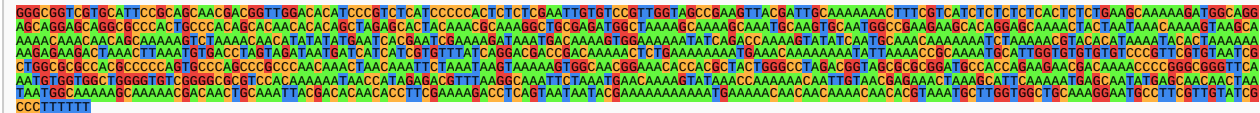


Drosophila parabiepectinata


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

Assembly: GCA_047116105.1_ASM4711610v1_genomic

Dro_par1 | CM120369.1:12135768-12136826 (-) | 1059 nt | lncRNA: noe consensus e-value: 3e-183
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84



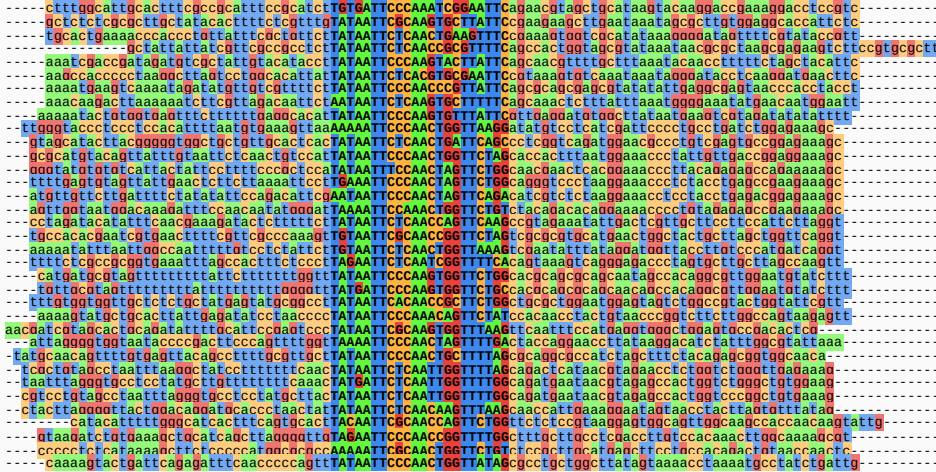
Dro_par2 | CM120372.1:44549648-44550177 (+) | 530 nt | lncRNA: noe consensus e-value: 3.9e-06
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.96



	Dro_par1	Dro_par2
Dro_par1	-	32
Dro_par2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

Dro_par1
Dro_par2
Arthropod_7SK
RNase_MRP
U6
U6
U6atac
tRNAsec
snoNAME18SA1806
U1
U1
U1
U1
U1
U1
U2
U2
U2
U2
U3
U4
U4atac
U5
U5
U5
U5
U7
U11
U12
OrCD1



Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoNAME18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.