## Glossina fuscipes

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

Assembly: GCA\_014805625.1\_Yale\_Gfus\_2\_genomic

## Glo\_fus1 | JACGUE010000051.1:387833-388274 (+) | 442 nt | IncRNA:noe consensus e-value: 3.7e-03

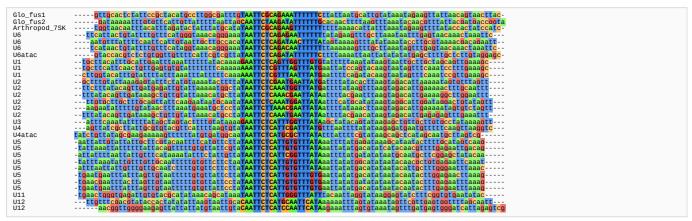
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.98

## Glo\_fus2 | JACGUE010000018.1:5050434-5050717 (-) | 284 nt | IncRNA:noe consensus e-value: 5.0e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.85

|          | Glo_fus1 | Glo_fus2 |
|----------|----------|----------|
| Glo_fus1 | -        | 43       |
| Glo_fus2 |          | -        |

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.