Drosophila imparisetae

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group

Assembly: GCA 035042265.1 ASM3504226v1 genomic

Dro_imp1 | JAWNLP010000769.1:3942810-3943808 (+) | 999 nt | IncRNA:noe consensus e-value: 2e-159

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

Dro_imp2 | JAWNLP010000146.1:5376168-5376409 (+) | 242 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 6nt PSE: 0.98

GCGCTCGAACAGCTCGCAGCACAAAGAGTTGATCACAACCTAAATTGTGATGCGCCCTGGGCAGCAGACGAACACATCTCCTCCTTGTCCCGTGAGAGGATCGAGATGAGTTCGATGGCACTCTTCTCACGCGCCCCGATAACACAAACAG

	Dro_imp1	Dro_imp2
Dro_imp1	-	15
Dro_imp2		-

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.