

APPENDIX 9. Maximum Likelihood (ML) trees of Arvicolinae mitochondrial genomes (excluding Control Region) and using the *Pliomys lenki* consensus sequences generated with regular ancient DNA mapping stringent parameters (STR sequence, left) and with relaxed parameters (REL sequence, right). Numbers in nodes indicate Maximum Likelihood Bootstrap (MLB) values. Circles indicate MLB=100. Genbank accession numbers are listed in Appendix 2 and partitioning scheme in Appendix 3.

