Drosophila seguyi

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

Assembly: GCA_008042675.1_UCB_Dseg_1.0_genomic

Dro_seg1 | VNJU01004884.1:230892-232124 (-) | 1233 nt | IncRNA:noe consensus e-value: 2e-189 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

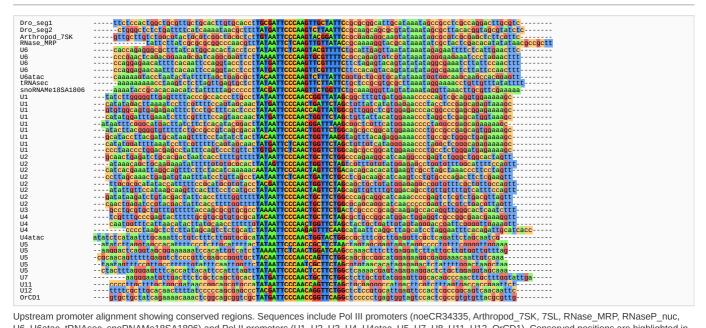
Dro_seg2 | VNJU01005337.1:165504-165935 (+) | 432 nt | IncRNA:noe consensus e-value: 4.2e-06

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

SECERTICA RECECTICA CARTITICA AGENTI SECCACECTOCTA CITATTE I SECANA CA CARACITETA A ACEATITA I ETE AACCA TETTE GECCAE AAAA TEATICE REALA TEATI

	Dro_seg1	Dro_seg2
Dro_seg1	-	18
Dro_seg2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.