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* You should state whether an appropriate sample size was computed when the study was being designed
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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High-throughput sequence data have been deposited at the European Nucleotide Archive under accession no. PRJEB24921

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Source data 1. Results of the recombination analysis using the methods RDP, GENECOV, Chimera, MaxChi, BootScan, SiScan, 3Seq within RDP v4 pakage (Martin et al., 2015).

Source data 2. Multi-fasta alignment of all modern and ancient genomes used to construct the network and perform recombination analysis.