## Drosophila anomelani

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

Assembly: GCA 035045905.1 ASM3504590v1 genomic

## Dro\_anome1 | JAWNOO010000165.1:13978393-13979605 (+) | 1213 nt | IncRNA:noe consensus e-value: 1e-193

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

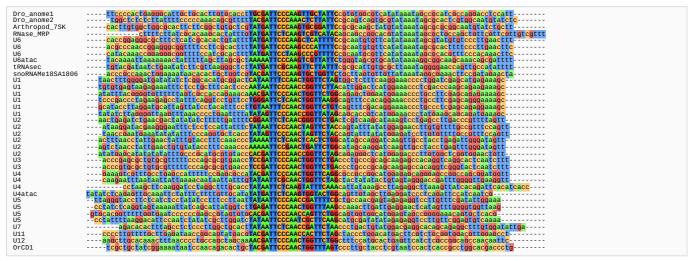
ESGE SETICATIC CELABCAACEACEACEATTES CALCATICCE CITICATICC COCTIC TOTE TO SETIES TACCES AND ACTITICES CATCECT CITICATIC CITICATIC CONTROL OF THE TACCES AND ACTITICES CATCECT CITICATIC CITICATIC CONTROL OF THE TACCES AND ACTIVATED AND ACCIDANCE CARREST AND ACCIDANCE CANDED AND ACCIDANCE CANDED AND ACCIDANCE CANDED ACCIDANCE ACC

## Dro\_anome2 | JAWNOO010000095.1:294850-295264 (+) | 415 nt | IncRNA:noe consensus e-value: 1.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.94

	Dro_anome1	Dro_anome2
Dro_anome1	-	18
Dro_anome2		-

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.