

## *Pollenia labialis*

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

**Assembly:** GCA\_949318255.1\_idPolLabi1.1\_genomic

Pol\_lab3 | OX439139.1:106034517-106034913 (+) | 397 nt | lncRNA: noe consensus e-value: 7.1e+00

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

5'GCGGTTTCATACCTCTGCAATGAAAGGGCTGTTACAGCTCCCTAACCAATGTGAAATCGTTAAAAAATTTCTCCTTAAACCGCTCTTAAACGCGGCGAAATTTGAGAAATATATAAAATAAAAAATAATTTCTAAAACAAAACGACCAATTTCTGCTAAATGCTTTAAAGATGATTTCTCACCATCAAAATAAAAAAGGCTAAGATGAATAAAGATACAAAAAAGAAAGATTTCAATTTCAATTTCAATTTCCAAATCCAAACACATTTCAAACTTTTACACGAAAAATATCTCAAACTTTCCAAACACTTTTCTGCTCAAAATTTGCGCTTAAATTTGAGCAATTTGAGCAATTCGAAATGACAAAGATACAAAAAAGGATTAATCGCAATTTTTTTTTTTT

**Pol\_lab4 | OX439140.1:74016369-74016590 (-) | 222 nt | lncRNA: no consensus e-value: 4.5e-04**

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

GGCGGGTCTTGATATCTCAGATGAACCGGTGTGTTACACGCCCTTTAATTGTAAAAATTAAACAGAGTTTATAAATTCAGATAAATTTTGTAGTTTAAAGTGGTGGAAACCCACAGTGGTGGAAACCCACCCCAATACCCGTTAAAAATTCAAACTTTGGCAGGCGCGGTGTATTAATTACAAAGTTTAAAGGGAGATTCAAAAGTTGTATCGCTTTTTT

**Pol\_lab5 | OX439139.1:112184100-112184324 (+) | 225 nt | lncRNA: noe consensus e-value: NA**

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

GGCGGTCAGGCATCTCCGGTGGAGAAGTTGTTCACAAACCCTTAATTGTGAACATTTCAAAATGAATCATTATGAATCGCTTATAAAATCTTGTAACTAAGAAAATCTTTAAAAATGTGTAAACCACAAAAATAAAATACACTCCATGGAAATTC  
CAGCTTCGGTAAGTGGCTGTGTATAAAAAACAAAGCTGTGGGGGATGTACAAAGTAATCGCCACCTTTTTTTTTTTT

Pol\_lab1 | OX439140.1:73996347-73996557 (+) | 211 nt | lncRNA: noe consensus e-value: NA

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

GGCGGCTTTATCTCTCCGGTGGAAAGGTTGTTCAACAACCTAAATTGTGAATTGAAAAAGGTGTGATTGCAGACCCATGTGTCTCAGTTAAATGAATGAAGCAAGAAATGTTGGAAAAACACCCGCTGAAATTTCAAGCTTTGGCAGG  
CGGCGTGTATAAATTACAAAGCTTTGAAGGGAGATTAAAAAATTGTGATCGCTTTCTTTTT

	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 lncRNA sequences.

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Pol_lab1 -----TccttttatacaaaacatttttgcgaatctctTATAATTCGCGATTCCTTTTAAaabaanaactactctataataaacacaaatcttccaccattac
Pol_lab3 -----attatgtctctttttcccccaacattttctTATAATTCGCATATCTTCTTCTTaaattattctatataaacacacattctcaaaagtataacatc
Pol_lab4 -----gtttttctcaaaaacattttttagtgttgtctTATAATTCGCGATCTTCTTTTAAcgaanaactctctataaacacacaaatctgtttttctttatcc
Pol_lab5 -----TcctttttctctctttctttttctttcttctcTACAATTCGCGATTCCTTTTATAaacaacattctttaaacacaaaacatcgaatcaacaacac
U6 -----TctttttatctctgaatacatataaaaattttttacACAATTCGCATATCTTCTTATAaaattgtctagctcaaaagtataataatgatactactctc
U1 -----TattttttttctatcatattattatcgtgtgttttcaCAAAAATTCGATTGGTTCACAaaatctactctatagatgtggaattttgctgatgaagc
U1 -----cccaadgaataatctctatctctcttaaaaattttctTATAATTCGATTGGTTCGATAttttctctccaaatgaatccacatttaaacccaacaaagc
U1 -----aagcttatgaatctctctctctctctctctctctctcTACAATTCGCGATCTTCTTTTAAcgaanaactctctataaacacacaaatctgtttttctttatcc
U1 -----TcttcccaaaacgtctctgtctgtacattttttacACAATTCGATTCTGTTATGATcatatccctgaagaagttaagttgtgtcctgaagaagc
U1 -----caacccctctttttttattatctctcttttaattttattTGAATCTCATTTGGTTCGAAAtttttctataaagttaacgtcttaaacacacacaaagc
U1 -----aaacataaaaataaaagtctgtctacatagattttttacACAATTCACACAGTTTAAATAgatatgtataagaagaatttaagctgtgccaaagaaatc
U1 -----TgatttttttaacatatattatcgtgtgttttcaCAAACTTCGATTGGTTCACAaaatctactctatagatgtggaattttgctgatgaagc
U1 -----aataatatacctctttttaaataatttttaaaatctTATAACTTCGATTGGTTCGATAttttctctcaaaatgaatccacatttaaacccaacaaagc
U1 -----ataaaaataaacgtctgtgtgtgtgtctatagcattctTGAATCTCATTTGGTTCGATAttttctctcaaaagttaagttgtgtcctgaagaagc
U1 -----TctcccaaaagtcttatataatctctctctctctctTATAATTCGATTAGTGGGAaaaatttttataaagaagaagaagaagaagaagaagaaga
U1 -----tttttgcgaagtattctattatctctctctctctctTATAACTTCGATTAGTAAAGCAaaattttgtataaagttaagttgtgtgaagaagaagaagc
U1 -----TattttttctctcaaaccttttgcacafaaatattctctctTATAATTCGAAATAGTAAAGaaatattttgttaaaatfannfannfannfannfann
U1 -----ctctgcatttttttctcacaagaattattttctctTAAAAATTCGATTGATTTGAAAtttttctttaaaagtatcaaaattgaacacataaaagc
U1 -----ttctctgatacaatatacaaaatttttactctctctcttataATAATTCGATTCTGTTTGAaaatgaatctgtactaagttttataagaacaaagc
U1 -----cacctacacataatcacaaatcttttactctctctTATAATTCGATTCTGTTTGAaaatgaatctgtactaagttttataagaacaaagc
U1 -----acacaaatataaaattctctctctctctctttttttacACAATTCGCGATTCGATTAATgaatatttgtataaagaatataattctctctgaagaagc
U1 -----cccaagaagctttttttttttttttttttttttttTATAATTCGCGATTCGATTAATgaatatttgtataaagaatataattctctctgaagaagc
U1 -----gcagaanaatattttttttttttttttttttttttTATAACTTCGATTGGTTCGATAttttctctcaaaatgaatctgtctgaagaagaagaagc
U2 -----tttgtatctctacatacaaaactcttttaattttctTATAATTCGCGATTCGATTAaaattatactataatctcgaattgccactctttatgct
U2 -----ttttctctcgaacataaaactctgaaaattctctTATAATTCGATTTCGATTAATtataatataataataatctcgaattgactatgatttgaatt
U2 -----TcacaacattttttttttttttttttttttttTATAATTCGATTTCGATTCGATTAATtataatataataataatctcgaattgactatgatttgaatt
U3 -----accocaaaaaacctttttgtctgcacataaaactTATAATTCGATTTCGATTAATtataatataataataatctcgaattgactatgatttgaatt
U3 -----TctttctctcgaacctctctctctctctctctctctctTATAATTCGATTTCGATTAATtataatataataataatctcgaattgactatgatttgaatt
U3 -----TctttctctcgaacctctctctctctctctctctctctTATAATTCGATTTCGATTAATtataatataataataatctcgaattgactatgatttgaatt
U4 -----taatacataaaattttttctctctctctctctctTACAATTCGATTAGTGTATGAGttttttctataaagaatatttcagtttatacacaacaaagatt
U4 -----tattctctgaatttttttataacattaaatctactctTGATAATTCGATTGGTTCGATAtttttataaataatgattctgaagatttgaactaagaattt
U4 -----atattttttttttttttttttttttttttttttTATAATTCGATTAGTGTATGATAaaatattatcattatattatgaattttctacacaaatatt
U4 -----taattttttttttttttttttttttttttttttTATAATTCGATTAGTGTATGATAaaatattatcattatattatgaattttctacacaaatatt
U5 -----attataacgaatttttgtttctctctcagctctctctTAAAAATTCGATTGGTTCGATAtttttataaagaatctctataaagaatcttaagctctcagaacaa
U5 -----TctatcattttttttttttttttttttttttttttTATAATTCGATTAGTGTATGATAaaatattatcattatattatgaattttctacacaaatatt
U12 -----TctctgcacacctctataaaaactctataaaatTATAATTCGATTGGTTCGATAtttttgtataaagaatcttaagctctcagaacaa

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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.