Drosophila kurseongensis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > rhopaloa subgroup

Assembly: GCA_018153305.1_ASM1815330v1_genomic

Dro_kur1 | JAECXX010000005.1:13736962-13738063 (-) | 1102 nt | IncRNA:noe consensus e-value: 3e-202

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

Dro_kur2 | JAECXX010000141.1:3046145-3046664 (+) | 520 nt | IncRNA:noe consensus e-value: 2.8e-02

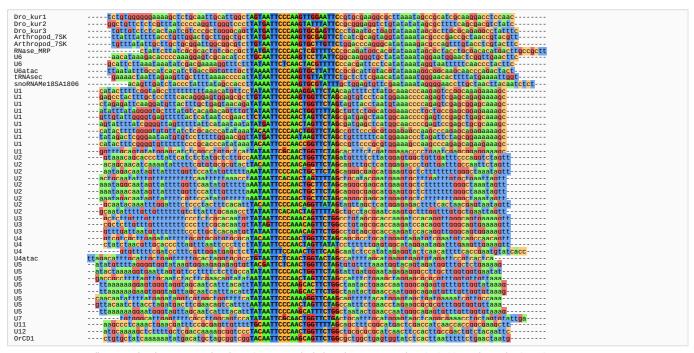
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.98

Dro_kur3 | JAECXX010000141.1:10956866-10957088 (-) | 223 nt | IncRNA:noe consensus e-value: 4.1e-04

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

	Dro_kur1	Dro_kur2	Dro_kur3
Dro_kur1	-	34	14
Dro_kur2		-	32
Dro_kur3			-

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.