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

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| --- | --- | --- | --- |
| **Primer name** | **Sequence (5’ to 3’)** | **PCR product size** | **Application** |
| Ins2.F1  Apple.R1  Ins2.R1 | GAGGTGCTTTGGTCTATAAAGG  GCATGAACTCCTTGATGATGG  CCAAGTTACTACCACCAAGGAC | Targeted: 713 bps  Wild type: 620 bps | Genotypingof *Ins2Apple* mice |
| SUR.PCR1  SUR.PCR2  Neo 5’ | CAATTCCTCAACTGAGGCTCTTAA  TCGCAGAGTGACCTCACAGCCTGT  AGCCTCTGTTCCACATACACTTCA | Targeted: 417 bps  Wild type: 457 bps | Genotypingof *Abcc8* KO mice |
| Ppargc1a-F  Ppargc1a-R | CTTTCTGGGTGGATTGAAGTGGTG  AGACTGTCCAGTGTCTCTGTGAG | 147 bps  (exons 2-3) | RT-qPCR of *Ppargc1a* |
| Bach2-F  Bach2-R | GCAAGCACTGGTTGGACAGAC  GAACTCAGCACAGCGGATGAC | 157 bps  (exons 4-5) | RT-qPCR of *Bach2* |
| Thra-F  Thra-R | CTGGACAAAGACGAGCAGTGTG  CACTGATTCCGGGTGATCTTGTC | 139 bps  (exons 4-5) | RT-qPCR of *Thra* |
| Myt1-F  Myt1-R | CCAGCAGCTCTATGACCTCAC  CTGGATACTTCCGCTCCTCAAAG | 201 bps  (exons 13-14) | RT-qPCR of *Myt1* |
| Actb-F  Actb-R | ACGATGCTCCCCGGGCTGCATTC  TCTCTTGCTCTGGGCCTCGTCACC | 115 bps  (exons 2-3) | RT-qPCR of *Actb* |
| mtCO1-F  mtCO1-R | TGCTAGCCGCAGGCATTAC  GGGTGCCCAAAGAATCAGAAC | 120 bps | mtDNA copy number |
| Ndufv1-F  Ndufv1-R | CTTCCCCACTGGCCTCAAG  CCAAAACCCAGTGATCCAGC | 120bp | mtDNA copy number |