Glossina pallidipes

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

Assembly: GCA_000688715.1_Glossina_pallidipes-1.0.3_genomic

Glo_pal1 | KK499996.1:192187-192632 (+) | 446 nt | IncRNA:noe consensus e-value: 1.1e-02

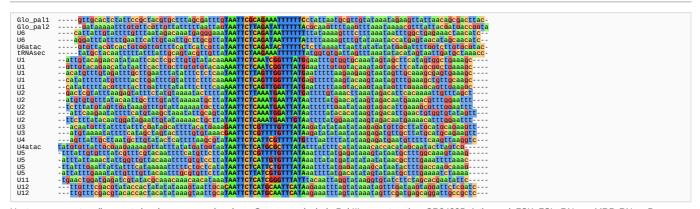
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.94

Glo_pal2 | KK499826.1:522416-522693 (-) | 278 nt | IncRNA:noe consensus e-value: 5.2e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.95

	Glo_pal1	Glo_pal2
Glo_pal1	-	38
Glo_pal2		-

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.