Drosophila rufa

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA_047115885.1_ASM4711588v1_genomic

Dro_ruf1 | CM120339.1:21628391-21629589 (+) | 1199 nt | IncRNA:noe consensus e-value: 6e-186

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

Dro_ruf2 | CM120342.1:21340690-21341208 (-) | 519 nt | IncRNA:noe consensus e-value: 6.2e-02

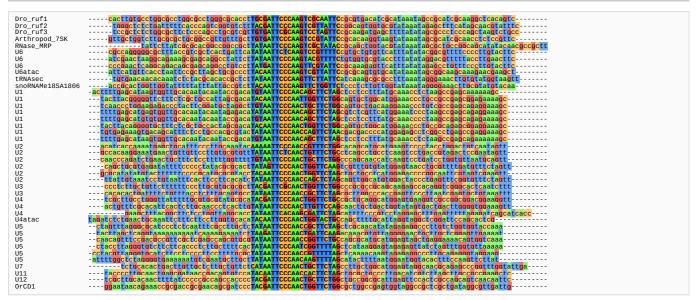
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

Dro_ruf3 | CM120338.1:34420108-34420432 (-) | 325 nt | IncRNA:noe consensus e-value: 6.2e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.88

	Dro_ruf1	Dro_ruf2	Dro_ruf3
Dro_ruf1	-	31	18
Dro_ruf2		-	47
Dro_ruf3			-

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.