Drosophila cyrtoloma

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > planitibia group > cyrtoloma subgroup

Assembly: GCA 035042485.1 ASM3504248v1 genomic

Dro_cyr1 | JAWNLH010000667.1:13409038-13410050 (-) | 1013 nt | IncRNA:noe consensus e-value: 6e-164

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

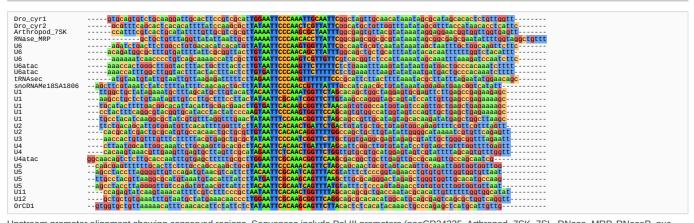
GCGGT 3' MOUT: ATCIGC IIITETHALIHAA. FOLY T. O.M. T. O

Dro_cyr2 | JAWNLH010000885.1:8129460-8129929 (-) | 470 nt | IncRNA:noe consensus e-value: 2.9e-13

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

	Dro_cyr1	Dro_cyr2
Dro_cyr1	-	30
Dro_cyr2		-

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.