## Glossina palpalis gambiensis

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

Assembly: GCA\_000818775.1\_Glossina\_palpalis\_gambiensis-2.0.1\_genomic

## Glo\_palp1 | KN796399.1:220653-221094 (-) | 442 nt | IncRNA:noe consensus e-value: 3.7e-03

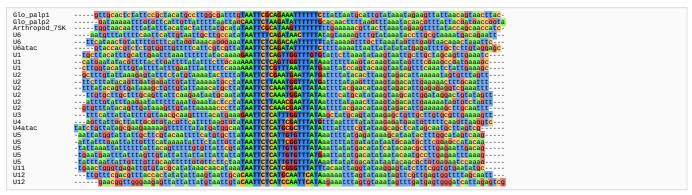
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.99

## Glo\_palp2 | KN796187.1:1323444-1323729 (-) | 286 nt | IncRNA:noe consensus e-value: 3.8e-10

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

	Glo_palp1	Glo_palp2
Glo_palp1	-	40
Glo_palp2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.