Drosophila villosipedis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > grimshawi group > orphnopeza subgroup

Assembly: GCA_035043025.1_ASM3504302v1_genomic

Dro_vil1 | JAWNNF010000027.1:1128056-1129063 (+) | 1008 nt | IncRNA:noe consensus e-value: 5e-160

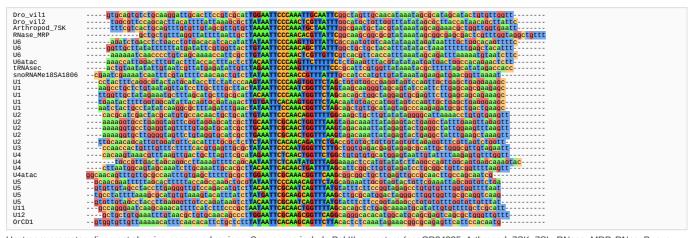
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_vil2 | JAWNNF010000024.1:14866201-14866711 (-) | 511 nt | IncRNA:noe consensus e-value: 1.3e-13

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

	Dro_vil1	Dro_vil2
Dro_vil1	-	31
Dro_vil2		-

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.