# 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 | IncRNA:noe consensus e-value: 5.0e+00

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

### Pol\_ped2 | OZ199114.1:138530911-138531148 (+) | 238 nt | IncRNA:noe consensus e-value: NA

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

GGCGGTTACGACATCTCCAGGGAAGAGGTTGTTCACAACCCTTGATTGTGAAACTTTCAAGAAAAGTCAATTAAGATCTCTGTTAATTCTTGTCGACTAAGAAAGTTTTAAAAAATGTGTACCCAACGTGACCCAAGCAAAAATAGCAA GCACTTCACGGAAATTTCCAGCTTTGGTAAGTGGCTGTGTATAAATACAAAGCTTTGGGGGGATGTCGCAAGTAAATCGCCATTTTTTT

## Pol\_ped3 | OZ199115.1:100177590-100177807 (+) | 218 nt | IncRNA:noe consensus e-value: NA

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

GGCGATCITGATCICICAGGIGGAAAGGITGITCACAACCCTICAATIGIGAAATIGAAACAGGCGITATIGCAGACCATGIGTCICAGITAATAAAGIGAAAAAAGIGIGAAAAAGIGIGAAAAACAATACACCCGCIGAAATIICAAGCI TIGGCAGGCGGCGIGTATAAATAACAAAGIIIGAAGGGAGATTAAAAAATIGIGAICGCITITIIIIII

# Pol\_ped4 | OZ199115.1:100191635-100191861 (+) | 227 nt | IncRNA:noe consensus e-value: 7.3e-06

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

#### Pol\_ped5 | OZ199115.1:100258397-100258621 (+) | 225 nt | IncRNA:noe consensus e-value: 4.2e-07

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

#### Pol\_ped6 | OZ199115.1:100271850-100272074 (-) | 225 nt | IncRNA:noe consensus e-value: 2.1e-02

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

#### Pol\_ped7 | OZ199115.1:100199950-100200171 (+) | 222 nt | IncRNA:noe consensus e-value: 1.9e-06

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

	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 IncRNA sequences.

Pol ped1	atttatuccttttttccaaaacattatttcctcTATAATTCGCATATTCTTTTTC
Pol_ped2	tatttt <mark>gctctag</mark> ttaactaattatacttt <mark>g</mark> ttct <mark>CATAATTCTCGTATTCTTTTTAA</mark> ttaaaaa <mark>g</mark> ttttgtatataaacaa <mark>g</mark> aaaat <mark>gccg</mark> tcataa <mark>gct</mark> -
Pol_ped3	<mark>qtttttctaacac</mark> attattttt <mark>qt</mark> qaa <mark>q</mark> tcct <b>TATAATTCTCGTATTCTTTTTAA</b> acaaaaa <mark>q</mark> tt <mark>ctq</mark> tataaataacacaaaatattttaattcattac
Pol_ped4	<mark>gattttc</mark> taaaacaataattttataaa <mark>g</mark> ttct <b>AACAATTCTCGTATTCTTTTAA</b> acaaatattact <mark>g</mark> tataaaatat <mark>cacg</mark> aaattttctttca <mark>g</mark> attac
Pol_ped5	t <mark>q</mark> ttttctaaaacattatttttatq <mark>taq</mark> ttct <b>TATAATTCTCGTATTCTTTTTTA</b> acqaaaat <mark>cac</mark> tqtataaaata <mark>qc</mark> ataaaatacttcccttcattac
Pol_ped6	<mark>gtttttctaaaaaattatttttac<mark>g</mark>aa<mark>gtcct<b>TATAATTCTCGTATTCTTTTTAA</b>acg</mark>aaaa<mark>g</mark>tt<mark>ct</mark>gtataaata<u>acacaaaatactatttc</u>ttatt<mark>c</mark>c</mark>
Pol_ped7	t <mark>u</mark> ttttctaaaacatattttttatutauttet <mark>TATAATICTCGTATTCTTTTTTA</mark> acuaaaatcactutataaata <mark>u</mark> cataaaatacttttcttcattac
U6 ·	attcaacttatttuttttucttettttctcacAGCAATTCCCATATTCTTTTTTGaaattttuttacacutacutacaactaaacaccttacttc
U6	ctattattttatc <mark>tqtaaacatttaaaatattttt<b>TACAATTCCCATAT<u>TC</u>TTTITAAq</b>aaaatt<mark>q</mark>tacqtacaaata<mark>q</mark>tatatttaa<mark>qcaactca</mark>cttt</mark>
U1	-c <mark>uacaacu</mark> aaaatat <mark>u</mark> taatcatt <mark>u</mark> tti <mark>u</mark> aatacattt <b>TATAACTCTCATTTGGTTTGAAT</b> tttttttctataa <mark>uaautcacu</mark> tttaau <mark>caucu</mark> aaaa <mark>uc</mark>
Ŭ1	-c <mark>uacaaqq</mark> aaaatatqtaatccttqtttqaatacattt <b>AATAACTCTCATTTGG</b> TTT <b>GAAT</b> ttcttttctataa <mark>qtaqtcacq</mark> tttaa <mark>qcaqcq</mark> aaaaq <mark>c</mark>
U1	-c <mark>aacaacu</mark> acaatatactatccatutttaatttaattt <b>attatttTatAACTCTCATTTGGTTTGAAT</b> tttttttctataa <mark>u</mark> ttauuttaau <mark>ccaucu</mark> aaaau <mark>c</mark>
U1	-adacaaddatadtacuttatccttutttaaatatattt <mark>TATAACTCTCATTTGG</mark> TTTGAATttttttttctataaadtadtcacutttaadcadcuaaaadc
U1	-tatttttt <mark>cac</mark> taaacttttatccttqatatcctttcq <b>tATACTTCTCATTTAGTTGGAAA</b> aatatttqcttaaataqttcaqtttqtqatqaqaaaaqc
U1	tttc <mark>gctgaqq</mark> tatgqtttttacttqttatcctttct <mark>AAAAATTCTCATTTTGTTGGGAA</mark> aaatatttqtgtataaataqttcaqtttqtqatqaqqaaa <mark>qc</mark>
U1	-c <mark>uacaaguatantacuttateettutttaaatatattt<b>TATAACTETEATTITE</b>TTIT<mark>EATT</mark>ttttttttetataa<mark>ntanteaeut</mark>ttaa<mark>ucane</mark>naaaa<mark>ue</mark></mark>
U1	tttc <mark>gccaaaq</mark> tat <del>qqtttttacttqttactttcct<b>AaTAATTCTCATTAA</b>GTT<b>GG</b>GA<mark>A</mark>aaatatttqtqtaaaata<mark>qttcaq</mark>ttt<mark>qtqaaqaq</mark>aaaa<mark>qc</mark></del>
U1	<mark>qctacaaaq</mark> atatttttatcct <mark>qq</mark> aatttttqtcctt <b>TATAATTCTCATTTGGAG</b> ttttttcatca <mark>q</mark> aaqtaqtcaaatttqa <mark>qcaac</mark> taaaa <mark>qc</mark>
U1	tttttdcatttacaaaatataattcadttttttca <mark>AATAACTCTCATTTGGTTTACAA</mark> aactacttdtactadatttddaadtttadcogatdaaadc
U1	ataaactaaaat <mark>u</mark> ttett <mark>e</mark> qttett <mark>u</mark> taattttttaq <mark>CACAATTCTCATTATGTTTATAC</mark> atqatate <mark>eq</mark> ttaa <mark>q</mark> atttqt <mark>qeeqaaq</mark> aaa <mark>u</mark> c
U1	<mark>ataaac</mark> taaatctttttc <mark>qqtcatqqttattttttaa<b>AACAATTCTTATTCAG</b>TTTA<b>TAA</b>atqatatccqttaa<mark>q</mark>aacttaaqtttqttcaqaqaaaaq<mark>c</mark></mark>
U2	<mark>coctotttootaaaottoaaaatacttttattttct<b>ATIAATCCCATTTAGTTAGTTAGTTA</b>GCTttoctacataaotttagottt<mark>occogaataaaott</mark></mark>
U2	<mark>actttccatccctqactqaaaqqacttttattctct<b>AAGAATTCTCATTTAGTTTAGTTA</b>actttqctacataaqtaatttaqqctttqqcqqaataaaqtt</mark>
U2	tttgtttgctggactaaaaccagttgaaattttctt <b>AATAATTTCCATTCAGTTAATAT</b> ttatttatactaatatattcgagcattggtttagtt
U4 U4	totttattttttattaaacatttottottetet <mark>TATAATTCTTATTAASTTGATA</mark> Tapaaattataegotatatttaagootttoetoecaattaa
U4atac	
	adutadudattudatdattittittitatudattiininin in
U5 U5	-autogo to to the total tract and the tract and tract an
U11	ctgatatatototoctaataacaagggggttotcttCTTAATTCTCATTTAGTGTATACaagaaaggtgtaagaaaatcgaatttataatucacatttaat
U11	
U12	tctggcaacgctgataaaaadgcatgctcatatgagTAGAATTCTCATGTGCTTCACATaaatttgtgttgaagtatttggggttgttcttcgtacaattc
OrCD1	tatcatccctqqttcaacttqtacqtcacttataCACAAGTCTCATTTGTTTTACATattattaaaaatatcaactqtaaaagcaaaccqttaaaaattt
0.001	catoutous agreement and control and a second contro

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.