## Epistrophe grossulariae

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

Assembly: GCA 929447395.1 idEpiGros1.1 genomic

## Epi\_gro1 | OV839568.1:104169864-104170163 (+) | 300 nt | IncRNA:noe consensus e-value: NA

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.78

## Epi\_gro2 | OV839568.1:31266418-31266709 (+) | 292 nt | IncRNA:noe consensus e-value: 1.3e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

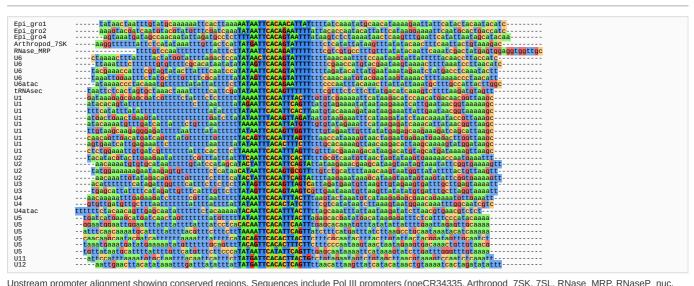
## Epi\_gro4 | OV839568.1:114372827-114373002 (+) | 176 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

GCBGTCCAATGTCTCAAACTATATAGGTTGACCACATTCCTCAATTGTGGGGGAAAAGTGAAAGCCTTTAAGCAAAAGTTTGAATTGAATTGAATGAGAGTATTGATTAGTTTGATTAGTTGATTAGTTGATTAACTAATAAAAAAGTATTGA GACAAATAAGATCGCAATCATTTTTT

	Epi_gro1	Epi_gro2	Epi_gro4
Epi_gro1	-	51	41
Epi_gro2		-	40
Epi_gro4			-

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.