**Trigoniidae**

**NeoMar**

. 1432 bp gap between COX2 and trnS2 only place for the ORF. ORF Finder biggest ORF is between pos 3029-3304.

**Hyriidae**

**EchMen\_F**

. Failed to detect trnA, tried Arwen, and cluster with trnA of WesCar\_F but without any results

**. DipSua\_F**

. MITOS Failed to detect trnQ, and ATP8. trnQ was annotated by ARWEN, ATP8 by alignment.

Still did not detected F-ORF.

**. PriObl\_F**

. MITOS Failed to detect trnI, and ATP8. MITOS detected a duplicated trnM. The trnM with lower e value was discarded. trnI and ATP8 were annotated by alignment. Still did not detected F-ORF.

**Mulleriidae**

**AnoTra**

**.** Failed to detect ND3, Detected by alignment with other ND3. trnK detected using Arwen. ATP8 detected by alignment with other ATP8.

. Mitos detects 2 trnNs and Arwen detects 2 trnGs

**Iridinidae**

**MutDub**

**.** MITOS:Genes not found: atp8, trnT. trnT was detected with Arwen. ATP8 by alignment with other atp8. No ORF is detected on the expected place

**ChaRub**

**.** MITOS:Genes not found: atp8, trnT. trnT and ATP8 were annotated by alignment with other species. No ORF is detected on the expected place

**Female**

**Unionidae**

**Anodontinae**

**AnoAna\_F**

. 16bp overlap between COX1 and COX2 giving a larger size to COX1 (Checked and COX1 starts earlier than usual)

. 26bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**LasCom\_F**

.Nothing out of the ordinary

**PygGra\_F**

. 71bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**UttImb\_F**

. 79bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and ND3 starts earlier than usual)

. did not detected trnT (Detected by Arwen and Updated in the Annotation)

. did not detected ATP8 (Annotated using original annotation and Blast)

**UttPen\_F**

. 64bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and ND3 starts earlier than usual)

. did not detected rrnL (Annotated using space between the adjacent tRNAs followed by Blast)

. did not detected ATP8 (Annotated using Anodontinae Alignment)

**CriPli\_F**

. 16bp overlap between COX1 and COX2 giving a larger size to COX1 (Checked and COX1 starts earlier than usual)

**SinLuc\_F**

. 37bp overlap between COX1 and COX2 giving a larger size to COX1 (Checked and COX1 starts earlier than usual)

. 44bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**SinWoo\_F**

.Nothing out of the ordinary

**AneArc\_F**

. 55bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and COX2 starts earlier than usual)

. did not detected trnK that should be included in the rrnS which has a longer size (Detected by Arwen and Updated in the Annotation)

**AneEus\_F**

. 38bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and COX2 starts earlier than usual)

. did not detected trnK that should be included in the rrnS which has a longer size (Detected by Arwen and Updated in the Annotation)

**ArcLan\_F**

. Duplication of ND3 (There are sequencing errors in ND3 Pos 221, 222 and 337 were missing annotation updated accordingly)

. Duplication of COB (There are sequencing errors in COB with two nucleotide insertions; annotation updated accordingly)

. Duplication of ND5 (There are sequencing errors in ND5 with one missing nucleotide; annotation updated accordingly)

**LanGra\_F**

.Nothing out of the ordinary

**Unioninae**

**AcuCor\_F**

. 76bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and COX2 starts earlier than usual)

. 26bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**AcuTor\_F**

. 34bp overlap between COX2 and ND3 giving a larger size to COX2 (Checked and COX2 starts earlier than usual)

. 26bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**CunPis\_F**

. 31bp overlap between ND4L and ATP8 (Checked and ND4L starts earlier than usual)

**LamGot\_F**

. 31bp overlap between ND4L and ATP8 (Checked and ND4L starts earlier than usual)

. Missing trnV (Arwen failed to detect trnV, annotated by alignment with the two most related species)

**NodDou\_F**

. 53bp overlap between COX2 and ND3 COX2 (Checked and COX2 starts earlier than usual)

. 10bp overlap between ND4L and ATP8 (Checked and ND4L starts earlier than usual)

**UniDel\_F**

. 79bp overlap between COX2 and ND3 COX2 (Checked and COX2 starts earlier than usual)

. 34bp overlap between ND4L and ATP8 (Checked and ND4L starts earlier than usual)

**UniFou\_F**

. trnF missing, trnA partial.

**UniPic\_F**

. 34bp overlap between ND4L and ATP8 (Checked and ND4L starts earlier than usual)

**Ambleminae**

**LamOrn\_F**

. Same annotation for COX1 and COX3 (total overlap) (Checked missing haplotype (N) on the stop codon of COX1, reannotated as a stop codon)

**VenEll\_F**

. 82bp overlap between COX1 and COX2 (Checked and COX1 starts earlier than usual)

**ToxPar\_F**

. 16bp overlap between COX1 and COX2 (Checked and COX1 starts earlier than usual)

**QuaQua\_F**

. 38bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**LamSil\_F**

. MITOS failed to detect FORF. Annotated by alignment with other species.

**LamPow\_F**

. MITOS failed to detect FORF. Annotated by alignment with other species.

**Gonideinae**

**SinCum\_F**

. 101bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

**SinSch\_F**

.Nothing out of the ordinary

**PotLit\_F**

. 38bp overlap between ND4 and ND4L (Checked and ND4 starts earlier than usual)

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**ProJap\_F**

. 94bp overlap between COX1 and COX2 (Checked)

. 38bp overlap between ND4 and ND4L (Checked)

. Duplication of ND3 (There are sequencing errors in ND3 with one nucleotide insertion; annotation updated accordingly)

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**LamLea\_F**

. 38bp overlap between ND6 and ND4 (Checked)

. 38bp overlap between ND4 and ND4L (Checked)

**SolCar\_F**

. 38bp overlap between ND4 and ND4L (Checked)

**SolOle\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**PilExi\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**PseVon\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**Rectidentinae**

**ConCon\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**HyrBia\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

**PhySup\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

. 17bp overlap between ND4 and ND4L (Checked)

**PhySup\_F**

. Missing ATP8 (Annotated by alignment with 6 gonideinae ATP8)

. 38bp overlap between ND4 and ND4L (Checked)

**Parreysiinae**

**LamCar\_F**

**.** MITOS filed to detect ATP8. ATP8 annotated by alignment. Failed to detect FORF.

**Margaritiferidae**

**MarMar\_F\_P2**

**MarMar\_F\_B155G**

**MarMar\_H\_MM63: Os tres anotados de foma perfeita atraves dos scripts e acertados com alinhamentos de todos os Margaritiferidae**

**MarDah\_F**

. Missing ATP8(Annotated by alignment with 6 gonideinae ATP8)

**MarFal\_F**

. Missing ATP8(Annotated by alignment with 6 gonideinae ATP8)

**MarMrc\_F**

. Missing ATP8(Annotated by alignment with 6 gonideinae ATP8)

. 44bp overlap between ND4 and ND4L (Checked)

**Male**

**Hyriidae**

**EchMen\_M**

. MITOS did failed to detect ATP8 and trnT. trnT was detected and annotated by ARWEN

**Unionidae**

**Anodontinae**

**AnoAna\_M**

. Missing ATP8(Annotated by alignment with 3 M-Anodontinae ATP8)

. 11bp overlap between ND4 and ND4L (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

. 44bp overlap between COX1 and COX2 (Checked)

. 2bp overlap between ND2 and trnM (Checked)

**PygGra\_M**

. Missing ATP8(two sequencing errors with missing nt’s at position 42 and 169 2 (Ns) were included. Annotated by alignment with 3 Anodontinae\_M ATP8)

. 41bp overlap between ND4 and ND4L (Checked)

. 62bp overlap between COX1 and COX2 (Checked)

. 107bp overlap between ATP6 and COX3 (Checked)

**UttPen\_M**

. Missing ATP8(Annotated by alignment with 3 M-Anodontinae ATP8)

. Missing ND4L(Annotated by alignment with 3 M-Anodontinae ATP8)

. 76bp overlap between ATP6 and COX3 (Checked)

. 29bp overlap between COX1 and COX2 (Checked)

. 256bp overlap between COX2 and NAD3 (Checked)

**Unioninae**

**AcuTor\_M**

**. Duplicated trnS1, I have maintained the second since it clusters with all other Unioninae in the annotation until further information**

**UniDel\_M**

. Missing ATP8(Annotated by alignment with 2 M-Ambleminae ATP8)

. 35bp overlap between ATP6 and COX3 (Checked)

. 13bp overlap between COX2 and NAD3 (Checked)

. 41bp overlap between ND4 and ND4L (Checked)

**UniElo\_M (Incomplete)**

. ATP8, and NAD6 incomplete. trnG missing.

**UniFou\_M\_UG7 (Incomplete)**

. trnC & trnQ missing.

**UniMan\_M (Incomplete)**

**UniPic\_M (Incomplete)**

. COX1, COX3 & NAD3 Gappy.

**UniTer\_M (Incomplete)**

. NAD1, NAD6, NAD2, COX3 & trnG Gappy, missing trnH, trnP

**Ambleminae**

**VenEll\_M**

. 70bp overlap between ATP6 and COX3 (Checked)

. 40bp overlap between COX2 and NAD3 (Checked)

**QuaQua\_M**

. Missing ATP8(Annotated by alignment with 2 M-Ambleminae ATP8)

. 10bp overlap between ND4 and ND4L (Checked)

**LamSil\_M**

. MITOS failed to detect MORF. Annotated by alignment with other species.

**LamPow\_M**

. MITOS failed to detect MORF. Annotated by alignment with other species.

**PotAla\_M**

. MITOS failed to detect MORF. Annotated by alignment with other species. COX2 seem to be quite small.

**Gonideinae**

**PotLit\_M**

. Missing ATP8(Annotated by alignment with 5 M-Gonideinae ATP8)

. Missing trnQ (Detected by Arwen and Updated in the Annotation)

. 121bp overlap between COX2 and NAD3 (Checked)

. 56bp overlap between NAD6 and NAD4 (Checked)

. 41bp overlap between ND4 and ND4L (Checked)

. 41bp overlap between COX1 and COX2 (Checked)

**ProJap\_M**

. Missing ATP8(Annotated by alignment with 5 M-Gonideinae ATP8)

. Missing trnC (Detected by Arwen and Updated in the Annotation)

. Duplication of ATP6 (Sequencing error has an additional G at position 199, it has to be removed for the alignment of all ATP6)

. 4bp overlap between NAD6 and NAD4 (Checked)

. 59bp overlap between ND4 and ND4L (Checked)

**SolCar\_M**

. Missing ATP8(Annotated by alignment with 5 M-Gonideinae ATP8)

. Missing trnQ (Detected by Arwen and Updated in the Annotation)

. 168bp overlap between NAD6 and NAD4 (Checked)

. 17bp overlap between ND4 and ND4L (Checked)

. 65bp overlap between ATP6 and COX3 (Checked)

**PilExi\_M**

. Missing ATP8(Annotated by alignment with 5 M-Gonideinae ATP8)

. Missing trnQ (Detected by Arwen and Updated in the Annotation)

. 4bp overlap between NAD6 and NAD4 (Checked)

. 41bp overlap between ND4 and ND4L (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

**PseVon\_M**

. Missing ATP8(Annotated by alignment with 5 M-Gonideinae ATP8)

. Missing trnV (Detected by Arwen and Updated in the Annotation)

. 154bp overlap between NAD6 and NAD4 (Checked)

. 92bp overlap between ND4 and ND4L (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

**Rectidentinae**

**ConCon\_M**

. Missing ATP8(Annotated by alignment with 4 M-Rectidentinae ATP8)

. 96bp overlap between NAD6 and NAD4 (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

. 22bp overlap between COX2 and NAD3 (Checked)

**HyrBia\_M**

. Missing ATP8(Annotated by alignment with 4 M-Rectidentinae ATP8)

. 25bp overlap between NAD6 and NAD4 (Checked)

. 50bp overlap between ND4 and ND4L (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

. 79bp overlap between COX2 and NAD3 (Checked)

**HyrBia\_M**

. Missing ATP8(Annotated by alignment with 4 M-Rectidentinae ATP8)

. 202bp overlap between NAD6 and NAD4 (Checked)

. 59bp overlap between COX3 and COX1 (Checked)

**RecSum\_M**

. Missing ATP8(Annotated by alignment with 4 M-Rectidentinae ATP8)

. 37bp overlap between NAD6 and NAD4 (Checked)

. 8bp overlap between COX3 and COX1 (Checked)

**Margaritiferidae**

**MarMrc\_M**

. Same annotation for COX1 and COX3 (total overlap) (Due to an absence of stop codon the gene was ended at the position 1521 (tat codon)

. Missing ATP8(Annotated by alignment with 4 M-Rectidentinae ATP8)

. 97bp overlap between NAD6 and NAD4 (Checked)