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| Supplementary Table 1. Annotation of mitochondrial DNA of female *R.Philippinaru\** |
| Gene | Start (nt) | End (nt) | Length(bp) | Length Difference | Strand | StartCodon | StopCodon | AntiCodon§ | Intergeniclength (bp) |
| *COX2* | 22138/21551 | 1432 | 1971 | 0 | H | ATT | TAA |  | 329 |
| *COX2* | 1762 | 3330 | 1569 | 0 | H | ATT | TAA |  | 66 |
| *tRNA-Pro* | 3397 | 3461 | 65 | 0 | H |  |  | UGG | -24 |
| *CYTB* | 3438 | 4685 | 1248 | 0 | H | ATG | TAA |  | 0 |
| *16S rRNA* | 4686 | 6093 | 1408 | 0 | H |  |  |  | 0 |
| *ND4* | 6094 | 7452 | 1359 | 0 | H | ATG | TAA/TAG |  | 0 |
| *tRNA-His* | 7453 | 7514 | 62 | 0 | H |  |  | GUG | -3/0 |
| *tRNA-Glu* | 7512/7515 | 7574 | 63/60 | -3 | H |  |  | UUC | 65 |
| *ATP6* | 7640 | 8377 | 738 | 0 | H | ATA | TGA |  | 22 |
| *ND3* | 8400 | 8804 | 405 | 0 | H | GTG | TAA |  | 89/90 |
| *ND5* | 8894/8895 | 10519/10520 | 1626 | 0 | H | ATA | TAA/TAA† |  | 14 |
| *tRNA-Tyr/-Asn* | 10534/10535 | 10593/10594 | 60 | 0 | H |  |  | GUU | 8 |
| *tRNA-Met* | 10602/10603 | 10669/10668 | 68/66 | -2 | H |  |  | CAU | 6/8 |
| *tRNA-Met* | 10676/10677 | 10741/10742 | 66 | 0 | H |  |  | CAU | 8 |
| *tRNA-Asp* | 10750/10751 | 10811/10812 | 62 | 0 | H |  |  | GUC | 20 |
| *tRNA-Val* | 10832/10833 | 10891/10892 | 60 | 0 | H |  |  | UAC | 19 |
| *ND6* | 10911/10912 | 11402/11403 | 492 | 0 | H | ATA | TAA |  | 8 |
| *tRNA-Lys/-Ser* | 11411/11412 | 11473/11474 | 63 | 0 | H |  |  | UCU | 0 |
| *tRNA-Val* | 11474/11475 | 11537/11538 | 64 | 0 | H |  |  | UAC | 0 |
| *tRNA-Phe/-Met* | 11538/11539 | 11602/11603 | 65 | 0 | H |  |  | UAU | 2 |
| *tRNA-Trp* | 11605/11606 | 11666/11667 | 62 | 0 | H |  |  | UCA | -1 |
| *tRNA-Arg* | 11666/11667 | 11728/11729 | 63 | 0 | H |  |  | UCG | 14 |
| *tRNA-Leu* | 11743/11744 | 11804/11805 | 62 | 0 | H |  |  | UAA | 2/-2 |
| *tRNA-Gly* | 11807/11804 | 11865/11867 | 59/64 | 5 | H |  |  | UCC | 4/3 |
| *tRNA-Gln* | 11870/11871 | 11937/11938 | 68 | 0 | H |  |  | UUG | 2 |
| *tRNA-Asn* | 11940/11941 | 12004/12005 | 65 | 0 | H |  |  | GUU | 0 |
| *tRNA-Thr* | 12005/12006 | 12067/12068 | 63 | 0 | H |  |  | UGU | 0 |
| *tRNA-Cys* | 12068/12069 | 12127/12128 | 60 | 0 | H |  |  | GCA | 19 |
| *tRNA-Ala* | 12147/12148 | 12209/12210 | 63 | 0 | H |  |  | UGC | 55/157 |
| *COX3* | 12265/12368 | 13140/13141 | 876/774 | -102 | H | GTT‡/ATG | TAA |  | 0 |
| *12S rRNA* | 13141/13142 | 14389/14390 | 1249 | 0 | H |  |  |  | 0/-120 |
| *COX1* | 14390/14271 | 15988/15959 | 1599/1689 | 90 | H | GTT‡/ATG | TAG |  | -1/29 |
| *tRNA-Leu* | 15988/15989 | 16051/16052 | 64 | 0 | H |  |  | UAG | 0 |
| *ND1* | 16052/16053 | 16981/16982 | 930 | 0 | H | ATA | TAA |  | 22/21 |
| *ND2* | 17004 | 18020 | 1017 | 0 | H | ATA | TAG |  | 1406/1141 |
| *ND4L* | 19427/19162 | 19834/19569 | 408 | 0 | H | ATG | TAG |  | 2183/1861 |
| *tRNA-Ile* | 22018/21431 | 22083/21496 | 66 | 0 | H | 　 | 　 | GAU | 54 |
| \*Mitocondrial genome of previously (Ref ID) and newly (ReSeq ID) sequenced was annotated and represented together (Ref/ReSeq)§Anticodon of tRNA annotated from newly sequenced mitogenome were only listed.†Stop codon, Taa, has been expected to be completed by addition of adenine residue to 3' of the mRNA.‡They were suggested to be exceptional start codon in previously reported mitochondria genome sequence. |