Supplementary Fig. S2. A maximum likelihood (ML) tree based on actin gene sequences. A representative of each actin species/genotype from 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 an actin 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.