Drosophila silvestris

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > planitibia group > planitibia subgroup

Assembly: GCA_035043445.1_ASM3504344v1_genomic

Dro_sil1 | JAWNMZ010000138.1:10655678-10656704 (+) | 1027 nt | IncRNA:noe consensus e-value: 1e-165

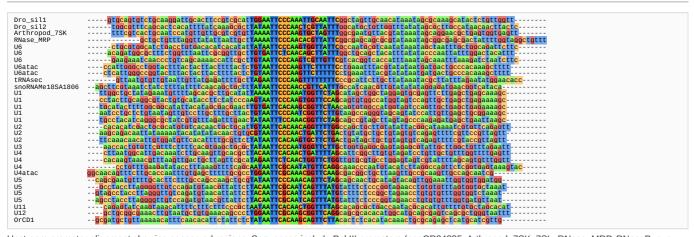
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

Dro_sil2 | JAWNMZ010000016.1:1457695-1458182 (+) | 488 nt | IncRNA:noe consensus e-value: 9.0e-12

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

	Dro_sil1	Dro_sil2
Dro_sil1	-	31
Dro_sil2		-

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.