## Drosophila crucigera

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

Assembly: GCA\_035041335.1\_ASM3504133v1\_genomic

## Dro\_cru1 | JAWNLG010000036.1:13219098-13220136 (-) | 1039 nt | IncRNA:noe consensus e-value: 3e-166

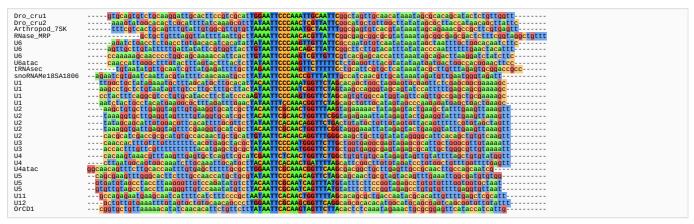
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

## Dro\_cru2 | JAWNLG010000031.1:4535620-4536131 (-) | 512 nt | IncRNA:noe consensus e-value: 5.8e-13

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

	Dro_cru1	Dro_cru2
Dro_cru1	-	31
Dro_cru2		-

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.