Pollenia amentaria

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

Assembly: GCA 943735925.1 idPolAmen1.1 genomic

Pol_ame4 | OX031006.1:175810696-175811100 (-) | 405 nt | IncRNA:noe consensus e-value: 1.5e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 15nt PSE: 0.88

Pol_ame2 | OX031006.1:159212051-159212285 (+) | 235 nt | IncRNA:noe consensus e-value: 7.3e-07

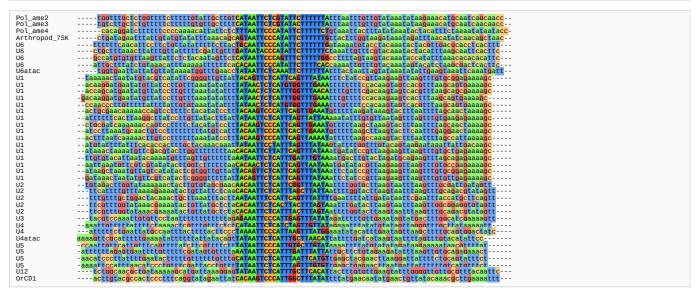
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.94

Pol_ame3 | OX031010.1:150780668-150780901 (-) | 234 nt | IncRNA:noe consensus e-value: 1.2e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.89

	Pol_ame4	Pol_ame2	Pol_ame3
Pol_ame4	-	41	40
Pol_ame2		-	90
Pol_ame3			-

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.