Melieria omissa

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

Assembly: GCA_963971225.1_idMelOmis1.1_genomic

Mel_omi1 | OZ020268.1:95161415-95162242 (-) | 828 nt | IncRNA:noe consensus e-value: 3.7e-28

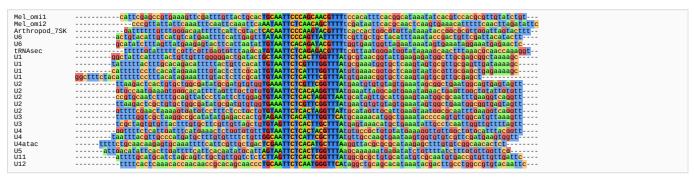
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 9nt PSE: 0.91

Mel_omi2 | OZ020269.1:18657880-18658366 (+) | 487 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.80

	Mel_omi1	Mel_omi2
Mel_omi1	-	40
Mel_omi2		-

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.