Melanostoma scalare

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Melanostoma

Assembly: GCA_949752695.1_idMelScal2.1_genomic

Mel_sca1 | OX456985.1:36110135-36110415 (-) | 281 nt | lncRNA:noe consensus e-value: 1.4e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.86

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GGGCGGTTCAGTGCCTCACAGTGCTTGCGGTTGGCTACATTCCGTTTCCTAAATTGTAGTATCTAAATCGTATGCTTTGACATCCATACTAAGTAAAACAAACACTGCAAAATTGTGTTTGAGTAAAAATAAGTTTCACCAAAAACAACG
CAAACAAAAAACGAAAAAAAACTCTCCTCTCTATCGTATAAGAATATCTATAATATAGAATAAGACAATTCAAACAAAAACGAGAACAAAAATAAAAATCTGCTGAGGTATTTCGTGATCGCCTTTTTTTT
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Mel_sca1          ------tagcacatctaaaatacctcaatttacaatcacaTATAATTCGCAGATACTTtttcataactaactacaaccttaacaaaacttaaatatactaaccatt----------
RNase_MRP         ---------------tatgtataagtttttttaactttTACAGTTCGCAGTATTTTtttgctaatgtgcttgttgatatacaaatcgaatgcttatccagtggtagtgttgtt
tRNAsec           ----agatgacaaatttaaataaataaaatttttgttgaaTATGATTCACAGTATTTTtttcgttgtctttactgtcaatatgcattattagctgagaaatgat-----------
snoRNAMe18SA1806  -----aaaatataaaaaatttcattactttttatcatcaaTATAGTTCACATATTTTTtttatcatctcacttttaaataattatatatatgaacatgactataa----------
U1                ---acccaagaaaacgtaaagaaattttgtattctattttTACAGTTCACATTTACTTtttgttgaaaaagtgacaagagatggtataaaatttgaagaaagc-------------
U1                ---tatgggtttagggtgtttttctctttttttttaaTACAGTTCACACTCGTTTagagcgagaaagtttgtatagctgagataatggttgggaaaatc-------------
U1                ---aacacaaaaaaatataaaaaaaatttatttctcttaTACAGTTCACATTTACTTtttatttaaaaaatataacaaaaatatataaaatttgaaaaaac-------------
U1                ---tacacaagaaaaaggaaagcatctactgtttttctattTAGAATTCACATTTACTTttggctgaaaaagccataaaggatagtggaaaatgtgaagaaagc-------------
U1                ---acccaagaaaacgcaaagaaattttgtattctttttatTACAGTTCACATTTACTTtttgttgaaaaagtgacaagagatggtttaaaatttgaagaaagc-------------
U1                ---acaaaacacaaaaacacaaaaaatattatttactttcaTTCAATTCACATTTTGTTgaagctaaaaagattacaagacatagtaaaaacaaaaaaaaaac-------------
U2                ---aattatttttatttttatgtatttatttcaatacatcttTCCAATTCACACAACACTcctgcaaaaaagtatacaagtaattgcttgttttcaaagaaaagtt-------------
U2                -----caacaacaaattctgagggattattattttttctTATAACTCACACCGTCTTactgttggtatagttgtgaagtaatagtagtttttcagtacaaagtt-----------
U2                ---actattttattttatgtattttatttcaatacatcttTCCAATTCACACAACACTcctgcaaaaaagtatacaagtaattgcttgttttcaaagaaaagtt-------------
U4                ---ttttttcaaaattttatttaatttatttttatacataTACAATTCACATTTTCATctttctgaaaatttttgaaaaaaaaaaaaaaaatttaaaaattatt-------------
U4                ----agccgaaaagaacacaaaataatttctttaaatttttAGAATTCACAGTGCCTTgttgtaggaaatgttataagagatcgagtgagttggttgtaaagtt-----------
U4atac            gtttgcagttttgcacccctttcaatattcttttaaatcaTACACTTCACATTCAGTTggtttaatttaattcataagacagcaaattgtgatcacatca----------------
U5                --caaatgaatccgacatgtttttttatactatatccttaaTTCAATTCACATTCACTCtttactcctgacatatcttataatgataatacttatatcatact--------------
U5                --aattatcgactttctatcaattctctgttgtttctttttTACAGTTCACACTTACTTtcatccgtcaagttgacaaagggaagtgagaaattgtttgcaaa-------------
U11               ---gagtcgatgtacattgtatagactgacttgtgttcctTACAATTCACATCAAGTTtctgtagccaacgctataggtaagagtgaaattgagtgagatatt-------------
U12               ------gtcaactgcaattggatattttattttgttaaaTACAATTCACACTCTCTTttgtcaattaaacgttatacttagatgtaaggaagtgcagttaacttc----------
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Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAMe18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.