Eupeodes luniger

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

Assembly: GCA_951509635.1_idEupLuni2.1_genomic

Eup_lun1 | OX608074.1:33996997-33997304 (+) | 308 nt | lncRNA:noe consensus e-value: NA
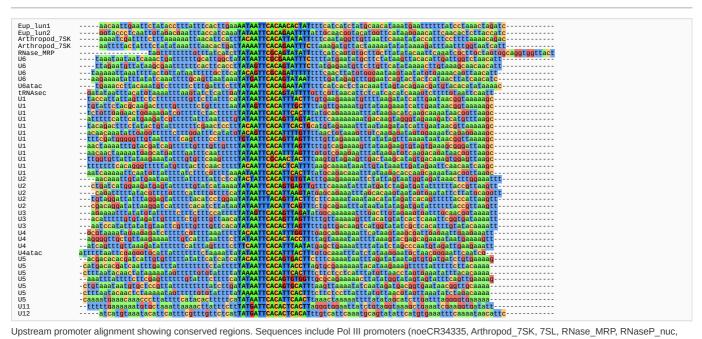
5' motif: GTGGT   3' motif: ATCAC   Internal max. Poly-T: 3nt   Trailing-T: 6nt   PSE: 0.80

Eup_lun2 | OX608074.1:116652321-116652615 (+) | 295 nt | lncRNA:noe consensus e-value: 7.8e-10

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

	Eup_lun1	Eup_lun2
Eup_lun1	-	54
Eup_lun2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.