. S6: Ancestry proportion patterns in Italy. Following Lazaridis et al. 2022, we estimated ancestry in different Eurasian broad regions. The left and right panel shows the ancestry composition using PANE and F4admix (as estimated by (Lazaridis et al., 2022)).

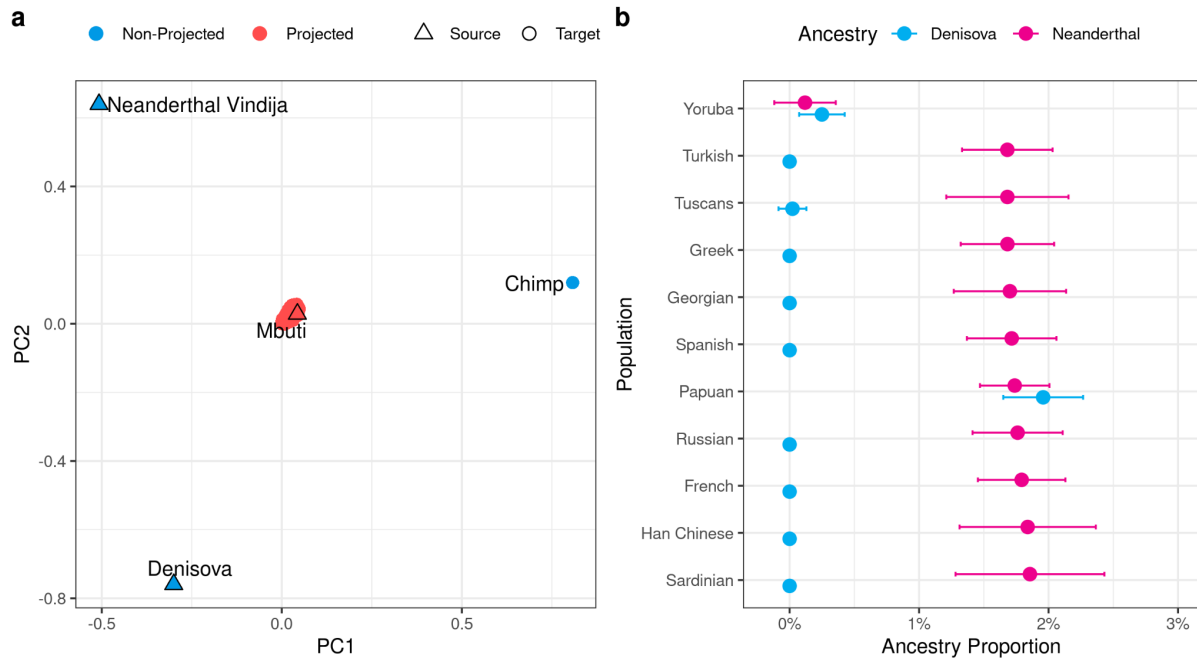


Fig. S7: Testing hybridization with other species. (A) Principal Component Analysis (PCA) used as input for the PANE framework. A total of 6,441 modern and ancient genomes are projected onto the genetic variability of Neanderthal, Denisovan, and chimpanzee genomes, using 182,314 SNPs for the projection. (B) PANE results showing average Denisovan and Neanderthal ancestry proportions (± 1 SD) in modern human populations, with populations sorted by Neanderthal ancestry levels.