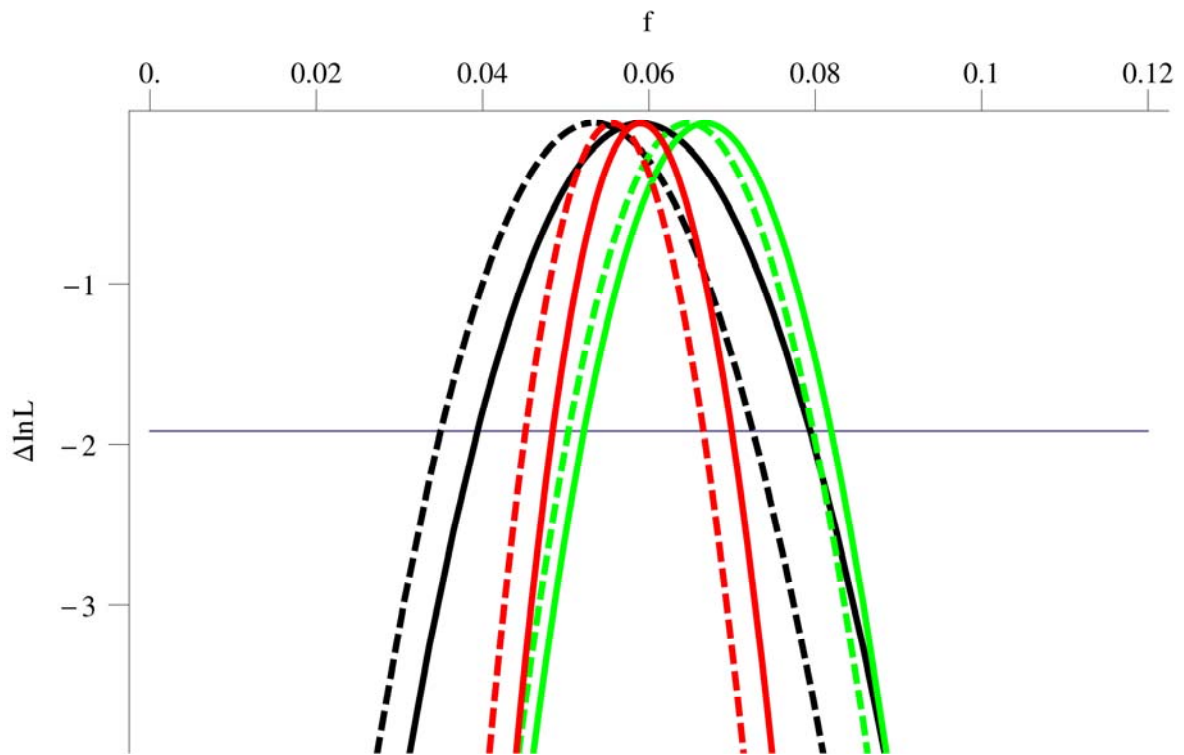
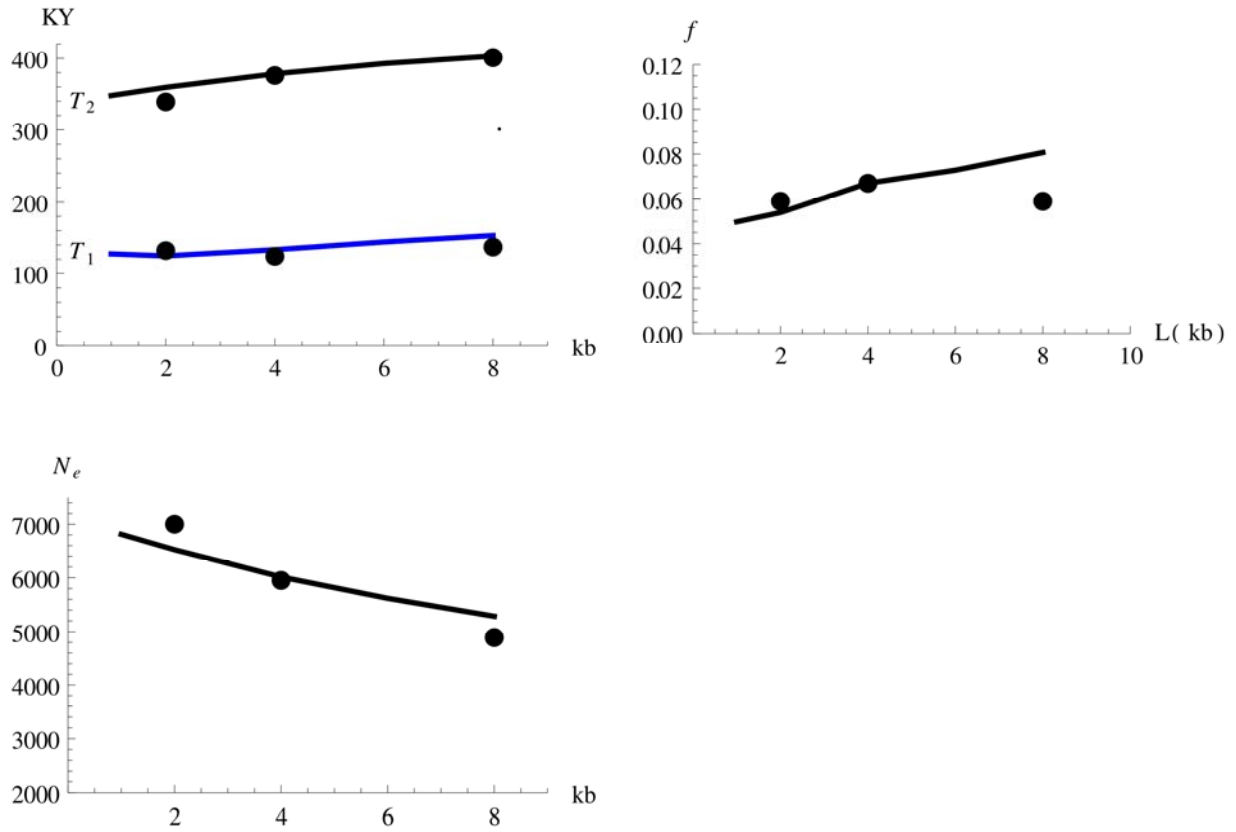


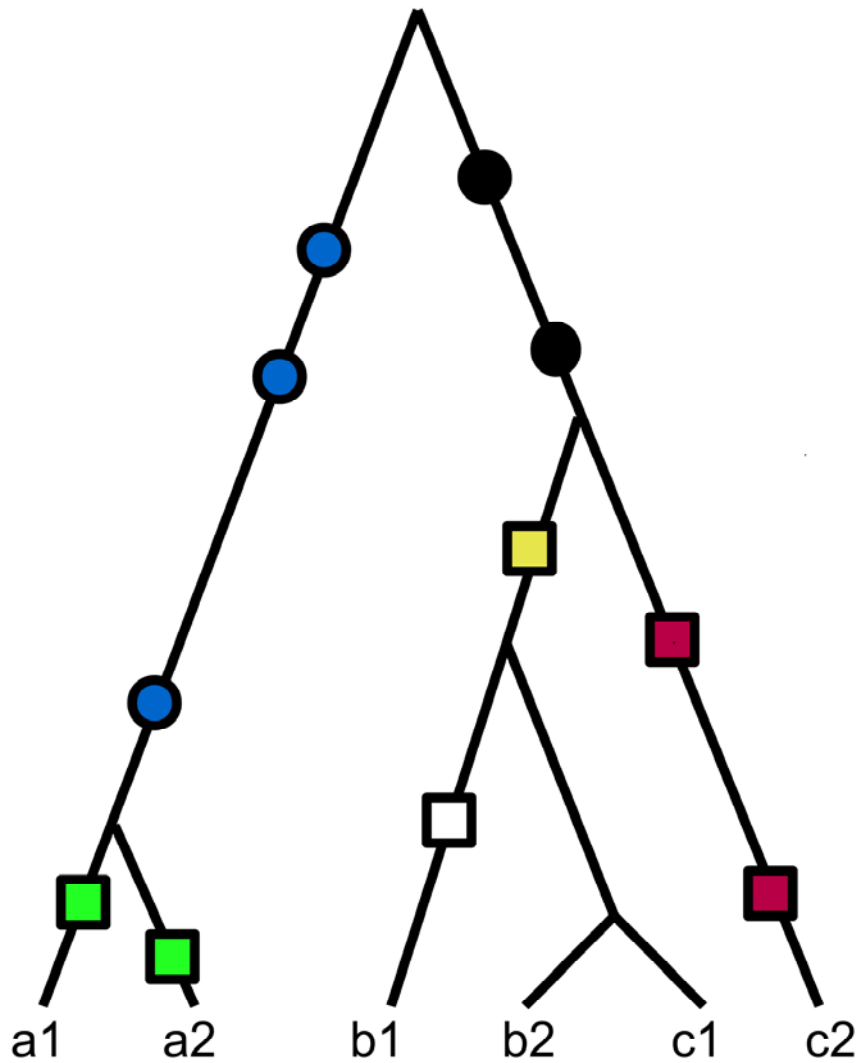
**Figure S1** (A) The expected information ( $E[\Delta \ln L]$ ) to distinguish the IUA model (Durand et al. (2011) parameters) from a null model of strict divergence. The dotted line shows the information contained in 10,000 unlinked SNPs. The grey line corresponds to 10,000 blocks each containing a single SNP on average analysed using maximum likelihood. Black, green and red show results for 2kb, 4kb and 8kb blocks respectively. (B) The expected standard deviation ( $E[SD]$ ) of  $f$  for the likelihood method plotted against block length.



**Figure S2**  $\Delta \ln L$  plotted against the admixture proportion  $f$  (from Neandertals into Eurasians) inferred from the 2 kb (black), 4kb (green) and 8kb data (red) for the CEU (dashed lines) and the CHB (solid) triplets. 95% confidence intervals are given by the horizontal line.



**Figure S3** Expected estimates of parameters from data simulated with recombination (1.3 cM/Mb) plotted against block length. The parameter estimates from the 2, 4 and 8kb analyses of the CEU dataset (assuming no intra-locus recombination) are shown as black dots.



**Figure S4** An example of a genealogy underlying sequence data from three diploid individuals (*a*, *b*, and *c*). Homozygous sites (filled circles) or single heterozygous sites in an individual (white square on the branch leading to *b1*) present no phasing problem. Random phasing of unique heterozygous sites (green and red squares) does not affect the inferred topology of an *a*, *b*, *c* triplet alignment which is uniquely determined by shared derived mutations which may be homozygous (black circles) or complex heterozygous sites (yellow square). Similarly, random phasing of unique heterozygous sites does not introduce biases if the branches of the underlying genealogy have the same length (green squares).

### Files S1-S2

Available for download as .zip files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.162396/-/DC1>

**File S1** Supporting *Mathematica* notebook

**File S2** Contains .txt files of mutational configurations (after filtering and correcting for the excess of Neandertal singletons) in 2kb, 4kb and 8kb autosomal blocks for two triplets: (CEU, YRI, Nean) and (HAN, YRI, Nean). More information can be found in the READ\_ME file included.

**Table S1 The expected information on parameters in the IUA model.** The second row gives the expected standard deviation of parameter estimates based on 10,000 blocks for the parameter values assumed by Durand et al. (2011) (bottom row in bold). Results are shown for 2kb and 4kb blocks.

Parameter	2kb				4kb			
	$T_1$	$T_2$	$T_{gf}$	$f$	$T_1$	$T_2$	$T_{gf}$	$f$
$E[I]$	0.733	0.701	0.003	0.477	1.27	1.22	0.008	0.838
$E[SD]$	0.0117	0.0119	0.178	0.0145	0.00886	0.0091	0.112	0.011
	<b>0.125</b>	<b>0.15</b>	<b>0.60</b>	<b>0.04</b>				

**Table S2 Maximum likelihood estimates of parameters under the IUA<sub>2</sub> model.** Time parameters are scaled in generations; the second row (in bold) gives absolute values, i.e. effective population sizes in individuals and divergence in KY. 95% confidence intervals are shown in brackets.

Data	$\theta$ ( $N_e$ )	$\theta$ ( $N_e$ )	$T_1$	$T_2$	$T_{gf}$	$f$
CEU, 4kb	0.71	0.98	0.411	1.28	0.411	0.065, (0.050–0.080)
	<b>5,910, (5,840–5,990)</b>	<b>8,180, (7,790–8,600)</b>	<b>121, (115–128)</b>	<b>377, (369–385)</b>	<b>121, (79.9– <math>T_1</math>)</b>	
CHB, 4kb	0.71	0.97	0.418	1.26	0.418	0.069, (0.054–0.084)
	<b>5,970, (5,880–6,030)</b>	<b>8,080, (7,700–8,500)</b>	<b>125, (118–131)</b>	<b>376, (368–383)</b>	<b>125, (81.6– <math>T_1</math>)</b>	
CEU, 8kb	1.17	1.84	0.411	1.27	0.411	0.056, (0.045, 0.067)
	<b>4,870, (4,820–4,920)</b>	<b>7,680, (7,360–8,040)</b>	<b>137, (132–142)</b>	<b>399, (393–405)</b>	<b>137, (111– <math>T_1</math>)</b>	
CHB, 8kb	1.17	1.86	0.415	1.26	0.415	0.059, (0.048–0.070)
	<b>4,890, (4,840–4,930)</b>	<b>7,750, (7,520–8,000)</b>	<b>137, (132–145)</b>	<b>401, (395–407)</b>	<b>137, (112– <math>T_1</math>)</b>	

**Table S3 Support  $\Delta \ln L$  relative to the best fitting model (IUA) for alternative models of history.** Strict divergence (Null), divergence with admixture (IUA) or ancestral population structure (AS). The IUA<sub>2</sub> model allows for different effective sizes in the two ancestral populations. The number of model parameters is shown in brackets. Models were estimated without the Neandertal singletons

Dataset	IUA <sub>2</sub> (5)	IUA (4)	AS (4)	Null (3)
CEU, 2kb	0	2.6	13.7	13.7
CHB, 2kb	0	1.9	13.9	13.9
CEU, 4kb	0	3.2	29.9	29.9
CHB, 4kb	0	3.4	32.9	32.9
CEU, 8kb	0	17.4	53.3	53.3
CHB, 8kb	0	18.2	52.7	52.7



**Table S4 Maximum likelihood estimates of parameters under the divergence with admixture (IUA) model.**

Neandertal singletons are excluded from the analysis. Time parameters are scaled in generations and measured from the present. The second row (in bold) gives absolute parameter values, i.e. effective population sizes in individuals and divergence in KY. 95% confidence intervals (in brackets) were calculated assuming that LD between blocks  $>100kb$  apart can be ignored.

Dataset	$\theta$ ( $N_e$ )	$T_1$	$T_2$	$T_{gf}$	$f$
CEU, 2kb	0.425	0.367	0.924	n/a	0.055, (0.036–0.073)
	<b>7,100, (6950–7250)</b>	<b>136, (131–141)</b>	<b>342, (336–349)</b>	n/a	
CHB, 2kb	0.423	0.370	0.930	n/a	0.057, (0.039–0.076)
	<b>7,070, (6930–7210)</b>	<b>136, (130–141)</b>	<b>341, (334–347)</b>	n/a	

**Table S5 Expected (top half) and observed (bottom half) frequencies of blocks with a total numbers of mutations  $S$  for each of the four topology classes.** The expectation is derived assuming the model that provided the best fit to the 2kb (N/YRI/CEU) data (Table 2) and closely fits the observed frequencies.

$S$	0	1	2	3	4	5	6	7	8	Total
(N,(YRI,CEU))	n/a	0.046	0.043	0.024	0.0099	0.0036	0.0012	0.00039	0.00012	0.13
(YRI,(N,CEU))	n/a	0.012	0.013	0.0083	0.0040	0.0016	0.00058	0.00019	0.000062	0.039
(CEU,(N,YRI))	n/a	0.0085	0.011	0.0071	0.0035	0.0014	0.00053	0.00018	0.000058	0.032
Unresolved	0.36	0.28	0.12	0.037	0.0099	0.0023	0.00050	0.00010	0.000020	0.80
(N,(YRI,CEU))	n/a	0.052	0.046	0.023	0.0097	0.0037	0.0013	0.00039	0.00014	0.14
(YRI,(N,CEU))	n/a	0.015	0.015	0.0084	0.0038	0.0016	0.00059	0.00018	0.000052	0.045
(CEU,(N,YRI))	n/a	0.013	0.013	0.0078	0.0036	0.0013	0.00054	0.00020	0.000045	0.040
Unresolved	0.36	0.26	0.11	0.036	0.011	0.0027	0.00078	0.00024	0.000063	0.78

Note that 80% of blocks are topologically unresolved.