## Drosophila serrata

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

Assembly: GCA\_002093755.2\_Dser1.1\_genomic

## Dro\_ser1 | MTTC01001344.1:4607650-4608898 (-) | 1249 nt | IncRNA:noe consensus e-value: 3e-190

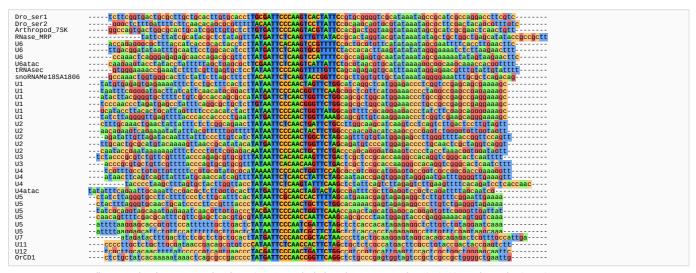
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

## Dro\_ser2 | MTTC01000064.1:1091924-1092458 (-) | 535 nt | IncRNA:noe consensus e-value: 1.4e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.99

	Dro_ser1	Dro_ser2
Dro_ser1	-	29
Dro_ser2		-

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.