

Supplementary figure S8. Alignment of the CN9E putative deduced capsid (Cp) amino acid (aa) sequences derived using the standard genetic code (shown as CN9E/Cp/STD_code) with ‘ATG’ as initiation codon and invertebrate mitochondrial genetic code (shown as CN9E/Cp/INV-Mit_code) with ‘ATG’ as the initiation codon. A ‘*’ denotes an identical aa residue. Numbers to the right indicate the positions of the aa for respective sequences.

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CN9E/Cp/STD_code      MRRRIRRFRRRYRLRTQRRYRKRVKTSSLVRHHRALSSTDNLTVYLTARVRLNLPEPNPS 60
CN9E/Cp/INV-Mit_code  MRRRISRFRRRYRLRTQSRYRKRVKTSSLVRHHRALSSTDNLTVYLTARVRLNLPEPNPS 60
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CN9E/Cp/STD_code      TPFYGSGKYDLSFFQNEAYTETNLPAVHRFFQYYRIHWIKEELKPAFNVIKNIDPYSYLN 120
CN9E/Cp/INV-Mit_code  TPFYGSGKYDLSFFQNEAYTETNLPAVHSFFQYYRIHWMKEELKPAFNVIKNIDPYSYLN 120
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CN9E/Cp/STD_code      SQTEQLTTWRNRNMTSYVCAPWKRQNPPANELELSITKGAKKIRAHQECRRKFKPAVYTA 180
CN9E/Cp/INV-Mit_code  SQTEQLTTWRNRNMTSYVCAPWKRQNPPANELELSMTKGAKKIRAHQECRRKFKPAVYTA 180
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CN9E/Cp/STD_code      QQSNTTQQYTFTDMKYSFKIASDANGVRVPHWCSYWFLPYFQITPTNPGTPETTDYPLFE 240
CN9E/Cp/INV-Mit_code  QQSNTTQQYTFTDMKYSFKMASDANGVRVPHWCSYWFLPYFQITPTNPGTPETTDYPLFE 240
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CN9E/Cp/STD_code      MWATAKVTTYKFSQYNVN 258
CN9E/Cp/INV-Mit_code  MWATAKVTTYKFSQYNVN 258
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