Episyrphus balteatus

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

Assembly: GCA 945859705.1 idEpiBalt1.1 genomic

Epi_bal1 | OX244018.1:44684435-44684738 (-) | 304 nt | IncRNA:noe consensus e-value: NA

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.83

Epi_bal2 | OX244018.1:100616528-100616830 (-) | 303 nt | IncRNA:noe consensus e-value: 3.1e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.99

	Epi_bal1	Epi_bal2
Epi_bal1	-	51
Epi_bal2		-

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.