

## *Eustalomyia histrio*

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

**Assembly:** GCA\_949748255.1\_idEusHist1.1\_genomic

**Eus\_his1 | OX456525.1:45440404-45440793 (+) | 390 nt | lncRNA: noe consensus e-value: 3.5e-06**

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

GGCGGTCCTGATCCTCTCAGTGAATGATGGTCACATCTCAATTATGTGACAAATTAGGAAAAATCTTAAATTCACTAAGGTGAATTAATGTGGTAAACTATATGTATATATATATAAAATTCCTATTGTTCCTATAAGGCBCAT  
AGAGCGATGAGGAGGATCAATCAACCTTTATTAAATCCCATCAACGACAAAAAAAGAAAAAATATAGAAAAAAGAAAAAATATAAAATAGAAACCAACCAACCAACCACTTCTCAAAAAATCAATTCTAGAAATAGAAAGCGAATTGAGAAAGAAATCC  
ACITCTAAAAATTTTATCTAGAAATAGAAAGCGAATTGAAAAAGAGTGGAAACGATAGGAGGGATCAAAATGGTGTGATCGCTTTTTTT

**Eus\_his2 | OX456525.1:45388594-45388954 (+) | 361 nt | lncRNA: noe consensus e-value: 2.9e-03**

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

[illegible]

	Eus_his1	Eus_his2
Eus_his1	-	71
Eus_his2		-

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.