



Supplementary Figure S2: **Phylogenetic tree of first and second codon position analyzed under $CAT + GTR + \Gamma_4$** . Bayesian phylogenetic reconstruction using PhyloBayes 3.0 [43]. The $CAT + GTR_{nt} + \Gamma_4$ substitution model was applied to first and second codon positions of the 33 taxa data set. *P. falciparum* and 2 of its relatives infecting great ape hosts, *P. reichenowi* and *P. gaboni*, formed a monophyletic clade with 3 rodent parasites, *P. yoelii*, *P. berghei* and *P. chabaudi* (posterior probability $PP = 0.92$). Posterior probabilities equal to 1 were removed.