| Gene name | ETC complex | Gene ID | Reference sequences | Forward primer | Reverse primer |
|---|---|---|---|---|---|
| Ndufa1 | Complex I | 54405 | NM_019443 | catccacaaattcaccaacg | caggcccttggacacatagt |
| Ndufa10 | Complex I | 67273 | NM_024197 | ccaaccaaggtggtagagga | ccggaatggtcgtgtaattc |
| Ndufa11 | Complex I | 239760 | XM_358948 | ccagatgacccccgaacta | agcttgccgatcttgaacag |
| Ndufa12 | Complex I | 66414 | NM_025551 | accgatgggtcatctacacc | gcagtcggtggattagtcgt |
| Ndufa12l | Complex I | 75597 | XM_001476048 | ctccacccactatggaggaa | tgcagtaggtgaaggcaaga |
| Ndufa13 | Complex I | 67184 | NM_023312 | tcttccaggcagagaaggac | cccatcgtgtggtatggaac |
| Ndufa2 | Complex I | 17991 | NM_010885 | aggtaaccagagccatgcag | gacccaaagcacacatttcc |
| Ndufa3 | Complex I | 66091 | NM_025348 | catgatcaacaaggccacac | gttcttcagccagtccaagc |
| Ndufa4 | Complex I | 17992 | NM_010886 | cagatgtcagctgggacaga | gtctgggccttctttcttca |
| Ndufa4l2 | Complex I | 407790 | NM_001098789 | cctgagtcccaatgaccagt | gcagggagcagaaagagtga |
| Ndufa5 | Complex I | 68202 | NM_026614 | ttgcttcagggtggtgaagt | tattggccacttccactggt |
| Ndufa6 | Complex I | 67130 | NM_025987 | gtcacagaccccagagtggt | agaaatcctttggccttggt |
| Ndufa7 | Complex I | 66416 | NM_023202 | gttgtgcctccctcaatcat | gacagctcccacctcttcat |
| Ndufa8 | Complex I | 68375 | NM_026703 | catgcagctgtttcgtcact | tctctggcaaaggacgatct |
| Ndufa9 | Complex I | 66108 | NM_025358 | caaaccggtacctgctcttc | tggactcagcccaaagagtt |
| Ndufab1 | Complex I | 70316 | NM_028177 | gatccagaaaagctctccgtaa | tcaggaatttcaaacccaaa |
| Ndufaf1 | Complex I | 69702 | NM_027175 | ggaagggtacgagatgtcca | gggctggatcagtaaacaca |
| Ndufb10 | Complex I | 68342 | NM_026684 | tggagcagttcaccaaagtg | gccttcctttcttccagcat |
| Ndufb11 | Complex I | 104130 | NM_019435 | ttttccatcgtcctggtctt | aggccattgacttctcggta |
| Ndufb2 | Complex I | 68198 | NM_026612 | tcacccgtctggtacctttc | tgtaccggggctgaatatgt |
| Ndufb3 | Complex I | 66495 | NM_025597 | agaaacggtgcagaagaagc | acccccatttgaatcctttt |
| Ndufb4 | Complex I | 68194 | NM_026610 | ttcagtacaacgaccccaaa | cctgccacagctcctaaaag |
| Ndufb5 | Complex I | 66046 | NM_025316 | accctggctatcctccagat | ccttttcaggggttggaaat |
| Ndufb6 | Complex I | 230075 | NM_001033305 | tcgctgtttctcatgtgctt | tctccagtctccagaattgtatca |
| Ndufb7 | Complex I | 66916 | NM_025843 | ctgaagtgcaagcgagacag | cgctcacgttcaaactcctt |
| Ndufb8 | Complex I | 67264 | NM_026061 | ggccgccaagaagtataaca | tgataccacggatccctctc |
| Ndufb9 | Complex I | 66218 | NM_023172 | gtggaagaagctgaggatgg | gcaagtcaccttcccttctg |
| Ndufc1 | Complex I | 66377 | NM_025523 | cctcggttttcatgtggatt | tccagaggaaggactgtgat |
| Ndufc2 | Complex I | 68197 | NM_024220 | tttgtatgctgtgaaggacca | tgaaaacttcaacgcactgg |
| Ndufs1 | Complex I | 227197 | NM_145518 | cttcagggaggcattcattc | gttggacacagctgcaagaa |
| Ndufs2 | Complex I | 226646 | NM_153064 | cacatgttggcagatgtcgt | ttgtctcccaccagacacag |
| Ndufs3 | Complex I | 68349 | NM_026688 | ttatggcttcgagggacatc | attcttgtgccagctccact |
| Ndufs4 | Complex I | 17993 | NM_010887 | ttctgaccttcagtgccaaa | tccaagaaaagtttgcacca |
| Ndufs5 | Complex I | 595136 | NM_001030274 | gcgaaaaaggagtgcaagat | tgaggtggaggggtgtattt |
| Ndufs6 | Complex I | 407785 | NM_010888 | cacaacagcctgtgaacgag | catgtccccgtttttgtttc |
| Ndufs7 | Complex I | 75406 | NM_029272 | ggcggtggctactaccacta | cagctgcaagatgccataaa |
| Ndufs8 | Complex I | 225887 | NM_144870 | cgacacgctatgacatcgac | cagcaactcctcgtgtgtct |
| Ndufv1 | Complex I | 17995 | NM_133666 | gactccctgtgggagatcag | aatcgttgcatccgatcct |
| Ndufv2 | Complex I | 72900 | NM_028388 | ctggaaaagttcccaaacca | caagttaaaggcctgcttgc |
| Ndufv3 | Complex I | 78330 | NM_030087 | gacagcaaagaagccaggtc | cgctttcctttcctgtcttg |
| Sdha | Complex II | 66945 | NM_023281 | acatgcagaagtcgatgcag | cattcccctgtcgaatgtct |
| Sdhb | Complex II | 67680 | NM_023374 | agctactggtggaacggaga | gcagcggtagacagagaagg |
| Sdhc | Complex II | 66052 | NM_025321 | cctttgggaaccacagctaa | acggacagtgccataggaag |
| Sdhd | Complex II | 66925 | NM_025848 | ggtcagacccgcttatgtgt | gagagatgcagccttggaac |
| Cyb5a | Complex III | 109672 | NM_025797 | gggcagtcagacaaggatgt | ttctccaccaggatgctctt |
| Cyb5b | Complex III | 66427 | NM_025558 | gtcacctactaccggctgga | gcttgttccagcagaacctc |
| Cyb5r1 | Complex III | 72017 | NM_028057 | ccttacaccccgtcaccag | cccaatcttcaggctatcca |
| Cyb5r2 | Complex III | 320635 | NM_177216 | aatgagccaggaacccttttt | agctgtagcatgggcgtaat |
| Cyb5r3 | Complex III | 109754 | NM_029787 | acatcctgggccttcctatt | ttgaccaccaagtccacaaa |
| Cyb5r4 | Complex III | 266690 | NM_024195 | ggcctcagttctccaagcta | ggagtcatcctggaggtcaa |
| Cyc1 | Complex III | 66445 | NM_025567 | gcatcagaaccagagcatga | ccagctttcgactcttcagg |
| Rieske | Complex III | 66694 | NM_025710 | ccacctgttctggatgtgaa | aaaacggacagaagcaggaa |
| Ucrc | Complex III | 66152 | NM_197979 | gcgatctacgagcacatcaa | actccaggcaaacagctgac |
| Uqcc | Complex III | 226849 | NM_018888 | agaagccatgggattcactg | tgaatgtatcgggcatctga |
| Uqcr | Complex III | 66594 | NM_025650 | gccttacatcaacggcaagt | ctccagtgtccagcttcctc |
| Uqcrb | Complex III | 432822 | XM_484346 | taagagagccctggacctga | gcccactcctctctctcctt |
| Uqcrc1 | Complex III | 22273 | NM_025407 | aagctttgccagagtttcca | ggtacataggcgcatccact |
| Uqcrc2 | Complex III | 67003 | NM_025899 | ccaccttctaccgtccttca | actcgtcgagaaaaggcgta |
| Uqcrh | Complex III | 66576 | NM_025641 | tactctggttgcgcttgttg | gggggtccactagttcttcc |
| Uqcrq | Complex III | 22272 | NM_025352 | cgccttcccaagctatttc | gccccatgtgtagatcaggt |

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|---|---|---|---|---|---|
| Cox10 | Complex IV | 70383 | NM_178379 | gatgatctgcctggcatttt | gaagcaggaccagtcgaaag |
| Cox11 | Complex IV | 69802 | NM_199008 | gagaacatggtgcctgtcaa | atgccagtgcagtctctcct |
| Cox15 | Complex IV | 226139 | NM_144874 | cagtctgtggacctccctgt | cacaaaagcccctgagagag |
| Cox4i1 | Complex IV | 12857 | NM_009941 | agtgttgtgaagagtgaagac | gcggtacaactgaactttctc |
| Cox4i2 | Complex IV | 84682 | NM_053091 | gttgactgctacgcccagcgc | ccggtacaaggccaccttctc |
| Cox5b | Complex IV | 12859 | NM_009942 | cagaagggactggacccata | ttcacagatgcagcccacta |
| Cox6a1 | Complex IV | 12861 | NM_007748 | gagggttcagctcggatgt | ggggtctctcgtgctcttc |
| Cox6a2 | Complex IV | 12862 | NM_009943 | ttcctagcctccctttgaca | gaagagccagcacaaaggtc |
| Cox6b1 | Complex IV | 110323 | NM_025628 | ccccaaccagaaccagacta | gacttgtacacacgccggta |
| Cox6c | Complex IV | 12864 | NM_053071 | cacagatgcgtggtcttctg | gcatacgccttctttcttgg |
| Cox7a1 | Complex IV | 12865 | NM_009944 | ccgacaatgacctcccagta | ccagcccaagcagtataagc |
| Cox7a2 | Complex IV | 12866 | NM_009945 | aagatgttgcggaatctgct | gcatcccattatcctcctga |
| Cox7b | Complex IV | 66142 | NM_025379 | ctaagccgtctccaagttcg | aagatggctccacctgctaa |
| Cox7c | Complex IV | 12867 | NM_007749 | ccagagtatccggaggttca | ggtcatcatagccagcaacc |
| Cox8a | Complex IV | 12868 | NM_007750 | atgtctgtcctgacgccact | gaagtgagcccaatggtgat |
| Atp5a1 | Complex V | 11946 | NM_007505 | ttatcccccgaatctctgtg | gcaatcgatgttttcccagt |
| Atp5b | Complex V | 11947 | NM_016774 | gaggtcttcacgggtcacat | atgggtcccaccatgtagaa |
| Atp5c1 | Complex V | 11949 | NM_001112738 | acaatctggccaacctcatc | gtgcggttgaaagtcaaggt |
| Atp5d | Complex V | 66043 | NM_025313 | aggggttcacacagaagacg | agcatgtccagtgtcacagc |
| Atp5e | Complex V | 67126 | NM_025983 | ccggtttgaggctactctga | cctcactgcttttgcacaga |
| Atp5f1 | Complex V | 11950 | NM_009725 | atcgcctggactaccacatc | ttggcaatggtctccttttc |
| Atp5g1 | Complex V | 11951 | NM_007506 | aaaaatgcagaccaccaagg | caggaaggctgcttagatgg |
| Atp5g2 | Complex V | 67942 | NM_026468 | tgggactgtttttgggagtc | tgagaaaggccaccattagg |
| Atp5g3 | Complex V | 228033 | NM_175015 | cccagaatggtgtgtgtcag | caccagaaccagcaactcct |
| Atp5h | Complex V | 71679 | NM_027862 | gaaaccacctgcgattgact | gtccaccagggctgtgtatt |
| Atp5i | Complex V | 27425 | NM_013795 | actacgccaaggttgagctg | aaccattcagcacagcttcc |
| Atp5j | Complex V | 11957 | NM_016755 | gtccttcggtcagcagtctc | agatgcctgtcgctttgatt |
| Atp5j2 | Complex V | 57423 | NM_020582 | tggataatgatgcgggattt | ctgccaggaccatgctaatc |
| Atp5k | Complex V | 11958 | NM_007507 | cggttcaggtctctccactc | cttcttttcctccgctgcta |
| Atp5o | Complex V | 28080 | NM_138597 | ctatgcaaccgccctgtact | gtgcgcttgatgtagggatt |
| Atp5s | Complex V | 68055 | NM_026536 | ccatggtcatgtgactccag | cacaccgaagtagccactca |
| Atpaf1 | Complex V | 230649 | NM_181040 | agacaaaactgcggaggaaa | aaatgttgggcaggactgag |
| Atpaf2 | Complex V | 246782 | NM_145427 | ggtgcttaccagccacttgt | gaagcacagcttgttccaca |
| LOC100040708 | Complex V | 100040708 | NM_001111335 | agaccatggccaagttcatc | aaccagctcaaccttggtgt |
| Ucp1 | UCP | 22227 | NM_009463 | ggcctctacgactcagtcca | ccttcacgacctctgtaggc |
| Ucp2 | UCP | 22228 | NM_011671 | ctcaaagcagcctccagaac | acatctgtggccttgaaacc |
| Ucp3 | UCP | 22229 | NM_009464 | cggtggatgtggtaaagacc | aaaggagggcacaaatcctt |
| Ucp4 | UCP | 74011 | NM_028711 | aggtcggatggtcacctatg | gtcagtggggttggctaaaa |
| Ucp5 | UCP | 20523 | NM_011398 | ggaatgctgggagacacaat | gtcccactattgccctctga |
| Sco1 | Chaperone | 52892 | NM_001040026 | ccacctgttcagagacgtt | ttccttgaccttagcgcagt |
| Sco2 | Chaperone | 100126824 | NM_001111288 | ctgctcaaccctgatggtct | acagggcctaggcaataggt |
| Surf1 | Chaperone | 20930 | NM_013677 | acttgggagtcaccatcctg | gggcttcctgttttctgtga |
| Actb | Reference | 11461 | NM_007393 | ctaaggccaaccgtgaaaag | ccatcacaatgcctgtggta |
| Hprt | Reference | 15452 | NM_013556 | gccccaaaatggttaaggtt | caagggcatatccaacaaca |
| Ppia | Reference | 268373 | NM_008907 | agcatacaggtcctggcatc | ttcaccttcccaaagaccac |
| Lonp1 | Control | 74132 | NM_028782 | acacatccaaggaggtgctc | gagggttcaaggcgatgata |
| Vegfa | Control | 22339 | NM_001025257 | caggctgctgtaacgatgaa | gcattcacatctgctgtgct |
| Bnip3 | Control | 12176 | NM_009760 | gcttggggatctacattgga | ccaaggaccatgctagctct |
| Gapdh | Control | 14433 | NM_008084 | aactttggcattgtggaagg | ggatgcagggatgatgttct |
| Slc2a1 | Control | 20525 | NM_011400 | agcagctgtcgggtatcaat | acagcgacaccacagtgaag |

**Gene Name =** scientifically recognized gene name abbreviation

**ETC Complex =** ETC complex (I, II, III, IV, V) of which gene is included (UCP = uncoupled protein gene; Chaperone = chaperone gene; Reference = housekeeping gene; Control = stress responsive/HIF1α responsive gene)

**Gene ID =** Entrez Gene identification number

**Reference Sequence =** NCBI reference sequence code

**Forward Primer =** primer designed to amplify sense (top) strand of template

**Reverse Primer =** primer designed to amplify antisense (bottom) strand of template

**Amp Size =** size of amplicon created by listed primers

| Amp size |
|---|
| 124 |
| 139 |
| 140 |
| 139 |
| 134 |
| 129 |
| 125 |
| 121 |
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| 140 |
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