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.