Drosophila murphyi

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > grimshawi group > orphnopeza subgroup

Assembly: GCA_018904325.1_ASM1890432v1_genomic

Dro_mur1 | JAEIFX010001249.1:980343-981373 (+) | 1031 nt | IncRNA:noe consensus e-value: 4e-166

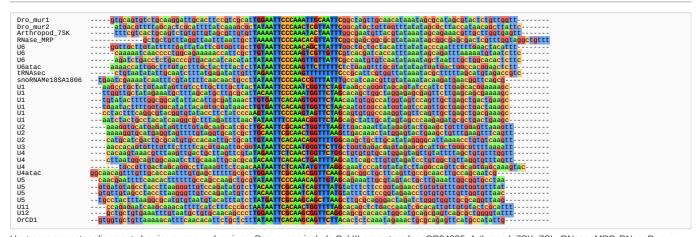
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_mur2 | JAEIFX010001255.1:2393072-2393566 (-) | 495 nt | IncRNA:noe consensus e-value: 4.8e-15

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

	Dro_mur1	Dro_mur2
Dro_mur1	-	30
Dro_mur2		-

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.