Drosophila trapezifrons

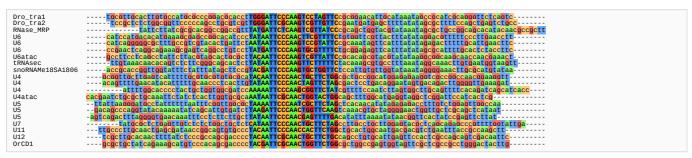
Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA_018874455.1_ASM1887445v1_genomic

| Dro_tra2 JAEIIF010027307.1:549-878 (-) 330 nt IncRNA:noe consensus e-value: 5.8e-07 | | | |
|--|--|--|--|
| 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.86 | | | |
| GCCGCTCGAGCCCCCCAAGTTCTCAAGGGTTGCCCACTTTTCCCAACTAATTGTGGTAGCACTGCCCCAACAACTGAAAACATGAAAACATGAAAAATGTTAAGAACTCAAAAACTGTTAAGAACTAATGAACAAAATTAATGAAAAATGAAAAATGAAAAATTAAGTGCCAAAAAATGAAAAATGAAAAAAAA | | | |

| | Dro_tra1 | Dro_tra2 |
|----------|----------|----------|
| Dro_tra1 | - | 18 |
| Dro_tra2 | | - |

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.