Lordiphosa andalusiaca

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

Assembly: GCA 035044965.1 ASM3504496v1 genomic

Lor_and1 | JAWNNM010003130.1:193849-194785 (+) | 937 nt | IncRNA:noe consensus e-value: 7e-183

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

Lor_and2 | JAWNNM010003314.1:38838-39313 (+) | 476 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

Lor_and3 | JAWNNM010003214.1:36845-37130 (+) | 286 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 7nt PSE: 0.85

Lor_and4 | JAWNNM010003214.1:51112-51397 (-) | 286 nt | IncRNA:noe consensus e-value: NA

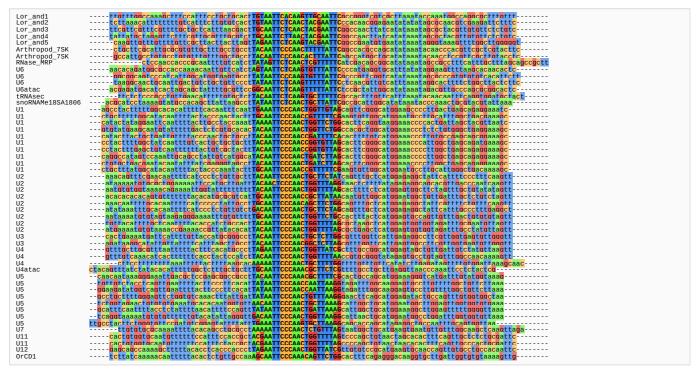
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.80

Lor_and5 | JAWNNM010002855.1:17068-17312 (-) | 245 nt | IncRNA:noe consensus e-value: 3.7e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 11nt PSE: 0.82

| | Lor_and1 | Lor_and2 | Lor_and3 | Lor_and4 | Lor_and5 |
|----------|----------|----------|----------|----------|----------|
| Lor_and1 | - | 32 | 18 | 18 | 15 |
| Lor_and2 | | - | 43 | 45 | 35 |
| Lor_and3 | | | - | 96 | 54 |
| Lor_and4 | | | | - | 54 |
| Lor_and5 | | | | | - |

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.