

Physocephala rufipes

Taxonomic lineage: Brachycera > Muscomorpha > Conopoidea > Conopidae > Physocephala

Assembly: GCA_963966595.1_idPhyRufi1.1_genomic

Phy_ruf1 | OZ016502.1:38018776-38019667 (+) | 892 nt | lncRNA: noe consensus e-value: 1.2e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.90

666c66tCGAAAAATGCCAGATTGTGAGGTTGATCGCATCCCCTTCCAAAAATTGCGACCCGAAACAACAACACAAAGTCTCAGTTTCTATGAAAAATTAATGAAATGCGCCCAAGCTCTTCAGTTGTGTGTGTGAGCCTTTCTTTCC

TCCCCACAACAACCCCAACCCCAATCAAAAAAAGGGAAGGGGAAAGAAAGGAGCAAGCATATAAGCGAAAAAGCAATAAACGCAAAATACGAAAAACAACAAAAATAACATCTATGATTTCCTTCTCATCGTCTTTTGAATGAAA

GATATACBATACTGAATGTTGATGAAAAAGAAAAAGACGACTAGAAAAACAACAAACCACCAACAACAACAACCAACCAACCCCTACAACAACAACGACACGAGAAAAAAGGAGGGTGGAGGACATTCCCTTTAAGCGGTGTTTGC

TGGGATGTCCCTTGGACATCTTAACAGACGACBATACTAAAAATTGTGCTCTCCTGTCTTACTGTGCTGCTATATGTACAGTGTATAGACACACAGAAAAACAACAACAAAAACAATTTCTCTCACTTAACAAACAACAACAAAA

CAACTGGAAACAATGAAAAAACAACATAAAAAATTCBATCBATCGTTTCATATCATTAAACGTGTTAAACGTGTATGCGACAGATTTCGCGAGCCAGTTGGAAAAAATTAAACAACGAAAAACBAAATCAATAAAAAATCGAAAAA

TGAATTCAAAAAATCGGGAACCTTTAGACACACTAATCAAAATGAAATCAACACACBACACTTAAAGAAACGAAACACATGTTCATGTCTCAATACTGTGGTGTGTGATCAGGAGTATTTGATCTGTGATCGCCACTTTTTT

Phy_ruf1	-----	taaacattttccttctcgtttcattcttcattatcctttAAAAATCATAATAATTTTTTccatctgataaccctataaaggataaacatccaaagtgaqcgctacc
Arthropod_7SK	-----	aaaaaccacaacaattgtgttcattttcaattttATAAATTCATAATAATTTATTtgccttaagtgaagataaaatcgtggtcaagaacgtcttgatttc
U6	-----	attcaagttaataaccttttttcttaaaotcatccttGTAATTCATAATAAATTTTCTccaaataaocotatatotaaotattctaatotcccaattc
U6	-----	aattcataataaaattttacttcaattgctcaggtTATAATTCATAGTTAGTTTTTccgattgaatgdcataaaattgaaaatttgaaaacgtacatttc
U6atac	-----	tgtaaagataaaaatgacaatagatttttagttgattTATAATTCATAAATTTTTTcgaattatggaataaagatttcgaatttcacactgaactcgc
U1	---	tcagaatattctttcattcttcttcaadaattcttTATAATTACAGAAATGGTTTTGgaadaaataatttgaataattdaatdgaadgaaccccaaaagc
U1	---	cacagcaagaatatttcacattctttatattcaacgtTATAATTACACAATGTTTTATGgaataatattggaagagatacactgcgaacgaagaaagc
U1	ttgcaatgcaataataattttaagcgaatgcatttgcattTAGAATTCACACTATGTTTAGagcataacgcgtttaagatttatgttttgaagcaagcct	
U2	-----	gagaacacatttttgccttgcgctcatgaaatctcATAAATTCACATCTGGTTTTATTgacttttgtttatataacctctgcatcagcggtgaaaagt
U2	-----	cttodaacaacaattttcatttaccattotataataacaaTATAATTACATCAGGTTTTTAATtttttcttaoctaatatacctctcatttaoctaototaott
U3	-----	tagacctgttgcgtatattatttagttttcagttctTATAATTACAAATATGTTTAAaagtttgaagttttgtagaacatggtgaataacggaaagtt
U3	-----	ataaaggcataatgataattaggttttaaaatcttTATAATTACATATATGTTTAAcagagtttgaagatttgcacagcataaaggaaggttaaaagtt
U4	-----	gaotaaagccacttttttcttaatatataaataccaTATAATTACACAGGGTTTTAGaaaaaatttgaatttaaaagaaatttttaotttcataactc
U4	-----	tttgaagcttttcattaaacaaaaatttgcgaatgctTATAATTACAAATCACTTTATTTTcaaaaagacacgaaggaagaaacatttgactactggt
U4atac	-----	tttttgcgaatttttgcggtattttaatttttctcgaTACAATTCATATAGGGTTTAAGtaaatgagccgtaaaaccagcaagaacatttgactcg
U5	-----	ggaaatotttcaatttttcttttcaattatadotcttaTAAATTCACGAGCGGTTTAATcotaatttotaacdaatductttttotcotootttat
U11	-----	attttgctcgttagcaattttgtagttgatttgcataTAATTCATAAAGTTTAAGtgaactagattttatatctccgacctagagaaggtttttat
U12	-----	cacctaatataattacataataatttgcagcaTACAATTCATACGGTTTAATatgaattacgtttaaagtacctcgcaaatacgtattacagctc

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.