

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

Assembly: GCA_018152265.1_ASM1815226v1_genomic

Dro_fic1 | JAECK010000106.1:5340779-5341890 (+) | 1112 nt | lncRNA: noe consensus e-value: 5e-198

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

GCGCGGCTGTCATATCCGACGACGACGGTTGGACATGCTCCGCTCTCATCCCATCTCTCTGAAATTTGTCGTTGGTATGCCCGAATTCATCATTTGCAAAAATCTCGTATCATCTTCACATCTCTGAGAGCAAAAAACGCGCGCGACGAC
 GCGCATCTGTCGATATCTCTTCCCCAAACAGAGCTGTTGTCGAGGTGTGTCAGATGCGACGAGGACACGAGACGATATAAATACAGAAACAAATCACTACGCGACGAAATATTAACCATGTATACCAATCGAAAA
 ATGATATGCAAAAAATGAGAAAAATATACGACGAGATATCAATTCGCAACCAAAAAATATCAAAAAATACACATAAAAATACATCAAAAAATGAGAACAGGATGATATGATGACATGATATGTCGACGAGT
 ATGAGGACGACCGCAAAAAATCTCTGAAAAATCTGCAAAAAAAATATATAAATCTCAAAATCTGATTTGGTGTGTTCTCCGCTCGTGATATCAGTGGCGGCGCGACGCCACCCCGCTGCTGCGCCATCGCGCGCCGCTGTCGCGCCGCT
 CATCATGCCCACGCGCCCCCTCCGAAAGCCCTACTGTCGCCCCCGCAAGAGCGGGATGACGCGGCAAAAAAGAGGCGGCGCATATGATATGACATATCATTAACACGCAAAAAACCAAGAACCAACACCAAAATCTGAAAGCGGCGG
 GACCCGAAAGAGGAAAAAGCGGTGCGCGGACGCGTGCACGAAAAAAGATGATGGCTGCTGCGGACGCGGTGCGCATTTGGGCGGACAGAGCGCGCGCGCTCCACAAAAATACCGCTATGAGACGCTTTTAAAGGAAAACTTGAATTAAGT
 AAGATTTAAACCAAAAAACATTTTAAAGCAAGAAAAACGAGTTTCAAAATGAGCAATATGAGCAACATTAATATGGCAAAAAACGCAAAACGACATGCAAAATACGACACACCTTCGAAAAAGACCTCAGTAATTAATAAACACCC
 AAAAAACACAGTGAATCTGGTGGTGCAGAAAGAAATGCTCTGTGATGCCCCTTTTT

Dro_fic2 | JAECK010000196.1:11363662-11364194 (-) | 533 nt | lncRNA: no consensus e-value: 7.5e-04

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

GCGGGCT CAGCGCCCT CACAGTACT CAGGGGGT GGGCCACT CT CACT GAGT GCT GCTG CCAAAAAAT TGAAGAAAAAT GAGGT GTT TCGGGGT CACAGAT TGA GGT CAG CCAAAAAAT CTT TAT GAAAT TGA GAGAAAT CBAAAACAGT TGA AAAAAAT
 TATGAGGAAGAGT CAGTCT TACATAAT TAT TGT GGG TAT TGAAGAAAAAT GCGCTA TAAAGAAAA GGGGGT TAT TCGGGAGAGAGT TGAACAAAT TGAAGAAAAAT CCGCBAAGAGGGG CAGAT TAT GAGGACAGAGT CAGT TGAACAGCAG
 CAGT TACT GCGGCGGT TACAAAT TCCCGCGT TGT GTT GTT CCCCCGGGAGT CAGCGT CAGT TACT TGAAGT GGT TAT TGAAGAAAAAT TCGAAGCGCCCT CAGT CCGCCTA TGA GCAACAAAAAAG CAGAAAAAAT TCAAAAAAATAAT TAAAC
 CAAAAAATAAAG CAAACAAATAAAT TAT TACTCTT GAGGACAGCT GGGAT GGT GGGAGT TAAAT TCCACCTT TCGATGT CAGTAT CAGCTAT TTTT

Dro fic3 | JAECK010000196.1:2754130-2754427 (-) | 298 nt | lncRNA:oe consensus e-value: 1.3e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.94

GGGCGGTCGAGCGCCCTCACAGTGTCAGGGGTGGCCACAGTTCCTGACTAATTGTGGTTGCTAGAATTGTAATACGAAACGCAAGTACATTGTGGGTGTCGGCGTATAAATTGTAATTTACGTTGTATACAAAAGCCAAATTGTTAAAT
ATAAATAAATTACACAAAAAGCGGCGCCGGAACAAACCAACAAAAAAACGAAAGTCAGTTAAATCGCCAAAAAAGAAACCAACACATAATTACACTGTGGGGTGCCTGGTAGAGGGGAATCCCCCCTTCCAGTGATCGCTATTTTT

	Dro_fic1	Dro_fic2	Dro_fic3
Dro_fic1	-	30	15
Dro_fic2		-	43
Dro_fic3			-

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, snoRNAm18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.