

Sampled Taxa	Support 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>P. fal. P. ber.</i>	0.007,	*	, 0.149	0.991,	0.86,	0.823	0.001,	*	, 0.028
<i>P. fal. P. cha.</i>	0.525,	0.13,	0.508	0.466,	*	, 0.429	0.009,	*	, 0.063
<i>P. fal. P. yoe.</i>	0.065,	*	, 0.285	0.922,	0.49,	0.601	0.013,	*	, 0.114
<i>P. gab. P. ber.</i>	0.153,	*	, 0.198	0.445,	*	, 0.393	0.402,	0.01,	0.385
<i>P. gab. P. cha.</i>	0.601,	0.13,	0.498	0.029,	*	, 0.076	0.369,	*	, 0.423
<i>P. gab. P. yoe.</i>	0.115,	*	, 0.226	0.101,	*	, 0.181	0.783,	0.54,	0.572
<i>P. rei. P. ber.</i>	0.000,	*	, 0.076	0.999,	0.94,	0.894	0.001,	*	, 0.029
<i>P. rei. P. cha.</i>	0.193,	*	, 0.386	0.798,	0.27,	0.557	0.008,	*	, 0.057
<i>P. rei. P. yoe.</i>	0.010,	*	, 0.151	0.984,	0.77,	0.745	0.005,	*	, 0.104

Supplementary Table S8: **Robustness of clade support in trees designed to display long branches.** Each of the 9 taxon samples comprised the three most distantly related *Leucocytozoon* species, the 14 primate parasites, and two single representatives of parasites of great apes and of rodents, respectively. In each case, 14 taxa were removed from the complete nucleotide data-set comprising 33 taxa and 3 concatenated genes, 3308 sites. Phylogenetic analyses were performed under models $GTR_{nt} + \Gamma_4 + I$ and $GTR_{nt} + \Gamma_4$, for maximum likelihood (ML) and Bayesian (BI) methods, respectively. Cells display support as follows: [*PP*, *SH*, *BS*], with *PP*: posterior probability (BI), *SH*: Shimodaira-Hasegawa-like support (“*”: not applicable, ML), and *BS*: bootstrap support (ML). Main lineages of mammal parasites are defined according to their host preference: “Rodent”, “Primate” and “Great Ape” (see Additional file 1, Table S1). “*P. fal.*”: *P. falciparum*, “*P. rei.*”: *P. reichenowi*, “*P. gab.*”: *P. gaboni*, “*P. yoe.*”: *P. yoelii*, “*P. ber.*”: *P. berghei*, “*P. cha.*”: *P. chabaudi*.