

Supplementary Materials for

Genomic insights into the complex demographic history and inbreeding Phenomena during Zhou Dynasty on the Central Plains of China

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2 Supplementary Figures

Figure S1. Layout overview of the Guanzhuang site. The site featured a distinctive 'convex' planar layout, comprising a large city (outer city) and a small city (inner city), with the latter positioned to the north of the former (Tang et al., 2022).

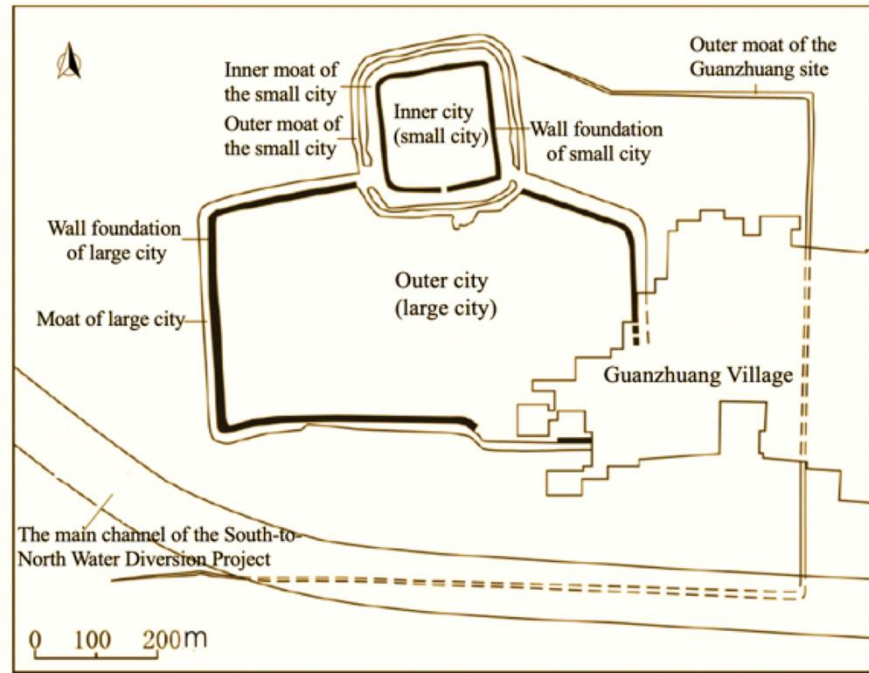


Figure S2. Ancient DNA damage patterns for the Guanzhuang samples. The left represented C to T misincorporations at the 5' end and the right represented G to A misincorporations at the 3' end.

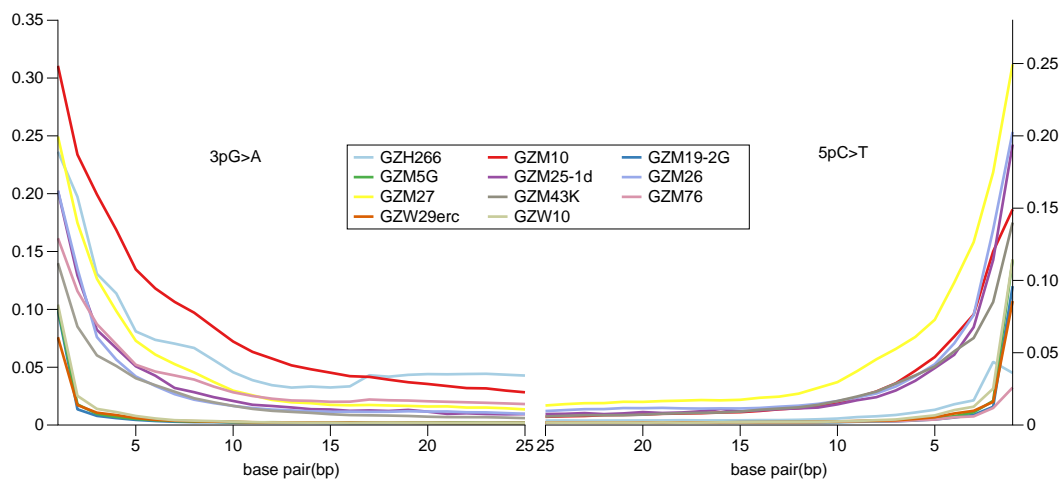


Figure S3. PMR estimation of genetic relatedness in Guanzhuang individuals. In general, for identical individuals ($r=1$), the PMR is roughly half of what it is for unrelated individuals ($r=0$, the baseline). For first-degree relatives ($r=0.5$) and second-degree relatives ($r=0.25$), the PMR is around $3/4$ and $7/8$ of the baseline, respectively. Through that, we confirmed that the Guanzhuang individuals were genetically unrelated individuals.

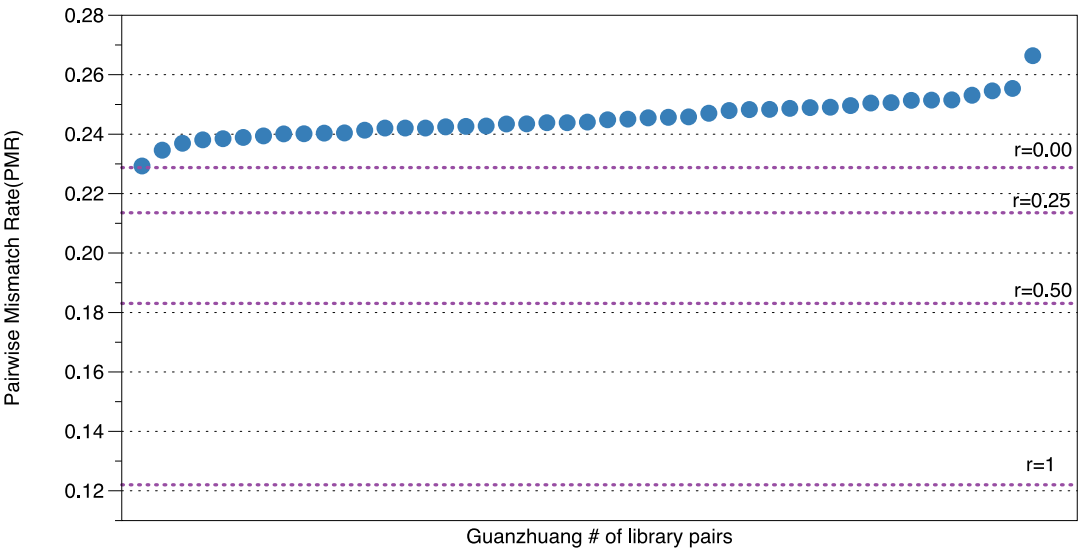


Figure S4. Distribution of Runs of Homozygosity (ROH) length (>4 cM) in sample GZW29erc. The solid line represents the expected ROH distribution for various scenarios of close-union offspring.

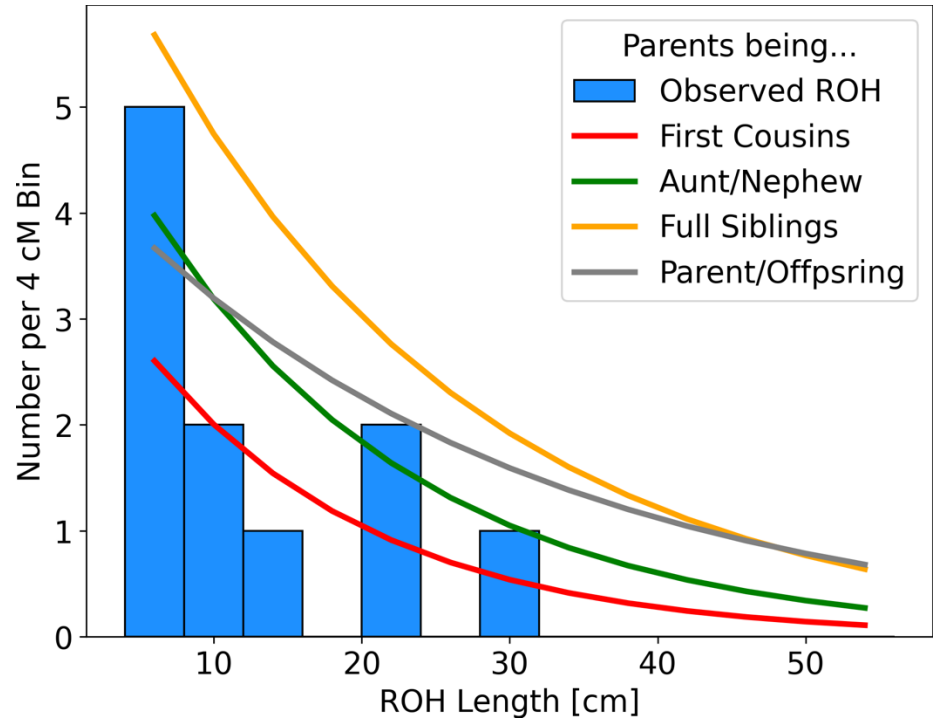


Figure S5. PCA results of Guanzhuang population with present-day and ancient East Asians. Ancient individuals were projected onto the top PCs. The individual GZM10, deviating from the Guanzhuang cluster, was marked as Guanzhuang_o.

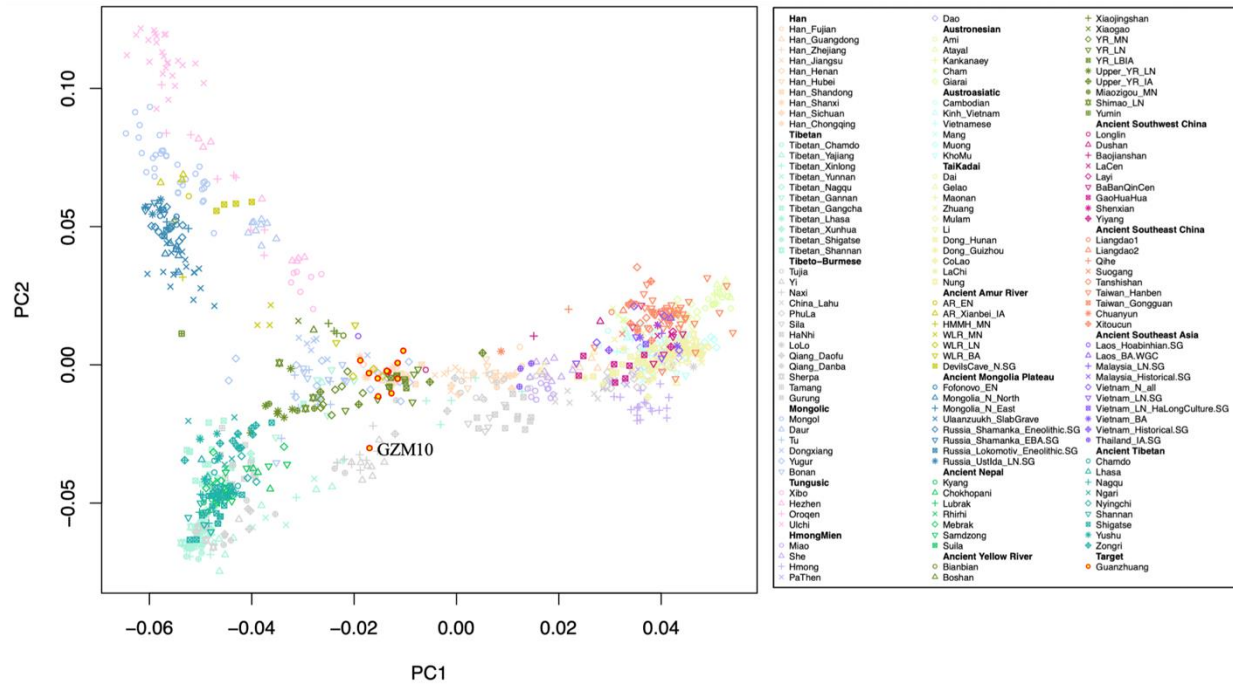


Figure S6. Cross-validation (CV) error estimates of ADMIXTURE for the "HO" dataset. The K values was ranged from 2 to 20, reaching a minimum at K=10.

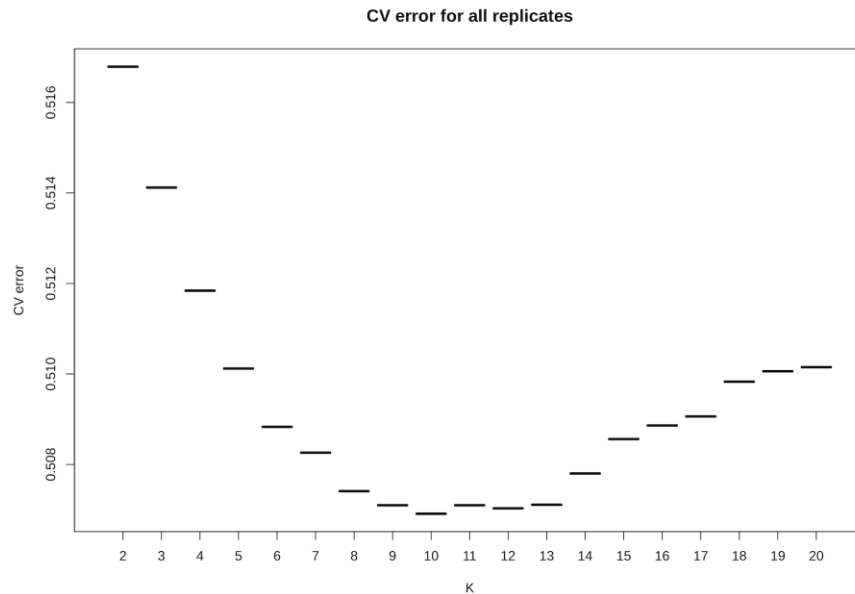


Figure S7. Outgroup f3-statistics of Guanzhuang outlier. Populations with fewer than 10,000 SNPs were excluded. The top 30 populations exhibiting the highest genetic drift with the Guanzhuang outlier were presented.

