Muscina stabulans

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Muscidae > Muscina

Assembly: GCA 051014185.1 ASM5101418v1 genomic

Mus_sta1 | CM117225.1:133927982-133928502 (-) | 521 nt | IncRNA:noe consensus e-value: 1.2e-01

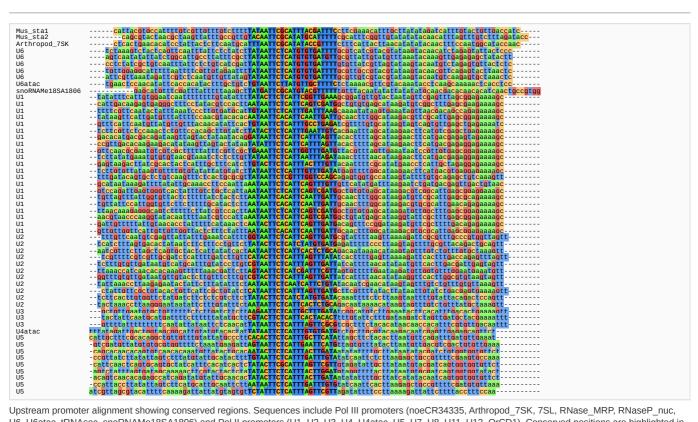
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

Mus_sta2 | CM117227.1:78543873-78544138 (-) | 266 nt | IncRNA:noe consensus e-value: NA

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

| | Mus_sta1 | Mus_sta2 |
|----------|----------|----------|
| Mus_sta1 | - | 38 |
| Mus_sta2 | | - |

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.