Drosophila prolongata

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

Assembly: GCA_036346975.1_ASM3634697v1_genomic

Dro_pro1 | JAYMZC010000379.1:2880095-2881196 (+) | 1102 nt | IncRNA:noe consensus e-value: 8e-202

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

Dro_pro2 | JAYMZC010000108.1:22455323-22455830 (-) | 508 nt | IncRNA:noe consensus e-value: 9.2e-03

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

Dro_pro3 | JAYMZC010000108.1:14958438-14958658 (+) | 221 nt | IncRNA:noe consensus e-value: 9.4e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.98

	Dro_pro1	Dro_pro2	Dro_pro3
Dro_pro1	-	33	14
Dro_pro2		-	33
Dro_pro3			-

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.