Hirtodrosophila histrioides

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Hirtodrosophila > quadrivittata group > confusa subgroup

Assembly: GCA_037075165.1_ASM3707516v1_genomic

Hir_his1 | JBAMCL010000727.1:1381506-1382437 (+) | 932 nt | IncRNA:noe consensus e-value: 1e-188

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

Hir_his2 | JBAMCL010000372.1:5664108-5664852 (+) | 745 nt | IncRNA:noe consensus e-value: NA

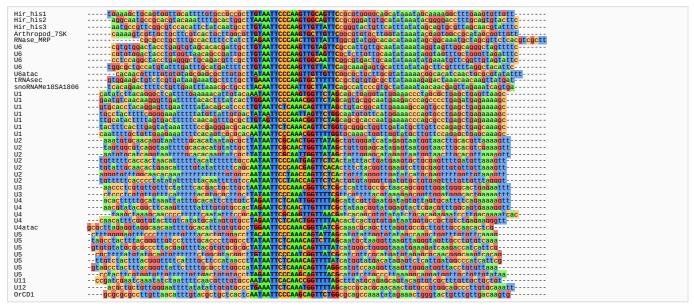
5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

Hir_his3 | JBAMCL010000054.1:1036228-1036845 (-) | 618 nt | IncRNA:noe consensus e-value: 3.9e-02

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

	Hir_his1	Hir_his2	Hir_his3
Hir_his1	-	43	39
Hir_his2		-	60
Hir_his3			-

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.