## Beris morrisii

Taxonomic lineage: Brachycera > Stratiomyomorpha > Stratiomyidae > Beris

Assembly: GCA 951812415.1 idBerMorr1.1 genomic

## Ber\_mor1 | OX638310.1:26839098-26839503 (-) | 406 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 1.00

## Ber\_mor2 | OX638310.1:26831179-26831583 (-) | 405 nt | IncRNA:noe consensus e-value: NA

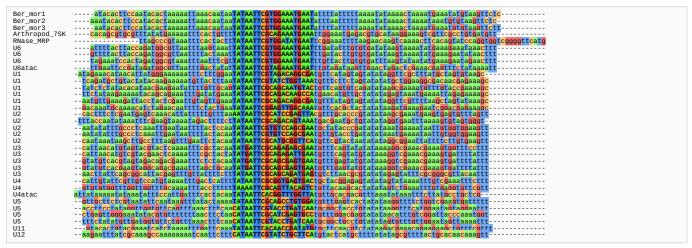
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

## Ber\_mor3 | OX638310.1:26851140-26851519 (-) | 380 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 1.00

	Ber_mor1	Ber_mor2	Ber_mor3
Ber_mor1	-	97	91
Ber_mor2		-	90
Ber_mor3			-

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.