## Dasysyrphus albostriatus

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

Assembly: GCA\_946251815.1\_idDasAlbo1.1\_genomic

## Das\_alb1 | OX276336.1:108813459-108813771 (-) | 313 nt | IncRNA:noe consensus e-value: 6.0e-05

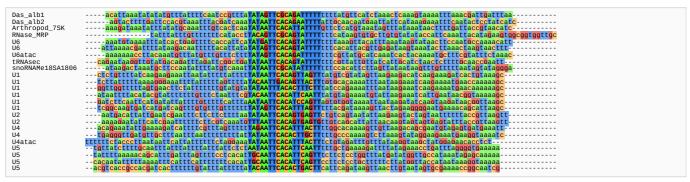
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.98

## Das\_alb2 | OX276336.1:31483031-31483324 (-) | 294 nt | IncRNA:noe consensus e-value: 1.3e-09

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

	Das_alb1	Das_alb2
Das_alb1	-	46
Das_alb2		-

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.