Supplemental Note 1

Bayesian phylogeographic analysis

We conducted the analyses in BEAST v1.10.4 [33]* using BEAGLE library v3.1.2 [34]* for accelerated, parallel likelihood evaluation. The coalescence time was estimated as a normally distributed prior with 6,681±680 years to the J2b2 root node and 5,362±600 to the E2a1 root node. We did not use any other topology constraint. For site model we used GTR substitution model and Gamma site heterogeneity model with 4 categories. We implemented uncorrelated relaxed log-normal clock model. For ucld.mean a log-normal prior was given with $M=5.0e^{-8}$ and $S=5.0e^{-8}$ in real space. For ucld.stdev we gave log-normal prior with $M=5.0e^{-9}$ and $S=5.0e^{-9}$ in real space. Bayesian skyline model was used as the tree model with group sizes of 5. Uniform distribution bounded by 0 and $1.0e^{15}$ was given as skyline.popSize prior. The Brownian random walk (BRW) model [30]* was implemented as the diffusion model in continuous space. We ran three sets of 300,000,000 chains with different random number seeds ensuring ESS values well above 200 for every run. The results were manually checked with Tracer v1.7 software. The trees of the three parallel chains were combined together with the software LogCombiner, leaving the first 10% of trees as burn-in. The maximum clade credibility (MCC) tree was generated with TreeAnnotator using -hpd2D 0.8 flag to summarize 80% of the highest posterior density (HPD) area for the tree nodes. The uncertainties of the MCC tree node locations were visualized with SpreaD3 v0.9.7.1rc software [35]* using the world map in the “geojson” format as base (downloaded from https://github.com/Stefie/geojson-world).

**Reference numbers according to the main text.*