Drosophila ambigua

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > obscura subgroup

Assembly: GCA_018150905.1_ASM1815090v1_genomic

Dro_amb1 | JAECWS010000002.1:20837630-20838962 (-) | 1333 nt | IncRNA:noe consensus e-value: 9e-145

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

Dro_amb2 | JAECWS010000094.1:1584119-1584696 (-) | 578 nt | IncRNA:noe consensus e-value: 3.7e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.96

| | Dro_amb1 | Dro_amb2 |
|----------|----------|----------|
| Dro_amb1 | - | 30 |
| Dro_amb2 | | - |

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.