Drosophila sproati

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > grimshawi group > orphnopeza subgroup

Assembly: GCA 018904355.1 ASM1890435v1 genomic

Dro_spr1 | JAEIFY01000109.1:1084934-1085965 (-) | 1032 nt | IncRNA:noe consensus e-value: 9e-166

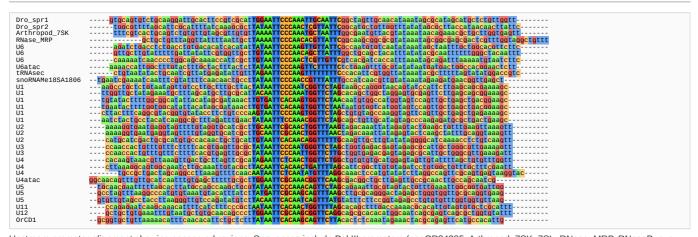
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_spr2 | JAEIFY010000119.1:4928429-4928927 (-) | 499 nt | IncRNA:noe consensus e-value: 1.1e-13

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

	Dro_spr1	Dro_spr2
Dro_spr1	-	31
Dro_spr2		-

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.