Drosophila auraria

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

Assembly: GCA_051940825.1_ASM5194082v1_genomic

Dro_aur1 | CM123407.1:21309787-21310984 (+) | 1198 nt | IncRNA:noe consensus e-value: 5e-187

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Dro_aur2 | CM123410.1:14197677-14198172 (-) | 496 nt | IncRNA:noe consensus e-value: 1.3e-02

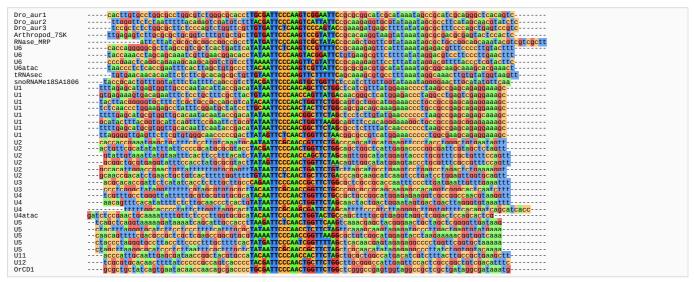
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

Dro_aur3 | CM123406.1:578062-578414 (+) | 353 nt | IncRNA:noe consensus e-value: 3.5e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.91

	Dro_aur1	Dro_aur2	Dro_aur3
Dro_aur1	-	22	19
Dro_aur2		-	53
Dro_aur3			-

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.