## Drosophila macrothrix

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > glabriapex group > conspicua subgroup

Assembly: GCA 035042055.1 ASM3504205v1 genomic

## Dro\_macr1 | JAWNLX010000261.1:4071165-4072192 (-) | 1028 nt | IncRNA:noe consensus e-value: 3e-165

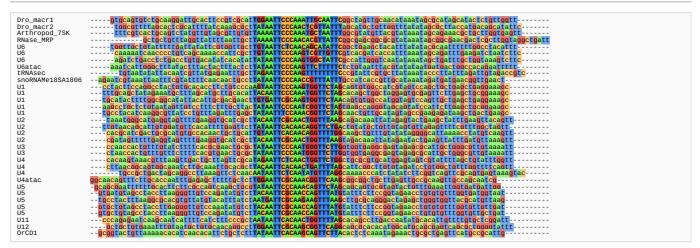
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

## Dro\_macr2 | JAWNLX010000587.1:14948494-14949018 (-) | 525 nt | IncRNA:noe consensus e-value: 3.7e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

	Dro_macr1	Dro_macr2
Dro_macr1	-	29
Dro_macr2		-

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.