Drosophila ercepeae

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

Assembly: GCA_018150545.1_ASM1815054v1_genomic

Dro_erc1 | JAECWL010000164.1:7291151-7292197 (+) | 1047 nt | IncRNA:noe consensus e-value: 2e-183

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

Dro_erc2 | JAECWL010000197.1:8102987-8103199 (+) | 213 nt | IncRNA:noe consensus e-value: 3.5e-06

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.91

	Dro_erc1	Dro_erc2
Dro_erc1	-	12
Dro_erc2		-

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.