



Additional file 1: Figure S1. Majority-rule consensus tree based on a PhyloBayes analysis of complete mitochondrial genomes from ape-infecting *Plasmodium* parasites. The alignment is based on the mitochondrial dataset from Liu et al. (2010) and only contains sequences from Clades C1 (from Chimpanzees) and G1 (from Gorillas; also contains human *P. falciparum*). Two contigs from the Gorilla genome assembly, which contain parasite-derived mitochondrial fragments, were added to the alignment. Bayesian posterior probabilities are given at the nodes. The tree was rooted with the C1 clade of Chimpanzee-infecting *Plasmodium* parasites. All EMBL/Genbank acc. nos. are given in parentheses.