

Coelopa pilipes

Taxonomic lineage: Brachycera > Muscomorpha > Sciomyzoidea > Coelopidae > Coelopa

Assembly: GCA_947389925.1_idCoePili4.1_genomic

Coe_pil1 | OX376696.1:61796596-61797280 (-) | 685 nt | IncRNA: noe consensus e-value: 2.5e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.98

666C66TC66GT6CTCCACAGC66CAAGGGT6TCBAGCAGCCCCCT6GAATT6CTGTAATTAAACGATAAC6CAACAAACCAAGAT6TTTTAATTACTCTTTCCACGAAAGCAGATTATGACATTGACAAATGGTTG6AAATCAAGCAACAAAAACAAAAACAAACAAACAAACAAAGAAATATTACATTAAATGACGACCAACACATACACTATACAAATATATAAAAAATATATCGAGCGAGAGGAGGCCACAGGTTCCCCCTCCCCAGTCTGTCCTCC66GGCCCTCCTCC66TC66GT6CTG6CATG6CAAGGGATCAGGTCAG6ACACTC6TC6TCATGAGGAGAGAGAGGGGGCC66GCTCGCACGGGATC66GT66GAGGGAGCTCCTCTCAGCG6GACAAAAACGAGAAATGATTGTACACACA

T6GATATTGATATTGAAAGAGAGCTAGCTAGTTGAAAAATTAACAAATGGGTAAGCTAAAACCTGAAAGTCGTGCAATTAACAAACAGT6ACAAAGTCAAAAATATCAACATACATTTGAGACTATGTTGTTGATTTTCAATTTCAAA

66CAATTGCTTTACCG6CAATG6GCTG6AGATTGTACAAAGGTCGTG6AGATCAAAATGATCGCCCTTTTTTT

Coe_pil2 | OX376700.1:26671956-26672235 (-) | 280 nt | IncRNA: noe consensus e-value: 1.8e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 1.00

66C66TCAATGCTCCAGTACCAAC66TTGGCCACATCCC6TAATTGAGGCAAGATATACTTGTATAAGCAAACTATAAAAAAATATTTCGAATCCAAAAACAAAAACAAACAAAAACATTTCAACTGGATAAAAATAAAACCCCACTTTCTAGATCACATTCTATCCATTAAAGATCGATTGAGGTTAAGAAACGTAAAAAATTCCTCTCTCAGTTTTCGTCBAGGGGTTAATTAAATAAGATACTGTATGAAGCAAAACG6ATCGCCTGCTTTTT

| | Coe_pil1 | Coe_pil2 |
|----------|----------|----------|
| Coe_pil1 | - | 26 |
| Coe_pil2 | | - |

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.

| | | | |
|---------------|-------|--|-------|
| Coe_pil1 | ----- | tttggagcggagcttttcgctcgaactggggtcgaaTAATCCCAAGACCTTTTTcgcacccgctcaggctatttgaggatcctccgaggttcgccttc | ----- |
| Coe_pil2 | ----- | tggtctatttttagatttttttcgcgcgttcctaTAATCCCAAGAAATTTTTcgagctcgaggtcttcaaaatagagaagcatcgagacagttgca | ----- |
| Arthropod_7SK | ----- | cacaaacacagatgaattttttcttcgaatttcgaATTCGCAAGAAATTTTTCgtgaagttagtcggtacacacggccactttggcgccatatgaattgggtggactgcgtt | ----- |
| RNAse_MRP | ----- | -----agttattactcatcgccgctttaTAATCCCAATATTTTTTCgtgaagttagtcggtacacacggccactttggcgccatatgaattgggtggactgcgtt | ----- |
| U6 | ----- | gtgttggtcaggcagagcactgcgctcgccgaccttaGATTCCCAAGAACCTTTTTcggtacgacgtcggtataaagggaacagatcgagcactgacttt | ----- |
| U6 | ----- | aaadaaatttcaacgaattttctaccgctccctaaCGATTGCGAATGATTTTTTcgaacccctccgcataaaadacaatcttadaatdaacatc | ----- |
| U6 | ----- | cagtcgattttatcgtccagcgccacgcagcgcgcgataAATTGCGAAGAAATTTCTTcggtaccgcatcaggtataaagggaacagctcgagcglttgacttl | ----- |
| U6 | ----- | aaacaaactacttaattatttttaccatgtcttcacttaAATTGCGAATAACTTTTTTCgtggagtgaaataaagaacatgtgataacgattcgacatc | ----- |
| U6atac | ----- | gttttcacgcccctaataatataattatatacgttcacttaAATTCCCAATAATTTTTTCaataccgctcaataaadaaaaaataattttttctdaantc | ----- |
| tRNAsec | ----- | aaacttttgtgtgtgtgtttttctttgcttcgataAATTCCCAATAACTTTTTTCgttaacggctcattctaaaaattatgtaactggagaaacctact | ----- |
| U1 | ----- | aaacccctcgagctgggatgcccaacttgatcgccgataTAATCCCAAGTGGTTAGTgacacgagcgctcaagagcccggaactgtgctggagaagaac | ----- |
| U1 | ----- | ttonttctotatatattttcattcaatcttccttttaCAATTCCCAATTTGGTTCAATtgaadaaacacaaataaadaactcactcactaocdaadgaadac | ----- |
| U1 | ----- | cccgaattgttccggaatttcctttctattctcgcgcataAAATCCCAACCGTTTGTggaaaacgcccgtcaagagatccalltgaagcgagggaagc | ----- |
| U1 | ----- | aaacacatcgactttcattcgcccatcgtaagaacacataAATTCCCAACTGGTTGGTggaacgcgattggaagtatggaatgaagaagcgatgaagac | ----- |
| U1 | ----- | gcacatattttttcttgcctcttccgctcaacataAATTCCCACTAGGTCATGtgaattatdaattgaadaaadttttotaacagcgaaagac | ----- |
| U1 | ----- | cctcgtcatatgcttctgccttggccgctgtgcgctttgtaattcccaactGGTTCGAGGAATGGTGGCatagaaggaccttcgagggcgcggaagc | ----- |
| U1 | ----- | taacctacccttagatttagacttcgactgcctgcttattGATTCCCAACGAGTTTCTGtaactctccgctcaagaagcccgcgagggcgcggaagac | ----- |
| U2 | ----- | cccttctctaaactaaaaadattcccaatotttaCAATTCCCACTTGGTTATgaaadaadacaattcaatdaatttcctttcaocccadaaadaac | ----- |
| U2 | ----- | ttagcgcatgttcgagctgtttatgcatactgttttaAATTCCAATTTGGTTCAATtggttcggtgacatagaaggctctgtagcactttcaagtt | ----- |
| U2 | ----- | actcgagtgaggtttcattccttttcgacgggttcacAAATTCCAATGTTGTCGtaggtttttactaatctattggcttggagcacttccagtt | ----- |
| U2 | ----- | gcacgaatattttatatattcatccacacttccgcataGATTCCCAACTGGTTGGAAGcaataatdaacatatataatctataaagacgtttcaott | ----- |
| U2 | ----- | tgagtcactactggcatttactaatctgttgcctgcgataGATTCCCAACTGGTTCTGtcatttgcgatatagagaccccgcaacctctgtaact | ----- |
| U3 | ----- | ttctataaatgaattcataccgtacgtattatgcttgaTAATCCCAATCGGTTTGTgttcgcgcgctctcttaggttggtctgtggggagccagaattt | ----- |
| U3 | ----- | ttatadacacacacgttctttcctccacacgtccataAATTCCAAATGGTTGAAGcaaatccatctcatotatdaatctttccacacdaaaatt | ----- |
| U3 | ----- | tttcagacacattttcattaccacgcgcagggcttgTAATTCCAATTTGGTTGTCgacggctgtcttaggttggtctgtatggggtatgaaatt | ----- |
| U3 | ----- | ttctattgtatgattccaccgatatggggttaacttgaATTGCGATGTTGTTATgaaattgttctgaagaagctgtctgtgtctatggggaatt | ----- |
| U4 | ----- | tcctttttatatattttccacatttttgaattttccataAATTCCAATTCGGTTGGTTTcaaaattttaaacttaaaodactcaotttaantaaatcatc | ----- |
| U4 | ----- | ttcgctactcgagctgcagttttttcttcgcggctcgataAATTCCAACAAAGTTGGTCacttcgcgcgctcttagtgccagactccgggtgagtcgtc | ----- |
| U5 | ----- | aaacttgctgactgcctgcacaaattggtataactcgtataGATTCCCAATTATGTTTTGcctaattgtctcaagtataaccttatgatagtttagtcagttc | ----- |
| U5 | ----- | acaacatafatototodaatatttttaattctttttgaacataGATTCCCAACAGGTTTATtgaacdaaattttadaaadtctctatdaaadtadaaag | ----- |
| U5 | ----- | atcagataaagaattgtttatgcaggttcagcagataAATTCCACTTGGTTGCTAaaacgatgaacatgaacaggtgttttaggttgggaat | ----- |
| U11 | ----- | catccgattgcttgccatgctgtcgtggttcgataAATTCCAATTTGGTTGGTgcaacgcgggttcattgctgcttgaagggtctgtgaggttc | ----- |
| U12 | ----- | cttaatttccttttttactttccatccaacctcaaaTAATTCCAAAATGGTTTACAcaaataccctatattcaottcacactdaocccaodcaatttc | ----- |
| OrCD1 | ----- | tttttcgcttatgcttctcgtttgtccataGATTCCCAACCGGTTGATGagattcgtcgacagaagagacttgggttgggtgctgagttgttcgaaa | ----- |

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.