Drosophila mojavensis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > mulleri subgroup

Assembly: GCA_018153725.1_ASM1815372v1_genomic

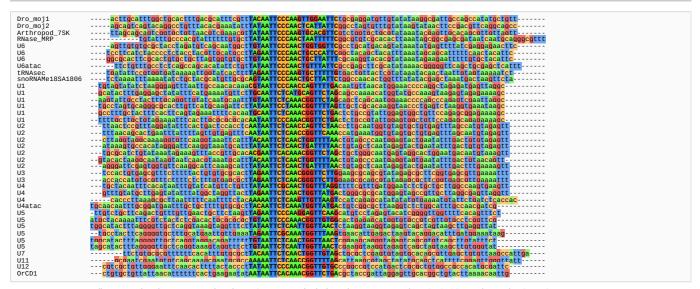
Dro_moj1 | JAECYD010000073.1:6667036-6667960 (+) | 925 nt | IncRNA:noe consensus e-value: 3e-170 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.82

Dro_moj2 | JAECYD010000135.1:21299511-21300193 (+) | 683 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 17nt PSE: 0.95

	Dro_moj1	Dro_moj2
Dro_moj1	-	43
Dro_moj2		-

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.