Table S2: Draft mitochondrial DNA genomes of six *Cryptolestes* species from Australia (*C. ferrugineus*, *C. pusilloides*, *C. pusillus*), China (*C. turcicus*, *C*. sp. 'WTT-2013'), and Malaysia and Vietnam (*C*. sp. 'WTT-2016'). The non-Australian individuals were all from biosecurity inspections at Australia's border interceptions. We identified the *C*. sp. WTT-2013 individual found in goods from China based on partial mtCOI sequence identity as reported in (Tay et al., 2016). The temporarily named '*C*. sp. 'WTT-2016' specimens found in goods from Malaysia and Vietnam represented a putative species based on partial mtCOI gene and concatenated mitochondrial DNA protein coding genes phylogenetic analyses (refer to main text). The estimated mitogenome sequence lengths, and percentage (%) AT content of 13 concatenated protein coding genes (11,024bp) are also provided. † indicates the A-T content of the full draft mitogenomes. Assembled mitogenomes of the six *Cryptolestes* species are available from CSIRO's Data Access Portal (Tay et al., 2024).

Species	**Country**	**Estimated length**	**Commodity**	**AT% (total†)**
C. ferrugineus	Australia	156,156 bp	Wheat	75.2% (76.6)
C. pusillus	Australia	15,319 bp	Wheat	74.0% (75.6)
C. pusilloides	Australia	15,213 bp	Wheat	75.3% (76.7)
C. pusilloides	Australia	15,179 bp	Oats	75.1% (76.5)
C. sp. WTT-2013	China	15,231 bp	Rhizomes (seized in mail)	74.2% (75.4)
C. turcicus	China	15,341 bp	Rhizomes (seized in mail)	75.2% (76.5)
C. sp. WTT-2016	Vietnam	15,186 bp	Personal effects	72.9% (74.6)
C. sp. WTT-2016	Malaysia	15,186 bp	Personal effects	72.9% (74.6)