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Supplemental Information

Ancient Maltese genomes and the genetic geography of Neolithic Europe

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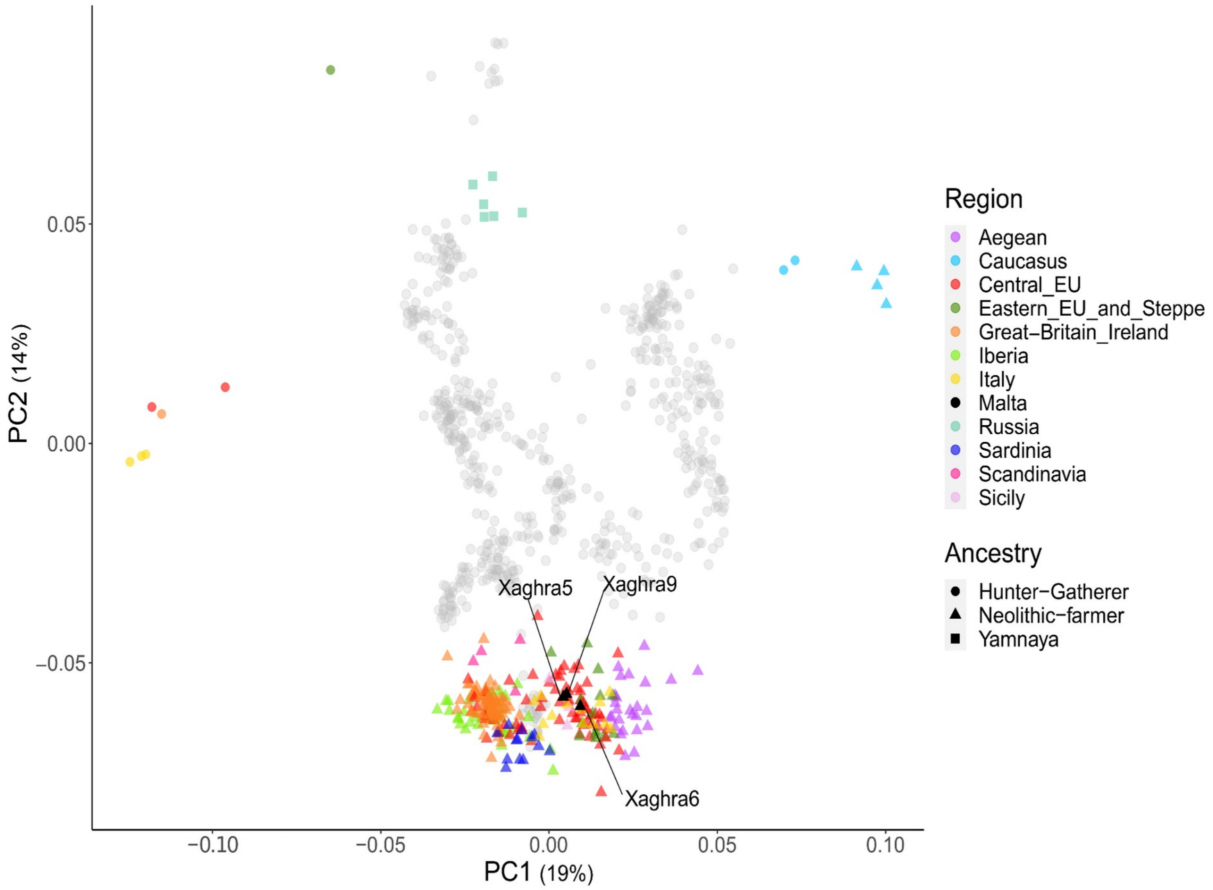

Figure S1: PCA for ancient Maltese and other ancient European populations. **Related to Star Methods and Data S2.** Maltese genomes as well as other published Neolithic and Mesolithic genomes were projected onto a principal component analysis plot using the Human Origins dataset as a modern reference. For each principal component the percentage of variance explained is indicated in parentheses. The ancient Maltese samples group together with Central and Southern European Neolithic genomes.

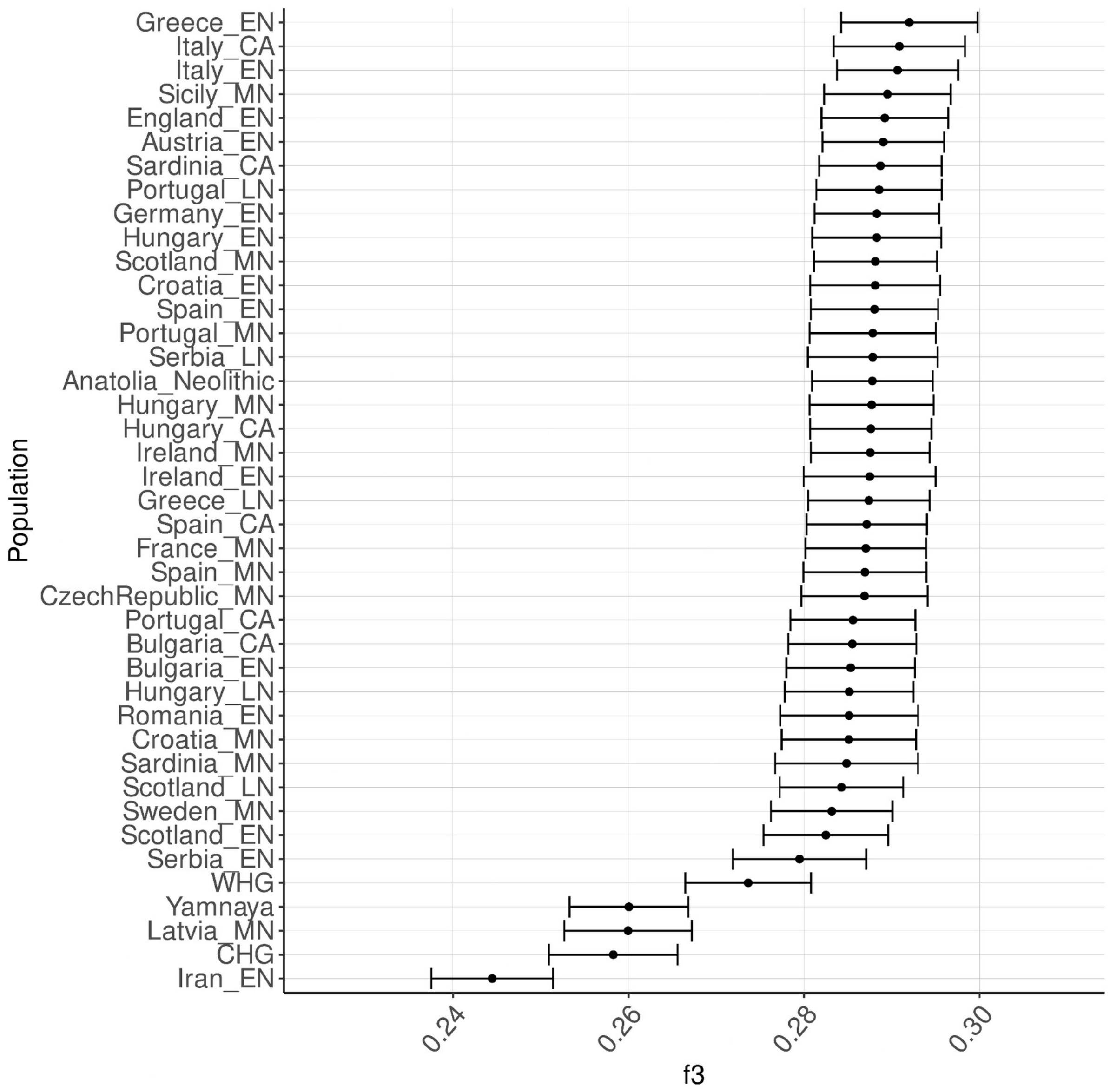

Figure S2: Shared drift measured using the outgroup-f3 statistics. **Related to Star Methods and Data S2F.** The results using outgroup-f3 statistics represented by circles with error bars in the form (Mbuti; X, Malta Neolithic) show the Maltese being closer to early Neolithic individuals from Greece and the Italian peninsula. (EN=Early Neolithic, MN=Middle Neolithic, LN=Late Neolithic, CA=Copper Age, WHG=Western hunter-gatherer, CHG=Caucasus hunter-gatherer, EHG=Eastern hunter-gatherer). The Anatolian Neolithic population is represented by individuals from Marmara, Barcın.

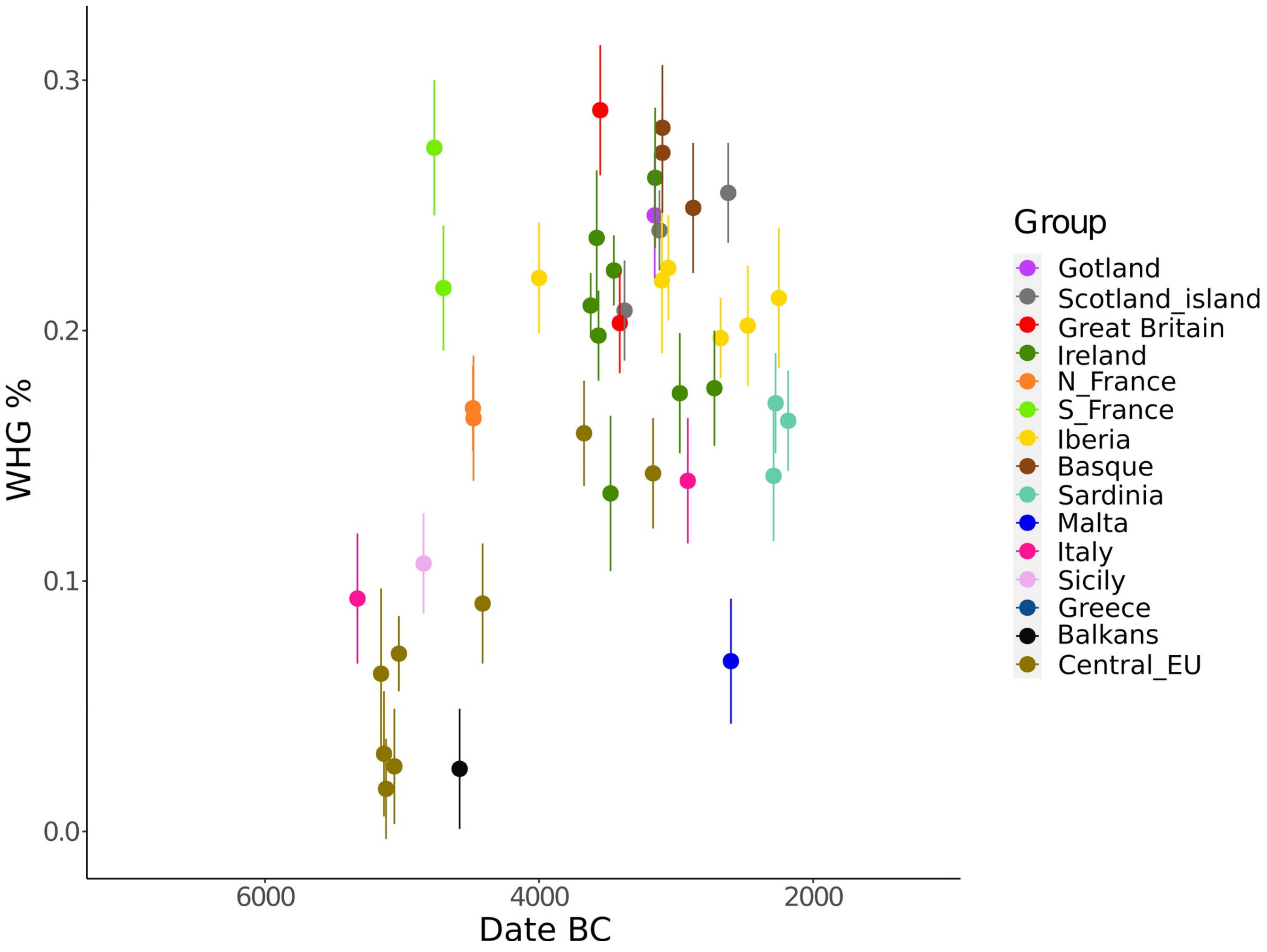

Figure S3: Temporal distribution of hunter-gatherer ancestry in Neolithic Europeans. Related to Star Methods and Data S2E. qpAdm was used to measure the quantity of Western Hunter-gatherer (WHG) populations, represented by the individuals KO1 and Loschbour, present in European Neolithic populations. Each point represents with its error bar a group with at least 2 individuals from an archaeological site and time period. The WHG percentages are reported with 95% error bars.

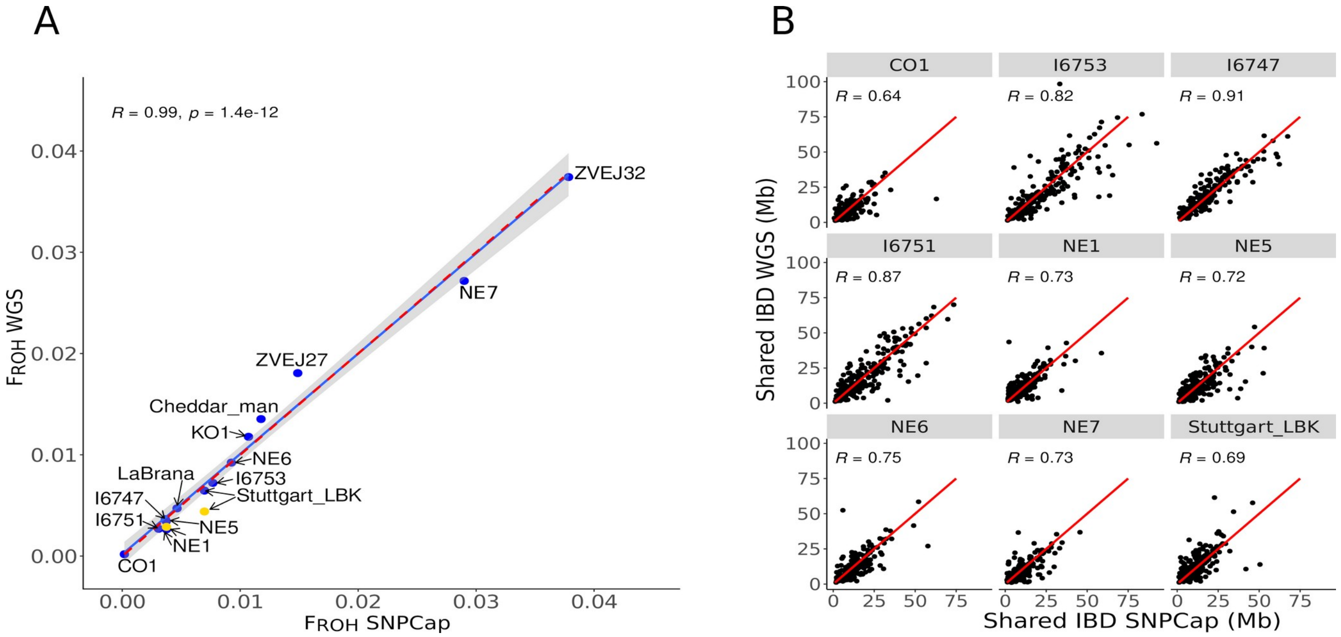

Figure S4: Comparisons of IBD and F_{ROH} estimates from imputed WGS and SNP captured data. Related to Star Methods and Data S1B, S1D. (A) F_{ROH} were compared between imputations of WGS and SNP captured data (respectively "F_{ROH} WGS" and "F_{ROH} SNPCap") where these are available from the same samples. These correlate with a P-value lower than and the regression line (coloured blue) error margins overlap with the 1:1 plot (red line). Also two yellow coloured points denote where three genomes (NE1, Stuttgart_LBK) also had WGS F_{ROH} estimates available from high coverage SNP calls - these are plotted Vs F_{ROH} SNPCap. (B) Plots of IBD sharing values involving each of nine Neolithic samples for which WGS and SNP capture - based estimates are available. For each, total estimates of the genome shared with all other Neolithic samples is plotted alternately using the two different data sets. The WGS and SNP-derived values correlate significantly (each at $p < 10^{-15}$) and vary around the 1:1 plotline, drawn in red.

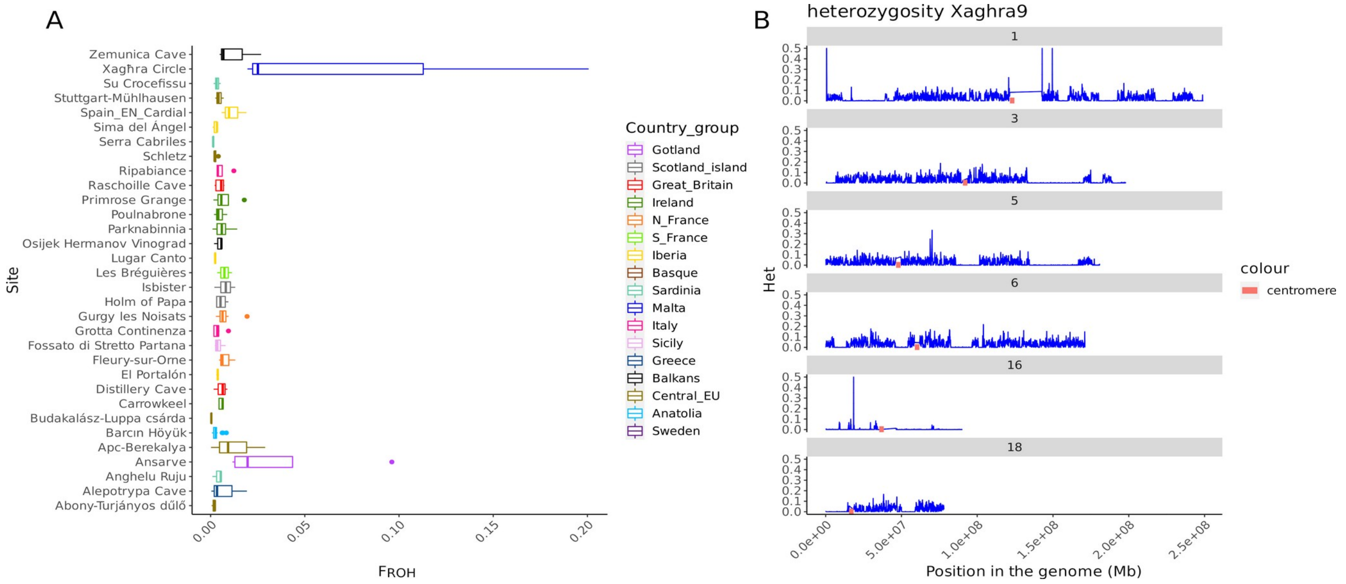

Figure S5: Inbreeding F_{ROH} coefficient estimates and chromosome heterozygosity plots for Xaghra9. Related to Figure 2A and Data S1D. (A) F_{ROH} coefficients within sites with a minimum of 3 individuals. The Maltese possess the highest median inbreeding coefficient followed by values from Gotland. (B) The average heterozygosity is plotted for Xaghra9 using a window size of 100 kb and illustrates examples of long genome tracts of homozygosity in selected chromosomes.

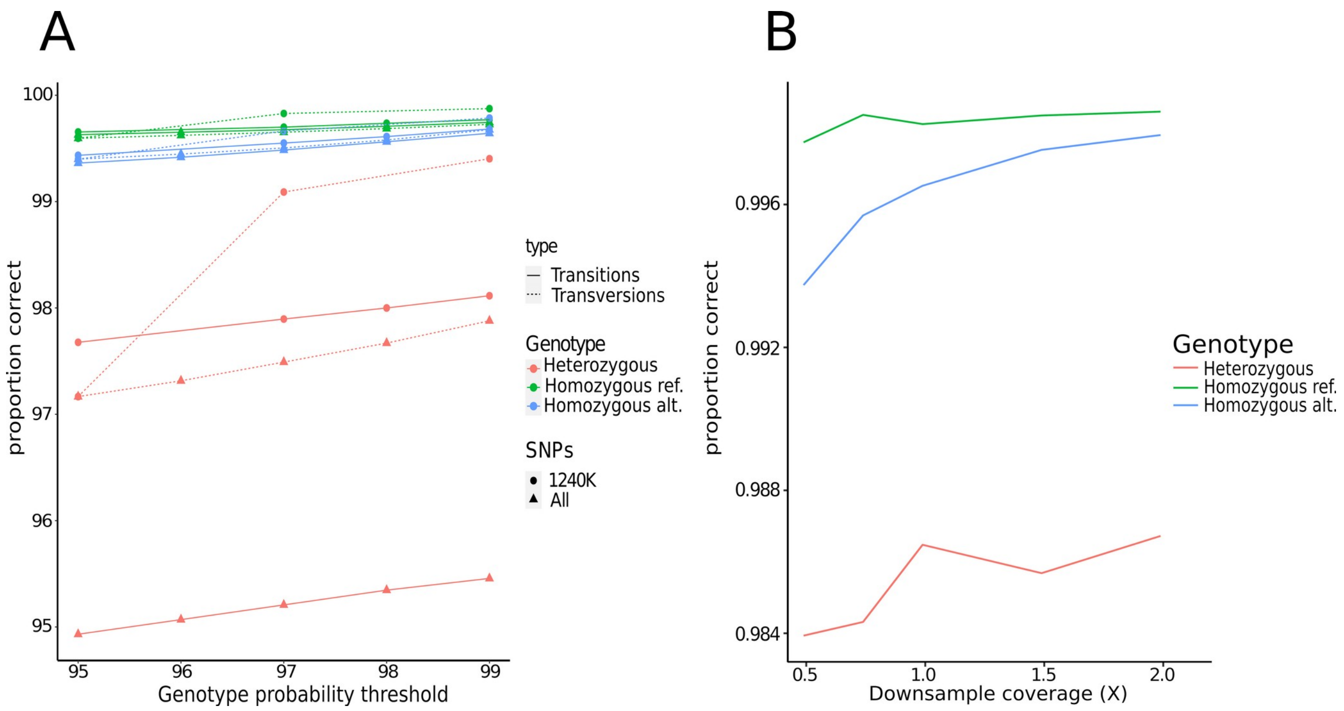

Figure S6: Accuracy of imputed genotypes. **Related to Star Methods.** (A) Genotypes imputed from a SNP captured genome (LBK) compared against those called from its high coverage genome sequence using the software SNPSift[S43]. Heterozygous and transversion SNPs show overall lower accuracy compared to homozygous and transition imputed SNPs. The SNPs corresponding to the 1240K positions were predicted overall with higher accuracy compared to other variants. (B) Genotypes imputed from a downsampled WGS genome (LBK) also here compared against its high coverage genome sequence. Only transversions are considered in this analysis and heterozygous calls show overall less accuracy than homozygous ones. Overall the percentage of safely imputed genotypes remains high for each genotype class across different probability thresholds.

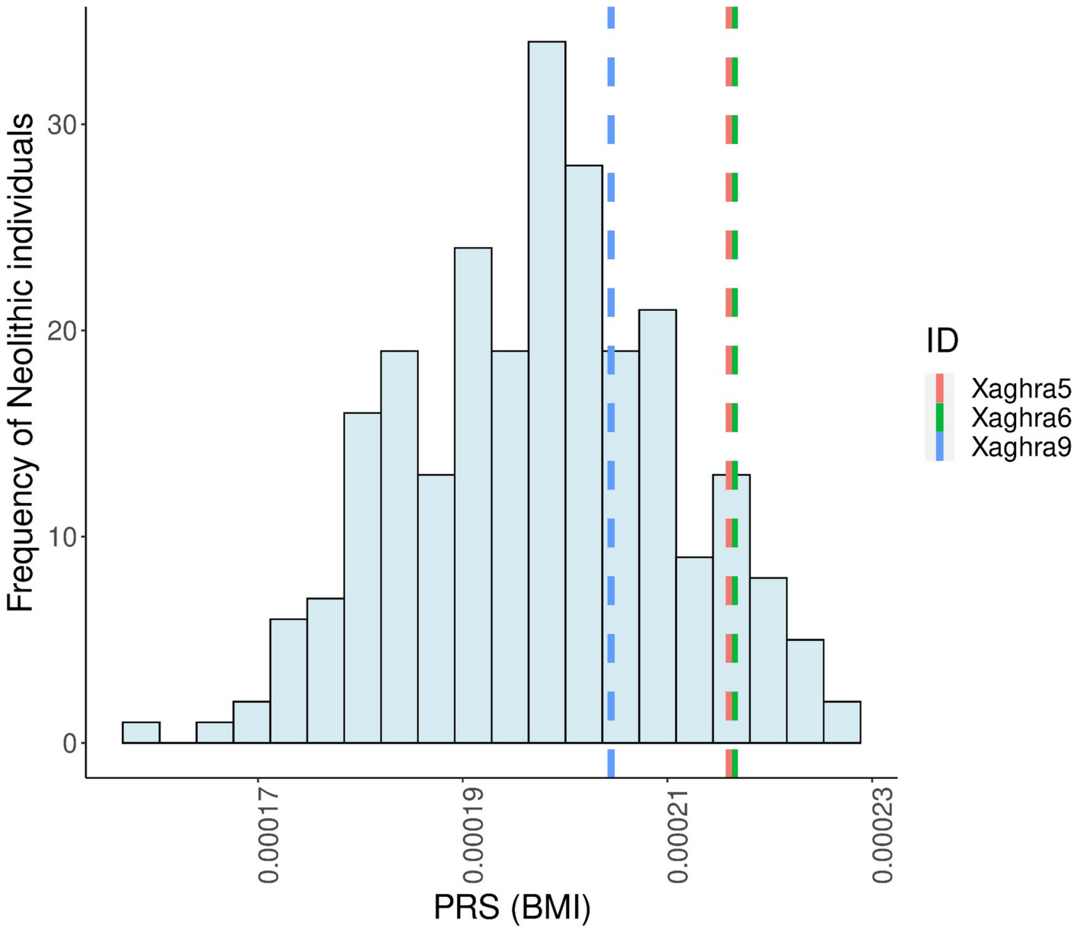

Figure S7: Body mass index in ancient Maltese. **Related to Star Methods.** Polygenic risk score (PRS) information calculated from the UK Biobank dataset was used to estimate body mass index (BMI) of the ancient Maltese together with 247 European Neolithic samples. None of the former showed extreme values.

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