Chrysopilus asiliformis

Taxonomic lineage: Brachycera > Tabanomorpha > Tabanoidea > Rhagionidae > Chrysopilus

Assembly: GCA_964034945.1_idChrAsil3.1_genomic

Chr_asi1 | OZ035962.1:27873585-27873814 (-) | 230 nt | lncRNA:noe consensus e-value: 1.7e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.81

```
GGCGGTCCGGTGTTTCGCAGTTGAACGGTTAGTTACAACCCGCAATTGTACGGAAATCCAAGAGTCGATATAATCATATTAAGCTCCTATATATAAAAAGCAAAAAAAAAAGAAATAAATGAAAATCTTGTCTGTTCTATTGTTCGGACT
TTAAAAATCAAAGCTCTATCCATAATTCGTCTTGATTAGAGGGCAAAGTTTACTGTGAGACGAATTTGATCGCCTTTTTT
```

```
Chr_asi1          -------ttgacgtaaaaagctacacgatttgaattaaaTATAATTCGCAGCGCGTAGAaaacttgattgattaatatatataaaagtttttagccgtcgcaattt
Arthropod_7SK     ------gcttttgctaaccctcaacttcgttcgtttccaTATAATTCGCGAGCAAGCAAaaattcctcacttactatataagaaagtttcaaagcacactgcctc-
U6                ------gacaaacacccagatgaacttttgttgactccagTATAGTTCGCATTTGAGAAActtagtcaaagttgaatatatataccagttccaaagtttaacactc-
U6atac            ------cgtagtgtaagtttgtgcagctttgtgttttagTATAGTTCGCATATTGTATAtctgttttgaccaatgtatatatacgaatttaaagacagtccagctt-
tRNAsec           -----agtgtggttcggagattcgatatttgaattgtgctTATAATTCACATATGTGGAAaattttcacgcttagtatatatagaaattcaacaaagcttccgtt--
snoRNAMe18SA1806  ------tttttgaaaacatttgtagtgtttcattctgcgaAATAATTCGCATGTTTAAGAatctttttcgataggtatatatacaatcccaaaatagaacagctgc-
U1                --agttgtcctatccagcgttgctttttttccattccctTATAATTCACCCATAAACAGtgcaatcggagtataaatagtcagcttcggaccaaagaattc-----
U1                --agttgttggtattctgcgttgattgttttccactcgctTATAGTTCACACAAAAACAGcgtaattgaagtataaatagtcagcttcggaccaaggaattc-----
U2                --tgactcacgcgtttggtatagaattctttcccctcgtaCATAATTCGCTTACAAACAGagacaacccagtataaataacaaattcagtgcttggttcggt-----
U2                --tgaataatgcgtttttgtatagaaatttttatattcgttTATAATTCGCTTACAAACTGcgaatacggagtataaataagcaaatgcaggatttgttccggt-----
U2                --tgactcacgcgtttggtatagaaatttttcccctcgttCATAATTCGCTTACAAACAGcgagaacccagtataaataacaaattcagtgcttggttcggt-----
U3                ---atgtgatttttttaaagaacattttcgccgtcgatTATAATTCACACAGAAACAGcaaaatcgtcgtataaatacctcggtcagtgctagtggagggc----
U3                ---aatacagaaattgcccatacaattgtttgcctttcttTATAATTCACACATAAACAGcaaaatcgtcgtataaatacctcggtcagtgctagtgcaaggt----
U4                ---taaagccataaatctcctatgtaaatttccttcaatTATAATTCGCACATGTTCTGggactatcggggtataaagtcttttcgaacgatgatcgtc----
U4atac            acattccataaaacattatattccaaaaatctccttcgctTATAATTCGTACATGGTCTGcacaatcgtggtataaaaggtcagctggaagctggttgag-------
U5                tctacttgtatttatatacaagcggttttttcgctcaaaTGTAATTCGCATATGGTCTGcgaaatcgaggtttaaatagcttaggctcgcttggtagca-------
U5                -actgccaacaaaagtccatatcaaatatttccctcgttCATAATTCGCACGTATTTAGcaacattgtagtataaatacctcggttcaggttgtgtttgg------
U5                -actggccaacaaaagtccatatcaaataattccctcgttCATAATTCGCATAGGTTTAGcaacattgtagtataaatacctcggttcaggttgtgtttgg------
U12               ---gtagtaataaaatgctttaaatttttttccttcaaaTACAATTCGCACATAAACAGcaatctcccagtataaataggtaagctttagtggaaagaattc----
```

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.