

Supplementary Information

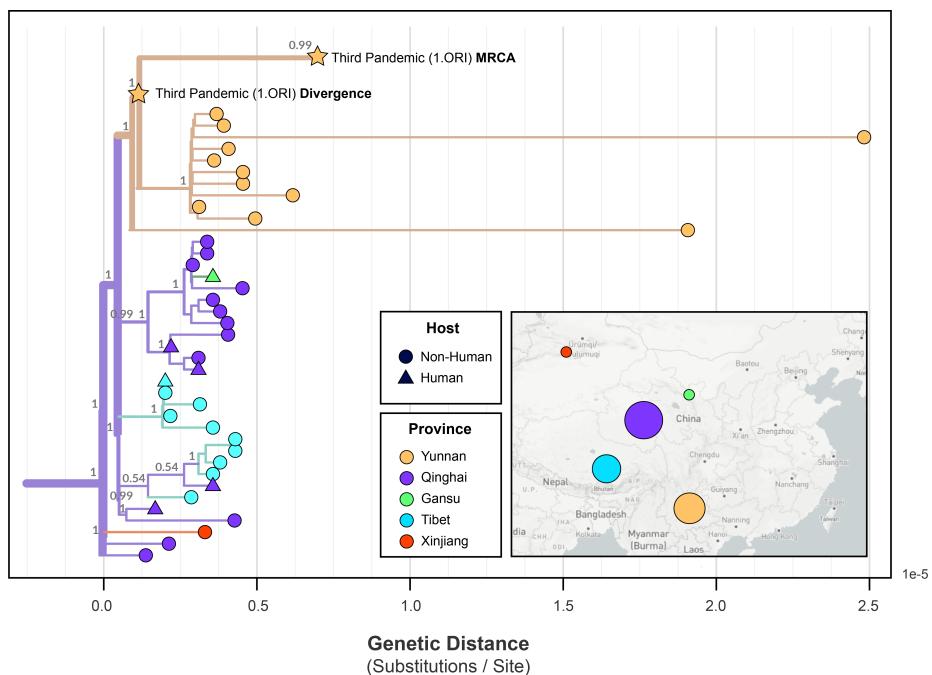


Figure S1: Geographic structure of the *Intermedium* (1.IN) population which is ancestral to the Third Pandemic (1.ORI). Branches are colored based on a discrete, ancestral state reconstruction using sampling location (province). Branch labels indicate the likelihood of the ancestral location given the data.

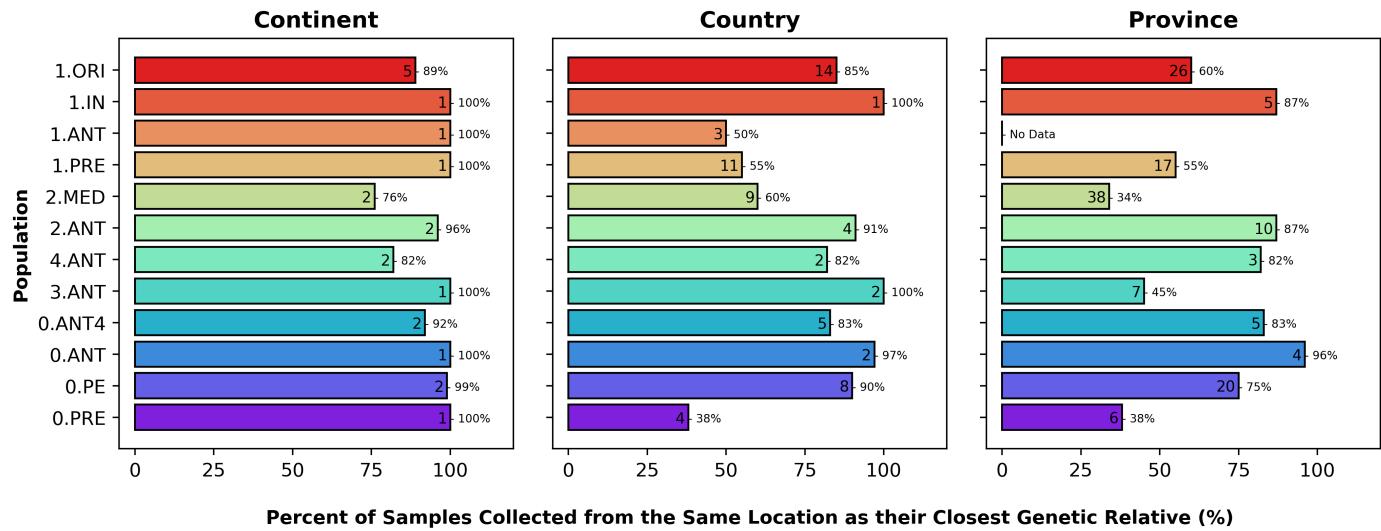


Figure S2: Geographic structure by population according to the percent of genomes sampled from the same location as their closest genetic relative. Internal bar labels indicate the number of locations sampled.

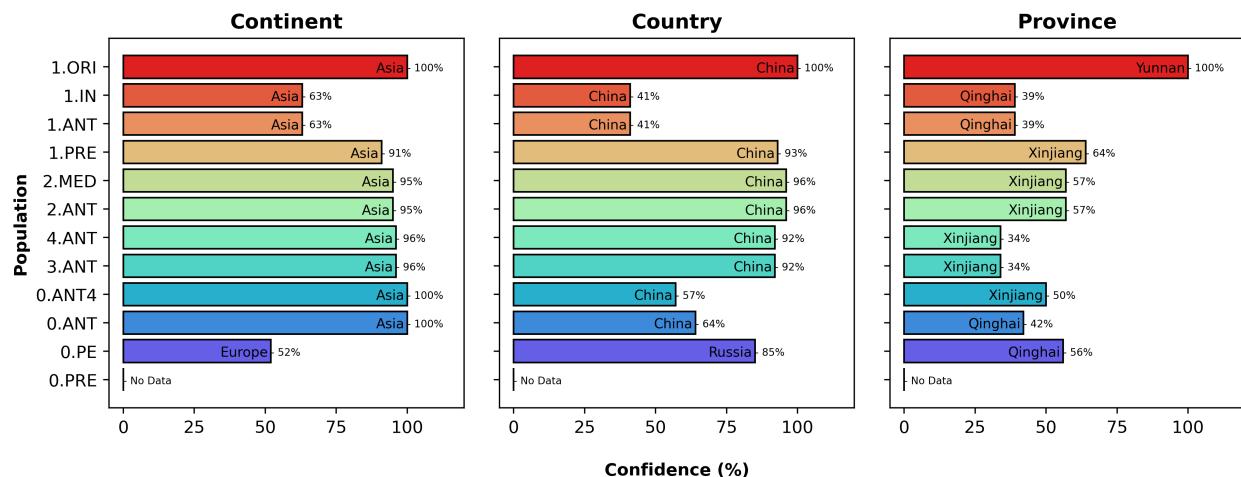


Figure S3: Geographic locations of the ancestral populations from which each population diverged. Ancestral locations were estimated by fitting discrete migration models to the maximum likelihood phylogeny using sampling locations. Internal bar labels indicate the location with the highest confidence given the data.

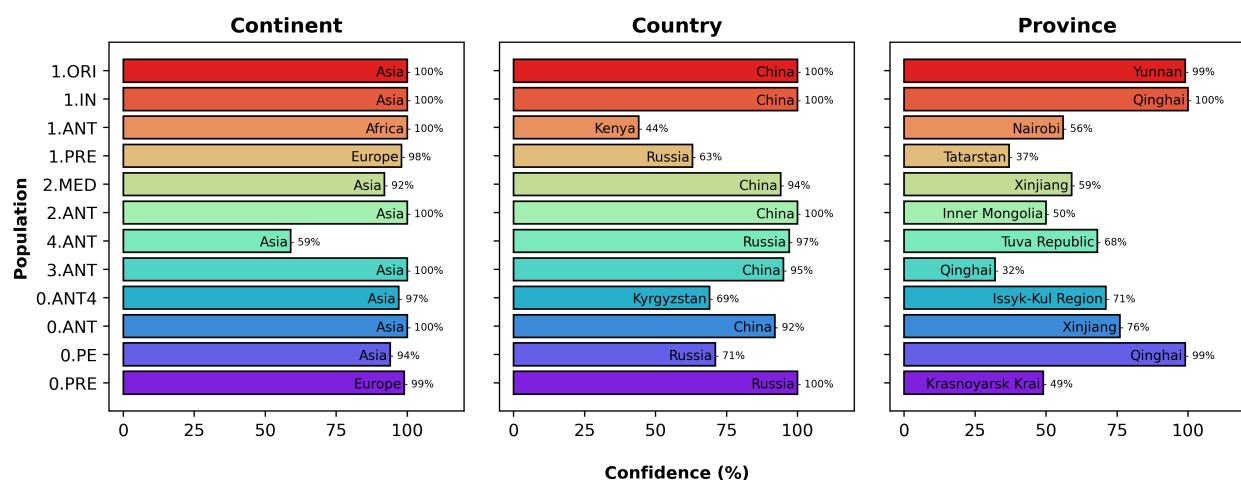


Figure S4: Geographic locations of the most recent common ancestors (MRCA) by population. Ancestral locations were estimated by fitting discrete migration models to the maximum likelihood phylogeny using sampling locations. Internal bar labels indicate the location with the highest confidence given the data.

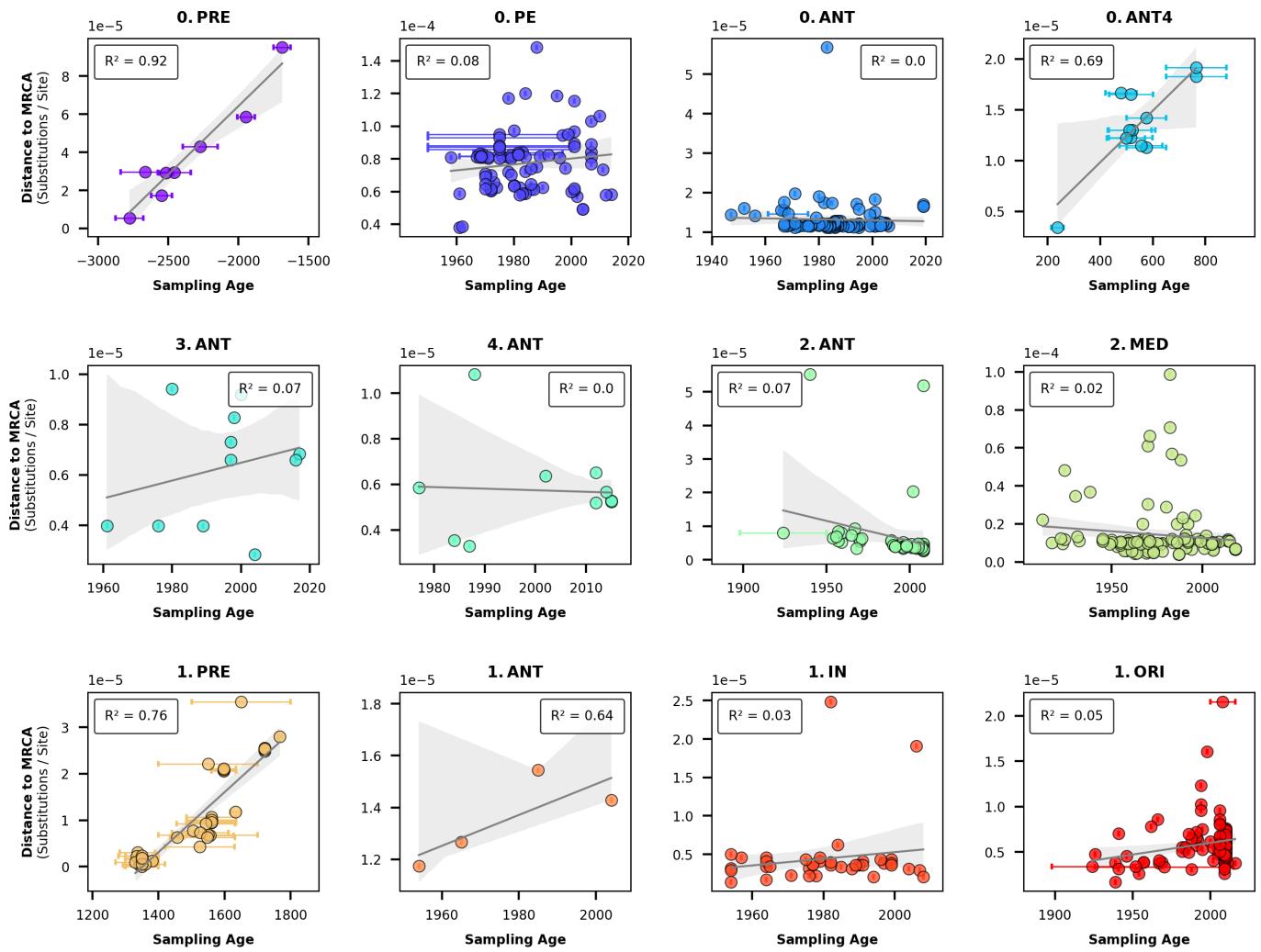
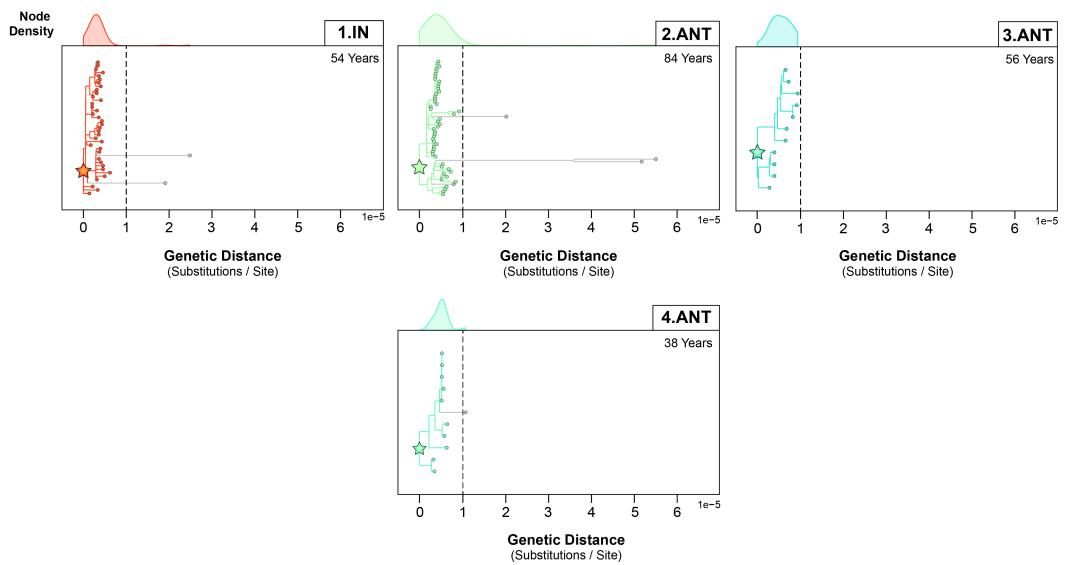
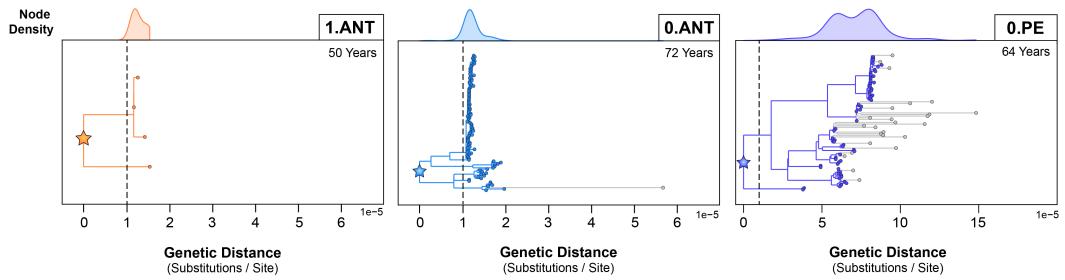


Figure S5: Population-specific rate variation in *Yersinia pestis* as observed through regressions of root-to-tip distance on sampling age. The distance to the population MRCA was calculated using subtrees extracted from the maximum likelihood phylogeny.

A. No Temporal Signal



B. Insufficient Internal Calibrations



C. Temporal Signal With Informative Dates

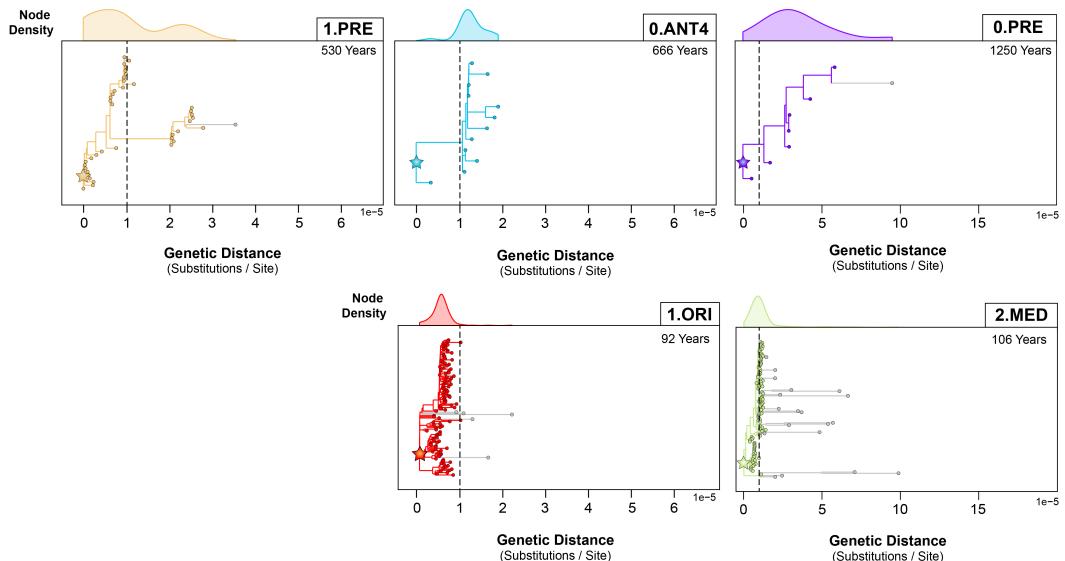


Figure S6: The subtrees extracted from the maximum likelihood phylogeny for the *Yersinia pestis* populations with (A) no detectable temporal signal, (B) ... Stars indicate the node representing the most recent common ancestor (MRCA). Grey branches indicate outliers, as defined by the 90% confidence interval of external branch lengths from all populations.

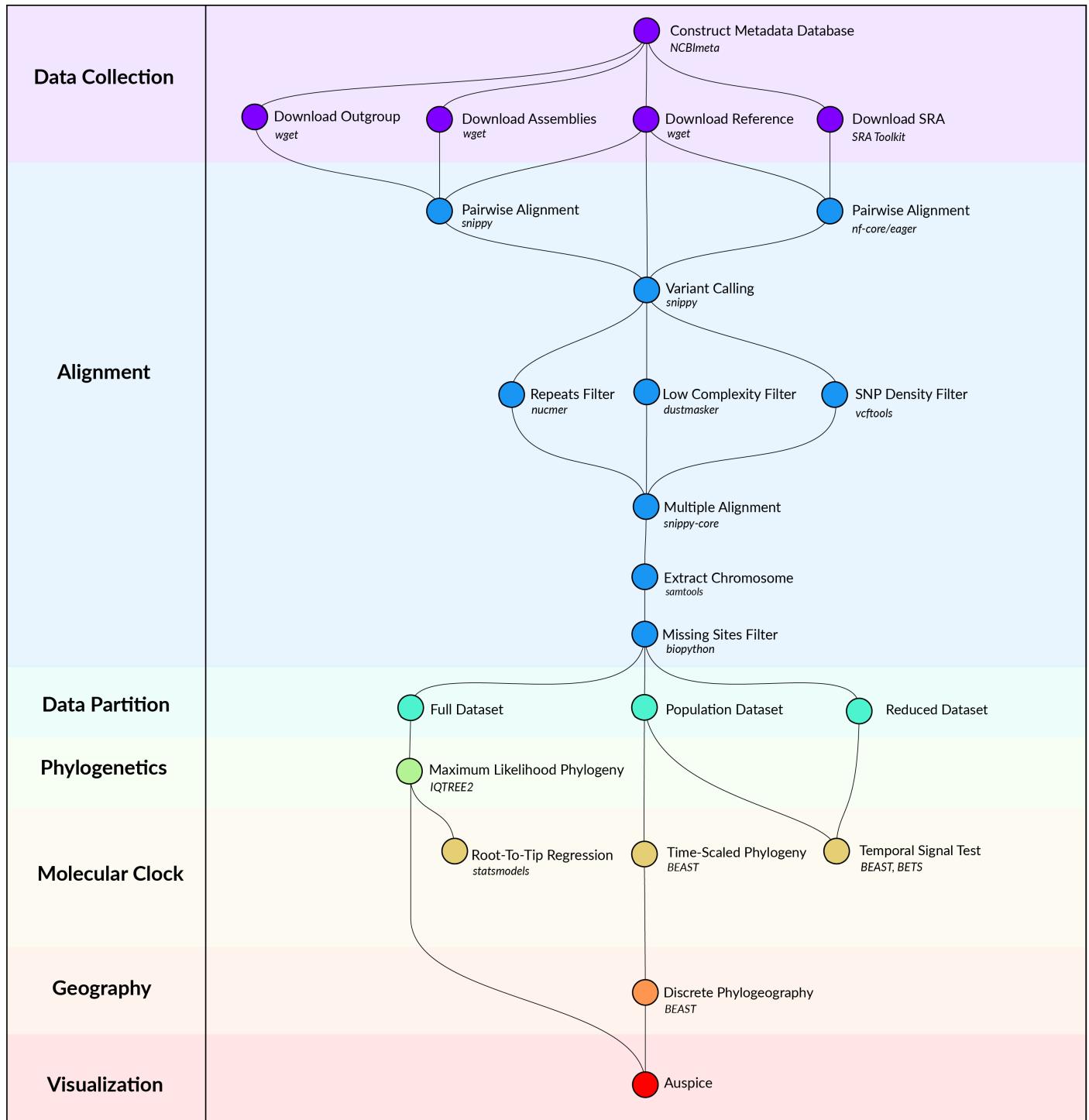


Figure S7: Computational methods workflow.