

Appendix Sequence Summary Table III. Summary of Sequence Variation across the 211 Lemurs Examined

Genes	All PAST	COIII	ND3	ND4L <sup>a</sup>	ND4 <sup>a</sup>	tRNAs	Gly	Arg	His	Ser	Leu	Phe	12s rRNA
Characters (nucleotides) for PAST Fragment	2378	30	348	297	1378	328	73	73	70	65	47		
Constant	1046	19	152	117	581	178	46	42	34	25	31		
Parsimony-uninformative	128	0	16	19	59	26	4	6	3	12	1		
Parsimony-informative	1204	11	180	161	728	124	23	25	33	28	15		
Informative proportion	0.51	0.37	0.52	0.54	0.53	0.38	0.32	0.34	0.47	0.43	0.32		
Insertions/deletions	21	0	0	0	0	21	5	5	3	8	0		
Retention index	0.92	0.91	0.90	0.81	0.92	0.88	0.90	0.89	0.93	0.86	0.88		
Characters (nucleotides) for 12s rRNA Fragment	877											22	855
Constant	513											5	508
Parsimony-uninformative	42											2	40
Parsimony-informative	322											15	307
Informative proportion	0.37											0.68	0.36
Insertions/deletions	33											6	27
Retention index	0.93											0.93	0.91
Characters (nucleotides) for Combined Sequence <sup>b</sup>	3255												
Constant	1530												
Parsimony-uninformative	199												
Parsimony-informative	1526												
Informative proportion	0.47												
Insertions/deletions	54												
Retention index	0.93												
Characters (nucleotides) for D Loop Fragment	554												
Constant	346												
Parsimony-uninformative	18												
Parsimony-informative	190												
Informative proportion	0.34												
Insertions/deletions	47												
Retention index	0.95												

<sup>a</sup>ND4 and ND4L overlap by seven bases.

<sup>b</sup>Combined sequences for PAST and 12s rRNA Fragments only.