

Table 8S. Test of substitution saturation for Pleuronectoidei PCGs mitogenome sequences

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OTU									
Number	Iss	Iss.cSym	T	d.f.	P	Iss.cAsym	T	d.f.	P
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4	0.309	0.854	87.831	7539	0.0000	0,845	86.405	7539	0.0000
8	0.310	0.846	77.125	7539	0.0000	0,766	65.633	7539	0.0000
16	0.310	0.842	72.880	7539	0.0000	0,680	50.723	7539	0.0000
32	0.314	0.815	66.858	7539	0.0000	0,570	34.233	7539	0.0000
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Note. Analysis performed on fully resolved sites only. Testing whether the observed Iss is significantly lower than Iss.c. IssSym is Iss.c assuming a symmetrical topology. IssAsym is Iss.c assuming an asymmetrical topology. Two-tailed t-tests are used (Xia et al. 2003; Xia and Lemey 2009).

Interpretation of results:

Significant Difference		

	Yes	No

Iss < Iss.c	Little saturation	Substantial saturation

Iss > Iss.c	Useless sequences	Very poor for phylogenetics