

Table S1. Best fit partitions and substitution models.

| | Set Partition (Conducted by PartitionFinder 2) | Best Model for BI (Selected by PartitionFinder 2) |
|---|---|--|
| Best Partition CDS genes (BIC=63,885) | <i>atp6-8</i> | MTMAM+I+G |
| | <i>cox1-2-3</i> | MTART+I+G |
| | <i>cob</i> | MTART+I+G |
| | <i>nad1-2-3-4-4L-5-6</i> | MTMAM+I+G+F |
| Best Partition to rRNA genes (BIC= 27648.25) | <i>rrnS-L</i> | GTR+I+G |

Table S2. Basic composition of mitochondrial genome of *Monoplex pilearis*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 13 |
| tRNA-Lys | H | 794-868 | 75 | | | 2 |
| tRNA-Ala | H | 871-940 | 70 | | | 33 |
| tRNA-Arg | H | 974-1042 | 69 | | | 0 |
| tRNA-Asn | H | 1043-1109 | 67 | | | 13 |
| tRNA-Ile | H | 1123-1194 | 72 | | | 2 |
| Nad3 | H | 1197-1550 | 354 | ATG | TAA | -1 |
| tRNA-Ser | H | 1550-1619 | 70 | | | -1 |
| Nad2 | H | 1619-2677 | 1059 | ATG | TAA | 154 |
| Cox1 | H | 2832-4367 | 1536 | ATG | TAA | 15 |
| Cox2 | H | 4383-5069 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 5067-5136 | 70 | | | 0 |
| Atp8 | H | 5137-5295 | 159 | ATG | TAA | 2 |
| Atp6 | H | 5298-5993 | 696 | ATG | TAA | 34 |
| tRNA-Met | L | 6028-6097 | 70 | | | 6 |
| tRNA-Tyr | L | 6104-6174 | 71 | | | -1 |
| tRNA-Cys | L | 6174-6239 | 66 | | | -2 |
| tRNA-Trp | L | 6238-6307 | 70 | | | -3 |
| tRNA-Gln | L | 6305-6374 | 70 | | | 1 |
| tRNA-Gly | L | 6376-6444 | 69 | | | 1 |
| tRNA-Glu | L | 6446-6515 | 70 | | | 0 |
| 12s | H | 6516-7494 | 979 | | | 0 |
| tRNA-Val | H | 7495-7564 | 70 | | | 0 |
| 16s | H | 7565-8932 | 1368 | | | 0 |
| tRNA-Leu | H | 8933-9002 | 70 | | | 0 |
| tRNA-Leu | H | 9003-9073 | 71 | | | -1 |
| Nad1 | H | 9073-10003 | 941 | ATG | TA | 10 |
| tRNA-Pro | H | 10014-10080 | 67 | | | 2 |
| Nad6 | H | 10083-10583 | 501 | ATG | TAG | 5 |
| Cytb | H | 10589-11728 | 1140 | ATG | TAA | 10 |
| tRNA-Ser | H | 11739-11805 | 67 | | | 1 |
| tRNA-Thr | L | 11807-11872 | 66 | | | 9 |
| Nad4L | H | 11882-12178 | 297 | ATG | TAG | 28 |
| Nad4 | H | 12207-13545 | 1339 | ATG | TAA | 6 |
| tRNA-His | H | 13552-13617 | 66 | | | 0 |
| Nad5 | H | 13618-15339 | 1722 | ATG | TAA | 4 |
| tRNA-Phe | H | 15344-15412 | 69 | | | 150 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S3. Basic composition of mitochondrial genome of *Tutufa bubo*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAG | 11 |
| tRNA-Lys | H | 792-864 | 73 | | | 40 |
| tRNA-Ala | H | 905-973 | 69 | | | 8 |
| tRNA-Arg | H | 982-1050 | 69 | | | 0 |
| tRNA-Asn | H | 1051-1116 | 66 | | | 21 |
| tRNA-Ile | H | 1138-1209 | 72 | | | 1 |
| Nad3 | H | 1211-1564 | 354 | ATG | TAA | 0 |
| tRNA-Ser | H | 1565-1634 | 70 | | | -1 |
| Nad2 | H | 1634-2692 | 1059 | ATG | TAA | 4 |
| Cox1 | H | 2697-4232 | 1536 | ATG | TAG | 14 |
| Cox2 | H | 4247-4933 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4931-5000 | 70 | | | 0 |
| Atp8 | H | 5001-5159 | 159 | ATG | TAA | 2 |
| Atp6 | H | 5162-5857 | 696 | ATG | TAG | 40 |
| tRNA-Met | L | 5898-5964 | 67 | | | 11 |
| tRNA-Tyr | L | 5976-6041 | 66 | | | 8 |
| tRNA-Cys | L | 6050-6113 | 64 | | | -2 |
| tRNA-Trp | L | 6112-6180 | 69 | | | -2 |
| tRNA-Gln | L | 6179-6245 | 67 | | | -1 |
| tRNA-Gly | L | 6245-6314 | 70 | | | -2 |
| tRNA-Glu | L | 6313-6383 | 71 | | | 0 |
| 12s | H | 6384-7355 | 972 | | | 0 |
| tRNA-Val | H | 7356-7425 | 70 | | | 0 |
| 16s | H | 7426-8819 | 1394 | | | 0 |
| tRNA-Leu | H | 8820-8890 | 71 | | | -1 |
| tRNA-Leu | H | 8890-8960 | 71 | | | -1 |
| Nad1 | H | 8960-9901 | 942 | ATG | TAA | 0 |
| tRNA-Pro | H | 9902-9969 | 68 | | | 1 |
| Nad6 | H | 9971-10471 | 501 | ATG | TAA | 24 |
| Cytb | H | 10496-11635 | 1140 | ATG | TAA | 4 |
| tRNA-Ser | H | 11640-11706 | 67 | | | 2 |
| tRNA-Thr | L | 11709-11774 | 66 | | | 13 |
| Nad4L | H | 11788-12084 | 297 | ATG | TAG | 10 |
| Nad4 | H | 12095-13451 | 1357 | ATA | TAA | 16 |
| tRNA-His | H | 13468-13532 | 65 | | | 0 |
| Nad5 | H | 13533-15254 | 1722 | ATG | TAG | -1 |
| tRNA-Phe | H | 15254-15321 | 68 | | | 151 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S4. Basic composition of mitochondrial genome of *Gyrineum natator*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 12 |
| tRNA-Lys | H | 793-861 | 69 | | | 10 |
| tRNA-Ala | H | 872-940 | 69 | | | 9 |
| tRNA-Arg | H | 950-1020 | 71 | | | 2 |
| tRNA-Asn | H | 1023-1090 | 68 | | | 11 |
| tRNA-Ile | H | 1102-1170 | 69 | | | 3 |
| Nad3 | H | 1174-1527 | 354 | ATG | TAA | -2 |
| tRNA-Ser | H | 1526-1595 | 70 | | | -1 |
| Nad2 | H | 1595-2653 | 1059 | ATG | TAA | 4 |
| Cox1 | H | 2658-4193 | 1536 | ATG | TAA | 16 |
| Cox2 | H | 4210-4896 | 687 | ATG | TAA | -2 |
| tRNA-Asp | H | 4895-4963 | 69 | | | 0 |
| Atp8 | H | 4964-5122 | 159 | ATG | TAA | 2 |
| Atp6 | H | 5125-5820 | 696 | ATG | TAA | 39 |
| tRNA-Met | L | 5860-5930 | 71 | | | 1 |
| tRNA-Tyr | L | 5932-5999 | 68 | | | 6 |
| tRNA-Cys | L | 6006-6070 | 65 | | | -2 |
| tRNA-Trp | L | 6069-6136 | 68 | | | -2 |
| tRNA-Gln | L | 6135-6199 | 65 | | | 0 |
| tRNA-Gly | L | 6200-6268 | 69 | | | 0 |
| tRNA-Glu | L | 6269-6339 | 71 | | | 0 |
| 12s | H | 6340-7295 | 956 | | | 0 |
| tRNA-Val | H | 7296-7363 | 68 | | | 0 |
| 16s | H | 7364-8747 | 1384 | | | 0 |
| tRNA-Leu | H | 8748-8816 | 69 | | | 0 |
| tRNA-Leu | H | 8817-8885 | 69 | | | 0 |
| Nad1 | H | 8886-9827 | 942 | ATG | TAA | 1 |
| tRNA-Pro | H | 9829-9896 | 68 | | | 1 |
| Nad6 | H | 9898-10392 | 495 | ATG | TAG | 23 |
| Cytb | H | 10416-11555 | 1140 | ATG | TAA | 4 |
| tRNA-Ser | H | 11560-11627 | 68 | | | 1 |
| tRNA-Thr | L | 11629-11696 | 68 | | | 9 |
| Nad4L | H | 11706-12002 | 297 | ATG | TAG | -7 |
| Nad4 | H | 11996-13369 | 1374 | ATG | TAA | 6 |
| tRNA-His | H | 13376-13441 | 66 | | | 0 |
| Nad5 | H | 13442-15163 | 1722 | ATG | TAG | -1 |
| tRNA-Phe | H | 15163-15231 | 69 | | | 354 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S5. Basic composition of mitochondrial genome of *Tonna sulcosa*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAG | 11 |
| tRNA-Lys | H | 792-864 | 73 | | | 13 |
| tRNA-Ala | H | 878-945 | 68 | | | 50 |
| tRNA-Arg | H | 996-1064 | 69 | | | 4 |
| tRNA-Asn | H | 1069-1136 | 68 | | | 27 |
| tRNA-Ile | H | 1164-1236 | 73 | | | 2 |
| Nad3 | H | 1239-1592 | 354 | ATG | TAG | 6 |
| tRNA-Ser | H | 1599-1666 | 68 | | | 0 |
| Nad2 | H | 1595-2653 | 1059 | ATG | TAA | 4 |
| Cox1 | H | 2738-4273 | 1536 | ATG | TAA | 17 |
| Cox2 | H | 4291-4977 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4975-5044 | 70 | | | 0 |
| Atp8 | H | 5045-5203 | 159 | ATG | TAA | 25 |
| Atp6 | H | 5229-5924 | 696 | ATG | TAA | 37 |
| tRNA-Met | L | 5962-6031 | 70 | | | 6 |
| tRNA-Tyr | L | 6038-6105 | 68 | | | 10 |
| tRNA-Cys | L | 6116-6181 | 66 | | | -2 |
| tRNA-Trp | L | 6180-6248 | 69 | | | -2 |
| tRNA-Gln | L | 6246-6314 | 69 | | | 0 |
| tRNA-Gly | L | 6315-6381 | 67 | | | -1 |
| tRNA-Glu | L | 6381-6453 | 73 | | | 0 |
| 12s | H | 6454-7414 | 961 | | | 0 |
| tRNA-Val | H | 7415-7482 | 68 | | | 0 |
| 16s | H | 7483-8879 | 1397 | | | 0 |
| tRNA-Leu | H | 8880-8948 | 69 | | | 0 |
| tRNA-Leu | H | 8949-9019 | 71 | | | -1 |
| Nad1 | H | 9019-9960 | 942 | ATG | TAG | 0 |
| tRNA-Pro | H | 9961-10029 | 69 | | | 1 |
| Nad6 | H | 10031-10531 | 501 | ATG | TAA | 9 |
| Cytb | H | 10541-11680 | 1140 | ATG | TAA | 5 |
| tRNA-Ser | H | 11686-11750 | 65 | | | 9 |
| tRNA-Thr | L | 11760-11829 | 70 | | | 7 |
| Nad4L | H | 11837-12133 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12127-13503 | 1377 | GTG | TAA | 12 |
| tRNA-His | H | 13516-13585 | 70 | | | -1 |
| Nad5 | H | 13585-15306 | 1722 | ATG | TAG | 0 |
| tRNA-Phe | H | 15307-15375 | 69 | | | 313 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S6. Basic composition of mitochondrial genome of *Lotoria lotoria*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 15 |
| tRNA-Lys | H | 796-869 | 74 | | | 10 |
| tRNA-Ala | H | 880-949 | 70 | | | 19 |
| tRNA-Arg | H | 969-1037 | 69 | | | 0 |
| tRNA-Asn | H | 1038-1105 | 68 | | | 15 |
| tRNA-Ile | H | 1121-1190 | 70 | | | 4 |
| Nad3 | H | 1195-1548 | 354 | ATG | TAG | 0 |
| tRNA-Ser | H | 1549-1616 | 68 | | | 0 |
| Nad2 | H | 1617-2675 | 1059 | ATG | TAG | 6 |
| Cox1 | H | 2682-4217 | 1536 | ATG | TAA | 15 |
| Cox2 | H | 4233-4919 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4917-4986 | 70 | | | 0 |
| Atp8 | H | 4987-5145 | 159 | ATG | TAA | 2 |
| Atp6 | H | 5148-5846 | 699 | ATG | TAA | 33 |
| tRNA-Met | L | 5880-5948 | 69 | | | 3 |
| tRNA-Tyr | L | 5952-6022 | 71 | | | 7 |
| tRNA-Cys | L | 6030-6095 | 66 | | | -2 |
| tRNA-Trp | L | 6094-6163 | 70 | | | -2 |
| tRNA-Gln | L | 6162-6229 | 68 | | | 2 |
| tRNA-Gly | L | 6232-6299 | 68 | | | 6 |
| tRNA-Glu | L | 6306-6376 | 71 | | | 0 |
| 12s | H | 6377-7336 | 960 | | | 0 |
| tRNA-Val | H | 7337-7403 | 67 | | | 0 |
| 16s | H | 7404-8764 | 1361 | | | 0 |
| tRNA-Leu | H | 8765-8834 | 70 | | | 0 |
| tRNA-Leu | H | 8835-8903 | 69 | | | 0 |
| Nad1 | H | 8904-9844 | 941 | ATG | TA | 0 |
| tRNA-Pro | H | 9845-9913 | 69 | | | 1 |
| Nad6 | H | 9915-10415 | 501 | ATG | TAA | 5 |
| Cytb | H | 10421-11560 | 1140 | ATG | TAA | 6 |
| tRNA-Ser | H | 11567-11631 | 65 | | | 2 |
| tRNA-Thr | L | 11634-11700 | 67 | | | 9 |
| Nad4L | H | 11710-12006 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12000-13373 | 1374 | ATG | TAA | 5 |
| tRNA-His | H | 13379-13443 | 65 | | | 0 |
| Nad5 | H | 13444-15165 | 1722 | ATG | TAA | 13 |
| tRNA-Phe | H | 15179-15246 | 68 | | | 575 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S7. Basic composition of mitochondrial genome of *Phalium glaucum*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 14 |
| tRNA-Lys | H | 795-863 | 69 | | | 14 |
| tRNA-Ala | H | 878-945 | 68 | | | 6 |
| tRNA-Arg | H | 952-1020 | 69 | | | 14 |
| tRNA-Asn | H | 1035-1105 | 71 | | | 1 |
| tRNA-Ile | H | 1107-1176 | 70 | | | 4 |
| Nad3 | H | 1181-1534 | 354 | ATG | TAA | 3 |
| tRNA-Ser | H | 1538-1607 | 70 | | | -1 |
| Nad2 | H | 1607-2665 | 1059 | ATG | TAA | 8 |
| Cox1 | H | 2674-4209 | 1536 | ATG | TAA | 21 |
| Cox2 | H | 4231-4917 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4915-4984 | 70 | | | -1 |
| Atp8 | H | 4984-5142 | 159 | ATG | TAA | 18 |
| Atp6 | H | 5161-5856 | 696 | ATG | TAA | 40 |
| tRNA-Met | L | 5897-5965 | 69 | | | 15 |
| tRNA-Tyr | L | 5981-6049 | 69 | | | 9 |
| tRNA-Cys | L | 6059-6122 | 64 | | | -2 |
| tRNA-Trp | L | 6121-6188 | 68 | | | 1 |
| tRNA-Gln | L | 6190-6251 | 62 | | | 5 |
| tRNA-Gly | L | 6257-6324 | 68 | | | 6 |
| tRNA-Glu | L | 6331-6402 | 72 | | | 0 |
| 12s | H | 6403-7370 | 968 | | | 0 |
| tRNA-Val | H | 7371-7441 | 71 | | | 0 |
| 16s | H | 7442-8849 | 1408 | | | 0 |
| tRNA-Leu | H | 8850-8918 | 69 | | | 0 |
| tRNA-Leu | H | 8919-8987 | 69 | | | 0 |
| Nad1 | H | 8988-9929 | 942 | ATG | TAA | 0 |
| tRNA-Pro | H | 9930-9998 | 69 | | | 3 |
| Nad6 | H | 10002-10502 | 501 | ATG | TAA | 11 |
| Cytb | H | 10514-11653 | 1140 | ATG | TAA | 8 |
| tRNA-Ser | H | 11662-11727 | 66 | | | -2 |
| tRNA-Thr | L | 11726-11793 | 68 | | | 7 |
| Nad4L | H | 11801-12097 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12091-13464 | 1374 | ATG | TAG | 14 |
| tRNA-His | H | 13479-13543 | 65 | | | 0 |
| Nad5 | H | 13544-15265 | 1722 | ATG | TAA | -1 |
| tRNA-Phe | H | 15265-15332 | 68 | | | 611 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S8. Basic composition of mitochondrial genome of *Semicassis bisulcate*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 15 |
| tRNA-Lys | H | 796-870 | 75 | | | 12 |
| tRNA-Ala | H | 883-951 | 69 | | | 3 |
| tRNA-Arg | H | 955-1023 | 69 | | | 2 |
| tRNA-Asn | H | 1026-1092 | 67 | | | 3 |
| tRNA-Ile | H | 1096-1164 | 69 | | | 4 |
| Nad3 | H | 1169-1522 | 354 | ATG | TAA | 6 |
| tRNA-Ser | H | 1529-1598 | 70 | | | -1 |
| Nad2 | H | 1598-2656 | 1059 | ATG | TAA | 9 |
| Cox1 | H | 2666-4201 | 1536 | ATG | TAA | 17 |
| Cox2 | H | 4219-4905 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4903-4972 | 70 | | | -1 |
| Atp8 | H | 4972-5130 | 159 | ATG | TAA | 14 |
| Atp6 | H | 5145-5840 | 696 | ATG | TAA | 34 |
| tRNA-Met | L | 5875-5941 | 67 | | | 17 |
| tRNA-Tyr | L | 5959-6026 | 68 | | | 10 |
| tRNA-Cys | L | 6037-6100 | 64 | | | -2 |
| tRNA-Trp | L | 6099-6176 | 69 | | | 3 |
| tRNA-Gln | L | 6171-6232 | 62 | | | 1 |
| tRNA-Gly | L | 6234-6304 | 71 | | | 0 |
| tRNA-Glu | L | 6305-6375 | 71 | | | 0 |
| 12s | H | 6376-7339 | 964 | | | 0 |
| tRNA-Val | H | 7340-7406 | 67 | | | 0 |
| 16s | H | 7407-8789 | 1383 | | | 0 |
| tRNA-Leu | H | 8790-8858 | 69 | | | 4 |
| tRNA-Leu | H | 8863-8931 | 69 | | | 0 |
| Nad1 | H | 8932-9873 | 942 | ATG | TAA | 0 |
| tRNA-Pro | H | 9874-9941 | 68 | | | 3 |
| Nad6 | H | 9945-10445 | 501 | ATG | TAA | 16 |
| Cytb | H | 10462-11601 | 1140 | ATG | TAA | 7 |
| tRNA-Ser | H | 11609-11677 | 69 | | | -3 |
| tRNA-Thr | L | 11675-11741 | 67 | | | 9 |
| Nad4L | H | 11751-12047 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12041-13414 | 1374 | ATG | TAA | 19 |
| tRNA-His | H | 13434-13499 | 66 | | | 0 |
| Nad5 | H | 13500-15221 | 1722 | ATG | TAA | -1 |
| tRNA-Phe | H | 15221-15289 | 69 | | | 544 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S9. Basic composition of mitochondrial genome of *Phalium flammiferum*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAA | 15 |
| tRNA-Lys | H | 796-865 | 70 | | | 18 |
| tRNA-Ala | H | 884-951 | 68 | | | 6 |
| tRNA-Arg | H | 958-1028 | 71 | | | 11 |
| tRNA-Asn | H | 1040-1110 | 71 | | | 1 |
| tRNA-Ile | H | 1112-1181 | 70 | | | 4 |
| Nad3 | H | 1186-1539 | 354 | ATG | TAA | 2 |
| tRNA-Ser | H | 1542-1611 | 70 | | | -1 |
| Nad2 | H | 1611-2669 | 1059 | ATG | TAG | 8 |
| Cox1 | H | 2678-4213 | 1536 | ATG | TAA | 19 |
| Cox2 | H | 4233-4919 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4917-4986 | 70 | | | -1 |
| Atp8 | H | 4986-5144 | 159 | ATG | TAA | 16 |
| Atp6 | H | 5161-5856 | 696 | ATG | TAA | 46 |
| tRNA-Met | L | 5903-5970 | 68 | | | 15 |
| tRNA-Tyr | L | 5986-6053 | 68 | | | 11 |
| tRNA-Cys | L | 6065-6129 | 65 | | | -2 |
| tRNA-Trp | L | 6128-6195 | 68 | | | 1 |
| tRNA-Gln | L | 6197-6258 | 62 | | | 2 |
| tRNA-Gly | L | 6261-6331 | 71 | | | 0 |
| tRNA-Glu | L | 6332-6402 | 71 | | | 0 |
| 12s | H | 6403-7382 | 980 | | | 0 |
| tRNA-Val | H | 7383-7452 | 70 | | | 0 |
| 16s | H | 7453-8862 | 1410 | | | 0 |
| tRNA-Leu | H | 8863-8931 | 69 | | | 0 |
| tRNA-Leu | H | 8932-9000 | 69 | | | 0 |
| Nad1 | H | 9001-9942 | 942 | ATG | TAA | 0 |
| tRNA-Pro | H | 9943-10011 | 69 | | | 3 |
| Nad6 | H | 10015-10515 | 501 | ATG | TAA | 13 |
| Cytb | H | 10529-11668 | 1140 | ATG | TAA | 8 |
| tRNA-Ser | H | 11677-11742 | 66 | | | -2 |
| tRNA-Thr | L | 11741-11809 | 69 | | | 6 |
| Nad4L | H | 11816-12112 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12106-13479 | 1374 | ATG | TAA | 11 |
| tRNA-His | H | 13491-13555 | 65 | | | 0 |
| Nad5 | H | 13556-15277 | 1722 | ATG | TAA | -1 |
| tRNA-Phe | H | 15277-15345 | 69 | | | 599 |

“H” indicates the heavy strand while “L” indicates the light strand.

Table S10. Basic composition of mitochondrial genome of *Tutufa rubeta*.

| Gene | Strand | Location | Size (bp) | Start codon | Stop codon | Intergenic nucleotides |
|----------|--------|-------------|-----------|-------------|------------|------------------------|
| Cox3 | H | 1-780 | 780 | ATG | TAG | 11 |
| tRNA-Lys | H | 792-865 | 74 | | | 38 |
| tRNA-Ala | H | 904-972 | 69 | | | 9 |
| tRNA-Arg | H | 982-1050 | 69 | | | 1 |
| tRNA-Asn | H | 1052-1117 | 66 | | | 27 |
| tRNA-Ile | H | 1145-1214 | 70 | | | 2 |
| Nad3 | H | 1217-1570 | 354 | ATG | TAA | -1 |
| tRNA-Ser | H | 1570-1639 | 70 | | | -1 |
| Nad2 | H | 1639-2697 | 1059 | ATG | TAA | 3 |
| Cox1 | H | 2701-4236 | 1536 | ATG | TAA | 15 |
| Cox2 | H | 4252-4938 | 687 | ATG | TAA | -3 |
| tRNA-Asp | H | 4936-5005 | 70 | | | 0 |
| Atp8 | H | 5006-5164 | 159 | ATG | TAA | 2 |
| Atp6 | H | 5167-5862 | 696 | ATG | TAG | 40 |
| tRNA-Met | L | 5903-5968 | 66 | | | 9 |
| tRNA-Tyr | L | 5978-6047 | 70 | | | 6 |
| tRNA-Cys | L | 6054-6119 | 66 | | | -2 |
| tRNA-Trp | L | 6118-6186 | 69 | | | -1 |
| tRNA-Gln | L | 6186-6250 | 65 | | | 1 |
| tRNA-Gly | L | 6252-6319 | 68 | | | 0 |
| tRNA-Glu | L | 6320-6390 | 71 | | | 0 |
| 12s | H | 6391-7359 | 969 | | | 0 |
| tRNA-Val | H | 7360-7428 | 69 | | | 0 |
| 16s | H | 7429-8824 | 1396 | | | 0 |
| tRNA-Leu | H | 8825-8893 | 69 | | | 0 |
| tRNA-Leu | H | 8894-8964 | 71 | | | -1 |
| Nad1 | H | 8964-9905 | 942 | ATG | TAA | 0 |
| tRNA-Pro | H | 9906-9974 | 69 | | | 1 |
| Nad6 | H | 9976-10476 | 501 | ATG | TAA | 24 |
| Cytb | H | 10501-11640 | 1140 | ATG | TAA | 5 |
| tRNA-Ser | H | 11646-11710 | 65 | | | 3 |
| tRNA-Thr | L | 11714-11779 | 66 | | | 13 |
| Nad4L | H | 11793-12089 | 297 | ATG | TAG | -7 |
| Nad4 | H | 12083-13456 | 1374 | ATG | TAA | 15 |
| tRNA-His | H | 13472-13537 | 66 | | | 0 |
| Nad5 | H | 13538-15259 | 1722 | ATG | TAG | -1 |
| tRNA-Phe | H | 15259-15326 | 68 | | | 654 |

“H” indicates the heavy strand while “L” indicates the light strand.