Drosophila affinis

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

Assembly: GCA_037356375.1_KU_Daffinis_5.1_genomic

Dro_aff1 | CM074802.1:47457733-47458991 (+) | 1259 nt | IncRNA:noe consensus e-value: 4e-180

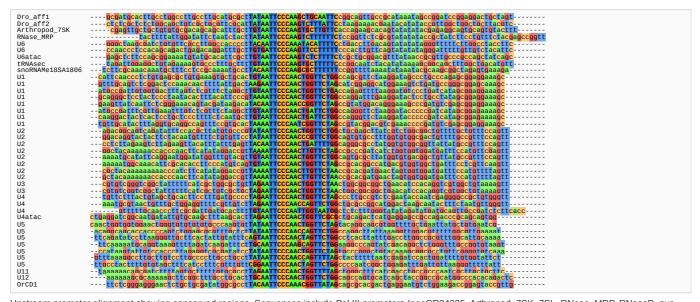
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Dro_aff2 | CM074800.1:44722454-44723019 (-) | 566 nt | IncRNA:noe consensus e-value: 1.0e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.95

	Dro_aff1	Dro_aff2
Dro_aff1	-	31
Dro_aff2		-

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.