

Appendix 7. Amount of unalignable sequence data in bp and the percentage deleted for each gene.

Data set	Gene	Sequence length, bp	Total deleted sequence, bp	Percentage (%) sequence deleted
Species-level comparisons				
Lepidoptera	COI	1545	75	4.9
	COII	790	50	6.3
	ND5	895	112	12.5
Arachnida	16S	1035	150	14.5
	COI	485	14	2.9
Cephalopoda	COI	657	0	0.0
	16S	580	123	21.2
Gastropoda	28S	1680	124	7.4
	COI	1220	11	0.9
Echinodermata	18S	1880	159	8.5
	28S	390	58	14.9
Platyhelminthes	18S	2620	911	34.8
	COI	960	150	15.6
Family-level comparisons				
Hymenoptera	28S	591	142	24.0
	COI	421	0	0.0
Bivalvia	18S	1819	106	5.1
	28S	3509	180	5.1
	COI	1074	63	5.9
Annelida	18S	1624	241	12.9
	H3	1270	55	4.2

Monogenea	18S	1898	242	11.3
	28S	930	405	30.3