

**APPENDIX 10.** Bayesian 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 Posterior Probability (PP) values. Circles in nodes indicate PP=1. Genbank accession numbers are listed in Appendix 2 and partitioning scheme in Appendix 3.

