## Drosophila paracracens

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > split tarsi subgroup **Assembly:** GCA 035044025.1 ASM3504402v1 genomic

## Dro\_para1 | JAWNMN010000192.1:5414577-5415592 (+) | 1016 nt | IncRNA:noe consensus e-value: 3e-155

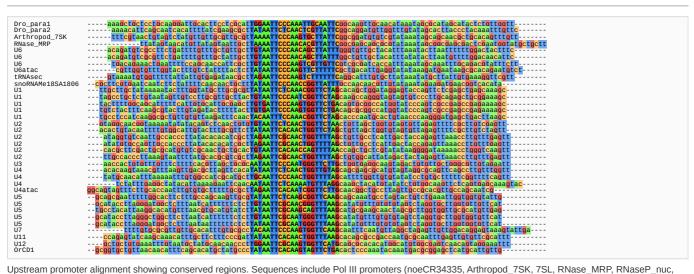
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

## Dro\_para2 | JAWNMN010000838.1:1619625-1619862 (+) | 238 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

	Dro_para1	Dro_para2
Dro_para1	-	15
Dro_para2		-

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.