Drosophila infuscata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified mouthparts group

Assembly: GCA 035042205.1 ASM3504220v1 genomic

Dro_inf1 | JAWNLR010000085.1:5668587-5669622 (+) | 1036 nt | IncRNA:noe consensus e-value: 1e-156

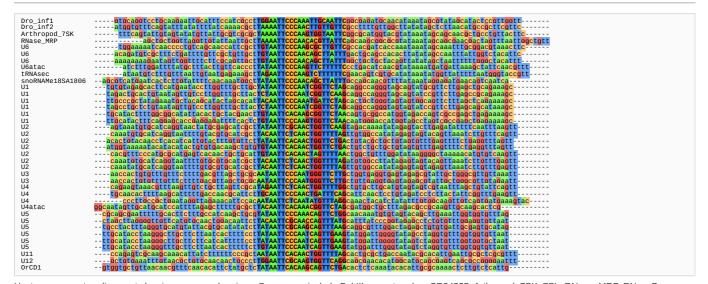
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.88

Dro_inf2 | JAWNLR010000086.1:3207495-3207778 (+) | 284 nt | IncRNA:noe consensus e-value: 2.5e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.98

	Dro_inf1	Dro_inf2
Dro_inf1	-	21
Dro_inf2		-

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.