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Rainbow trout, classified as abhd5 by BLAST search
GTGAAGAATGGCTGACCAAGCGGTGACTACTGAGAGAGGACTGGCTCAGCGAATACTGAT
GTTTCTTGGTATTCATAGTCTTTTCTACAATTTGTTGAGTATCCTGGACAGAACGTTGAG
GTCCTGGACTTCCACGGCATGGATCACCAGCTGGCTGCCCTCCTGGTGCCCCACCTCCCA
GAACCAGCTCAAGACTGCAGAGGAGAAGATGCTGCAATGCATCACAGGCAAGGTGTCCCA
GCAGTATGTCCCAATCTCGGATGGTAACATGCTGTGGACCCTCACATTGAATGGAAACAT
GAAGAACCAGACTCCCCTGGTGCTGCTGCATGGCTTCGGTGGAGGGGTGGGCCTGTGGGC
CCTCAACCTAGACGCCCTGGCCCAACAGAGGCCCGTCTATGCCTTTGACCTGCTGGGCTT
CGGCCAGAGCAGCCCTACTTCAGCTCCGACGCCAAGGAGGCTGAGGCCCAGTTTGT
GGACTCCATCGAGCAGTGGAGGGCTAAAGTCGGCCTGGAAGCCATGGTCATGCTGGGACA
TAACTTTGGAGGTTATTTGGCAGCTGCTTATTCGCTCAAGTATCCCACCAGGGTGCAACA
TATGGTGCTGGTTGAGCCGTGGGGCTTACCTGAGCGTCCAGACACAGAAGACCAGGACAG
GCCCACCCCGTGTGGATCAAAGCCCTGGGAGCCATGTTGAGCCCGTTCAACCCCCTGGC
                                             TAAGACCAGACTT
GAATGTCCAGACTCCCAGTGGTGAGACAGCCTTCAAGAACATGACCATCCCATACGGGTG
GGCCAAGAGGCCTATGCTGCAGAGGATTGGCCTGCTCCATGCTGACATCCCTATTACTGT
GATATATGGGTCACGCTCCAGCATCGACGGTAACTCGGGCAACGCTATCAAAGAAATGAG
GCCAAACTCTCATGTGGAGATCATAGCTATCAGAGGAGCGGGCCACTACGTCTATGCTGA
CCAGCCAGAGGACTTCAACCACAGAGTGCTTCAGGTGTGACGCGCTGGGCTGATGGGG
GGGGGTGGGCACTAGTTAACCTGCGGAGAGTGACTT
TGTCCTCTCAGTGAGCATGTGATCTGTGAGGATAGAGGGGCTGGGCATACAGCTCAATA
GGGCTTTATTTTACCTCGATCATCCTCACTTTAGGTCCTCAGTAGTAGACCTACCACCAC
CAGCACAGCAGACCTGCTAACTAGGGAAGGACCCCGTGTTGAAAAGATGATTCTCCTGGA
TTGGTTGGTTTGACACTTGTATTCATTCTACTGACAAAAGAGAATGGCTCATAGTTGTTA
CTGCTTGTT
mfe: -23.8 kcal/mol
position 1251
abhd5
                    CA G
                 AGCU AUAG GCUUUAUUUUA
                 UCGA UGUC CGAAGUAGAGU
omv-miRNA-143 3' C
                        Д
mfe: -23.0 kcal/mol
position 426
                   A GCCCUA G C 3'
abhd5
                GAGC GCAG CUUCA CUC
CUCG UGUC GAAGU GAG
omy-miRNA-143 3'
                  A AC A U5'
mfe: -21.6 kcal/mol
position 152
                     ccuccu cc c c 3'
abhd5
                GGCUGC GGUGC CA CUC
UCGAUG UCACG GU GAG
omy-miRNA-143 3' C
                             AA A U5'
mfe: -20.2 kcal/mol
position 1176
                    CCU CAUGCCCAGA UG C
abhd5
                 GCUACA GU GCU UC UCUCA
CGAUGU CA CGA AG AGAGU
omy-miRNA-143 3' CU
mfe: -19.1 kcal/mol
position 721
abhd5
                        ACUGGUGGGGCCACU GGUCCCACACU
                                                     G
                 GGGCUACG G UGUUUCA CUC
CUCGAUGU C ACGAAGU GAG
                                                   ACGAAGU GAG
omv-miRNA-143 3'
                                                        A U 5'
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Fig. S1. Predicted binding sites for omy-miR-143 on rainbow trout *abhd5*. The sequence for *omy-miR-143* was obtained from Salem et al. (Salem et al., 2010) and *abhd5* was retrieved from the trout database in the Gene Index project (http://compbio.dfci.harvard. edu/tgi/) under accession number TC114063. Predicted binding sites (six) are highlighted in purple; start and stop codon location, highlighted in green, was predicted by translation of the trout *abhd5* sequence into AA and comparison with the full protein sequence in zebrafish. Criteria and methods used for the identification of binding sites are explained in the main text.