Pollenia labialis

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Calliphoridae > Pollenia

Assembly: GCA 949318255.1 idPolLabi1.1 genomic

Pol_lab3 | OX439139.1:106034517-106034913 (+) | 397 nt | IncRNA:noe consensus e-value: 7.1e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 9nt

Pol_lab4 | OX439140.1:74016369-74016590 (-) | 222 nt | IncRNA:noe consensus e-value: 4.5e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt

Pol_lab5 | OX439139.1:112184100-112184324 (+) | 225 nt | IncRNA:noe consensus e-value: NA

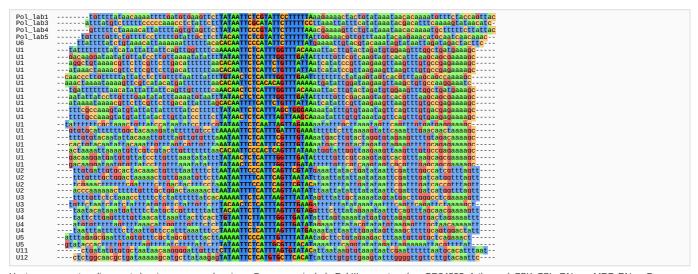
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 11nt

Pol_lab1 | OX439140.1:73996347-73996557 (+) | 211 nt | IncRNA:noe consensus e-value: NA

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

	Pol_lab3	Pol_lab4	Pol_lab5	Pol_lab1
Pol_lab3	-	38	37	38
Pol_lab4		-	59	70
Pol_lab5			-	62
Pol_lab1				-

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.