

Additional file 1 for:

**Mitochondrial phylogenomics provides conclusive evidence that the family
Ancyrocephalidae is deeply paraphyletic**

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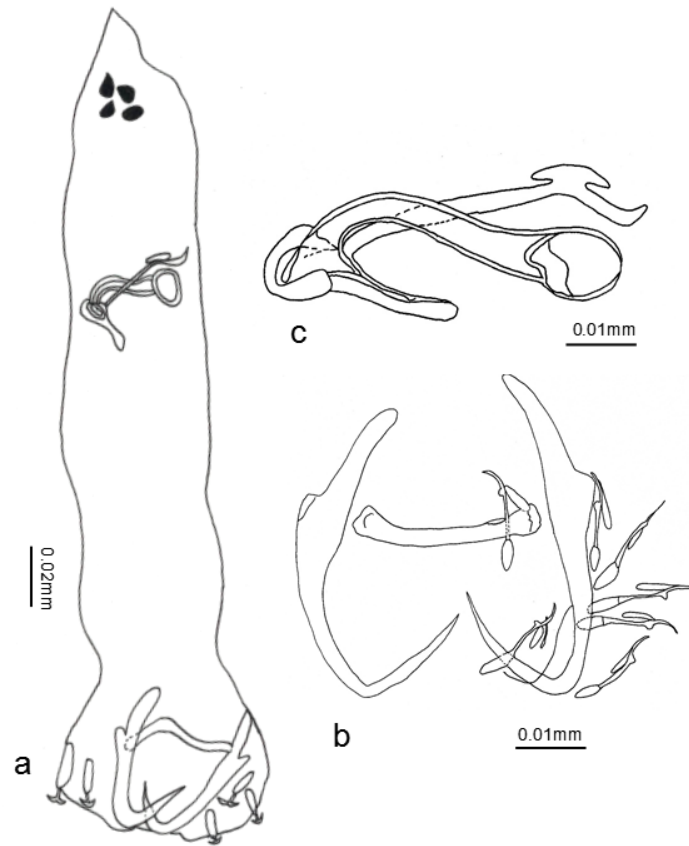


Figure S1. The drawing of a *Dactylogyrus simplex* Bychowsky, 1936 specimen. a) The entire specimen. b) Opisthaptor elements. c) Copulatory organ. Size bars are shown within the figure.

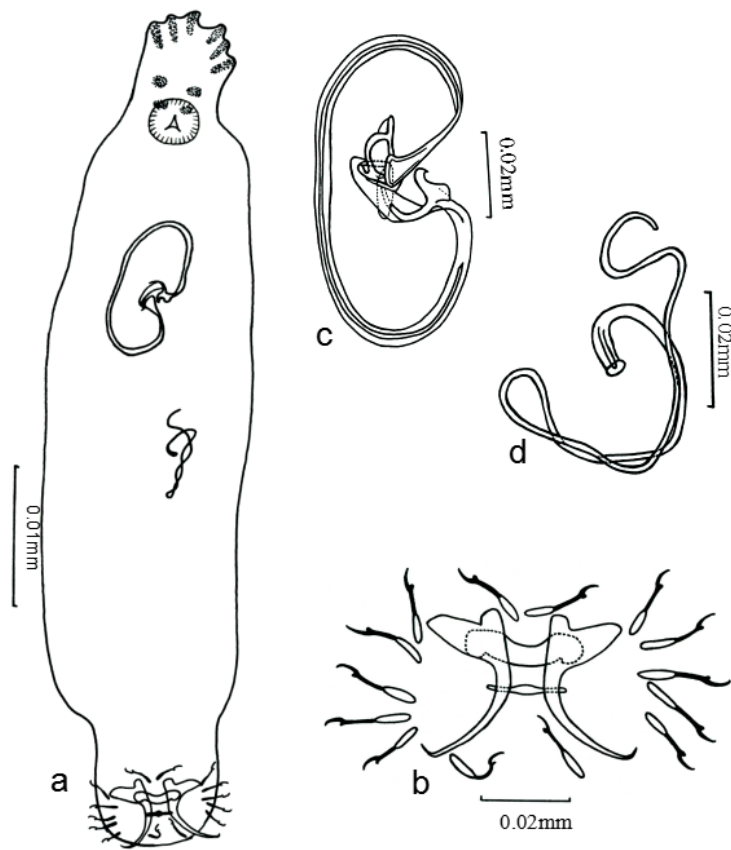


Figure S2. The drawing of a *Dactylogyrus tuba* Linstow, 1878 specimen. a) The entire specimen. b) Opisthaptor elements. c) Copulatory organ. d) Vagina. Size bars are shown within the figure.

Dactylogyrus simplex OP058752

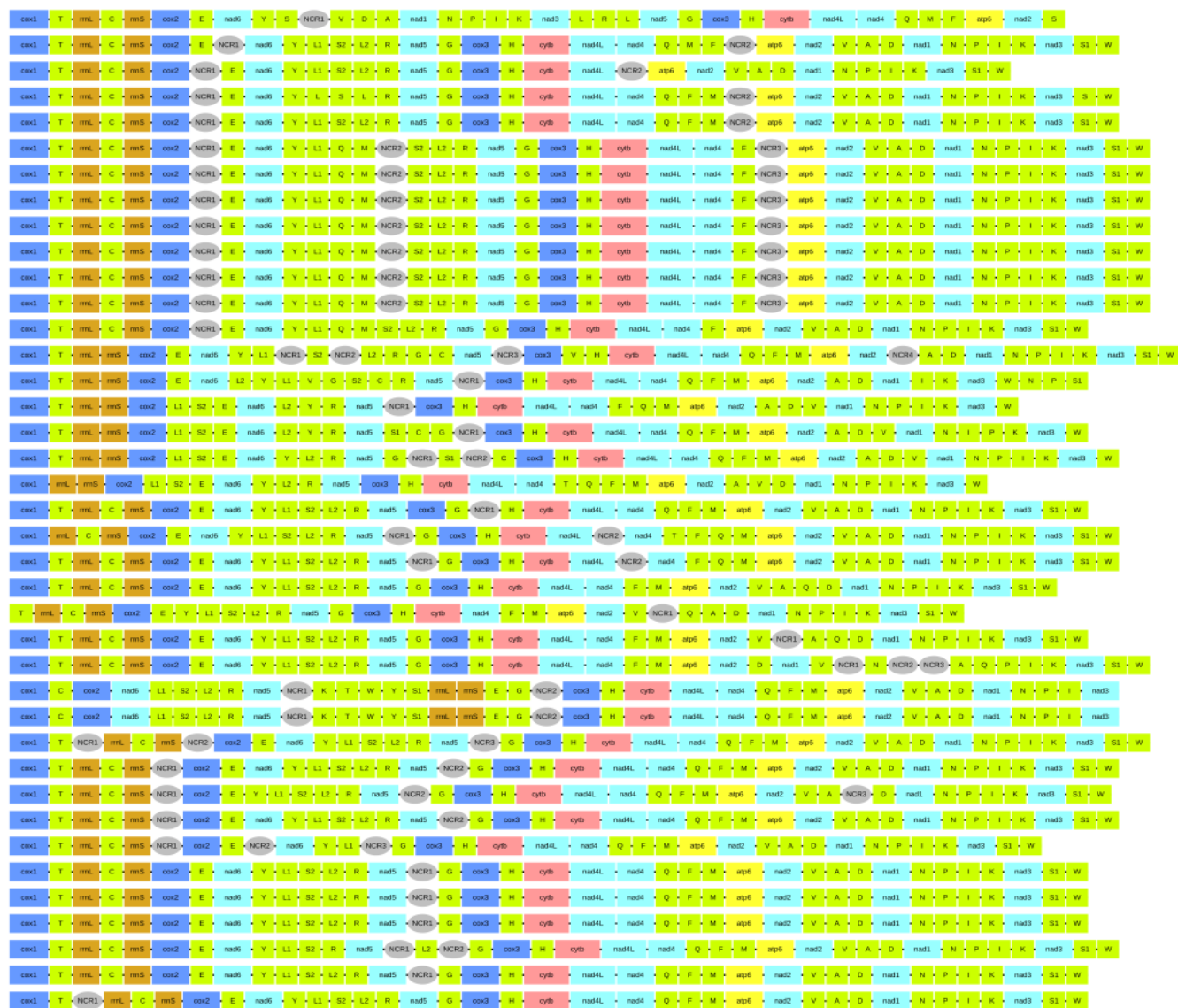


Figure S3. The mitogenomic architecture of the studied Monopisthocotylea dataset. The three *Dactylogyrus* mitogenomes are highlighted in yellow. Mitogenomes are shown linearized and rearranged to start with *cox1*.

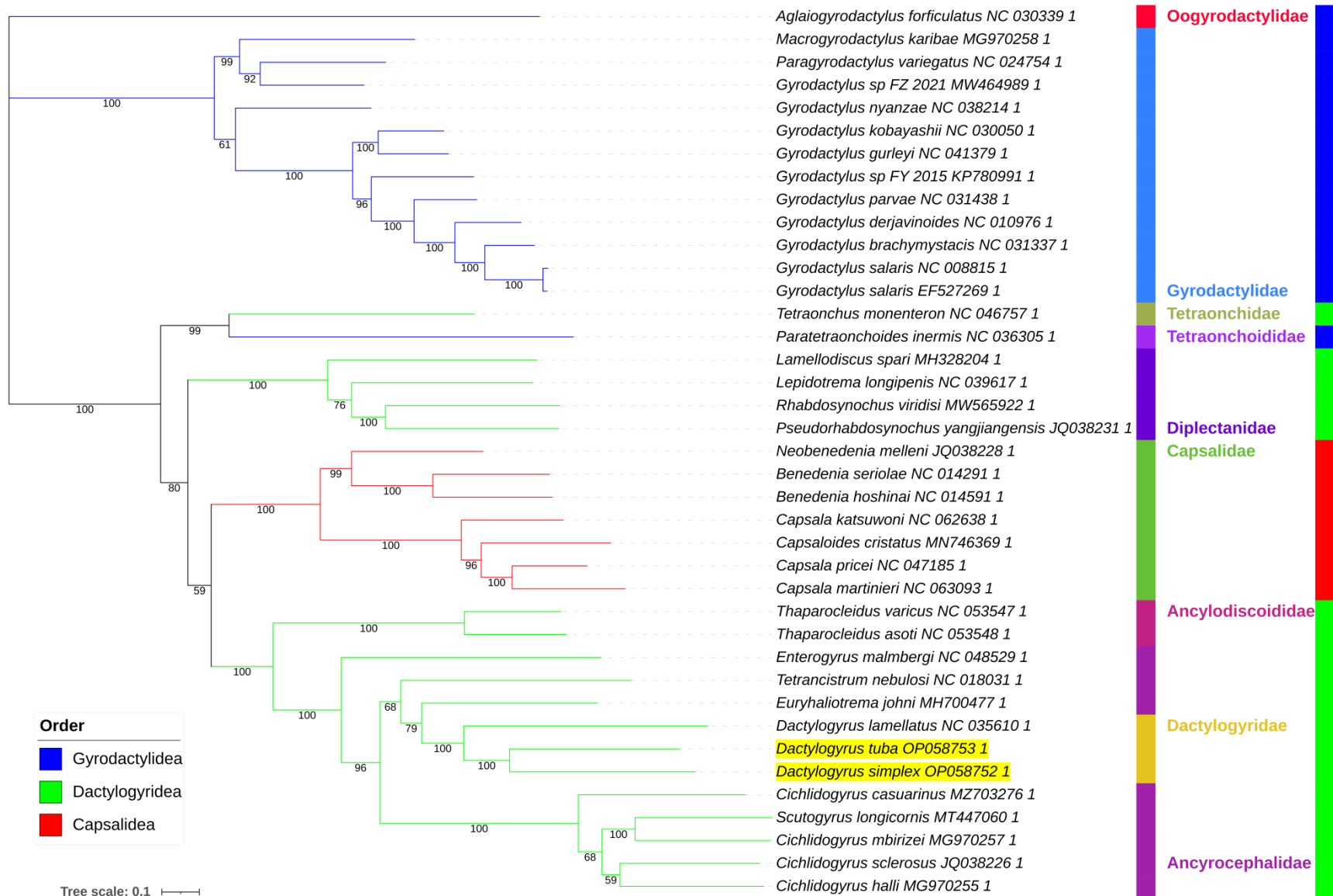


Figure S4. The NUC_ML mitochondrial phylogenomic analysis of the Monopisthocotylea. The NUC dataset comprised concatenated (partitioned) nucleotide sequences of 12 PCGs and 2 rRNAs. IQ-TREE was used to conduct the Maximum-Likelihood (ML) analysis. Bootstrap support is shown next to the nodes. The family-level taxonomy is shown to the right. Orders are indicated by a coloured strip and coloured branches, with the legend included in the figure. The two newly-sequenced species are highlighted by a yellow background.

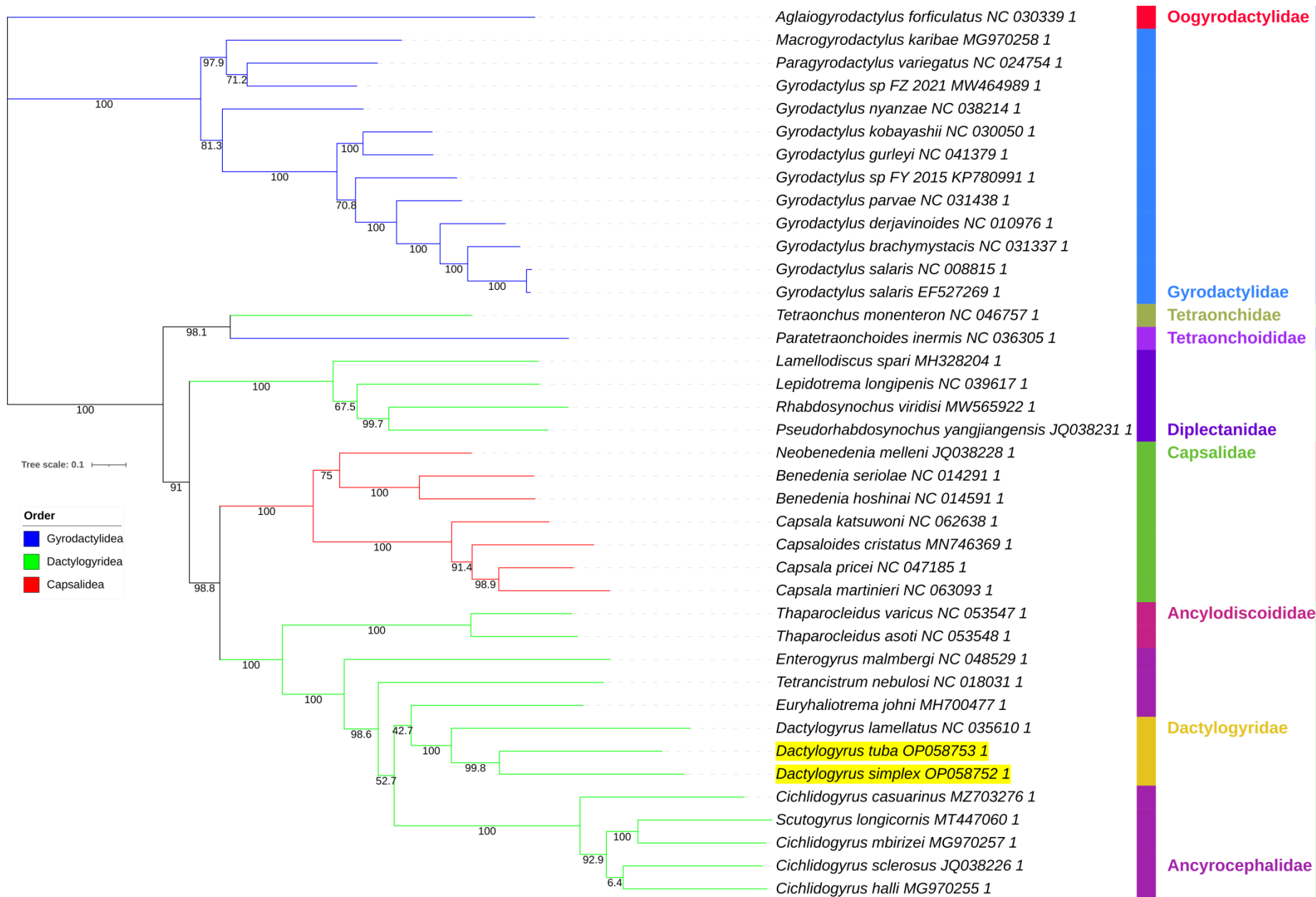


Figure S5. The NUC_ML_12PCGs mitochondrial phylogenomic analysis of the Monopisthocotylea. The NUC dataset comprised concatenated (partitioned) nucleotide sequences of 12 PCGs (2 rRNAs were not included). For other details please see Figure S4.



Figure S6. The ITS1-based BI phylogenetic analysis of the Dactylogyridea. Two Gyrodactylidae species are outgroups. GenBank accession numbers are shown next to species names. Posterior probability support values are shown next to nodes. The family-level taxonomy is shown to the right. The two newly-sequenced species are highlighted by a yellow background.

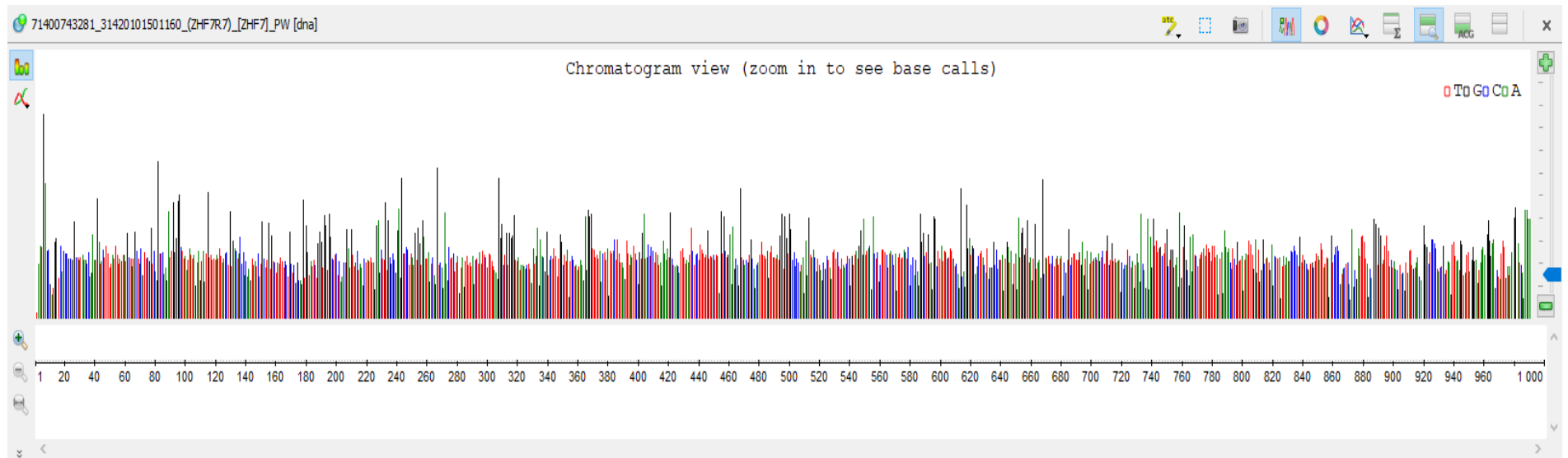


Figure S7. Sequencing chromatogram comprising ‘problematic’ the segment covering the 3’ end of *cytb*, 5’ end of *nad4L*, and the 10 bp intergenic space between them in *D. simplex*.