## Drosophila rhopaloa

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

**Assembly:** GCA\_018152115.1\_ASM1815211v1\_genomic

## Dro\_rho1 | JAECXI010000150.1:2680758-2681857 (+) | 1100 nt | IncRNA:noe consensus e-value: 1e-201

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

## Dro\_rho2 | JAECXI010000003.1:21551852-21552358 (-) | 507 nt | IncRNA:noe consensus e-value: 1.3e-02

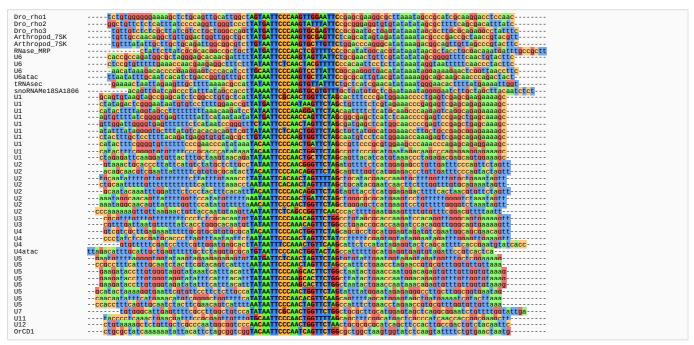
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.98

## Dro\_rho3 | JAECXI010000003.1:13989492-13989708 (+) | 217 nt | IncRNA:noe consensus e-value: 3.7e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.98

		Dro_rho1	Dro_rho2	Dro_rho3
	Dro_rho1	-	34	12
	Dro_rho2		-	34

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.