Drosophila neoperkinsi

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

Assembly: GCA_037043555.1_ASM3704355v1_genomic

Dro_neop1 | JBAMBG010005539.1:17729-18745 (-) | 1017 nt | IncRNA:noe consensus e-value: 1e-162

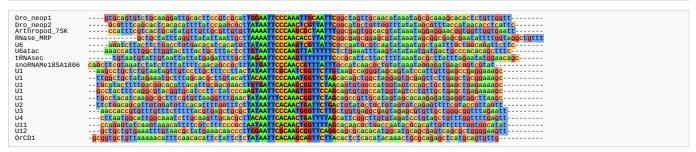
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Dro_neop2 | JBAMBG010001491.1:3265-3741 (+) | 477 nt | IncRNA:noe consensus e-value: 2.5e-14

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

	Dro_neop1	Dro_neop2
Dro_neop1	-	30
Dro_neop2		-

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.