Drosophila asahinai

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

Assembly: GCA_008042795.1_UCB_Dasa_1.0_genomic

Dro_asa1 | VNJZ01005298.1:18120-19320 (-) | 1201 nt | IncRNA:noe consensus e-value: 1e-186

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

SEGUEST CESCATITUCECASCALGEA CESTI GESCACATUCCE TOTAT COCCACACTUCT CEASTI TECCESASTI TACEA TISCA ANACTITUSTICAT COCTUCT COTACTUCT SEASCALAS CANAGE CASSAS CANAGE CASSAS CANAGE CASSAS CANAGE CASSAS CANAGE COCCUCACAC COCCES CANAGE CANAG

Dro_asa2 | VNJZ01013349.1:11607-12134 (-) | 528 nt | IncRNA:noe consensus e-value: 1.9e-02

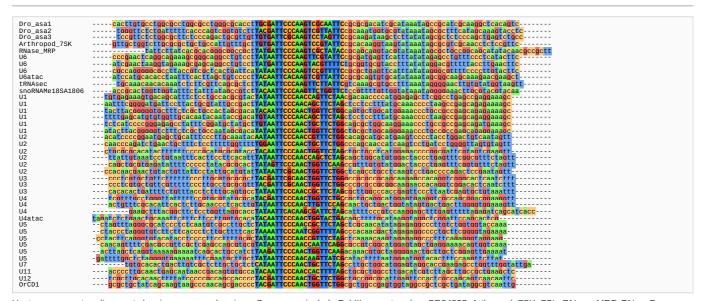
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.98

Dro_asa3 | VNJZ01006488.1:557450-557779 (-) | 330 nt | IncRNA:noe consensus e-value: 4.9e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.89

	Dro_asa1	Dro_asa2	Dro_asa3
Dro_asa1	-	31	18
Dro_asa2		-	44
Dro_asa3			-

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.