

## 2. Base composition bias assessed in PAUP.

Dataset	Gene	Length (bp)	Full nt coding	RY coding
Dataset 1	12S	360	0.00000000	0.00018845
	16S	437	0.00000000	0.89975358
	18S	1768	0.75730695	---
	28S	1825	0.00000000	1.00000000
	H3 1 <sup>st</sup> &2 <sup>nd</sup> pos.	228	1.00000000	---
	H3 3 <sup>rd</sup> pos.	114	0.00000000	0.98849718
Dataset 2	12S	337	0.00000904	0.25868942
	16S	462	0.19044689	---
	COII 1 <sup>st</sup> &2 <sup>nd</sup> pos.	456	0.99921741	---
	COII 3 <sup>rd</sup> pos.	228	0.00000000	0.00000052
	18S	1798	0.46180295	---
	28S	1699	0.00000057	0.99999563
	H3 1 <sup>st</sup> &2 <sup>nd</sup> pos.	222	1.00000000	---
	H3 3 <sup>rd</sup> pos.	111	0.00000000	0.89687779
	EF1a 1 <sup>st</sup> &2 <sup>nd</sup> pos.	714	1.00000000	---
	EF1a 3 <sup>rd</sup> pos.	357	0.00000000	0.67399420