## Drosophila fuyamai

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

Assembly: GCA\_018153365.1\_ASM1815336v1\_genomic

## Dro\_fuy1 | JAECXW010000446.1:2076647-2077748 (-) | 1102 nt | IncRNA:noe consensus e-value: 9e-203

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

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## Dro\_fuy2 | JAECXW010000062.1:17836801-17837289 (-) | 489 nt | IncRNA:noe consensus e-value: 6.0e-03

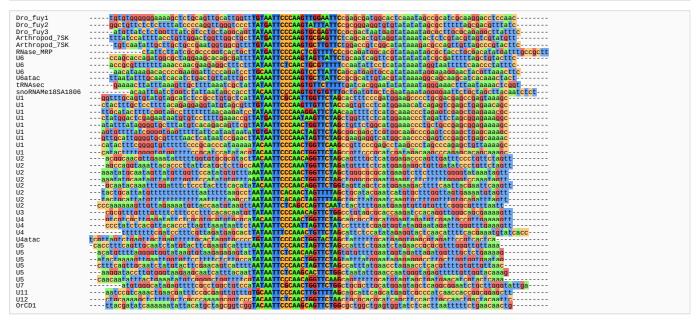
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.98

## Dro\_fuy3 | JAECXW010000062.1:10568426-10568645 (+) | 220 nt | IncRNA:noe consensus e-value: 1.3e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.99

	Dro_fuy1	Dro_fuy2	Dro_fuy3
Dro_fuy1	-	24	13
Dro_fuy2		-	34
Dro_fuy3			-

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.