Lordiphosa stackelbergi

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

Assembly: GCA 018904235.1 ASM1890423v1 genomic

Lor_sta1 | JAEIFU010003043.1:20245-21159 (+) | 915 nt | IncRNA:noe consensus e-value: 7e-190

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.81

Lor_sta2 | JAEIFU010000056.1:23153-23401 (-) | 249 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.77

Lor_sta3 | JAEIFU010000056.1:39034-39280 (-) | 247 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.77

GGCGGTCGAACGTCTCAACAGCGTCAAGGGTTGGCATCATCCCCAACTAATTGAACTGCAAAGTTATACCGTACAACAGCTATACAAAAAACAAGTCATTGAGAAATGCAAAATACCCCGCAGAAATGCAAAAAACACAGCAGAAATGCTAAACACAGGAGATACACCCACGAATGCAAAAAAACACGCAGTTGATGAGAAAAACACAGCAGAATGATCGCCACTTTTTT

| | Lor_sta1 | Lor_sta2 | Lor_sta3 |
|----------|----------|----------|----------|
| Lor_sta1 | - | 19 | 17 |
| Lor_sta2 | | - | 95 |
| Lor_sta3 | | | - |

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.