

## *Drosophila elegans*

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

**Assembly:** GCA\_018152505.1\_ASM1815250v1\_genomic

**Dro\_ele1 | JAECL010000156.1:11281814-11282921 (-) | 1108 nt | lncRNA: noe consensus e-value: 1e-200**

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

[illegible]

**Dro\_ele2 | JAECXL010000098.1:900967-901437 (-) | 471 nt | lncRNA: noe consensus e-value: 1.7e-04**

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

GCGCCCTCGACGCGCTACAGATTTGTGAAGG6TGGCCACATTCCTCATTAAT18TGGCAGCAAAAAATTGAAGAAAGATCTGGGTCTATTGAAAGAAAGCCCTCACAGAGAGGGTTATTCCGGGACAGAGGAACAATTTGAAGAACAGCAAGAGGA  
 AGCCGCGAGACGCGCCTACGAGATCAAGATTTGGGGACATTTTGGGTCATTTTGGTCTTATGTGCTCTCTACGACAAATTCGTGGGCTTTATTGAAGCAATTTGTGGTCGTCTTAATTTGAAGAACAGGATTATACTCGGGTTTATTAACTCAGCA  
 AAAAAAGCTCTACTACATCAAGCAAAAAGACCCCAATACATTTGAAAGGCCAGAAAAGCCAGAGAGGCAAAACAAACAAAGCAAAAAATCCAAAAAATAAACAAATCAAGAAATTAACACACTGTGAAGGCGCTGGAGGGGGAGAAACTC  
 TCTCCAGTATCGCATTTT

	Dro_ele1	Dro_ele2
Dro_ele1	-	22
Dro_ele2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.