## Hirtodrosophila confusa

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

Assembly: GCA 035043065.1 ASM3504306v1 genomic

## Hir\_con1 | JAWNNI010000213.1:6110214-6111137 (-) | 924 nt | IncRNA:noe consensus e-value: 2e-188

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

## Hir\_con2 | JAWNNI010000164.1:442624-443354 (-) | 731 nt | IncRNA:noe consensus e-value: 4.8e-02

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.94

## Hir\_con3 | JAWNNI010000006.1:1911753-1912328 (-) | 576 nt | IncRNA:noe consensus e-value: 7.5e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

	Hir_con1	Hir_con2	Hir_con3
Hir_con1	-	44	40
Hir_con2		-	57
Hir_con3			-

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.