**Figure S3.** Phylogenetic relationships of the *12S-16S* mtDNA lion haplotypes. Neighbour-joining tree of the 1,882 bp *12S-16S* mtDNA sequences. Bootstrap values are placed at each branchpoint for the minimum evolution/maximum parsimony/maximum likelihood analyses, respectively (ME/MP/ML). Outgroups: Ppa – leopard, *Panthera pardus*; Pun – snow-leopard, *Panthera uncia*. The symbol (●) represents nodes with bootstrap support < 50 or an inferred polytomy in the bootstrap 50% majority-rule consensus tree.