

Melanostoma mellinum

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

Assembly: GCA_914767635.1_idMelMell2.1_genomic

Mel_mel1 | OU612059.1:35330741-35331024 (-) | 284 nt | lncRNA: noe consensus e-value: 7.8e-12

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt

666c66ttcagtgccctcacagtgcttgc66ttggctacattccgittccataattgtatgtatctaaatcgatgctttgacatccattactaagtataaaacaaaaaacactgcataattgtgtttgagtaaaaaaagtttcacccaaaaac
aacgataaaacaaaaaacgaaaaaacctcctctctatcgataaagaatatctataattatagaataagacattcaaacaaaaacgagaacaaaaacaaaaatctgttgaggattatgatgtgatcccttttttt

Mel_mel1 ----taccacatctaaaaatccctcaatttgcgaatcccaTATAATTGCGAGATACttttcttaacccactgcaaccttaacadaacttgaatatactgaccatt

U1 ---tcggttttaggttttaggggtgttttttccatttttttaTACAATTTCACACTCGtttagagcggaagaattgtatagcctgagatattcgctcagaatttc---

U1 ---acccaaagaaaacgtagagaaattttgtattcttttctTACAATTTCACATTACttttgttgaaaaagtgcacagagatgggtataaaatttgaggaagc---

U1 ---acccaadaaatctgaagaattttgtattctttttTACAATTTCACATTACttttgttgaaaaagtgcacagagatgggtataaaatttgaggaagc---

U3 ---acacttctttatctctgtggattcaattttgttcACAAATTCACATTACtttgcgcacaaaagttgacttaatagtgttatttgggtggagaattt---

U4 ---tttttccaaattttgtttgtttatttttatacataTACAATTTCACATTTCATcttgcctgaaaaatcttgaaaaaggggaagaaaaattgaaatcatc---

U4 ---aotcdaaaadaacacaaaataattttttcaattttTAGAATTTCACATTGCGTTGctggaadaaatgttataagadaatdaotdaottotaotaaaatt---

U4atac gtttgcaattttgcaccccttcaattgtcttttaaatcaTACAATTTCACATTTCAGtttctttaatttaattcataagacagcaaatgtgatcacatca-----

U5 ---atcgaattgtattgtatttaattcttttcgtttctttTACAATTTCACATTGCGttttctctgtaaaattgacataggggaagtgaataattgtgaaaaag---

U5 ---aatatcgaacttctgaatcattctcttctttttTACAATTTCACACTTACTttccctccatcaatttgaataaadaaatataaaaattattagaaa---

U12 -----aacatcatgggagtacattttattttcgttttaaTACAATTTCACACTCCCTCattcaattaaacgttatacttagatgcaagaagtgcaatttaacttc

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.