Drosophila basisetae

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > glabriapex group > punalua subgroup

Assembly: GCA 035041595.1 ASM3504159v1 genomic

Dro_bas1 | JAWNLB010000174.1:4180640-4181676 (-) | 1037 nt | IncRNA:noe consensus e-value: 9e-165

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

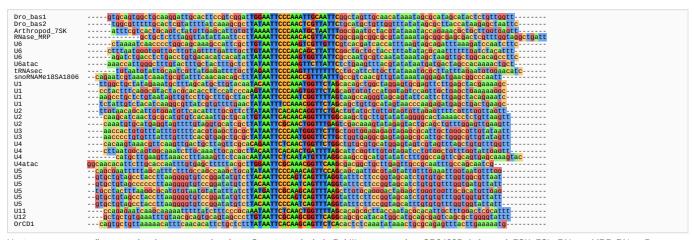
Dro_bas2 | JAWNLB010000174.1:14957601-14957955 (-) | 355 nt | IncRNA:noe consensus e-value: 3.1e-10

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

CATCCCCGACCETETGACAAATTETGETTATAAAAGAACAATGAAAGATATCATAAGACATTGAACAGAAATCAACAAAAAAACAACAAAAAAACTETETETGAGTGAAAA ATATATCGAAGAAAAAAAACACCAATAAAACAGAGAAAAACCAAAAAAATATAAAACACAGCCAGAACACGAAAAAAGGACGCACAACAGCTETTGATGCTCCGAGAG TTGGTTGATCGCTTTTTT

	Dro_bas1	Dro_bas2
Dro_bas1	-	25
Dro_bas2		-

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.