Drosophila cognata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila

Assembly: GCA 035041535.1 ASM3504153v1 genomic

Dro_cog1 | JAWNLC010000823.1:2108912-2109905 (+) | 994 nt | IncRNA:noe consensus e-value: 8e-158

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Dro_cog2 | JAWNLC010000235.1:8981948-8982306 (-) | 359 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

	Dro_cog1	Dro_cog2
Dro_cog1	-	24
Dro_cog2		-

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.