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region was the COI gene (687 bp) amplified for 31 individuals (Veliz et al., 2012; Genbank Accession Numbers: FJ380197 to FJ380116). Both fragments showed 100% alignment to the expected Control region and COI gene, respectively. Additionally, 34,385 contigs (14.46 million reads, 2.13 Gb) obtained from a de novo assembly performed with the sequences of an RNA-Seq performed in Ion Torrent and Ion Proton platform were mapped to the novel Basilichthys mitogenome, checking at the same time potential indels against depth and quality of NGS 454 reads.

Finally, the validations yielded a mitogenome assembly of 16,544 bp, similar in size to the Odontesthes sp. (16,527 bp) and the Menidia menidia mtDNA genomes (16,456 bp). Annotations were confirmed by comparing with Dual Organellar GenoMe Annotator (DOGMA) (Wyman et al., 2004) and MITochondrial genome annotation Server (MITOS)-generated annotations (Bernt et al., 2013). The complete mitochondrial genome of the silverside B. microlepidotus has a gene order typical of fishes and it contains 22 tRNA genes, 13 protein-coding genes, two rRNA genes and a non-coding control region (Table 1). The nucleotide composition was: A, 27.2%, T, 27.5%, G, 17.0% and C, 28.2%.

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Table 1. Continued

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<tr>
<th>Gene</th>
<th>Direction</th>
<th>From</th>
<th>To</th>
<th>Size (bp)</th>
<th>Start</th>
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<tr>
<td>ND6</td>
<td>-</td>
<td>13,817</td>
<td>14,359</td>
<td>536</td>
<td>ATC</td>
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<td>ATG</td>
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<tr>
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<td>16,543</td>
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Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article.

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References


