

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group
Assembly: GCA_035045355.1_ASM3504535v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.94

GGGCGGCTCGTCAATCCGACGTAACGACGGTGGACAGGCCCTCAACCCGACACTGCAAAATGTGTCCCGTGGGTTGCGAGGACGAAGTGTACGATGTAGGGTGAAGAGAGAGAGAGAGAGAGAGGGAGAGGGAAGAACACCTCGCGCA
AGGCTTTCGTCAATATCTGAGCAAAAAGCAAAATGACCAAGTAATGCAAAATGACAAATAATGACAGAGAGCAAACTATATATATATACCAAAATAATATAGATGACACAAAGATCTAAACAGCAAGATATACGAATGCT
CAATGATAATATCAAGACAAAAATATCTATACAGCCAAAGATATCAATGACCAAAAAAATTTATAAGAGCACTAAAAATAATCAAAAAAATGAAAGCAAACTATCTTAAGTGACCTAGTAGTGTAAAGATATCATCTGCT
GTTTTCAGGAGCAAAATGAAAACTCTAAAAATCTCTAAAAAAATATATAAAAACTGCAAAATGCAATGGTGTGTGTCCCGTTGCGTGTATGCGTGCACGGCGGCAAGAGCCGCGCAAAATCGGGAGATCTAGCAAAAATCTTGGCTGTG
AAAAAGAGGGCGCGGAGCAAGGGGGCTAGTCTGTGGCCCCAAAGATGTGCTGTGCAAAAAAATAAAAAATAAATCAAAAAAATGCGCATATCTGAGACCGGGGTGTGAGGGCTCGCCCCCAAGATCCCGACAGCCCA
AAAAACAGCAGCAAGGACAGCATGTCGATGATCCCAATGACCCAGAGAAATGCTGTGGAAATGACGATGACGAATGCGCGCTCCCAAAAAATACCCCATAGAGACGTTTAAAGGCAAAATTTAATTAACAAAAA
TGAAAAAATACCAATGAAAAAGAAATCAATGTAACTGACGCAACAGATATCAAAAATATGAGCAATATGAGCAATATGAGCAACATCACTAATTAATGGCAAAAAAGCAAAAATGAAAAATGCAAAATACGACACAACACCTTCGAAAAAGACCTCA
GTATATACCAATCAATCGCTGGGTGCTGAAAGGAATGCGTTTATGCTGTGCTCCCTTTTTTTT

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

GGGCGGCTCSABCBCTCTCCACACAAATAGGTTGATCAATCCCCGCTAAATG18GGACAAATAGGGAATACCAAGGACCAAGGCTCCAAATCAATAAAGATTCATATGTTATAGAAGAGAGAGATTCGCCCTAATATATATG1TGAATATG
GACCAATCAACCAACCCGCAATGAATTCGATCAATAGAAACGTATACGCGAAGAAACCAACATATGTGAAACCAATG18TGATAGCTTCCGAGGGGAATAAAGCTATATCGGCACAGCTGGAAATATATATATGATG1GGG
AGTTCCTTTATG18GGGATGATACCTGCACBACATGTTATACCATGAGAAAAAGGATACCGTTGAAATTTGATGATGATGAAAAACCTACCTACGTGTGTTAAACCTGTATAAAGAGAAAAATCAGAAGTGTTTATATATATGCBAAATTTG
ACGATTACCCTACTACTACATGAACAAATACCCCTATGTTATATCTGCAATCTACGATATGAAGAAGAGCTATGATGGGCTATCTTCAABCCCAATCGCAAAACCTAACAGAAAAATCCAAAAAAGAAAAAACAACAA
TAAAAAAAAGACACCGCTCGATCGGCAACAGCAATCCGGAAGAAACAACACGCTTTATATATGGAATCAAAATACACAAACCAATGACAAACCTTACCAGCGCACCAAAAAACAACAACCCACCACCAACCAACCAAC
CCCCAAAACGACTCTCTGTCTGCTGTGCGCCAGGAGAAATGATGGGAGAAATATCCCCCBBCTTCTCGGATATATCGCCTTTTT

	Dro_laci1	Dro_laci2
Dro_laci1	-	41
Dro_laci2		-

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.