Figure S3: Schematic representation of the published *C. turcicus* (KT070712; Sun, Liu, et al. (2016)) mitogenome aligned to the mitogenomes of: **[a]** *C. turcicus* (this study, see Tay et al. (2024)), and **[b]** *C.* sp. WTT-2013 (this study, see Tay et al. (2024)). **[a]** The *C. turcicus* mitogenome showed overall high level of nucleotide homologies with the *C. turcicus* mitogenome assembled from this study, as indicated by the bi-directional arrow with low *p*-dist values (0.3%) expected for intra-specific comparisons (see Tables S4 & S5). The red rectangle boxed region at the 5' end of the mtCOI partial gene region (*ca*. 700bp) showed high *p*-dist value (17.36%) expected at the inter-specific level (see Table S4 & S5). **[b]** Comparison between the published *C. turcicus* and *C.* sp. 'WTT-2013' (this study, see Tay et al. (2024)) mitogenomes, showing overall high nucleotide dissimilarity expected for inter-specific difference except for the box region which showed low *p*-dist value (1.36%) due to high nucleotide homology expected at the intra-specific level. The overall patterns suggested that the *C. turcicus* (KT182067) mitogenome consists of sequences from both *C. turcicus* and *C.* sp. 'WTT-2013'. The 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.

