

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Lordiphosa > miki group

Assembly: GCA_018904275.1_ASM1890427v1_genomic

Lor_cla1 | JAEIGQ010000100.1:383087-383987 (+) | 901 nt | lncRNA: noe consensus e-value: 6e-187

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

[illegible]

Lor_cla2 | JAEIGQ010000154.1:280157-280495 (-) | 339 nt | lncRNA: noe consensus e-value: 9.9e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.94

GGCGGTGAAAGCTCTCAACACGCTCAAAGGGTGGTCGATTCCCCACATAATTGCGGCAAAACACAAATGAATGGAAATTTGTTATGAAGCCACAAAAACAAAGCAAGAAATACCAAAAAAAATCAAAACACAAACAAAGAAACCTTTG
AACACACATAGAAAAGATCTCAATGAAATATCTTGGCAAAAGGGGTGAAAGACAAAAACAAATGAAGAAACCAACAAACAAATGAAGGACAAAAACCGAAACTTAAAAATGATCGAAAAATATACCGCTCTGTTGAGAAATGTTGTAAT
TTGGACTTAATTTGCAATCTTCTTGTATGACGCCACTTTT

Lor_cla3 | JAEIGQ010000133.1:377306-377554 (-) | 249 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATTGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.78

GGCGGGTCGAACGCTCTCAACAGCTTCAAAGGTTGGCATATCCCCAACTAATTGAACAGCAAGTTAAATCGTCAACCGTACATATCAAAAAACAAGTCATTGAAAAATGCAAAACAACCCGCAGAAATGCAACAAAAACAGCAGAAATGCTAACTAAACAACAGAGCTAATTCAGATTGATTAGCCAACAACAAAGCTGTTGAGATGATCGGAGAGGGTAACACCCACGAATGATTGCCACTTTTTT

Lor_cla4 | JAEIGQ010000201.1:186948-187192 (-) | 245 nt | lncRNA: no consensus e-value: 8.6e-13

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

GGCGGTGGAACGTTTCAACAGCTTCAAGGGTTGGTCTCATCCCCGACTAATTGAGGCAAAACCACTAAACAATGCAAAAGCAAGGTATATACAAACCTGCGCAAGCAGAAAACCACTAAGAAAGCAGAAATGCAATGTGAGCTCACCCCTT
TGAGGTGGGTGTTAATGTACACTAAATTCGATAATCTCGAATTTAGTTATAAAACAAAAACCAAGCTGTTGAGAGAAATTGTATCGCCTCTTTT

	Lor_cla1	Lor_cla2	Lor_cla3	Lor_cla4
Lor_cla1	-	25	20	19
Lor_cla2		-	52	51
Lor_cla3			-	63
Lor_cla4				-

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.