Glossina austeni

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

Assembly: GCA_000688735.1_Glossina_austeni-1.0.3_genomic

Glo_aus1 | KK502436.1:403533-403980 (+) | 448 nt | IncRNA:noe consensus e-value: 2.0e-03

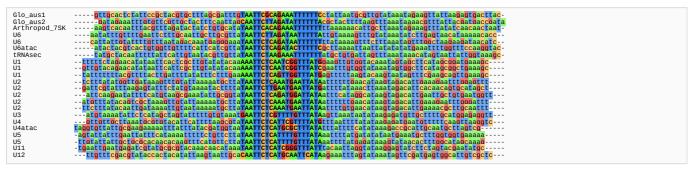
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.95

Glo_aus2 | KK502411.1:1863709-1863988 (-) | 280 nt | IncRNA:noe consensus e-value: 3.5e-09

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

	Glo_aus1	Glo_aus2
Glo_aus1	-	38
Glo_aus2		-

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.