**Table S1. Primers used in this study.**

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| --- | --- | --- | --- |
| **Primer name** | **Sequence (5’ to 3’)** | **PCR product size** | **Application** |
| Ins2.F1Apple.R1Ins2.R1 | GAGGTGCTTTGGTCTATAAAGGGCATGAACTCCTTGATGATGGCCAAGTTACTACCACCAAGGAC | Targeted: 713 bpsWild type: 620 bps | Genotypingof *Ins2Apple* mice |
| SUR.PCR1SUR.PCR2Neo 5’ | CAATTCCTCAACTGAGGCTCTTAATCGCAGAGTGACCTCACAGCCTGTAGCCTCTGTTCCACATACACTTCA | Targeted: 417 bpsWild type: 457 bps | Genotypingof *Abcc8* KO mice |
| Ppargc1a-FPpargc1a-R | CTTTCTGGGTGGATTGAAGTGGTGAGACTGTCCAGTGTCTCTGTGAG | 147 bps(exons 2-3) | RT-qPCR of *Ppargc1a* |
| Bach2-FBach2-R | GCAAGCACTGGTTGGACAGACGAACTCAGCACAGCGGATGAC | 157 bps(exons 4-5) | RT-qPCR of *Bach2* |
| Thra-FThra-R | CTGGACAAAGACGAGCAGTGTGCACTGATTCCGGGTGATCTTGTC | 139 bps(exons 4-5) | RT-qPCR of *Thra* |
| Myt1-FMyt1-R | CCAGCAGCTCTATGACCTCACCTGGATACTTCCGCTCCTCAAAG | 201 bps(exons 13-14) | RT-qPCR of *Myt1* |
| Actb-FActb-R | ACGATGCTCCCCGGGCTGCATTCTCTCTTGCTCTGGGCCTCGTCACC | 115 bps(exons 2-3) | RT-qPCR of *Actb* |
| mtCO1-FmtCO1-R | TGCTAGCCGCAGGCATTACGGGTGCCCAAAGAATCAGAAC | 120 bps | mtDNA copy number |
| Ndufv1-FNdufv1-R | CTTCCCCACTGGCCTCAAGCCAAAACCCAGTGATCCAGC | 120bp | mtDNA copy number |