Drosophila monieri

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group >

ananassae subgroup

Assembly: GCA_035047585.1_ASM3504758v1_genomic

Dro_mon1 | JAWNPJ010000106.1:12241816-12242739 (-) | 924 nt | IncRNA:noe consensus e-value: 4e-179

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.83

Dro_mon2 | JAWNPJ010000061.1:1578675-1579198 (+) | 524 nt | IncRNA:noe consensus e-value: 1.2e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

| | Dro_mon1 | Dro_mon2 |
|----------|----------|----------|
| Dro_mon1 | - | 38 |
| Dro_mon2 | | - |

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.