Drosophila pallidosa

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

ananassae subgroup

Assembly: GCA_040805635.1_ASM4080563v1_genomic

Dro_pall1 | JBEQPO010007407.1:28594-29644 (+) | 1051 nt | IncRNA:noe consensus e-value: 9e-185

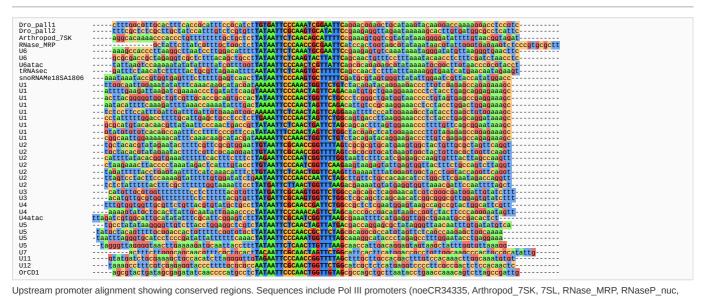
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

Dro_pall2 | JBEQPO010006469.1:18866-19336 (+) | 471 nt | IncRNA:noe consensus e-value: 2.5e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt PSE: 0.96

	Dro_pall1	Dro_pall2
Dro_pall1	-	34
Dro_pall2		-

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.