Drosophila ironensis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila

Assembly: GCA 021223825.1 ASM2122382v1 genomic

Dro_iro1 | JAJJHQ010003614.1:668445-669469 (+) | 1025 nt | IncRNA:noe consensus e-value: 3e-188

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

Dro_iro2 | JAJJHQ010005613.1:377571-377918 (-) | 348 nt | IncRNA:noe consensus e-value: 1.0e-07

5' motif: GCGGT 3' motif: ACTGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.82

Dro_iro3 | JAJJHQ010010328.1:461092-461325 (-) | 234 nt | IncRNA:noe consensus e-value: 3.3e-01

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.77

	Dro_iro1	Dro_iro2	Dro_iro3
Dro_iro1	-	21	14
Dro_iro2		-	49
Dro_iro3			-

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.