

Drosophila colorata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > melanica group

Assembly: GCA_035041545.1_ASM3504154v1_genomic

Dro_col1 | JAWNLD010000564.1:7214924-7216090 (+) | 1167 nt | lncRNA: noe consensus e-value: 3e-183

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

[illegible]

Dro_col2 | JAWNLD010000490.1:16422224-16422940 (+) | 717 nt | lncRNA: noe consensus e-value: 8.8e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.97

GGGCGGTCBACBCTGACGACBCTGCAAGGGTGTATCTACACBCCCCCATTAATTGTGATAATGATATGAAATCATTTTGAAGACATTTGCCACAGCATTTGGACAACTATATATGATATATAAAGACTATATGTTATAAAGATATAAGGGT
 ATATTGTAAATTTGAAGAAAAAATGGATGAAAAAATAATACAGATATGAAGACBGAACGATACATTCATTATATACAAACCAACACAAAAAAGAGAAAGCGAAAGAAATTAACATTCCTTATCTTATATATAATATAAGATTATAA
 CTTTATAGCAATATATTATATAGATGAGGAGAACTAATGATTATGAAGTAAAAAAAGATTTACCAACCGGGCCCAACACCCCCCAACCACTCATGTAAAAAAATTTGCTTTACTTTTATGTTAGTATGTTATGTTATGGAAG
 TCGCAGAGAAAAAAGAAATTCCTAATTCACTTATGAGAGAAAAAATCTTAATTAAGAGAAAAAAGCAAGCAACACACAACTAACAGAGAAATAGAGAAAAAAGACGGGGGAAAAAAAATGCCCCCTCGCTTGCGCTGGCCTGGCCGGG
 GAGACATCTTCCGCAAAATGACCCGCTGTGAGACBCTGCGAGTTAGAGGCTGGGGAGAGAAAAATCCTATCCATCTCCCGGCCCCCTTCCTGATATATGATCGCCTTTTTTTT

	Dro_col1	Dro_col2
Dro_col1	-	37
Dro_col2		-

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.