**Figure S10. Alignment of nucleotide sequences corresponding to two *mtco2* paralogues and the probe C060R108 from the Agilent 44K salmonid microarray (GEO accession number: GPL11299).**

 1 50

mtco2a\_BT044012 (1) CACAACTAGGATTCCAAGACGCGGCCTCCCCTGTAATAGAAGAACTCCTT

mtco2b\_DW556807 (1) --------------------------------------------------

 C060R108\_mtco2 (1) --------------------------------------------------

 51 100

mtco2a\_BT044012 (51) CATTTTCACGACCATGCTCTTATGATTGTTCTTCTTATCAGCACACTAGT

mtco2b\_DW556807 (1) --------------------------------------------------

 C060R108\_mtco2 (1) --------------------------------------------------

 101 150

mtco2a\_BT044012 (101) GCTTTATATCATTGTAGCAATAGTCTCTACTAAACTCACTAACAAGTATA

mtco2b\_DW556807 (1) -------------------------------AAACTCACTAACAAGTATA

 C060R108\_mtco2 (1) --------------------------------------------------

 151 200

mtco2a\_BT044012 (151) TCCTTGATTCTCAAGAAATCGAAATCGTTTGGACTGTCCTTCCAGCAGTT

mtco2b\_DW556807 (20) TCCTTGATTTTCAAGAAATTGAAATCGTTTGGACTGTCCTTCCAGCAGTT

 C060R108\_mtco2 (1) --------------------------------------------------

 201 250

mtco2a\_BT044012 (201) ATCCTCATTCTTATTGCCCTCCCCTCCCTTCGAATTCTTTACCTTATAGA

mtco2b\_DW556807 (70) ATCCTCATTTTTATCGCCCTCCCCTCCCTTCGAATTTTTTCCCTTATAGA

 C060R108\_mtco2 (1) --------------------------------------------------

 251 300

mtco2a\_BT044012 (251) **CGAAATTAATGACCCACACCTTA**CTATTAAAGCAATGGGTCACCAATGAT

mtco2b\_DW556807 (120) GGAAATTAATGACCCACCCCTTATTATTAAAGCAATGGGTCACCAATGAT

 C060R108\_mtco2 (1) --------------------------------------------------

 301 350

mtco2a\_BT044012 (301) ACTGAAGCTATGAATACACCGACTACGAAGACTTAGGCTTTGACTCTTAT

mtco2b\_DW556807 (170) ACTGAAGCTATGAATACCCCGACT**ACGAAGACTTGGGCTTTGATT**TTTAT

 C060R108\_mtco2 (1) --------------------------------------------------

 351 400

mtco2a\_BT044012 (351) ATAGTCCCCACCCAAGACTTAACGCCCGGTCAATTTCGTCTTCTAGAAAC

mtco2b\_DW556807 (220) ATAGTCCCCACCCAAGACTTAACGCCCGGTCAATTTTGTTTTTTAGAAAC

 C060R108\_mtco2 (1) --------------------------------------------------

 401 450

mtco2a\_BT044012 (401) AGACCATCGAATGGTTGTCCCTG**TAGAATCTCCAATCCGCGTC**CTAGTTT

mtco2b\_DW556807 (270) AGACCATCGAATGGTTGTCCCTGT**AGAATTTCCAATCCGCGTC**CTAGTTT

 C060R108\_mtco2 (1) --------------------------------------------------

 451 500

mtco2a\_BT044012 (451) CAGCTGAAGACGTCCTTCACTCCTGAGCCGTCCCTTCCTTAGGTGTAAAA

mtco2b\_DW556807 (320) CAGCTGAAGACGTCCTTCACTCCTGAGCCGTCCCTTCCTTAGGTGTAAAA

 C060R108\_mtco2 (1) --------------------------------------------------

 501 550

mtco2a\_BT044012 (501) ATGGACGCAGTCCCAGGACGATTAAACCAAACAGCCTTTATTGCCTCTCG

mtco2b\_DW556807 (370) ATGGACGCAGTCCCAGGAGGATTAAACCAAACAGCCTTTATTGCCTCTCG

 C060R108\_mtco2 (1) --------------------------------------------------

 551 600

mtco2a\_BT044012 (551) ACCTGGAGTATTCTACGGACAATGTTCTGAAATCTGCGGGGCCAACCACA

mtco2b\_DW556807 (420) ACCTGGAGTATTTTACGGACAATGTTTTGAAATTTGGGGGGCCAACCACA

 C060R108\_mtco2 (1) --------------------------------------------------

 601 650

mtco2a\_BT044012 (601) GCTTCATACCCATCGTTGTTGAAGCAGTGCCCCTAGAACACTTCGAGAAA

mtco2b\_DW556807 (470) GCTTCATACCCATGGTTGTTGAAGCAGTACCCCTAGAACACTTCGAGAAA

 C060R108\_mtco2 (1) ------------------TTGAAGGGGTACCCCTAGAACATTTTGGGAAA

 651 684

mtco2a\_BT044012 (651) TGATCCACTATAATACTTGAAGATGCCTAAAAAA

mtco2b\_DW556807 (520) TGATCCACTATAATACTTGAAGATGCCT------

 C060R108\_mtco2 (33) TGATCCATTTTGATATTTGAAGATGCCT------