

Model	Type of Data Set	Supports for Great Ape parasites sister group of:								
		Rodent			Primate+ Rodent		Primate			
		<i>PP</i>	<i>SH</i>	<i>BS</i>	<i>PP</i>	<i>SH</i>	<i>BS</i>	<i>PP</i>	<i>SH</i>	<i>BS</i>
<i>GTR<sub>nt</sub></i> + $\Gamma_4$ (+ <i>I</i> )	Cod. pos. 1, 2, 3	0.999	0.93	0.821	0.001, *	0.174	0.000, *	0.004		
	Cod. pos. 1, 2	0.961	0.78	0.681	0.039, *	0.316	0.000, *	0.003		
	Cod. pos. 3	0.793	0.39	0.587	0.146, *	0.249	0.060, *	0.104		
<i>CAT</i> + <i>GTR<sub>nt</sub></i> + $\Gamma_4$	Cod. pos. 1, 2, 3	0.995,			0.003,		0.001,			
	Cod. pos. 1, 2	0.921,			0.057,		0.022,			
	Cod. pos. 3	0.648,			0.108,		0.054,			
<i>GTR<sub>nt</sub></i> + <i>BP</i> + $\Gamma_4$	Cod. pos. 1, 2, 3	0.949,			0.005,		0.001,			
	Cod. pos. 1, 2	0.987,			0.012,		0.000,			
	Cod. pos. 3	0.717,			0.221,		0.062,			
<i>JTT</i> + $\Gamma_4$ (+ <i>I</i> )		0.919	0.46	0.416	0.081, *	0.571	0.000, *	0.007		
<i>GTR<sub>aa</sub></i> + $\Gamma_4$		0.978,			0.022,		0.000,			
<i>CAT</i> + $\Gamma_4$	Amino Acid	0.629,			0.352,		0.018,			
<i>CAT</i> + <i>JTT</i> + $\Gamma_4$		0.802,			0.195,		0.003,			
<i>CAT</i> + <i>BP</i> + $\Gamma_4$		0.747,			0.241,		0.011,			

Supplementary Table S2: **Analyses of the 33 taxa and 3 mitochondrial gene data sets.** Dependency of clade support on codon positions (“Cod. pos.”), amino-acid translation and on assumptions of various probabilistic models of substitution (*GTR<sub>nt</sub>*, *GTR<sub>aa</sub>* and *JTT*: single matrix model, *CAT*: site heterogeneous mixture model, *BP*: time heterogeneous model). Rates across site model components are defined as + $\Gamma_4$  + *I* under maximum likelihood (ML) and as + $\Gamma_4$  under Bayesian (BI) methods. Cells display support as [*PP*, *SH*, *BS*], with *PP*: posterior probability (BI), *SH*: Shimodaira-Hasegawa-like support (ML), and *BS*: bootstrap support (ML). “\*”: not applicable. Main lineages of mammal parasites are defined according to their host preference: “Rodent”, “Primate” and “Great Ape” (see Additional file 1, Table S1).