Table 6. Evolutionary model and mutation rate estimated for each locus

Locus	Evolutionary model	Mutation rate (per site per yr)
T2557	TIM + I	1.34×10^{-9}
T2191	GTR + I	1.83×10^{-9}
T2568	HKY	6.84×10^{-10}
T1636	K81uf + I	2.60×10^{-9}
T2020	HKY	1.20×10^{-9}
T1584	TVM	1.75×10^{-9}
T2019	HKY	9.18×10^{-10}
T2986	HKY	9.22×10^{-10}
T953	K81uf + I	5.17×10^{-10}
T2021	TrN	1.61×10^{-9}
T2472	TVM + I	1.21×10^{-9}
T1469	K80	2.75×10^{-10}
T151	HKY	1.09×10^{-9}
T1364	F81	7.08×10^{-10}
T2609	GTR + I	1.54×10^{-9}
T2659	HKY + I	7.46×10^{-10}
T1251	F81	1.60×10^{-9}
T24894	HKY	1.39×10^{-9}
T2041	F81 + I	1.33×10^{-9}
T2294	K80	9.48×10^{-10}
T2984	TIM + I	1.74×10^{-9}
T10604	HKY	6.17×10^{-10}
T812	TrN	1.13×10^{-9}
T2920	TVM	1.12×10^{-9}
T2012	TVM	7.25×10^{-10}
T784	K81uf + I	1.76×10^{-9}
T787	K81uf	1.03×10^{-9}

Locus	Evolutionary model	Mutation rate (per site per yr)
T813	K81uf	7.22×10^{-10}
T2085	TVMef + I	1.05×10^{-10}
T2064	TrN	4.11×10^{-10}
T2352	TrN + I	1.01×10^{-10}
T2560	HKY	3.79×10^{-10}
T1412	HKY	9.16×10^{-10}
T1419	TrN + I	9.38×10^{-10}
T1482	TrN + I	1.25×10^{-10}
T2963	TrN	2.86×10^{-10}
T2265	HKY + I	9.49×10^{-10}
T2266	HKY	7.78×10^{-10}
T2558	HKY	8.44×10^{-10}
T2906	HKY	3.06×10^{-10}
T2987	JC	9.17×10^{-10}
T946	HKY	1.26×10^{-9}
T2988	HKY	1.18×10^{-9}
T866	K81uf	1.37×10^{-9}
T1506	F81	4.46×10^{-10}
T2563	HKY + I	1.31×10^{-9}
T2018	HKY	1.45×10^{-9}
T2924	HKY	1.62×10^{-9}
T1386	TrN	1.74×10^{-9}
T864	HKY	1.59×10^{-9}
Average	-	1.10×10^{-9}

Mutation rates were estimated from DNA sequences inferred with PHASE 2.0
[Stephens M, Smith NJ, Donnelly P (2001) *Am J Hum Genet* 68:978-989] and an
expectation maximization algorithm [Excoffier L, Slatkin M (1995) *Mol Biol Evol*
12:921-927], two phasing methods shown as being accurate [Marchini J, Cutler D,
Patterson N, Stephens M, Eskin E, Halperin E, Lin S, Qin ZS, Munro HM, Abecasis G R,

et al. (2006) *Am J Hum Genet* 78:437-450]. Whenever the two phasing methods resulted in different estimates (which occurred for 15 human and 16 chimpanzee loci) the method suggesting the smallest number of different haplotypes was preferred. Human and chimpanzee haplotypes were then aligned, and the best sequence evolutionary model was selected by using ModelTest [Posada D, Crandall KA (1998) *Bioinformatics* 14:817-818]. The mutation rate for each locus was estimated byb using the average genetic distance between human and chimpanzee haplotypes under the most likely evolutionary model and by assuming a generation time of 25 years and a divergence time of 6 million years [Haile-Selassie Y, Suwa G, White TD (2004) *Science* 303:1503-1505] between the two species. The full names, references, and parameters for the evolutionary models can be found in the ModelTest manual (http://darwin.uvigo.es/software/modeltest.html).