



Additional file 4: Figure S4

Bayesian inference tree of *CytB* lineages (474 bp) belonging to the genus *Plasmodium*. Bayesian posterior probabilities and Maximum likelihood bootstrap values are indicated at most nodes. A sequence of *Haemoproteus tinnunculi* was used as outgroup. The scale bars indicate the expected number of substitutions per site according to the model of sequence evolution applied. Lineage names in bold letters were found in accipitriform raptors. Species names indicate that the lineages were already linked to the respective morphospecies.