# Lordiphosa fenestrarum

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

Assembly: GCA 035044985.1 ASM3504498v1 genomic

### Lor\_fen1 | JAWNNO010005060.1:149410-150324 (+) | 915 nt | IncRNA:noe consensus e-value: 4e-186

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

## Lor\_fen2 | JAWNNO010005088.1:97581-97905 (+) | 325 nt | IncRNA:noe consensus e-value: 6.1e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.94

### Lor\_fen3 | JAWNNO010003157.1:820-1133 (-) | 314 nt | IncRNA:noe consensus e-value: 8.7e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.83

#### Lor\_fen4 | JAWNNO010002742.1:659328-659607 (-) | 280 nt | IncRNA:noe consensus e-value: 3.7e-04

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

### Lor\_fen5 | JAWNNO010002742.1:141983-142197 (-) | 215 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.80

	Lor_fen1	Lor_fen2	Lor_fen3	Lor_fen4	Lor_fen5
Lor_fen1	-	25	24	19	15
Lor_fen2		-	60	54	45
Lor_fen3			-	61	49
Lor_fen4				-	52
Lor_fen5					-

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.