Drosophila differens

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > planitibia group > planitibia subgroup

Assembly: GCA 037043665.1 ASM3704366v1 genomic

Dro_dif1 | JBAMAZ010000097.1:1420106-1421134 (-) | 1029 nt | IncRNA:noe consensus e-value: 6e-167

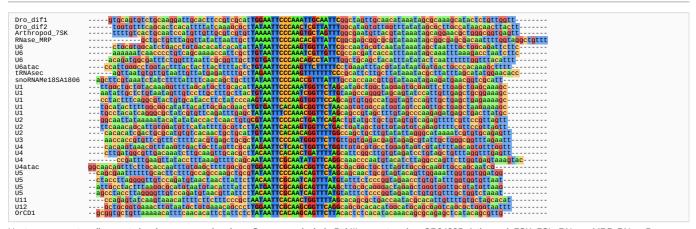
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

Dro_dif2 | JBAMAZ010000022.1:3035926-3036415 (-) | 490 nt | IncRNA:noe consensus e-value: 2.1e-10

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

	Dro_dif1	Dro_dif2
Dro_dif1	-	31
Dro_dif2		-

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.