Drosophila carrolli

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

Assembly: GCA 018152295.1 ASM1815229v1 genomic

Dro_carr1 | JAECXJ010000001.1:7458585-7459678 (-) | 1094 nt | IncRNA:noe consensus e-value: 1e-202

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

Dro_carr2 | JAECXJ010000002.1:4962517-4963024 (+) | 508 nt | IncRNA:noe consensus e-value: 8.7e-03

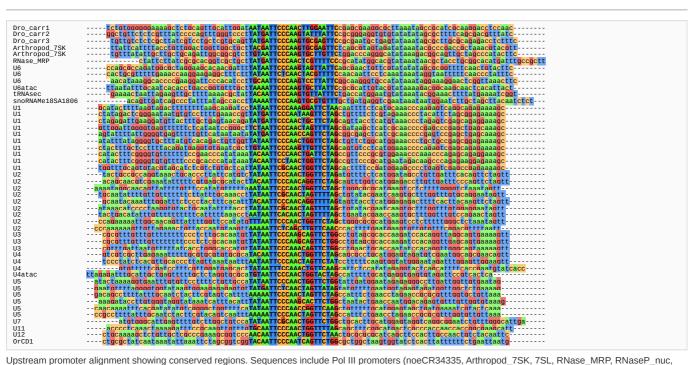
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.98

Dro_carr3 | JAECXJ010000002.1:12515505-12515727 (-) | 223 nt | IncRNA:noe consensus e-value: 8.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.98

	Dro_carr1	Dro_carr2	Dro_carr3
Dro_carr1	-	32	13
Dro_carr2		-	32
Dro_carr3			-

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.