Drosophila triauraria

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

Assembly: GCA_014170255.2_RU_Dtri_1.1_genomic

Dro_tri1 | CM024336.1:4712011-4713200 (-) | 1190 nt | IncRNA:noe consensus e-value: 1e-187

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

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Dro_tri2 | CM024333.1:13498851-13499346 (-) | 496 nt | IncRNA:noe consensus e-value: 2.7e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

Dro_tri3 | CM024335.1:568399-568750 (+) | 352 nt | IncRNA:noe consensus e-value: 7.3e-08

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.88

	Dro_tri1	Dro_tri2	Dro_tri3
Dro_tri1	-	22	20
Dro_tri2		-	52
Dro_tri3			-

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.