Drosophila yooni

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > antopocerus group > diamphidiopoda subgroup

Assembly: GCA_035043035.1_ASM3504303v1_genomic

Dro_yoo1 | JAWNNG010000410.1:1173333-1174349 (+) | 1017 nt | IncRNA:noe consensus e-value: 3e-157

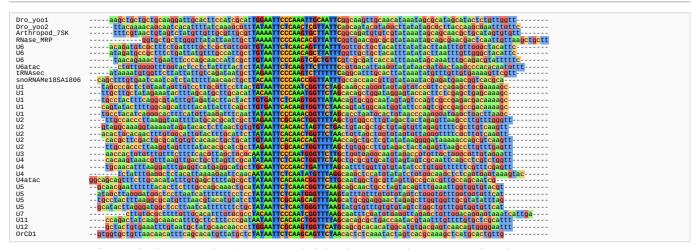
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Dro_yoo2 | JAWNNG010000736.1:117451-117789 (-) | 339 nt | IncRNA:noe consensus e-value: 3.0e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

	Dro_yoo1	Dro_yoo2
Dro_yoo1	-	22
Dro_yoo2		-

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.