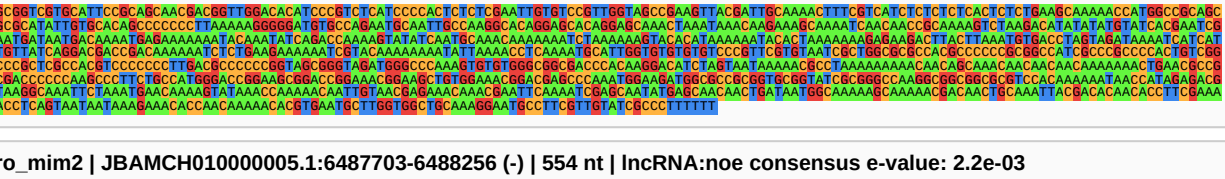
Drosophila mimetica

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

Assembly: GCA_037075245.1_ASM3707524v1_genomic

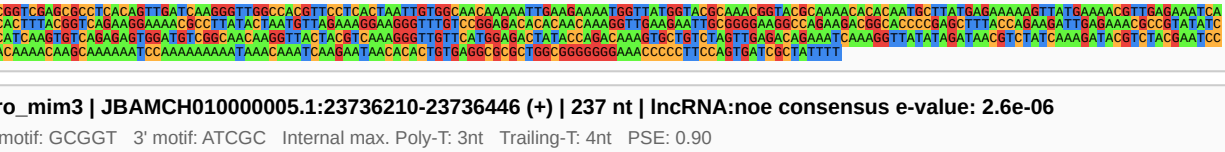
Dro_mim1 | JBAMCH010000004.1:16747324-16748462 (+) | 1139 nt | lncRNA:noe consensus e-value: 1e-194

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



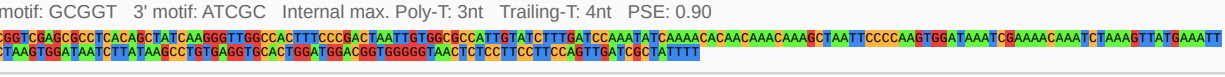
Dro_mim2 | JBAMCH010000005.1:6487703-6488256 (-) | 554 nt | lncRNA:noe consensus e-value: 2.2e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 1.00



Dro_mim3 | JBAMCH010000005.1:23736210-23736446 (+) | 237 nt | lncRNA:noe consensus e-value: 2.6e-06

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.90



	Dro_mim1	Dro_mim2	Dro_mim3
Dro_mim1	-	34	14
Dro_mim2		-	35
Dro_mim3			-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.