Meliscaeva auricollis

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

Assembly: GCA 948107695.1 idMelAuri2.1 genomic

Mel_aur1 | OX403617.1:67170950-67171265 (+) | 316 nt | IncRNA:noe consensus e-value: 3.0e-06

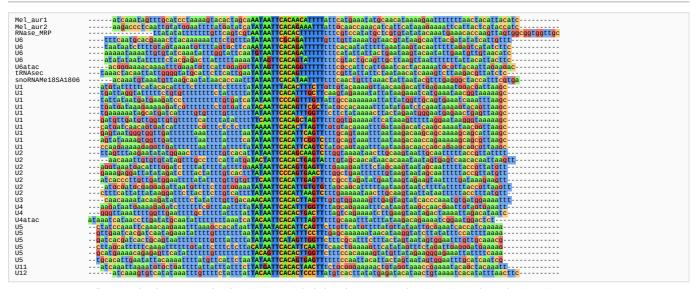
5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.89

Mel_aur2 | OX403617.1:20407763-20408055 (-) | 293 nt | IncRNA:noe consensus e-value: 4.4e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

		Mel_aur1	Mel_aur2
M	el_aur1	-	50
M	el_aur2		-

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.