## Epistrophe eligans

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Epistrophe

Assembly: GCA 951394125.1 idEpiElig2.1 genomic

## Epi\_eli1 | OX596029.1:92403565-92403857 (+) | 293 nt | IncRNA:noe consensus e-value: 2.0e-10

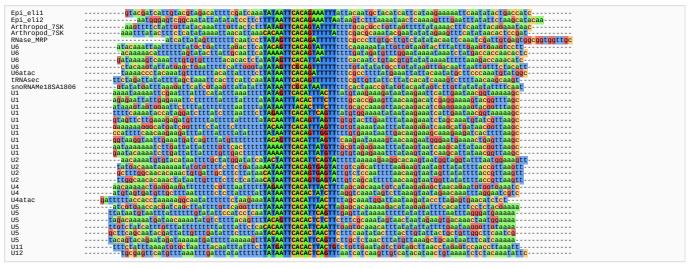
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

## Epi\_eli2 | OX596029.1:26314504-26314676 (+) | 173 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.89

	Epi_eli1	Epi_eli2
Epi_eli1	-	38
Epi_eli2		-

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.