Lordiphosa collinella

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

Assembly: GCA 018904265.1 ASM1890426v1 genomic

Lor_col1 | JAEIFV010000093.1:108590-109499 (+) | 910 nt | IncRNA:noe consensus e-value: 1e-190

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Lor_col2 | JAEIFV010000731.1:22901-23399 (+) | 499 nt | IncRNA:noe consensus e-value: 6.9e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.94

Lor_col3 | JAEIFV010000346.1:270063-270351 (+) | 289 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.81

Lor_col4 | JAEIFV010001011.1:10552-10809 (-) | 258 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.90

GGCGGTCGAACCACTCAACAGCAACAAGGGTTGGTCTCATCCCCAGCTAATTGAGGCAAAACCAGTTAAACAATGCGCAAAGCTAATAACAACTACAAACTGCGAAAGCAGCAAGAAACAATGCTAGACTTCACCTTATACGGTGTTTGTCA

Lor_col5 | JAEIFV010001011.1:2390-2635 (+) | 246 nt | IncRNA:noe consensus e-value: NA

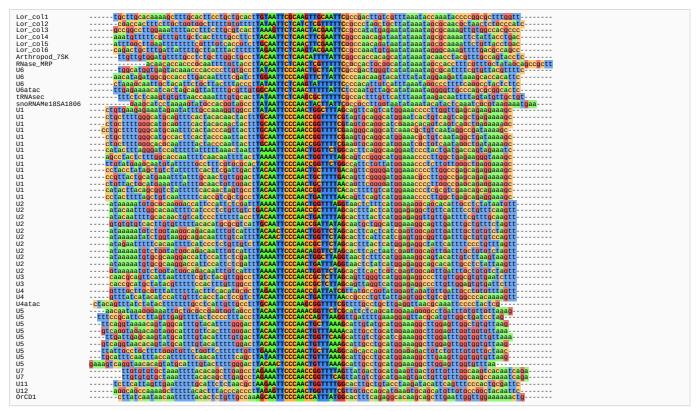
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.89

Lor_col6 | JAEIFV010001023.1:105284-105501 (-) | 218 nt | IncRNA:noe consensus e-value: 5.4e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.89

	Lor_col1	Lor_col2	Lor_col3	Lor_col4	Lor_col5	Lor_col6
Lor_col1	-	38	18	19	19	15
Lor_col2		-	41	38	36	31
Lor_col3			-	59	57	55
Lor_col4				-	87	57
Lor_col5					-	57
Lor_col6						-

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.



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.