

Paragus haemorrhous

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Paragus > Pandasyophthalmus

Assembly: GCA_965637125.1_idParHaem1.hap1.1_genomic

Par_hae1 | OZ280903.1:126515921-126516223 (-) | 303 nt | lncRNA: noe consensus e-value: 2.0e-09

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

666CGGTTGCTTGCCTCACAGTTGATACGGTTGACTACATTCCGTTCCCAAAATGTGATGATCTAAATCGTATGCTTTGACATCCATACAAAAATGACAACTAGAAAAAACACTGCAAAATGTGTTTGAGAAATAAAATATAAGTTT
CACCACAAAAACAAGCAAAAAACAACGCAAAACAAATCTCTCCCTCTATCGTATAAGATATCTATAATATAGAAATTAAGCCAATTCAATAAAAATGAGATAAAAATATCTATCAAAAAATGATATCTGCTGAGGTAGGTGTGATCGCCTT TTT

```
Par_hae1 -----gaacttaccatttotaagtaaatcatatcaaoTACAATTACAGAAATTAattcttcaotacattotacataatdaaatlccatcaccacaatcatc-----
RNase_MRP -----ttgtttgaattgtttttatctgtTACAATTCACAGAAATGTTTTcatcgtttgtcgaagcttatatacaaacgaattttataatadggcagtagttgc
U6 -----taataaaaaatttggttaggttaataatgcgaattcaTATAGTTACAGAAATTTgtttactacatatgtgaatttaagtaaaaaacttaaacatgtattttc
U6 -----atacttaaatatttcaatatttttttgaataaaTATAATTCCAGCAATTTatttcaaaacacatgaataaagttatdaaaattatccatatacaatt
U6 -----aatlccaaactatttcaatttctttttgacttaaaTATAATTCCAGAAATTTatttcaagaagacatgagaataaagttttcaaatlcaaccatacttc
U6 -----actacattttttaaaccctgataatagcaataataatcgttaTATAATTCCAGAAATTTattttaaagaataattagaataaaattatgaatagtttaac-----
U6atac -----taotadaactatatacaatttttttattattctTATAATTCCAGAAATTTttctcadcacccaatttatatacaaaaaaaaataaadttdtattt
tRNAsec -----caatcaatcgttaagttgatcaatgtttacttgttgaTATAGTTACAGAAATTTtttctgtaaatgttctaaacacatcaacatcttctagtggatcc
U1 -----gggtgttaaatattatattttatatttagtggttaTATAGTTACAGAAATTTgtttactgcaaaaatgataaaggtcaaatattatgttagaaaagc
U1 -----caaacacaactatcacatctttttatcttttactttTATAGTTACAGAAATTTatttcaaaaaaatttactataaannnnacdaaacgaatttaac
U1 -----cgactaggcgtgttttaggttttttttaaatcttctTATAATTCCAGAAATTTatttgcacaaaattttgtatagtttgaagaagtggaattttaagc
U1 -----gtctgtttttgcagggtattttttcttctgttttaTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----tgatgtttttccctgaagggtttttttcttctgttttaTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----tttttttttatttagadcaatttttcaatttttaTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----caacaaaaagggtatgtttatttttttttgaagcttTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----attttctacagacagatatttttactttttttttTATAGTTACAGAAATTTatttcaaaaaaatttataagatatagtgaaaaatccggttatagc
U1 -----caatcctatgatttgaatttttttcaattctTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----gtctgtttttgcagggtattttttcttctgttttaTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----tcccgtgcatggcaattgttttttatttctgtttttTACAATTCCAGAAATTTatttcaaaaaaatttataagatatagtgaaaaatccggttatagc
U1 -----atctcttttccctcaaaaattttttctctctctTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----gtcttttcttccctcaagggtattttttcttctgtttttTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U1 -----tctttctacagacagatatttttactttttttttTATAATTCCAGAAATTTatttcaaaaaaatttataagatatagtgaaaaatccggttatagc
U2 -----tttttttatcgcatttttttgaatttttttttTATAATTCCAGAAATTTatttcaaaaaaatttataagatatagtgaaaaatccggttatagc
U2 -----acacagaatacaaggctatttttaagggtttgtctgattTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U2 -----aatatfaattccaataadatttttcttcttcaataTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U3 -----aatlcaatttgcacagatcttccatcgtttctcttaTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U3 -----tgaatgaatttcaagaagatctttttactgttcttTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U3 -----tgaattttaaaaataatttttttcttctcttTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U4 -----tgaatgaatttcaagaagatctttttactgttcttTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U4 -----gggttgatgttctatgatacttttttcaattgtattctTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U4atac -----tttttcaaaactttttdttadcaatttttcttcttTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U5 -----ctattttgatttctactacaaattttaaagttcatltaTACAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U5 -----cttgcgaattgatactgattttttttagtttttagttttTACAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U5 -----attacacatccatataaatttttttcttcttctTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U5 -----aaagtgaataacacgggacattttttgattttacagtttaTACAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U5 -----ttaagactttttttgcatatttttcatatttcaaaaaTATAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U11 -----ttcaotdottttaaataattttacaattttdttttctTATAGTTACAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
U12 -----ggttagcatgacatagaattttttcacttcagtttcatTACAATTCCAGAAATTTgttgcataaataattataagatatagtgaaaaatccggttatagc
```

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.