Musca domestica

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Muscidae > Musca > Musca subgenus Musca

Assembly: GCA_030504385.2_Musca_domestica.polishedcontigs.V.1.1_genomic

Mus_dom1 | JARAKG010000123.1:723956-724575 (+) | 620 nt | IncRNA:noe consensus e-value: 5.0e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.91

Mus_dom2 | JARAKG010000046.1:2819895-2820509 (-) | 615 nt | IncRNA:noe consensus e-value: 1.2e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.89

BECSETT CEAN-SECTOTT CACEANASEGTTECT SECAT COCCTTANANTETE ATTANCANATIC CTACCACE CATTETEC ACTOC CATTETE CATTETE CATTETE CATTET CAACCACATT CATTET CATTE CATTET CATTE CATTET CATTE CATTET CATTET CATTE CATTET CA

Mus_dom3 | JARAKG010000035.1:4793754-4794300 (-) | 547 nt | IncRNA:noe consensus e-value: 3.7e-01

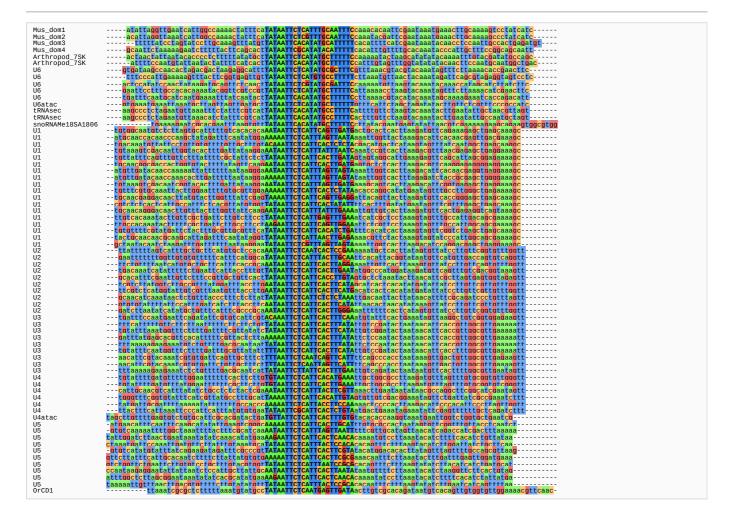
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

Mus_dom4 | JARAKG010000002.1:42695277-42695609 (-) | 333 nt | IncRNA:noe consensus e-value: 8.9e-12

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 26nt PSE: 0.87

	Mus_dom1	Mus_dom2	Mus_dom3	Mus_dom4
Mus_dom1	-	96	47	36
Mus_dom2		-	48	36
Mus_dom3			-	36
Mus_dom4				-

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.