Drosophila repleta

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > repleta subgroup

Assembly: GCA_018903745.1_ASM1890374v1_genomic

Dro_rep1 | JAEIGN010000753.1:171415-172342 (+) | 928 nt | IncRNA:noe consensus e-value: 4e-169

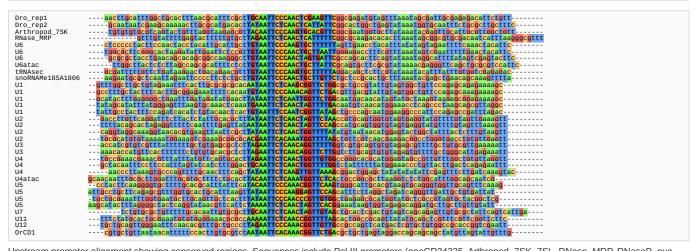
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.92

Dro_rep2 | JAEIGN010000488.1:1699155-1699794 (+) | 640 nt | IncRNA:noe consensus e-value: 3.7e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 10nt PSE: 0.96

	Dro_rep1	Dro_rep2
Dro_rep1	-	40
Dro_rep2		-

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.