Figure S2: Schematic representation of the published *C. ferrugineus* (KT182067; (Sun, Li, et al., 2016) mitogenome aligned to the mitogenomes of: **[a]** *C.* sp. 'WTT-2013' (Tay et al., 2024), and **[b]** *C. pusilloides* (Tay et al., 2024). **[a]** The *C. ferrugineus* (KT182067) mitogenome showed high level of nucleotide homologies with *C.* sp. 'WTT-2013' (Tay et al., 2024) as seen from two randomly selected regions indicated by the two bi-directional arrows with low *p*-dist values (0.52-1.42%) expected at the intra-specific level (see Table S5). The red rectangle boxed region showed high *p*-dist value (15.61%) expected for inter-specific nucleotide difference (see Table S5). **[b]** Comparison between the published *C. ferrugineus* of Sun, Li, et al. (2016) and the *C. pusilloides* mitogenome from this study (see (Tay et al., 2024), showing overall high nucleotide dissimilarity as expected for inter-specific difference except for the boxed region which showed high nucleotide homology expected at the intra-specific level. The overall patterns suggested that the *C. ferrugineus* (KT182067) mitogenome consists of sequences from two divergent species (i.e., *C.* sp. 'WTT-2013', *C. pusilloides*) and that it does not belong to *C. ferrugineus*. PCGs, tRNAs, and rRNAs are indicated by yellow, pink and red arrow bars, respectively. High levels of sequence identity are indicated by a solid green bar.

