

APPENDIX 8. Genome characteristics, missing data and PCGs stop codons of the two mitochondrial genomes generated for *Pliomys lenki* using stringent (STR) and relaxed (REL) parameters in the BWA iterative mapping.

Missing data per gene (?)		219A <i>Pliomys</i>		Stop codon
ESTIMATED TOTAL LENGTH (bp)		STR	REL	
tRNA-Phe	67	11	11	
12S_rRNA	947	45	45	
tRNA-Val	70	0	0	
16S_rRNA	1560	237	80	
tRNA-Leu	75	0	0	
ND1	955	144	80	T**
tRNA-Ile	68	0	0	
tRNA-Gln	75	0	0	
tRNA-Met	69	0	0	
ND2	1035	575	178	TAA
tRNA-Trp	67	0	0	
tRNA-Ala	69	0	0	
tRNA-Asn	70	0	0	
Origin of replication	36	0	0	
tRNA-Cys	68	0	0	
tRNA-Tyr	65	0	0	
COXI	1545	937	14	TAG
tRNA-Ser	69	0	0	
tRNA-Asp	68	0	0	
COX2	684	0	0	TAA
tRNA-Lys	66	66	0	
ATP8	204	59	0	TAA
ATP6	681	100	100	UNKNOWN
COX3	784	511	167	T**
tRNA-Gly	68	0	0	
ND3	348	237	237	TAA
tRNA-Arg	68	0	0	
ND4L	297	86	0	TAA
ND4	1378	919	214	T**
tRNA-His	68	68	0	
tRNA-Ser	59	39	0	
tRNA-Leu	69	0	0	
ND5	1812	333	177	TAG
ND6	525	190	182	TAA
tRNA-Glu	69	0	0	
CYTB	1143	386	7	TAA
tRNA-Thr	66	17	0	
tRNA-Pro	68	0	0	
Contro Region	960	341	329	