## Drosophila insularis

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > willistoni group > willistoni subgroup

Assembly: GCA\_047116485.1\_ASM4711648v1\_genomic

## Dro\_ins1 | CM120417.1:1616732-1618380 (-) | 1649 nt | IncRNA:noe consensus e-value: 5.8e-90

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

## Dro\_ins2 | CM120420.1:25527833-25528378 (+) | 546 nt | IncRNA:noe consensus e-value: NA

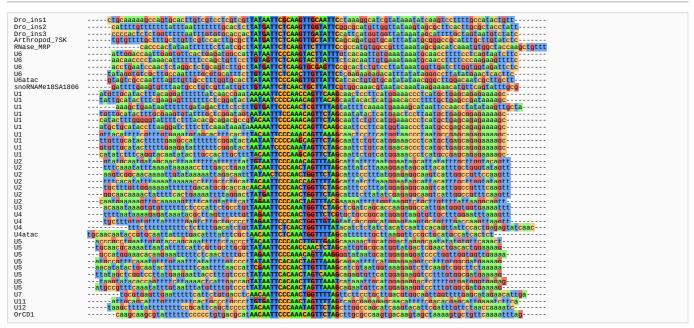
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.98

## Dro\_ins3 | CM120420.1:25921026-25921280 (-) | 255 nt | IncRNA:noe consensus e-value: 7.0e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.95

	Dro_ins1	Dro_ins2	Dro_ins3
Dro_ins1	-	21	9
Dro_ins2		-	35
Dro_ins3			-

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.