



Appendix II(q). Maximum likelihood phylogram derived from the 12S rRNA sequence data from 55 haplotypes from the 216 *Lepilemur* individuals with 19 out-group taxa. The phylogram presented with branch lengths proportional to the number of changes (values specified on the branches). The maximum likelihood phylogram (-ln likelihood = 6137.946) was obtained from the D-loop and PAST combined sequence alignment from a transition/transversion ratio of 3.86 ($\kappa = 8.230$) and a gamma shape parameter of 0.27.