## Eupeodes latifasciatus

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

Assembly: GCA\_920104205.1\_idEupLati1.1\_genomic

## Eup\_lat1 | OV049926.1:156844906-156845214 (-) | 309 nt | IncRNA:noe consensus e-value: NA

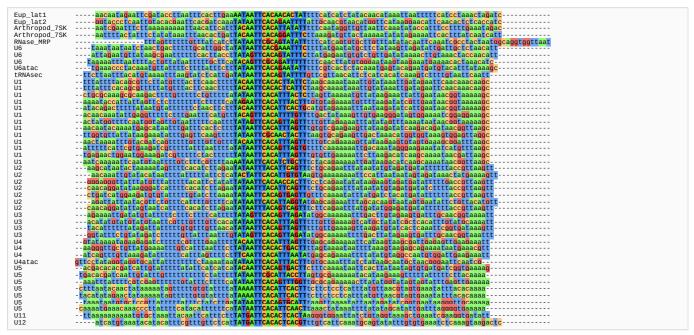
5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.76

## Eup\_lat2 | OV049926.1:39451434-39451725 (+) | 292 nt | IncRNA:noe consensus e-value: 2.3e-10

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

	Eup_lat1	Eup_lat2
Eup_lat1	-	52
Eup_lat2		-

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.