Drosophila algonquin

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > affinis subgroup

Assembly: GCA_035041765.1_ASM3504176v1_genomic

Dro_alg1 | JAWNKY010003069.1:88241-89491 (-) | 1251 nt | IncRNA:noe consensus e-value: 1e-180

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.82

Dro_alg2 | JAWNKY010003123.1:323814-324411 (+) | 598 nt | IncRNA:noe consensus e-value: 5.5e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

	Dro_alg1	Dro_alg2
Dro_alg1	-	32
Dro_alg2		-

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.