Drosophila truncata

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

Assembly: GCA_008042515.1_UCB_Dtru_1.0_genomic

Dro_tru1 | VNJQ01004759.1:112506-113758 (-) | 1253 nt | IncRNA:noe consensus e-value: 6e-191

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

Dro_tru2 | VNJQ01002014.1:39770-40179 (-) | 410 nt | IncRNA:noe consensus e-value: 4.6e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 1.00

	Dro_tru1	Dro_tru2
Dro_tru1	-	20
Dro_tru2		-

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.