Pollenia pediculata

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

Assembly: GCA_964300415.1_idPolPedi2.hap1.1_genomic

Pol_ped1 | OZ199114.1:152632306-152632697 (-) | 392 nt | lncRNA:noe consensus e-value: 5.0e+00

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 8nt   PSE: 0.87

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GGCGGTTCATAACCTCTGCATTGAAAGGGCTGTTCACACTCCCTAACCAATTGTGAAATTCGTTAAAAAAATTCCTCCTTAAAGCCGTCTTAACGACGACGAAATTTCAGAAATACATAAAATAAAAAATAATTTCTAAAACAAAAACAC
AATTTCTCTCTCATGCTTTAACATTGATTCTCACCTTCAAAATAAAAAAGGCTATAGAATAAATATAGAAAAAAAGAATTCAAATTTCAATTCAAATTCCAAACACATTTCAAACTTTACACCAAAAATATCTCAAAACTTTCCAAACAC
TTTCCTCTCAAATGTGCGCTTCAAATTTGAGCCAATTTGAAAATAATTCAAATGACAAGAGGTTACAAAAAGGGTTAATCGCCATTTTTTTT
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Pol_ped2 | OZ199114.1:138530911-138531148 (+) | 238 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 7nt   PSE: 0.83

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GGCGGTTACGACATCTCCAGGGAAGAGGTTGTTCACAACCCTTGATTGTGAAACTTTCAAGAAAAGATCAATTAAGAATCTCTGTTAATTCTTGTCGACTAAGAAAGTTTTAAAAATGTGTACCCAACGTGACCCAAGCAAAAATAGCAA
GCACTTCACGGAAATTTCCAGCTTTGGTAAGTGGCTGTGTATAAATACAAAGCTTTGGGGGATGTCGCAAGTAAATCGCCATTTTTTT
```

Pol_ped3 | OZ199115.1:100177590-100177807 (+) | 218 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGAT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 9nt   PSE: 0.86

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GGCGATCTTGATCTCTCAGGTGGAAAGGTTGTTCACAACCCTTCAATTGTGAAATTGAAACAGGCBTTATTGCAGACCATGTGTCTCAGTTAATAAAGTGAAAAATGTTGAAAAAGTGTGAAAACAATACACCCGCTGAAATTTCAAGCT
TTGGCAGGCGGCGTGTATAAATAACAAAGTTTGAAGGGAGATTAAAAAATTTGTGATCGCTTTTTTTTTT
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Pol_ped4 | OZ199115.1:100191635-100191861 (+) | 227 nt | lncRNA:noe consensus e-value: 7.3e-06

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 9nt   PSE: 0.91

```
GGCGGTCTTGATCTCTCAGATGAAACGGTTGTTCACAGCCCTTTAATTGTGAAATTTAAAAAGAGTTTATAATTGCAGATAATTTGTGGCTCAAAGAAGTTTCAGTGGTGGAAGACCCCACAGTGAAGATAAAAAATACACCCGTTGAAA
TTTCAAACTTTGGCAGGCGGCGTGTATAAATTACAAAGTTTAAGGGGAGATTGAAAAATTGTGATCGCTTTTTTTTT
```

Pol_ped5 | OZ199115.1:100258397-100258621 (+) | 225 nt | lncRNA:noe consensus e-value: 4.2e-07

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

```
GGCGGTCTTGTTCTCTCCGGTGGAAAGGTTGTTCACACCCCTTTAATTGTGAAATTGAAACAGGTGTGATTGCAGACCATGTGTCTCAGTTAATAAAGTTGAACTAAAAATGTTGAAAAAGTGTGAAAACAATACACCCGCTGAAATTTC
AAGCTTTGGCAGGCGACGTGTATAAATTACAAAGCTTTGAAGAGAGGTTAAAAAATAATGATCGCTTTCTTTTTT
```

Pol_ped6 | OZ199115.1:100271850-100272074 (-) | 225 nt | lncRNA:noe consensus e-value: 2.1e-02

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 9nt   PSE: 0.86

```
GGCGGTCTTGATCTCTCATGTGAAAAGGTTGTTCACAACCCTTAATTGTGAAATTAAAACAGAGTTTATATAATTGCAGATAATTTGTGGCTCAAAGAAGTTTCAGTGGTGGAATACCCCACAGTGAAGAAAAATACACCCGTTGAAATT
TCAAACTTTGGCAGGCGGCGTGTATAAATTACAAAGTTTAAGGGGAGATTGAAAAATTGTGATCGCTTTTTTTTT
```

Pol_ped7 | OZ199115.1:100199950-100200171 (+) | 222 nt | lncRNA:noe consensus e-value: 1.9e-06

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

```
GGCGGTCTTGATCTCTCCGGTGGAAAGGTTGTTCACAACCCTTTAATTGTGAAATTGAAACAGGTGTGATTGCAGACCATGTGTCTCAGTTAATAAAGTTGAACTAAAAATGTTGAAAAAGTGTGAAAACAATACACTCGCTGAAATTTC
AAGCTTTGGCAGGCGGCGTGTATAAATTACAAAGCTTTGAAGGGAGATTAAAAAATTGTGATCGCTTTTTTT
```

	Pol_ped1	Pol_ped2	Pol_ped3	Pol_ped4	Pol_ped5	Pol_ped6	Pol_ped7
Pol_ped1	-	41	40	39	40	40	40
Pol_ped2		-	58	64	58	66	60
Pol_ped3			-	78	90	79	93
Pol_ped4				-	75	94	77
Pol_ped5					-	76	95
Pol_ped6						-	78
Pol_ped7							-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.