

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group
Assembly: GCA_037075305.1_ASM3707530v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.91

GAGGTCGGTCTGTCATCCGACGTAAGCAACGGTGGACAGCCGCTCAACCCCAACACATCTGAATATGTCCTCGTGGGTGAGAGCAGCAGGGTGTGAGATGTGGAGGGAGATGAAGAGAGGAGCAACCGCCGCGCAATCTCTGT
 CAGATCTCTGTCAGGACAGCAATACGCCAAATACGCAATATGCAAAATATGCAAAAATATGATGCAAGAAACAGCTATATCATATATATGATGCAAAATATATATGCAAGACCAAAAGCTTAAAGCAAGATACGCAATCT
 CGCAATGATCAATCAAGCAAAAAATACCTATCAGCCAAAGGATATCAATGCAAAACAAAAACGATATAAAGCAACATAAAATACCTATAAAATATGAAGCAAACTAATCTAAATGTGACATGATAGTGTAAAGATATCATCATCTG
 GTTATCAGGACAGCAATGAAATCTGAAAAATCTAAAAAAATATGAAAAATGCAAAATCTGATGGTGTGTGTGTCGCGTGGTCTGCTGACGCGCCGCGCCAGGACAGCAATCCGGAATCTTGCAACATCTGGTGGGGA
 CAGTCAAGCCGCCCTGGGGGGGGCTACTCTGTGGCCCAAGCAATCTGTGCTGATCAAAAAAAACGATAAAAAACAAAAAACAAAAAACACCAAAATACGCAATATGATGAGAGAGACGGCGGGGTGGACAGCAAGCAACCCGAA
 AGTCTCTGACCAACCAAGCAAGCAAGAGAAAGCAATCTGCGATATCCCAATCAGCCGGGAGAGATGCTCTGGAGTACGACAAATGGGCGGTGCCAAAAATTAACCATAGATATTAAGCAAAATCTATAGCAAAATCTAT
 AATGACAAAAAAGCTATAAACAAAAATGATAGCAAAAAACATACCAAGCAATCAATCTGAATCTGAAACAAAGATATCAAAATATGACCAATATGAGCAACAACTAATATGCAAAAAAGCAAAATGAAAAATGCA
 AATTACGACCAACACACGCTGAAAAAGCCCTCAGTATATACCAACATTAATAATGCTGGGTGTGCAAGGGAATGCGCTTAGCGATCTCGCCCTCTTTT

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

[illegible]

	Dro_kane1	Dro_kane2
Dro_kane1	-	43
Dro_kane2		-

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.