

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

Assembly: GCA_018153835.1_ASM1815383v1_genomic

Dro_eug1 | JAECYE010002138.1:4169492-4170692 (+) | 1201 nt | lncRNA: noe consensus e-value: 3e-194

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

[illegible]

Dro_eug2 | JAE010002131.1:5554-56138 (-) | 585 nt | IncRNA: no consensus e-value: 2.0e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.99

AGCGGTCGACGCGCCCTACAGATCTTACGAGG6GTGGCCACCTTCCACCTAATTTGTCGACCAAAAAAATTTGAAGAAACAAAACTTGGTTTATATATGGTATCTAAATTTTCTGCGCAAAAGAAAAAGCAGCATATATGAGAGAAATTTGTAT
 TTATGAGAAAGCTTGAAGAAAGAAATGCTGACGAGTGGAGTAAAGAACGCGCTATTTCCGAGAGAGAGGTTTCTCCGAGAGAGAAAGAAAGTATTAATTTGCCAGGCCAAGAAAGCAATCTAATAGAGTTTGGTGGTGAAGAAAAAGTACGCTCGAGATCGACGACCGAC
 AGCGCTCCAGATTTGAGAAAAAGGAGTTTATATTTGTCGATGTCTGATATCTCCCCCTGCGCATCTCCGATCTCTCGCTCTCTGCTGGTCTTACAGGACGAGAGAGAGGTTTCTCTGAAAAATTAAGAGCAACCAATCTATGAAAAAAATATTTCCAA
 GCGCCCAACCAAGCTAGTGAAGAAAGCAAAATAAAATACCAAAAAAATTTCCAAAAAATTAACCTCAAAACAACTATTAATAACAACTGTGATAGCGCTCGCTGGTGTAGGAGAAATCCACCTTTCCAGTGTACGCTATTTT

Dro_eug3 | JAECYE010000496.1:653658-653933 (+) | 276 nt | lncRNA: noe consensus e-value: 5.4e-08

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.91

GGCGGTCGAGCGACTCACAGTTACCAAGGGTTGGCCACTTTCTGACTAATTGTGGACCAAAATGATGATGTAAAGGGTAAAAAGATTATATGATATATGATATTCTACATTACACGTGAAACGATAAACTACAATGAAAATATGA
ATATGAAACGAACACAAAAAGACCACAGAAAAAAGAAATACCAAGAAAGGTTTTATAAATAATGATTACAAATACAAATTGAAGTGTGAGGCGTTGGAATAAAATATCTTTCCAAGTATCGCTTTT

	Dro_eug1	Dro_eug2	Dro_eug3
Dro_eug1	-	36	17
Dro_eug2		-	38
Dro_eug3			-

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.