Drosophila mayri

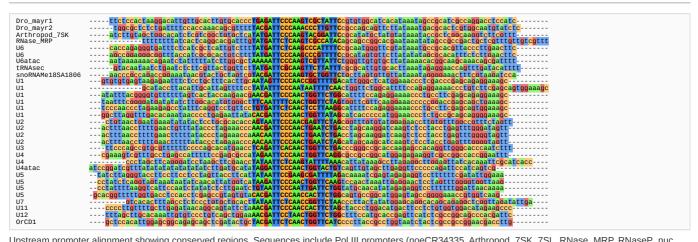
Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA_008042485.1_UCB_Dmay_1.0_genomic

Dro_mayr1 | VNJN01005554.1:238742-239956 (+) | 1215 nt | IncRNA:noe consensus e-value: 3e-193 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt | Trailing-T: 6nt PSE: 0.93 seccent is called a consensus e-value: 3e-193 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt | Trailing-T: 6nt PSE: 0.93 seccent is called a consensus e-value: 3e-193 scales a consensus e-value:

	Dro_mayr1	Dro_mayr2
Dro_mayr1	-	18
Dro_mayr2		-

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.