Supplemental Figure S2A: Mapping of the 5′ end of a *cox1* transcript species in accession Co. CR-RT-PCR was done with primer pair Atcox1-2/Atcox1-4. Sequencing of the 250 bp product (corresponds to the 340 bp product in Fig. 1) was obtained with oligonucleotide Atcox1-2. The 5′ end can be identified around position -49, where the sequence switches to predominantly ambiguous signals. Below the diagram the terminal sequence of the *cox1* RNA species is shown in capital letters. Upstream sequence, which cannot be read in the diagram is given in lower case letters. The position of the 5′ end is indicated by a bent line.
Supplemental Figure S2B: Mapping of the 5′ end of a *cox1* transcript species in accession Bur-0. CR-RT-PCR was done with primer pair Atcox1-1/Atcox1-4. Sequencing of the 390 bp product was obtained with oligonucleotide Atcox1-1. The 5′ end can be identified around position -105, where the sequence switches to predominantly ambiguous signals. Below the diagram the terminal sequence of the *cox1* RNA species is shown in capital letters. Upstream sequence, which cannot be read in the diagram is given in lower case letters. The position of the 5′ end is indicated by a bent line. A similar result was obtained by the analysis of the 390 bp product in Blh-1, which suggests a 5′ terminus around position -102 (data not shown).
Supplemental Figure S2C: Mapping of the 5’ end of the cox2 transcript in accession Cal. Sequencing of a 420 bp CR-RT-PCR product obtained with primer pair Atcox2-5/Atcox2-6 was performed with oligonucleotide Atcox2-2. The 5’ end can be identified around position -305, where the sequence switches from the 5’ end to 3’ terminal sequences, separated by a C that is not present in the reference sequence of mtDNA from accession C24. The terminal sequences of the RNA are given below the diagram (sense orientation). Sequence given in lower case letters cannot be read in the diagram.
Supplemental Figure S2D: Mapping of the 5’ end of the *cox2* transcript in accession Bur-0. A CR-RT-PCR product obtained with primer pair Atcox2-5/Atcox2-6 was cloned and 14 individual clones were sequenced. Most of the 5’ ends found in these clones cluster between positions -299 and -306. The numbers above the sequence indicate the numbers of clones that contain a distinct end. Number at the 5’ and 3’ ends of the sequence refer to accession number nc_001284.
Supplemental Figure S2E: Mapping of the 5’ end of the *nad2* transcript in accession Can-0. Sequencing of a 400 bp CR-RT-PCR product amplified with primer pair Atnad2ab-6/Atnad2cde-3 was performed with oligonucleotide Atnad2ab-6. The 5’ end can be identified around position -409, where the sequence switches from the 5’ end to the 3’ terminus. The terminal sequences of the RNA sense strand are given below the diagram. The positions of the 5’ and 3’ ends are indicated by bent lines.
Supplemental Figure S2F: Mapping of the 5' end of a nad2 transcript species in accession Can-0. A 300 bp CR-RT-PCR product obtained with primer pair Atnad2ab-6/Atnad2cde-3 was sequenced with oligonucleotide Atnad2ab-6. The 5' end can be identified at position -292, where the sequence switches from the 5' to the 3' terminus. The terminal sequences of the RNA sense strand are given below the diagram. The positions of the 5' and 3' ends are indicated by bent lines.
nad3-rps12

Ct-1
5’ ends at -184 and -197

Supplemental Figure S2G: Mapping of the 5’ ends of nad3-rps12 transcript species in accession Ct-1. A CR-RT-PCR product (400 bp) was amplified with primer pair Atnad3-2/Atbps12-6 and sequenced with oligonucleotide Atnad3-2. The 5’ ends can be identified around position -184, where the peak height decreases and where background peaks start to increase. An additional 5’ end is suggested around position -197, where background peaks reach the same intensity as the main sequence. However, a few nucleotides are still read before sequence switches into ambiguous peaks. The terminal sequence of the RNA sense strand are given below the diagram. Sequence given in lower case letters cannot be read in the diagram.
Supplemental Figure S2H: Mapping of the 5' end of a *nad3-rps12* transcript species in accession Tsu-1. A 360 bp CR-RT-PCR product was obtained with primer pair Atnad3-2/Atrps12-6 and sequenced with oligonucleotide Atnad3-2. The 5' end can be identified around positions -140 to -142, where the peak height decreases and where the *nad3-rps12* upstream sequence switches into mainly ambiguous signals. The terminal sequence of the RNA sense strand is given below the diagram. The A at position -142 could derive also from the 3' terminus.