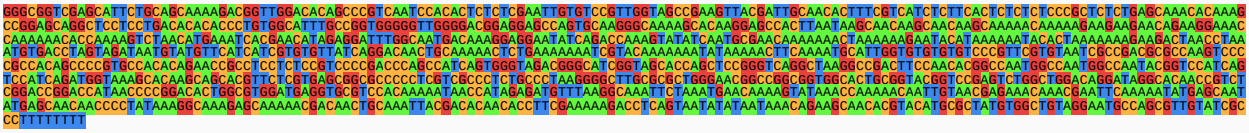
Drosophila lowei

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > pseudoobscura subgroup

Assembly: GCA_008121275.1_UCBerk_Dlow_1.0_genomic

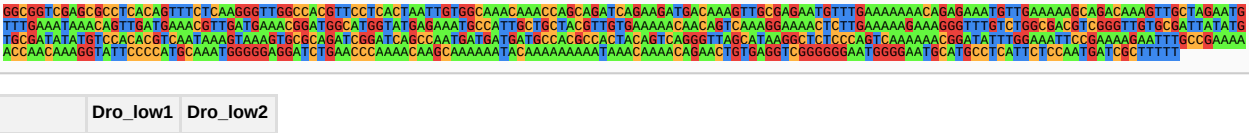
Dro_low1 | CM017781.1:7371203-7372412 (+) | 1210 nt | lncRNA:noe consensus e-value: 9e-180

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.89



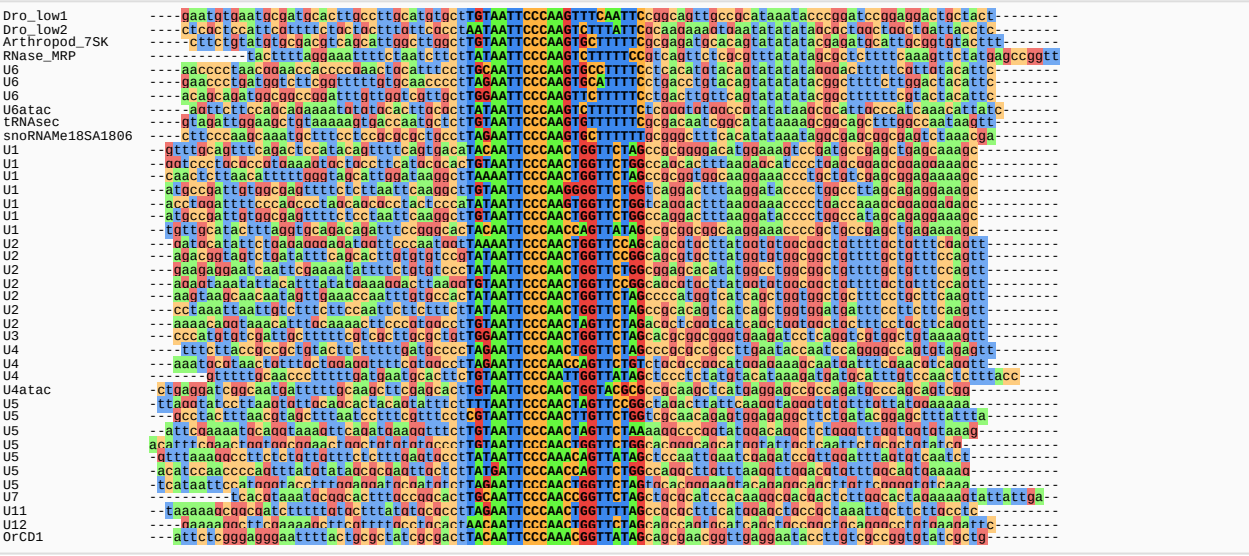
Dro_low2 | CM017779.1:14866476-14867067 (-) | 592 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.90



	Dro_low1	Dro_low2
Dro_low1	-	32
Dro_low2		-

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.