

Table S1. Divergence or Coalescence distance estimates

Group	Root height (μt_{MRCA})	SE
Synonymous sites (3324)		
Europeans - H1	0.00092	0.00026
Australians	0.00311	0.00049
Humans	0.00551	0.00057
Human/Neanderthal	0.01719	0.00045
Human/Chimpanzee	0.25768	0.00127
Nonsynonymous sites (7122)		
Europeans - H1	0.00039	0.00012
Australians	0.00082	0.00017
Humans	0.00116	0.00019
Human/Neanderthal	0.00233	0.00009
Human/Chimpanzee	0.01201	0.00012
RNA (4006)		
Europeans - H1	0.00050	0.00018
Australians	0.00096	0.00022
Humans	0.00187	0.00033
Human/Neanderthal	0.00304	0.00002
Human/Chimpanzee	0.04389	0.00007
D-loop (1084)		
Europeans - H1	0.00214	0.00068
Australians	0.00796	0.00152
Humans	0.01171	0.00156
Human/Neanderthal	0.02185	0.00173
Human/Chimpanzee	0.25954	0.00020

Evolutionary rate estimation using BEAST

Rate of evolution was estimated using BEAST (Drummond and Rambaut, 2007). Models of substitution for different sites were obtained using *Modeltest* (Posada and Crandell, 1998) (Table S2). Using an appropriate model for each type of site, strict molecular clock and constant population size models were chosen. Also the model that accommodate for sequence errors was used. The time ranges in table 1 were used as priors for most recent common ancestor (*tMRCA*) and we used the default values for other priors. An input BEAST XML file can be found at

Table S2. Modeltest parameters for BEAST analysis

Sites/Region	Europeans - H1	Australians	Humans	Human/ Neanderthal	Human/ Chimpanzee
Synonymous sites	HKY	TN93	TN93+G	TN93+G	TN93+I
Nonsynonymous sites	HKY	TN93+G	TN93+G+I	TN93+G+I	TN93+G+I
RNA	HKY	HKY	HKY+G	HKY+G	HKY+G+I
D-loop	HKY	HKY+G+I	HKY+G+I	HKY+G+I	HKY+G+I

Table S3. Estimates of rate of molecular evolution using BEAST

Group (No. of genomes)	Calibration times (intervals) KYr	Rate of evolution (x 10 ⁻⁸ s/s/year)			
		Synonymous sites	Nonsynonymous sites	RNA	D-Loop
European - H1 (83)	18 (11-25)	5.8 (10.2-2.1)	2.2 (4.2-0.6)	2.0 (4.6-1.8)	18.5 (34.2-4.9)
Australian (33)	45 (40-65)	7.0 (9.8-4.2)	1.8 (2.6-1.0)	2.1 (3.3-1.1)	22.2 (33.3-13.0)
Humans (100)*	150 (100 -200)	4.4 (6.3-2.6)	0.9 (1.4-0.5)	1.5 (2.3-0.8)	12.7 (18.8-7.0)
Human/Neanderthal	500 (300-700)	3.5 (5.1-2.0)	0.7 (1.1-0.4)	0.8 (1.2-0.4)	6.8 (10.8-3.1)
Human/Chimpanzee	6000 (5000-7000)	4.3 (5.4-3.2)	0.3 (0.4-0.2)	0.6 (0.9-0.4)	5.5 (8.2-3.3)
Ratio H1/Human-chimp		1.3 (0.7-1.9)	7.3 (3.0-10.5)	3.3 (2.6-4.5)	3.4 (1.5-4.2)

Figure S1

