Drosophila anomalipes

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

Assembly: GCA 035041615.1 ASM3504161v1 genomic

Dro_anom1 | JAWNKZ010000166.1:11422748-11423770 (+) | 1023 nt | IncRNA:noe consensus e-value: 2e-163

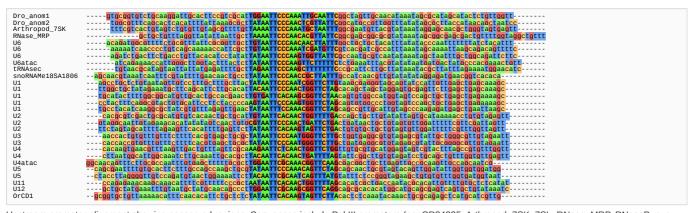
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.92

Dro_anom2 | JAWNKZ010000254.1:3299551-3300035 (+) | 485 nt | IncRNA:noe consensus e-value: 6.8e-12

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

	Dro_anom1	Dro_anom2
Dro_anom1	-	30
Dro_anom2		-

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.