

Table S4 Counts of polymorphic (*P*) and divergent (*D*) nonsynonymous (*N*) and synonymous (*S*) sites along with summary statistics of the MK table using 36 of the 38 mitochondrial haplotypes in our sample that were independently sequenced and assembled by Richardson *et al.* (2012). MK counts are from the “more inclusive” method.

Gene	P_N	P_S	D_N	D_S	NI^a	$Z^*{}^b$	$P_{FET}{}^c$
<i>ATPase6</i>	5	2	11	35	7.95	-0.78	0.021
<i>ATPase8</i>	1	0	2	8	6.00	-0.78	0.273
<i>COI</i>	1	16	8	101	0.79	-0.12	1.000
<i>COII</i>	0	5	6	39	0.95	0.02	1.000
<i>COIII</i>	1	9	8.5	47.5	0.62	-0.01	1.000
<i>Cyt-b</i>	2	5	17.5	67.5	1.54	-0.27	0.641
<i>ND1</i>	2	3	11	45	2.73	-0.46	0.287
<i>ND2</i>	1	5	23	39	0.34	0.26	0.413
<i>ND3</i>	0	1	5	22	1.92	-0.28	1.000
<i>ND4</i>	1	6	23	63	0.46	0.12	0.673
<i>ND4L</i>	1	1	1	7	7.00	-0.60	0.378
<i>ND5</i>	2	10	61.83	107.17	0.35	0.33	0.218
<i>ND6</i>	0	4	21.5	22.5	0.21	0.68	0.114

^a A count of 1 was added to each cell when calculating $NI = \frac{D_S P_N}{D_N P_S}$ for any locus with a zero count in any cell.

^b $Z^* = \text{Log}_{10} \left(\frac{(D_N+1)(P_S+1)}{(D_S+1)(P_N+1)} \right)$, as in (Presgraves 2005).

^c *P*-value from Fisher’s Exact Test of the MK table.