

Drosophila melanica

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

Assembly: GCA_004143765.1_ASM414376v1_genomic

Dro_mel1 | SCDT01000590.1:16380-17730 (+) | 1351 nt | lncRNA: noe consensus e-value: 3e-170

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 10nt PSE: 0.76

[illegible]

Dro_mel2 | SCDT01003066.1:4722-5343 (-) | 622 nt | lncRNA: no consensus e-value: 5.4e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.90

GGGCGGTCGAGCGCTTTACAGCGTCAAGGGTGATCACACCTCCCGGACTAATTGTGATGGAAATATGGCAAAAAATAAAAAGAGCTATATATACATACAACBTGGTGATCTTATAAAAAGCAGCAAGCAAGAAAAACAGAAAAATG
CGAGATTTTATAAATAATCTATAATATATATASGATCTGTGTTAGATAGAGGGGATAGAGGAGATATATATATATATATATGATGATGATGATCACTATGAAGCGTTTCTAGAAATTTATTTATATAATGTATTGGATGATGAAGCA
AAAAATACAGCCCGGACATCTCAAGCAAGTTTATATATATATTTAAAAAGAAAAAGCAAAAAATGTAAAAATCAAGAGCAAGAAAAAGAGAGAAAAATCCAACTCTTCAATAAAACTCCGACCAACATCGAATATG
ACCAAGCAATATCTCTACGCBAGATTTGAGGTGGGATCCCAATACACCTTCAACTGTGCAAGCAAAAAAAAATAACAAAAATAGCTGTGAGAGCGTTCGAGAAAGGGGAGATGGTTGGGAGGTTTCACGCCCTCCCTTTCTCTCCCTTC
CCGATATGATCGCTTTTTTTT

	Dro_mel1	Dro_mel2
Dro_mel1	-	28
Dro_mel2		-

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

Dro_mel1 -----
Dro_mel2 -----
Arthropod_7SK -----
RNase_MRP -----
U6 -----
U4atac -----
tRNAsec -----
snRNome18S1A906 -----

U1 -----
U1 -----
U1 -----
U1 -----
U2 -----
U2 -----
U2 -----
U3 -----
U3 -----
U4 -----
U4 -----
U4atad -----
U5 -----
U7 -----
ORC1 -----

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.