Drosophila emarginata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > saltans group > elliptica subgroup

Assembly: GCA_037075365.1_ASM3707536v1_genomic

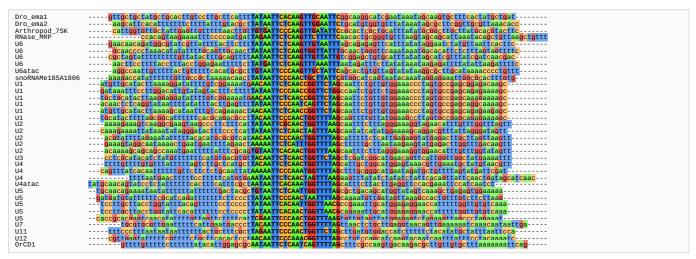
Dro_ema1 | JBAMCD010000296.1:1689919-1691142 (-) | 1224 nt | IncRNA:noe consensus e-value: 5e-136 5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.95

Dro_ema2 | JBAMCD010000160.1:3495524-3496303 (-) | 780 nt | IncRNA:noe consensus e-value: 4.5e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

	Dro_ema1	Dro_ema2
Dro_ema1	-	38
Dro_ema2		-

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.