

Glossina morsitans morsitans

Taxonomic lineage: Brachycera > Muscomorpha > Hippoboscoidea > Glossinidae > Glossina > Glossina subgenus Glossina

Assembly: GCA_001077435.1_ASM107743v1_genomic

Glo_mor1 | CCAG010013027.1:43894-44342 (+) | 449 nt | lncRNA: noe consensus e-value: 1.9e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.99

[illegible]

Glo_mor2 | CCAG010007674.1:40152-40430 (+) | 279 nt | lncRNA: no consensus e-value: 3.5e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.90

GGCGGGTTCATATCCCTTCAAGTTGAAAGCGTTGGCTGCATCCCCGGTTCATAATGATCCGAATTGCAACAAACAAAATGTGTCTCCAAATTAACCTTAGCCAAATAAAATTTGGCATTACCAAATACATAAATTATAATCTCTCTCTATGGTAG
AGCACACTTCTGACAAAAAGCAATATACAACACTCTAGCTGTTATCTTTGTAAGATAAAATTTGCATAATATGTATAAGCAAAAAAAAAAAAAAAAAAGGACGCTGTAAAGGATAACTGTGATCGCTTTTTT

	Glo_mor1	Glo_mor2
Glo_mor1	-	44
Glo_mor2		-

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.