Pollenia angustigena

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

Assembly: GCA 930367215.1 idPolAngu1.1 genomic

Pol_ang1 | OV884058.1:108948837-108949067 (+) | 231 nt | IncRNA:noe consensus e-value: 2.2e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.86

Pol_ang2 | OV884058.1:108974527-108974753 (+) | 227 nt | IncRNA:noe consensus e-value: 2.0e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

Pol_ang3 | OV884058.1:109027351-109027577 (+) | 227 nt | IncRNA:noe consensus e-value: 2.2e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

GGCGGTCTTGATCTCTCCGGTGGAAAGGTTGTTCACAATCCTTTAATTGTGAAACAGGTGTGACCACTGCGTCTCAGTTAATAAAGTTGAAATAGAATGGTTGAAAAAGTGTGAAAAAGTGTGAAAACAATACACCCGCTGAAATT
TCAAGCTTTGGCAAGCGGCGTGTATAAATTACGAAGCTTTGAAAGTGTGAAAAATTATGAACACTCTTTTTTT

Pol_ang4 | OV884058.1:108967750-108967975 (+) | 226 nt | IncRNA:noe consensus e-value: 4.8e-07

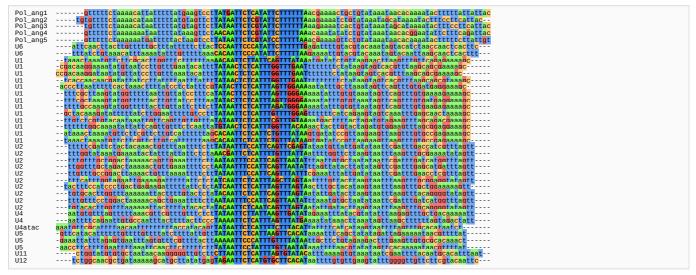
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

Pol_ang5 | OV884058.1:109087645-109087870 (-) | 226 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.82

	Pol_ang1	Pol_ang2	Pol_ang3	Pol_ang4	Pol_ang5
Pol_ang1	-	88	86	74	73
Pol_ang2		-	98	76	76
Pol_ang3			-	75	69
Pol_ang4				-	92
Pol_ang5					-

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.