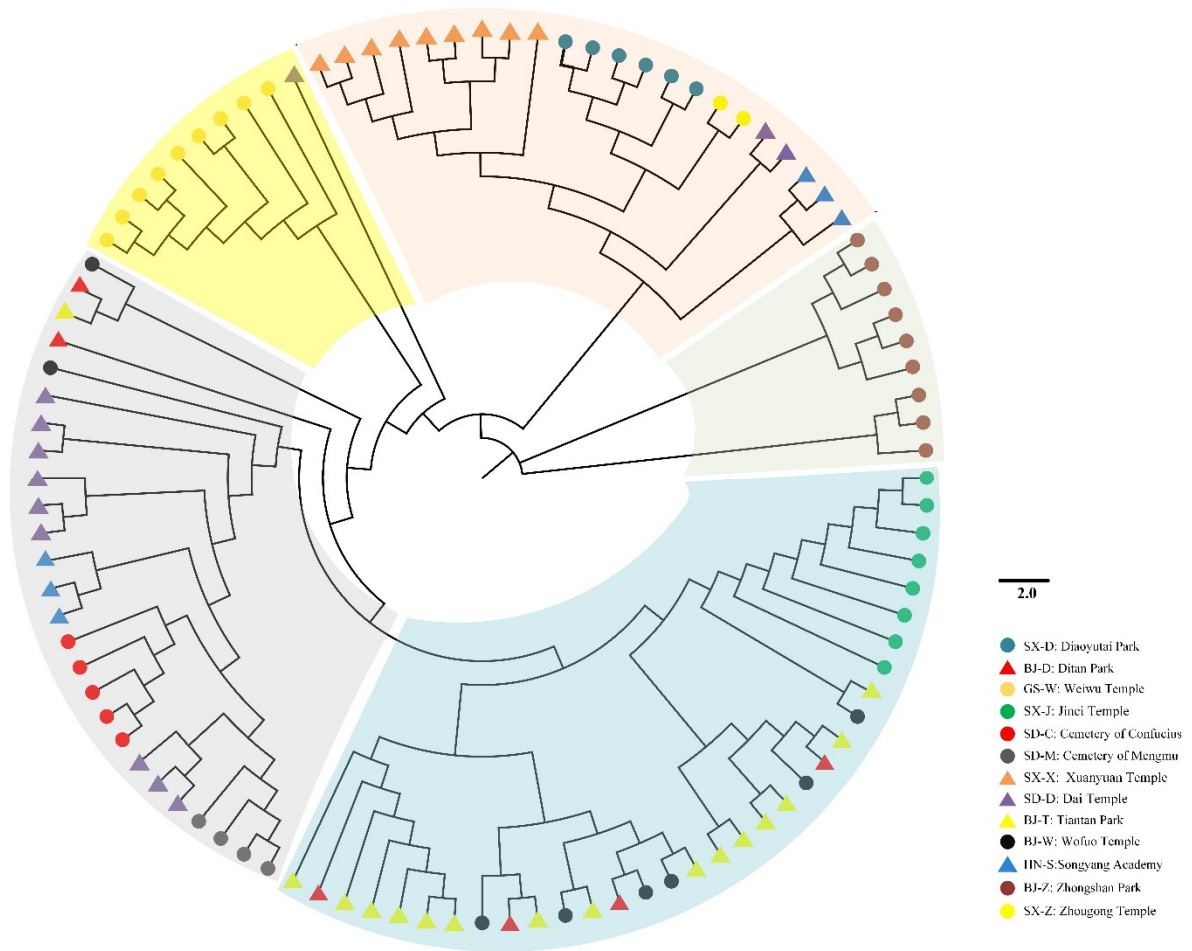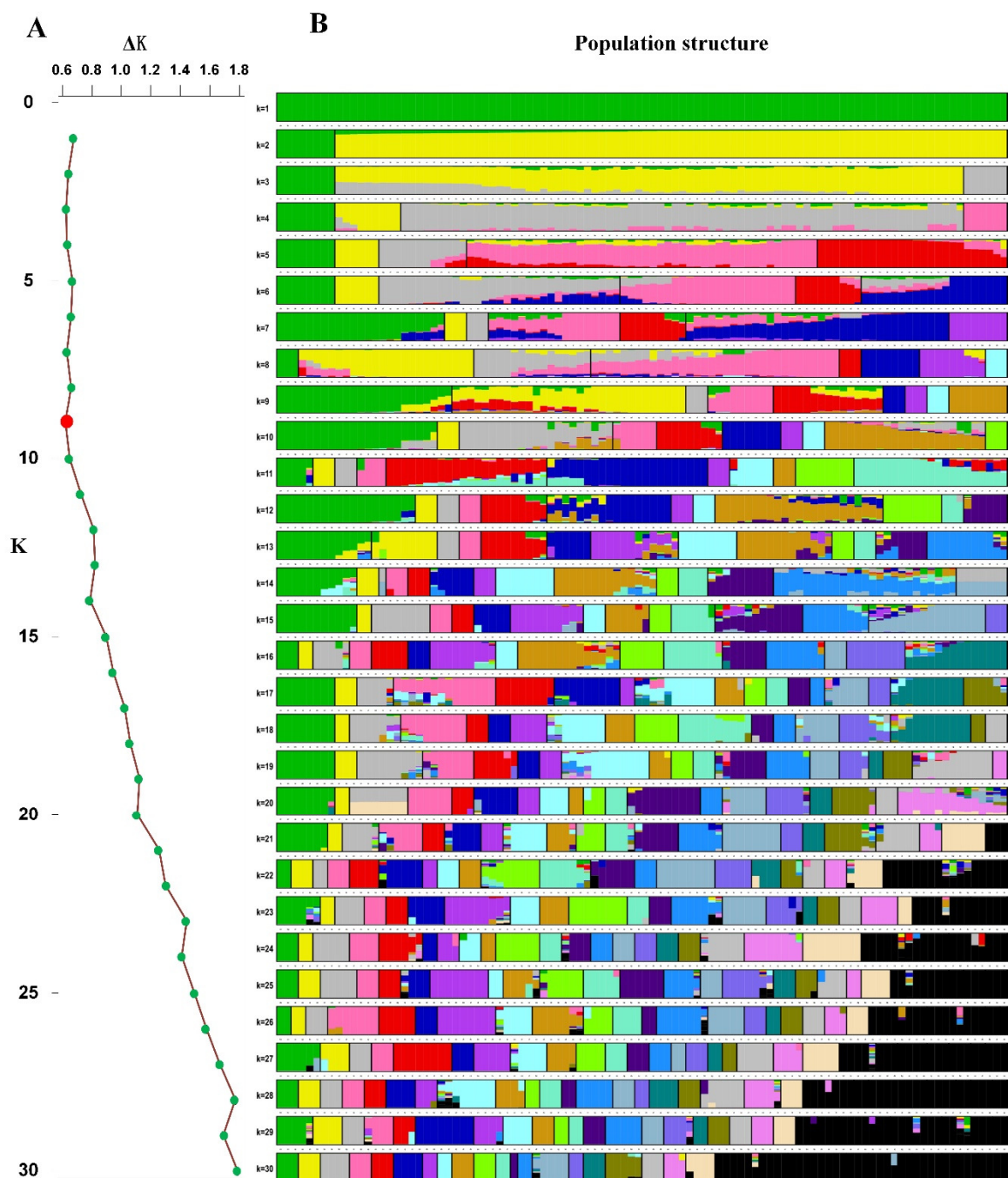**Supplementary Figure S1:** Sequence base distribution of ancient *P. orientalis*.

Supplementary Figure S2: Phylogenetic tree comprising 100 accessions constructed according to the neighbor-joining method with polymorphic SNPs.

Supplementary Figure S3: Population structure of 100 accessions (**A**) and the individual clusters corresponding to each K value as determined with the Admixture software (**B**).
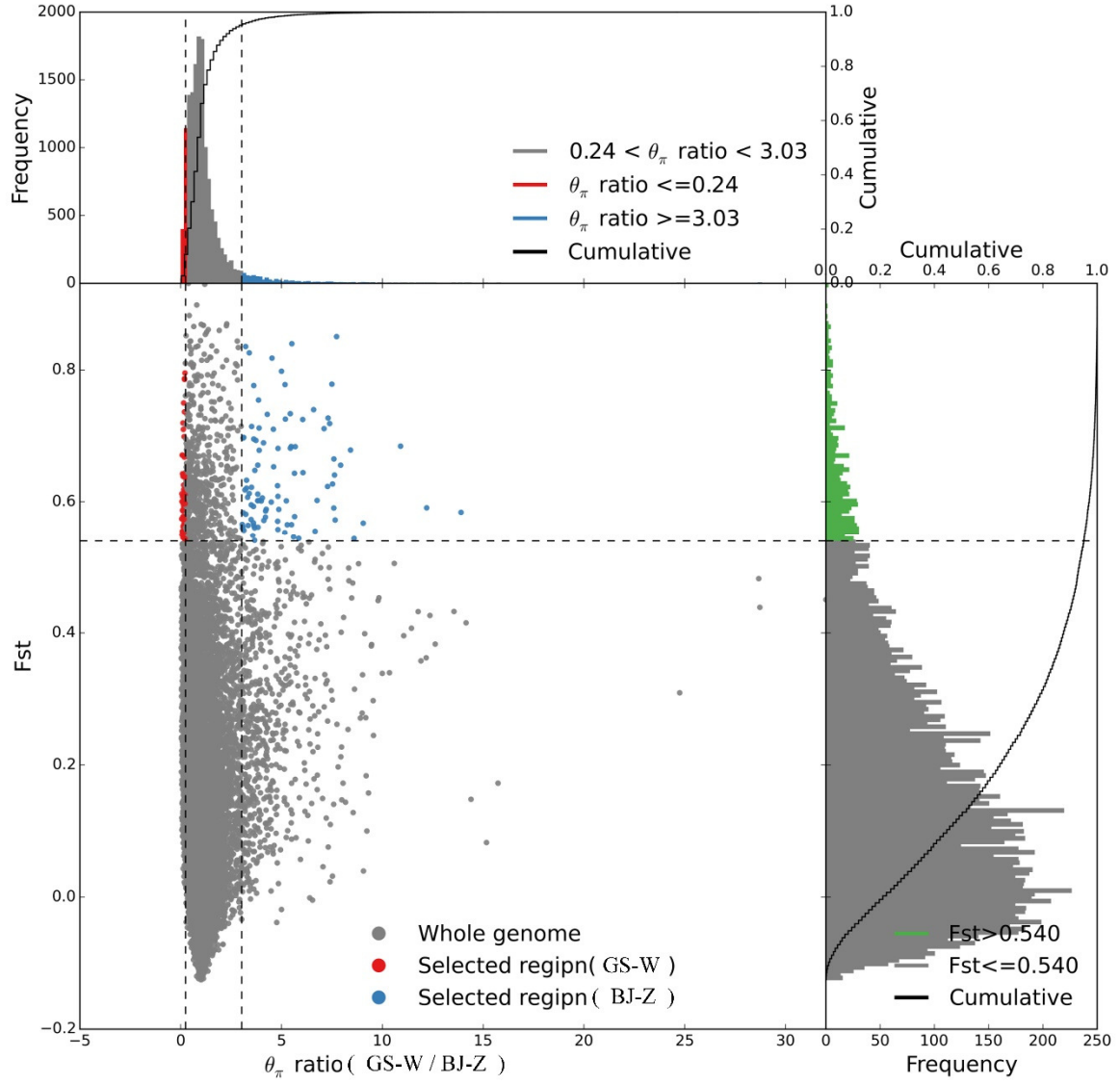
Supplementary Figure S4: Distribution of θπ ratios and Fst values and the regional distribution of population differentiation. Blue and green points represent the selected regions for the BJ-Z and GS-W populations.