## Eupeodes corollae

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Eupeodes > Eupeodes subgenus Eupeodes

Assembly: GCA 945859685.1 idEupCoro1.1 genomic

## Eup\_cor1 | OX244024.1:132028758-132029065 (+) | 308 nt | IncRNA:noe consensus e-value: 5.7e-06

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

## Eup\_cor2 | OX244024.1:32007215-32007507 (-) | 293 nt | IncRNA:noe consensus e-value: 5.6e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

	Eup_cor1	Eup_cor2
Eup_cor1	-	55
Eup_cor2		-

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.