## Drosophila tropicalis

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

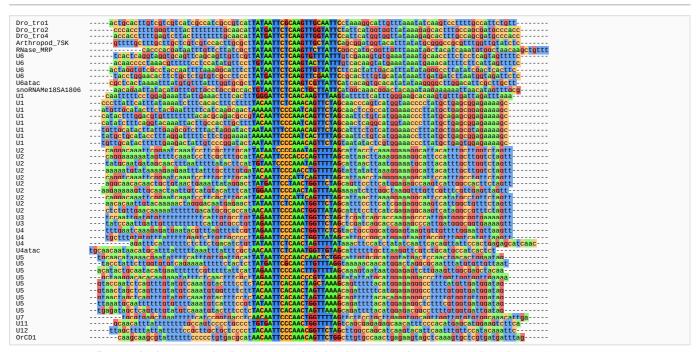
Assembly: GCA\_018151085.1\_ASM1815108v1\_genomic

## 

Dro\_tro2 | JAECWH010000366.1:468709-468963 (-) | 255 nt | IncRNA:noe consensus e-value: 1.6e-01
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98
66.661.651.466.071.666.46666.47667.6766.4767.6767.6

	Dro_tro1	Dro_tro2	Dro_tro4
Dro_tro1	-	9	9
Dro_tro2		-	96
Dro_tro4			-

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.