Drosophila ochracea

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

Assembly: GCA_035044125.1_ASM3504412v1_genomic

Dro_och1 | JAWNML010000047.1:12258834-12259867 (-) | 1034 nt | IncRNA:noe consensus e-value: 1e-165

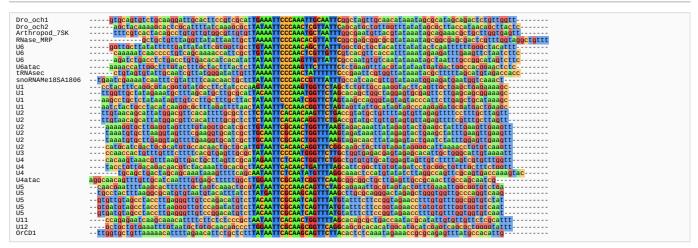
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_och2 | JAWNML010000021.1:10975270-10975779 (+) | 510 nt | IncRNA:noe consensus e-value: 2.9e-13

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

	Dro_och1	Dro_och2
Dro_och1	-	30
Dro_och2		-

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.