Figure S2. The mitochondrial genome of *Ziphius cavirostris*. The gene order is depicted and linearised starting from *cox1*. Genes encoded on the α-strand (right to left orientation) are underlined in green, while those encoded on the β-strand are underlined in red (left to right orientation). Gene nomenclature: *atp6* and *atp8*: ATP synthase subunits 6 and 8; *cob*: apocytochrome b; *cox1*-3: cytochrome c oxidase subunits 1–3; *nad1*-6 and *nad4L*: NADH dehydrogenase subunits 1–6 and 4L; *rrnS* and *rrnL*: small and large subunit ribosomal RNA (rRNA) genes; and X: transfer RNA (tRNA) genes, where X is the one-letter abbreviation of the corresponding amino acid. In particular, L1 identifies the CTN codon family, L2 the TTR codon family, S1 the AGY codon family, and S2 the TCN codon family. CR, Control Region. OL, origin of duplication of the light strand. A black circle located between two adjacent genes denotes the presence of an intergenic spacer (in white is the number of nucleotides forming the spacer). A white circle located between two adjacent genes denotes the presence of an overlapping segment (in red is the number of nucleotides forming the segment). Isp, intergenic spacer; start, start of the gene; end, end of the gene; size, size of the gene. For protein-coding genes, the start codon is provided in cyan and the stop codon in red (with incomplete stop codons written in parentheses). The anticodon is provided for every tRNA (e.g., tga for *trnS2*).