Supplementary Table S2: Analyses of the 33 taxa and 3 mitochondrial gene data sets. Dependency of clade support on codon positions (“Cod. pos.”), amino-acid translation and on assumptions of various probabilistic models of substitution ($GTR_{nt}$, $GTR_{aa}$ and $JTT$): single matrix model, $CAT$: site heterogeneous mixture model, $BP$: time heterogeneous model. Rates across site model components are defined as $+\Gamma_4 + I$ under maximum likelihood (ML) and as $+\Gamma_4$ under Bayesian (BI) methods. Cells display support as $[PP, SH, BS]$, with $PP$: posterior probability (BI), $SH$: Shimodaira-Hasegawa-like support (ML), and $BS$: bootstrap support (ML). “*”: not applicable. Main lineages of mammal parasites are defined according to their host preference: “Rodent”, “Primate” and “Great Ape” (see Additional file 1, Table S1).