Eustalomyia histrio

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Anthomyiidae > Eustalomyia

Assembly: GCA 949748255.1 idEusHist1.1 genomic

Eus_his1 | OX456525.1:45440404-45440793 (+) | 390 nt | IncRNA:noe consensus e-value: 3.5e-06

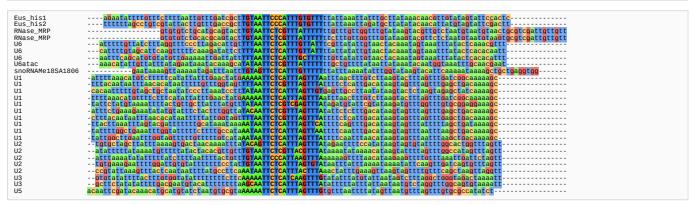
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.89

Eus_his2 | OX456525.1:45388594-45388954 (+) | 361 nt | IncRNA:noe consensus e-value: 2.9e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 7nt PSE: 0.89

	Eus_his1	Eus_his2
Eus_his1	-	71
Eus_his2		-

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.