Drosophila melanosoma

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > haleakalae group > scitula subgroup

Assembly: GCA 035042045.1 ASM3504204v1 genomic

Dro_melano1 | JAWNLY010000030.1:2375746-2376750 (-) | 1005 nt | IncRNA:noe consensus e-value: 7e-158

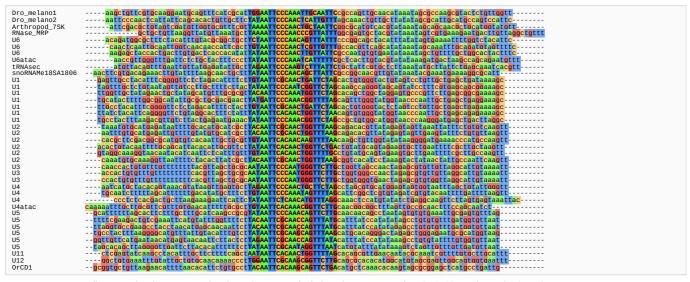
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.91

Dro_melano2 | JAWNLY010000179.1:2730169-2730613 (-) | 445 nt | IncRNA:noe consensus e-value: 5.5e-13

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

	Dro_melano1	Dro_melano2
Dro_melano1	-	28
Dro_melano2		-

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.