

Assembly: GCA_008121235.1_UCBerk_Dsub_1.0_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

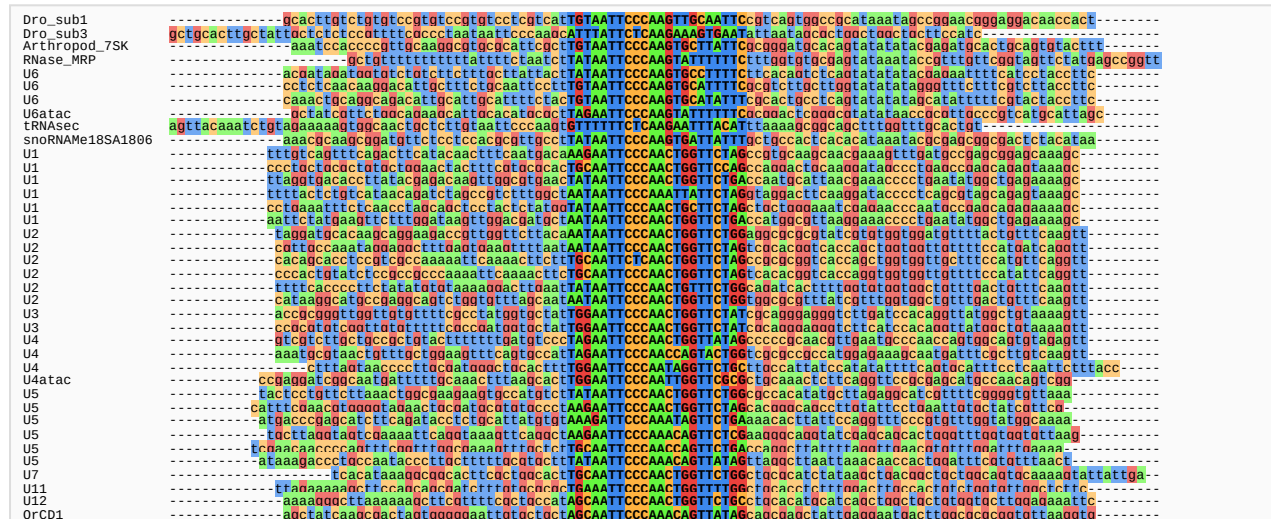
[illegible]

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.76

GGCGGTGGCCGCTCAGACCTCTCAAGGGTTGGCCACGACCTTGACTAATTGTGGCAAAAAACAACGGTCAATTGCGCAATACGCGAATACGCCAATGCCAATACAGTCCGCGATCAGTGGATCCCACACCAATTACAGGGGATAGTGTCT
 AGATCATCTCCCCAGTCAACCTGACGGATGCCAATCACAAGAAATGTGATTCCTCATGACAATACATGGTGGTGTATGATCAAAACCCCAAAACAGCCAAAAATACCAAAAAAAATAAAACAAACCGAACGTGTGAGGTCCGAGGAACCTGA

	Dro_sub1	Dro_sub3
Dro_sub1	-	14
Dro_sub3		-

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.