

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified mouthparts group > mimica subgroup
Assembly: GCA_037043585.1_ASM3704358v1_genomic

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

[illegible]

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

GGGCGGTGAGCATCTAGCAACATAAAGGGTGTATCATTCCCGCAGAGGTGTTGACCTGAAATAAATTTGTGTGAGCAAAAAAGAAACAAACTGTGTTAAAAAATAAATTTGTTATCTTCTCTCTTAAGAGCTATAAGGATATTAC
GAGCAACGACCAAAATGTGGCTTTCTTAGAGCCTTAAACAGCATTAACAATTAACTGAAAAATAAGGCCCAACAAAAAATAAAGCTGCTTAAAGATGCTACGAAGGGGGGAGGGGGAGGAGTGGTAACATCTTCCCCCATCCCTCCTTGTGTTGATCGCTTTTTTT

	Dro_mimi1	Dro_mimi2
Dro_mimi1	-	18
Dro_mimi2		-

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

[illegible]

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.