

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

Assembly: GCA_035043285.1_ASM3504328v1_genomic

Dro_subs1 | JAWNNB010001337.1:71573-72894 (-) | 1322 nt | lncRNA: noe consensus e-value: 5e-145

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.84

[illegible]

Dro_subs2 | JAWNNB010000717.1:1545922-1546513 (-) | 592 nt | lncRNA: noe consensus e-value: 3.6e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

[illegible]

Dro_subs3 | JAWNNB010000960.1:551336-551585 (+) | 250 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.88

GGCGGGTCGGTGCCTCACAGTTCTCAGGGTTGACCACTTTCCCGACTAAATTGGTACCAATGCCAATACCACACACGGATATTTGGAAATTCGTACAAGAAATTTGCCAAAACACCAGCCCAATCCAACAGGCCAGCCAATCACAACAAATGTGTGGAAAGCCCAAGAAATGGGCGGAAATAAAACGGAACGTTTGGCGCGGAGGAAACGGAGGGATGTAATGCATTCCTAAACCTCCTAAGATCGCTTTT

Dro_subs4 | JAWNNB010000960.1:528781-528961 (+) | 181 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

GGCGGTCAAAGTGCTCACGGTTGCAAGGGTTGACCACTTTCCAAACTAATTGTGGCTATGACTAGCGCCAATATGCCGTTGCTATAGGCCAGGCCAAGTCGATAAAACAAACAATAAAACTGTGTGGCGCGGGAAGGAAAGGAATGG
CATGCTCAAACTCCTTAGATCGCTTTTTT

Dro_subs5 | JAWNNB010000960.1:901068-901239 (+) | 172 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

GGCGGTCGGTGCCTCACAGTTGCGAAGGGTTGACCACCTTCCAAACTAATTGTGGCTATGACTAGCGCCAATATGCCGTTGCTATAAGCCAGTCAATAAAAAAAGCAAAAAAAGCTGTGTGGCGCGGAGGAACGGAAGGAATGCATTCTC
AAACCTCCTAAAGATCGCTTTT

	Dro_subs1	Dro_subs2	Dro_subs3	Dro_subs4	Dro_subs5
Dro_subs1	-	22	13	8	9
Dro_subs2		-	34	26	26
Dro_subs3			-	58	59
Dro_subs4				-	91
Dro_subs5					-

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.