

Dataset	Figure	Model	G	I	Reference (see below)
<i>nr28S</i> rDNA	Figure 3A; Figure S1	GTR	0.449	0.119	[1]
<i>cp23S</i> rDNA	Figure S2	TN	0.3486		[2]
<i>coI</i>	Figure 3B; Figure S3	GTR	0.2749		[1]
<i>calmodulin</i>	Figure 3C; Figure S4	HKY	0.1701		[3]
<i>rad24</i>	Figure 3D; Figure S5	J2 (TIM)	0.7432	0.3227	[4]
<i>actin</i>	Figure 3E; Figure S6	GTR	0.3884		[1]

1. Lanave C, Preparata G, Saccone C, Serio G (1984) A new method for calculating evolutionary substitution rates. *J Mol Evol* 20: 86-93.
2. Tamura K, Nei M (1993) Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol Biol Evol* 10: 512-526.
3. Hasegawa M, Kishino H, Yano K (1985) Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *J Mol Evol* 22: 160-174.
4. Rodriguez F, Oliver JL, Marin A, Medina JR (1990) The general stochastic model of nucleotide substitution. *J Theor Biol* 142: 485-501.