Drosophila paucipuncta

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > glabriapex group > punalua subgroup

Assembly: GCA 035043875.1 ASM3504387v1 genomic

Dro_pau1 | JAWNMP010000139.1:3726046-3727078 (+) | 1033 nt | IncRNA:noe consensus e-value: 5e-165

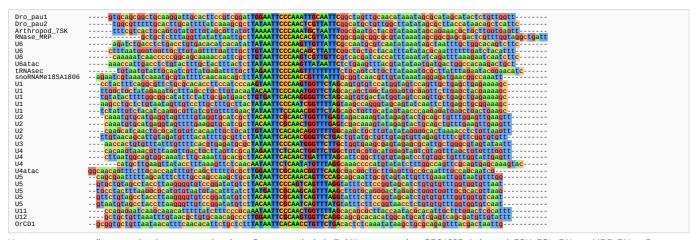
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_pau2 | JAWNMP010000268.1:24726132-24726486 (+) | 355 nt | IncRNA:noe consensus e-value: 6.5e-10

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

	Dro_pau1	Dro_pau2
Dro_pau1	-	25
Dro_pau2		-

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.