Drosophila anomalata

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

Assembly: GCA 035046425.1 ASM3504642v1 genomic

Dro_ano1 | JAWNNY010000605.1:2430392-2431443 (-) | 1052 nt | IncRNA:noe consensus e-value: 7e-184

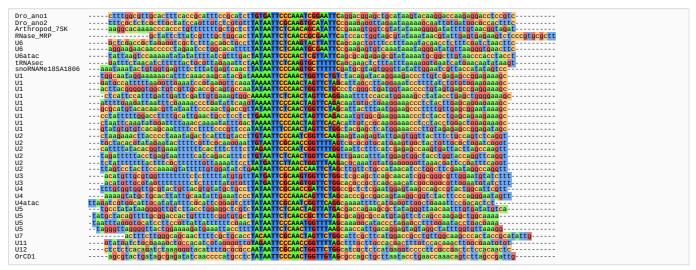
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

Dro_ano2 | JAWNNY010001851.1:46007-46468 (-) | 462 nt | IncRNA:noe consensus e-value: 1.3e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

| | Dro_ano1 | Dro_ano2 |
|----------|----------|----------|
| Dro_ano1 | - | 32 |
| Dro_ano2 | | - |

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.