Drosophila lacteicornis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA_008044355.1_UCB_Dlac_1.0_genomic

Dro_lact1 | VNKF01002184.1:17451-18666 (+) | 1216 nt | IncRNA:noe consensus e-value: 7e-187

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.90

Dro_lact2 | VNKF01008565.1:132554-133087 (-) | 534 nt | IncRNA:noe consensus e-value: 1.1e-02

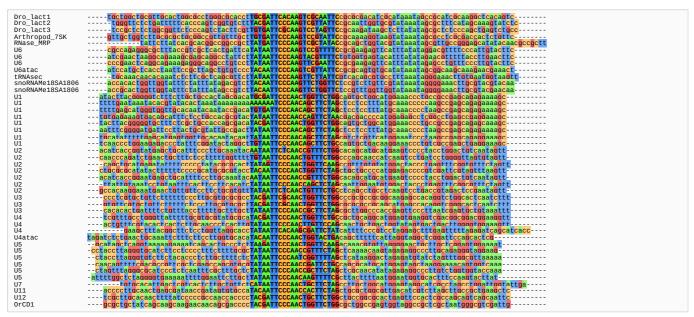
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.98

Dro_lact3 | VNKF01009512.1:76952-77280 (-) | 329 nt | IncRNA:noe consensus e-value: 1.7e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.92

	Dro_lact1	Dro_lact2	Dro_lact3
Dro_lact1	-	22	17
Dro_lact2		-	44
Dro_lact3			-

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.