## Musca vetustissima

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

Assembly: GCA 032173495.1 APGP CSIRO Mvet v1 genomic

#### Mus\_vet7 | JAUZEB010008635.1:217432-218115 (-) | 684 nt | IncRNA:noe consensus e-value: NA

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

## Mus\_vet8 | JAUZEB010010213.1:40013-40564 (-) | 552 nt | IncRNA:noe consensus e-value: 4.6e-02

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

### Mus\_vet1 | JAUZEB010009242.1:107233-107561 (+) | 329 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

# Mus\_vet2 | JAUZEB010009242.1:75460-75656 (-) | 197 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.86

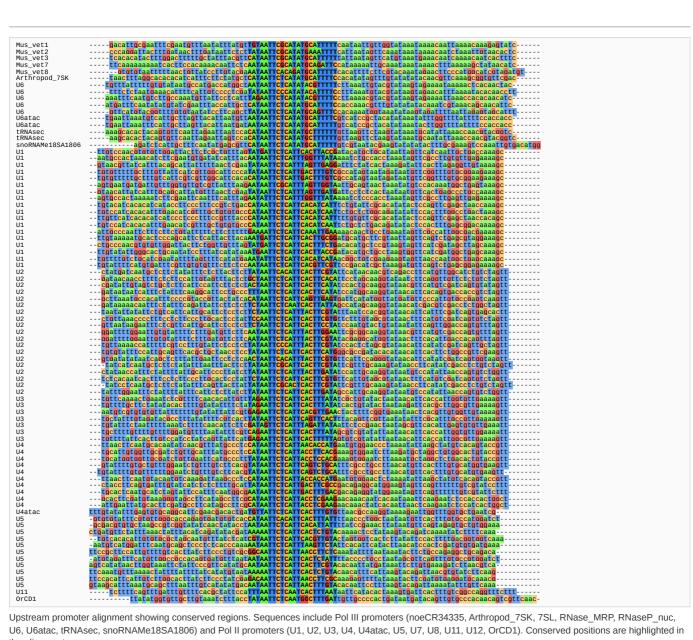
GGCGGTCCGGTTCTCCCCACCGAAAAGGTTGTCACATCCCTTAATTGTGTACCCCGTTGAAAATGTGCGAATATGGTGAAATTGTGGAAATTAAAGAGGTTTAATGGGTGTCACCTCGATACGTCAAGCTTCGGTCGAGAGTGGTACGTTAAA AATTAATAAGCTGTTGGGGAGAGTCTTGTAACCGATCGCCTTTTTTT

### Mus\_vet3 | JAUZEB010009242.1:103735-103920 (+) | 186 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

	Mus_vet7	Mus_vet8	Mus_vet1	Mus_vet2	Mus_vet3
Mus_vet7	-	44	33	17	16
Mus_vet8		-	35	18	19
Mus_vet1			-	49	48
Mus_vet2				-	85
Mus_vet3					-

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.