



Supplementary Figure I. Maximum likelihood tree (lnL = -2062.54) of 478 bp of cytochrome b sequenced from *Leucocytozoon* lineages hosted by South African birds. The tree was inferred using an HKY model of evolution with a discrete gamma distribution for rate variation among sites (5 categories; $G = 0.2285$). Nodal support is based on 1000 bootstrap replicates; bootstrap support >50% is shown. Numbers in parentheses indicate the number of individuals per species that hosted each *Leucocytozoon* lineage; lineage names are given after each bracket.