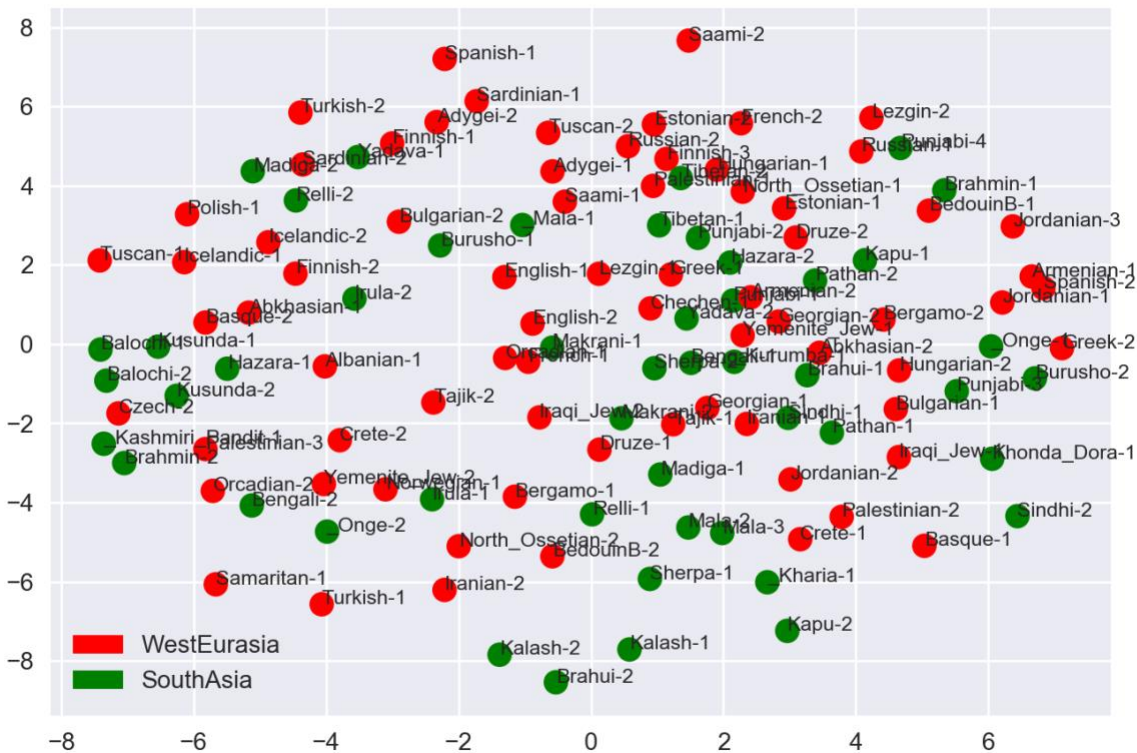


A scatter plot showing genetic variation across populations from West Eurasia and Central Asia/Siberia. The x-axis represents genetic variation (ranging from -8 to 6) and the y-axis represents genetic variation (ranging from -8 to 8). Populations are labeled with names and numbers (e.g., Samaritan-1, Turkish-1, Hanian-2, etc.). A legend indicates that red dots represent WestEurasia and yellow dots represent CentralAsiaSiberia. The plot shows a clear separation between the two groups, with WestEurasia populations generally clustered on the left and CentralAsiaSiberia populations generally clustered on the right.

WestEurasia vs. SouthAsia



Supplementary Information Figure 6. Multidimensional scaling of 73 individuals from WestEurasia and 27 individuals from CentralAsiaSiberia and B) 49 individuals from SouthAsia. Data used includes all DNA source types in the SGDP dataset. The metric used for scaling was based on the Euclidean distance between the set of alleles of each individual. Individuals are labeled by an abbreviated version of their sample ID in the SGDP dataset.