Figure 1: The spatiotemporal and genetic diversity of 601 *Y. pestis* genomes. Circles represent genomic samples and stars represent internal nodes. Colors distinguish the 12 populations of *Y. pestis*, based on an integrative approach using the major branches, biovar, and time period. **Phylogeny**: The maximum-likelihood phylogeny with branch lengths scaled by genetic distance in substitutions/site. The tree was rooted using two genomes of the outgroup taxa *Y. pseudotuberculosis*, which were subsequently pruned before visualization. **Timeline**: The mean sampling age of each genome. Internal node dates are bounded by ancient DNA calibrations. **Geography**: The sampling location of each