Supplementary Fig. S1. A maximum likelihood (ML) tree based on sequences of the gene encoding the small ribosomal subunit rRNA (SSU). A representative of each SSU species/genotype sequenced in this study is highlighted in bold and boxed. GenBank accession numbers, host species (Latin name) and country of isolate origin are shown in after the isolate identifier. The ML tree was rooted with a SSU sequence from *Plasmodium falciparum* [Acc. No.: EF472536]. Numbers at the nodes represent the bootstrap values gaining more than 50% support. Branch length scale bar indicates the number of substitutions per site.