**Supplementary Materials**

**Table A: PCR details**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Primer Sequence** | **Tm** | **Name** | **Length** | **Amplicon Length (bp)** |
| 5'- TCA CGG GAG CTC TCC ATG CAT -3' | 60.9 | Mi1F | 21 | 1651 |
| 5'- TAG GTT TAG CTC AGA GCG GTC AAG -3' | 58.3 | Mi1R | 24 |
| 5'- CTG GAA AGT GCA CTT GGA CGA A -3' | 57.7 | Mi2F | 22 | 1751 |
| 5'- AGT AGG AGG TTG GCC ATG GGT ATG -3' | 60.4 | Mi2R | 24 |
| 5'- GAG CCC GGT AAT CGC ATA AAA CTT -3' | 57,6 | Mi3F | 24 | 1690 |
| 5'- AGA AGG CTT ACG TTT AGT GAG GGA G -3' | 58 | Mi3R | 25 |
| 5'- TCT GAC ATC CGG CCT GCT TCT -3' | 60.8 | Mi4F | 21 | 1640 |
| 5'- CTG TGA TTA GGA CGG ATC AGA CGA -3' | 57.8 | Mi4R | 24 |
| 5'- GTG TCT CCT CTA TCT TAG GGG CCA TC -3' | 59.7 | Mi5F | 26 | 1733 |
| 5'- TAA GCC TAA TGT GGG GAC AGC TCA T -3' | 59.8 | Mi5R | 25 |
| 5'- ACG TTG ACA ATC GAG TAG TAC TCC CGA -3' | 60.5 | Mi6F | 27 | 1783 |
| 5'- TCG GAA ATG GTG AAG GGA GAC T -3' | 57.9 | Mi6R | 22 |
| 5'- TCA GGA GTA TCA ATC ACC TGA GCT CA -3' | 58.9 | Mi7F | 26 | 1707 |
| 5'- CAG GAG TTT GAT AGT TCT TGG GCA GTG -3' | 59.3 | Mi7R | 27 |
| 5'- CTC CCT TCC CCT ACT CAT CGC A -3' | 60.4 | Mi8F | 22 | 1738 |
| 5'- GCT TGG ATT AGC GTT TAG AAG GGC T -3' | 59.2 | Mi8R | 25 |
| 5'- CTA TAC AAC CGT ATC GGC GAT ATC GGT -3' | 59.4 | Mi9F | 27 | 1725 |
| 5'- ATT GTT AGC GGT GTG GTC GGG T -3' | 61.2 | Mi9R | 22 |
| 5'- AGC CAT CGC TGT AGT ATA TCC AAA G -3' | 56.4 | Mi10F | 25 | 1685 |
| 5'- TGG TAC CGT ACA ATA TTC ATG GTG GCT G -3' | 60.2 | Mi10R | 28 |
| 5'- GAA GCA GAT TTG GGT ACC ACC CAA G -3' | 59.8 | Mi11F | 25 | 679 |
| 5'- CAG ATA CTG CGA CAT AGG GTG CT -3' | 58.5 | Mi11R | 23 |

**Table B: Post-sequencing read characteristics**

|  |  |
| --- | --- |
| Total read count | 20,514,117 |
| Raw read count per sample *(mean ± sd )* | 47,050.73 ± 16,656.96 |
| Mapped read count per sample *(mean ± sd )* | 27,452.83 ± 10,703.89 |
| Raw Read length *(bp, mean ± sd )* | 136.8934 ± 55.49467 |

**Table C: Post-sequencing mitochondrial genome coverage**

|  |  |  |
| --- | --- | --- |
| **Coverage threshold *T*** | | **Proportion of mtGenome covered less than *T* *(%, mean ± sd )*** |
| 5 X | 0.3 ± 1.9 |
| 10 X | 0.8 ± 3.7 |
| 20 X | 2.4 ± 7.0 |
| 50 X | 10.7 ± 13.3 |

Figure A: Coverage Distribution along mitochondrial Genome.

Mean +/- Standard deviation over the 436 samples

Coverage in overlapping amplicon regions is divided by a factor 2

