



Supplementary Figure S3: **Phylogenetic tree of 18 ASL genes.** Bayesian reconstruction under the  $GTR_{nt} + \Gamma_4$  model. Edges with  $PP < 0.9$  were collapsed, and  $PP = 1$  are not shown. The ASL phylogeny is not congruent with a monophyly of mammal malaria parasites.