Drosophila atroscutellata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > spoon tarsi subgroup Assembly: GCA_035041605.1_ASM3504160v1_genomic

Dro_atro1 | JAWNLA010000105.1:12957671-12958694 (-) | 1024 nt | IncRNA:noe consensus e-value: 3e-155

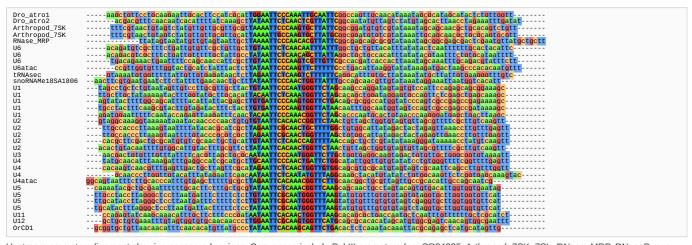
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Dro_atro2 | JAWNLA010000108.1:24190484-24190770 (+) | 287 nt | IncRNA:noe consensus e-value: 3.1e+00

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

	Dro_atro1	Dro_atro2
Dro_atro1	-	17
Dro_atro2		-

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.