Melieria crassipennis

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Ulidiidae > Melieria

Assembly: GCA_963668005.1_idMelCras1.1_genomic

Mel_cra1 | OY764962.1:93279139-93279931 (-) | 793 nt | IncRNA:noe consensus e-value: 1.1e-25

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 11nt PSE: 0.91

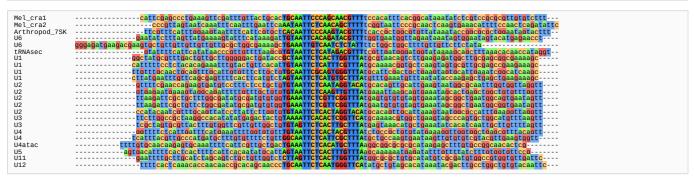
Mel_cra2 | OY764963.1:102011085-102011560 (+) | 476 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.81

SGCGGTCGTAGTACTCCGAGTTGAAAGGGTTGAACTGCACACAGCCCCGAATTGTCGCAGCGAATAGAGCACACATAAACGTGGTCTCTAAGGTTTTACCTTTGCCCCGTGAAGTTCTCTTACCCGTATATACAATTAACATAA AACGCATACACACAATTAATTGATGATTGTAATGTGTTATATAAGTAGGTACCACAGAGTTGGCCAAGTGTGATAAAGCAGTAACAGCACCAGCACTTGCGTCTGCATATCTTCCTTATATAAGTAGGTATCATCTCCATTAACT GATGTTGGTCGGGAGGAGAATATATGGGCGCATTCTCCTCCGTTCCCCACAATTAATGAAGATGAAATTTCCAATAGGTCACCTTGCCCCGAACCCGGCAGGTATGACGCTTGTTTCGCCATAACAAGAGTTTCAGTTGGTTTACTGCGG GGTGCGACTGTGATCGCCACATTTTT

	Mel_cra1	Mel_cra2
Mel_cra1	-	39
Mel_cra2		-

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.



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.