## Drosophila tani

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

Assembly: GCA\_008042535.1\_UCB\_Dtan\_1.0\_genomic

## Dro\_tan1 | VNJO01009974.1:414552-415740 (+) | 1189 nt | IncRNA:noe consensus e-value: 2e-185

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

## Dro\_tan2 | VNJO01000263.1:16168-16673 (+) | 506 nt | IncRNA:noe consensus e-value: 1.9e-03

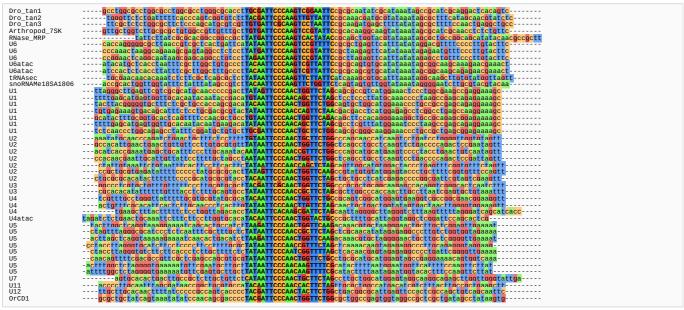
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.98

## Dro\_tan3 | VNJO01008473.1:16306-16627 (+) | 322 nt | IncRNA:noe consensus e-value: 2.8e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.89

	Dro_tan1	Dro_tan2	Dro_tan3
Dro_tan1	-	31	18
Dro_tan2		-	45
Dro_tan3			-

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.