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Supplemental Information

Spatial and temporal heterogeneity in human mobility patterns in Holocene Southwest Asia and the East Mediterranean

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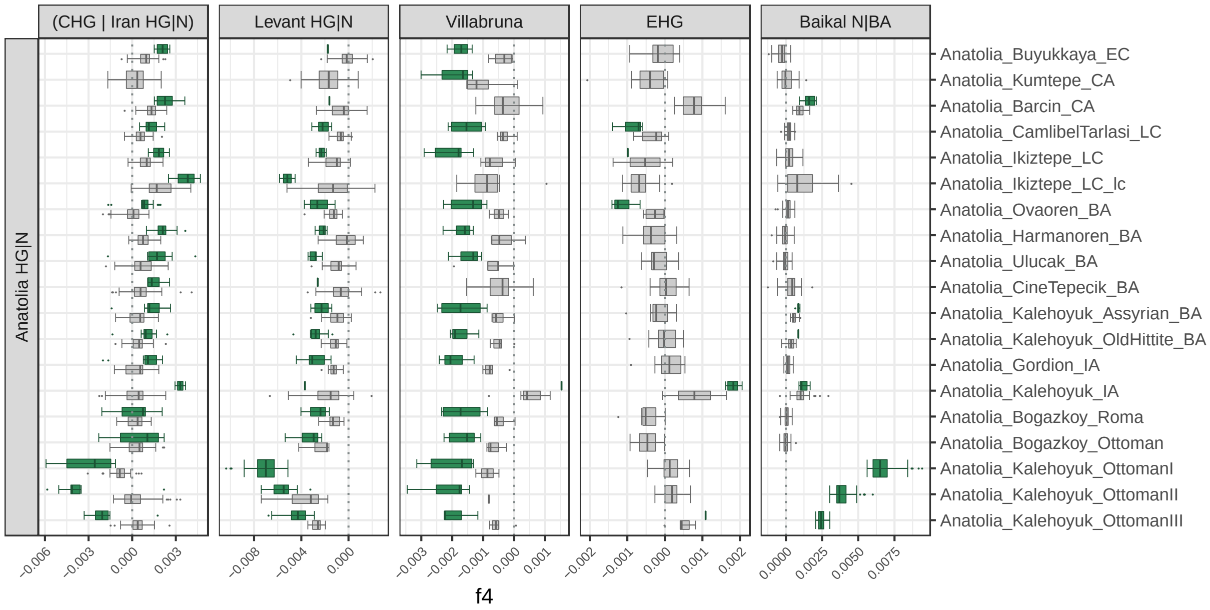

Figure S1: Genetic affinities of post-Neolithic Anatolian populations, **related to Table S3-S4 and Figure 3**. Results from the model f_4*(YRI, Test; Anatolia HG|N, Post Neolithic Anatolian)*, where *Test* refers to the South Caucasus/Iran or Levant pre-Neolithic/Neolithic populations, Villabruna, EHG and Baikal populations (Table S3). The Dataset 1 (STAR Methods) was used in the analysis. Boxplots show all f_4 statistics calculated by at least 10K overlapping SNPs. Green colour boxplots show nominally significant f_4-statistics with $|Z| > 3$ and grey colour boxplots show non-significant f_4-statistics with $|Z| < 3$.

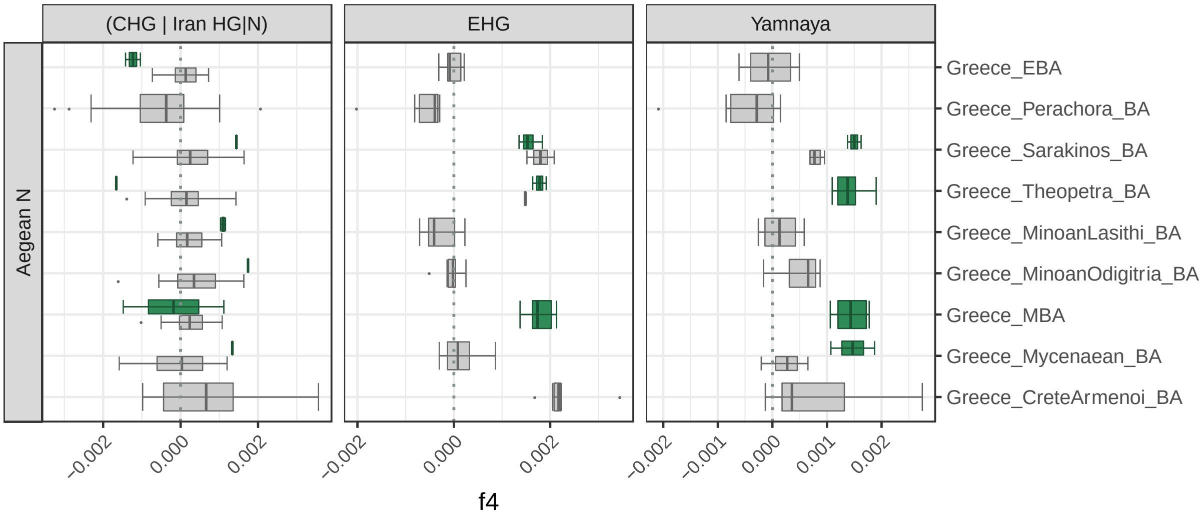

Figure S2: Genetic affinities of post-Neolithic Aegean populations, related to Table S3-S4 and Figure 3. Results from the model f_4*(YRI, Test; Aegean N, Post Neolithic Aegean)*, where *Test* refers to the South Caucasus/Iran pre-Neolithic/Neolithic populations, EHG and Yamnaya populations (Table S3). The Dataset 1 (STAR Methods) was used in the analysis. Boxplots show all f_4 statistics calculated by at least 10K overlapping SNPs. Green colour boxplots show nominally significant f_4-statistics with $|Z| > 3$ and grey colour boxplots show non-significant f_4-statistics with $|Z| < 3$.

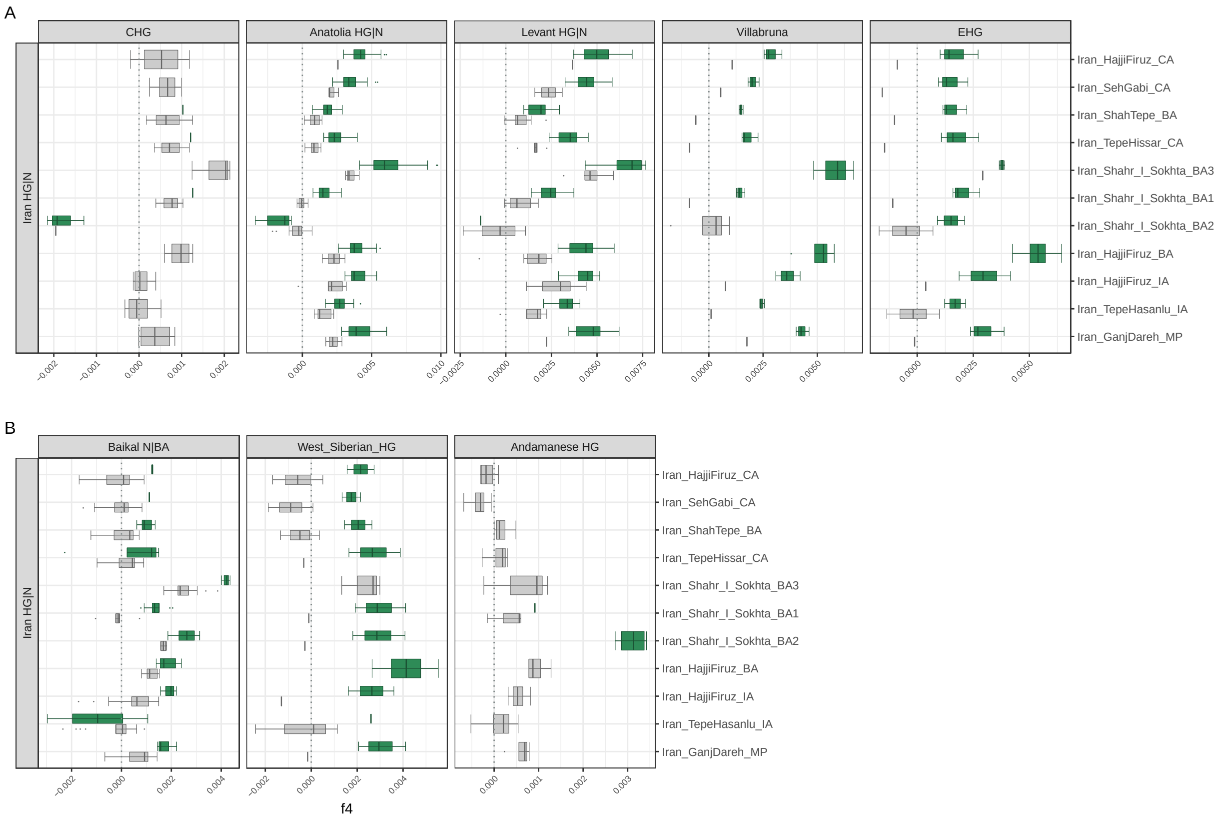

Figure S3: Genetic affinities of post-Neolithic Iran populations, related to Table S3-S4 and Figure 3. Results from the model f_4*(YRI, Test; Iran HG|N, Post Neolithic Iran)*, where *Test* refers to (A) the Anatolian or Levant pre-Neolithic/Neolithic populations, CHG, EHG and Villabruna populations, and (B) Baikal, WSHG and Andamanese HG (Table S3). The Dataset 1 (STAR Methods) was used in the analysis. Boxplots show all f_4 statistics calculated by at least 10K overlapping SNPs. Green colour boxplots show nominally significant f_4-statistics with $|Z| > 3$ and grey colour boxplots show non-significant f_4-statistics with $|Z| < 3$.

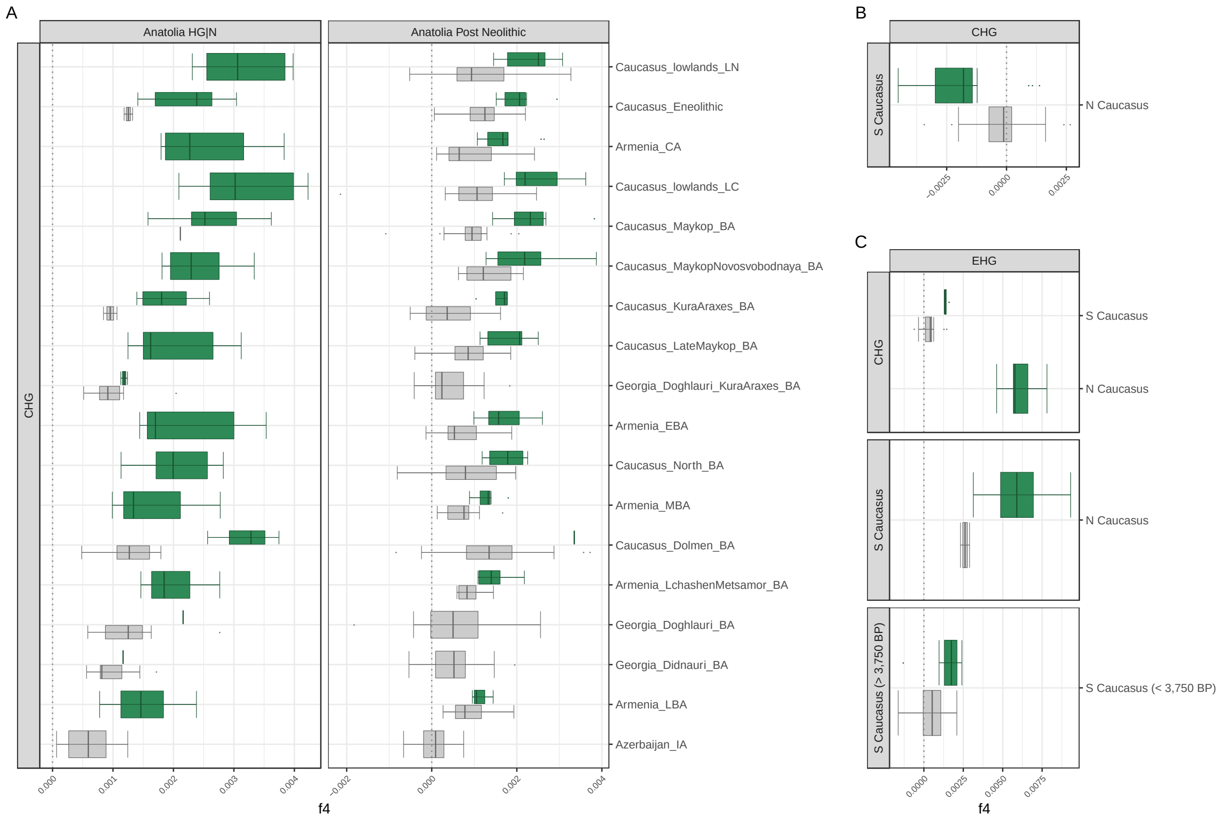

Figure S4: Genetic affinities of post-Neolithic South Caucasus populations, related to Table S3-S4 and Figure 3. Results from (A) f_4*(YRI, Anatolia HG|N or Anatolia Post Neolithic; CHG, South Caucasus Post Neolithic)*, (B) f_4*(YRI, CHG; South Caucasus, North Caucasus)*, and (C) f_4*(YRI, EHG; Pop1, Pop2)*, where *Pop1* or *Pop2* refer to CHG, South Caucasus or North Caucasus populations. The Dataset 1 (STAR Methods) was used in the analysis. Boxplots show all f_4 statistics calculated by using at least 10K overlapping SNPs. Green colour boxplots show nominally significant f_4-statistics with $|Z| > 3$ and grey colour boxplots show non-significant f_4-statistics with $|Z| < 3$.

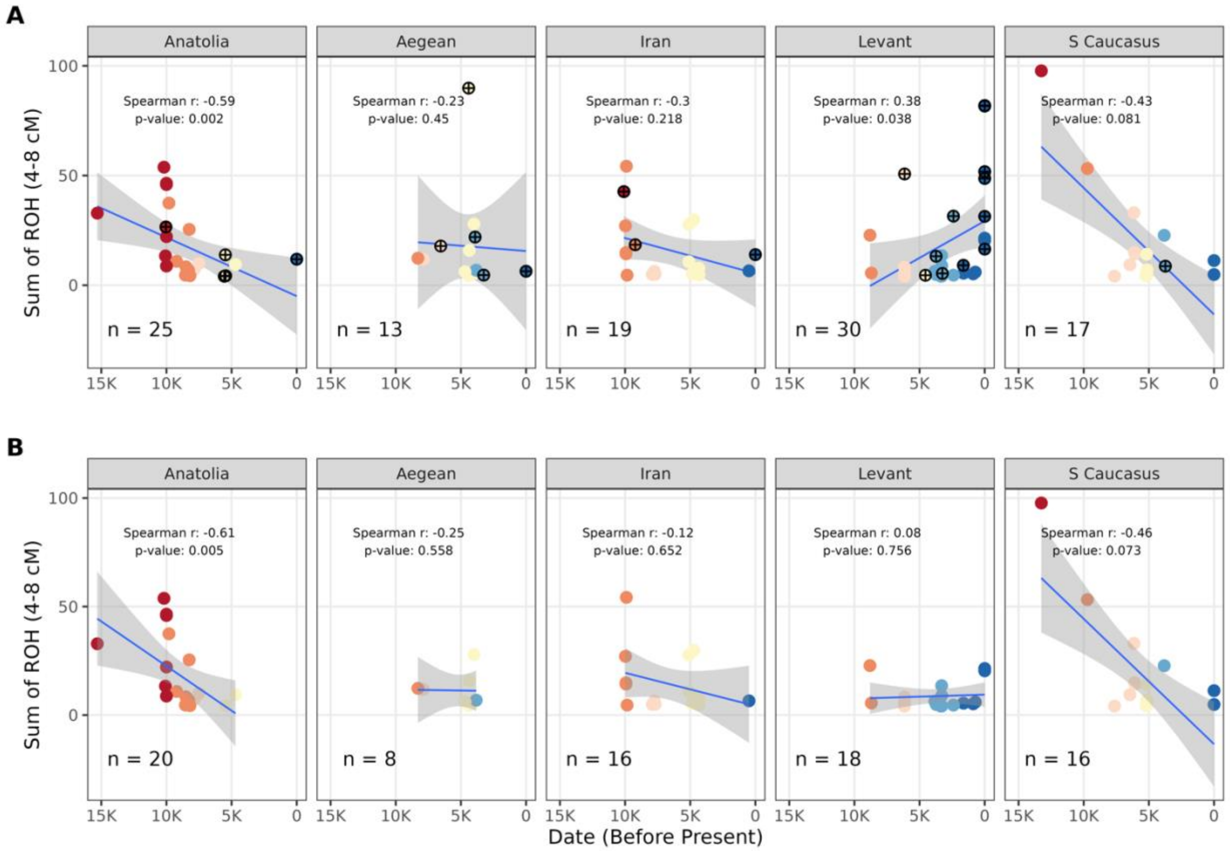

Figure S5: Sum of short (4-8 cM) runs of homozygosity (sROH) among ancient genomes, related to STAR Methods. Panel A shows all individuals for which ROH could be called (with minimum 400,000 SNPs), where individuals with ROH > 20cM, representing consanguinity, are indicated with a plus symbol. Panel B is the same as panel A but after removing likely consanguineous individuals (with ROH > 20cM). The Dataset 2 (STAR Methods) was used in the analysis. The lines in each panel represent linear regression lines. Each point represents an ancient individual and is colour coded based on its time period (Figure 1). We note that we detect no decrease in the sROH values (4-8 cM) for the Aegean, but this is likely because we did not have Aegean genomic samples from the first half of the Holocene with sufficient SNPs to determine ROH. The increase of the sum of ROH in the Levant we observed has been well-documented before and is likely due to an increase in consanguineous marriages in the region in recent times[S1] (see also Table Z11 in Zenodo).

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