

Drosophila micromelanica

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > melanica group

Assembly: GCA_004143825.1_ASM414382v1_genomic

Dro_mic1 | SCDY01000520.1:40439-41689 (+) | 1251 nt | lncRNA: noe consensus e-value: 8e-176

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.89

[illegible]

Dro_mic2 | SCDY01001774.1:15598-16192 (+) | 595 nt | lncRNA: no consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.99

[illegible]

	Dro_mic1	Dro_mic2
Dro_mic1	-	30
Dro_mic2		-

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

[illegible]

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.