

Zaprionus megalorchis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Zaprionus > Zaprionus subgenus Zaprionus > armatus group > vittiger subgroup

Assembly: GCA_051940805.1_ASM5194080v1_genomic

Zap_meg1 | JBNRRO010000750.1:1018422-1019876 (+) | 1455 nt | lncRNA: noe consensus e-value: 1e-167

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.92

GGGGCGGTGCTGATTCAGCAGTAACGACGGTTGGGCACATCCCGTCTACCCCTCAGCTGAAATTTGTGCTGCTAGGGGCAGACGTTTGAATAAAGAGAGAGGAGCAACAACAACAACAACAACAACATACACAAGAGGAGGAGGAG
TTTAGCAAAATTTTCGTCATATTTCTGAAAGCAAAAAGCAAAAGCBAAGCBAAGGCAAGCAAAAGCAGACGAAAGCAAAAAGCTTTTACAAAGCAGGACCAACAACAACAAGTGGATGCAACTAGTCTGCTGCGCTTCCBCAAAAATGC
TCCAAACACBAACAACATAAATGABAAAGCACAAGAGCAAAAACATATATAAACCACTATAAAACAAAGAAACCAACAACAAGCTTAAACACAGAAATCACBAACACCAATGATAAAAAACCAAGACAAAAACAAATATCAGA
CCAACTCBAATATCAATGCAACCAAAAAAATATATAAACCACTATAAATACACTAAAAAACCAACAACAGAAACATGAGGAAAAACCAACAACACTAAATGTGACCTAGTAGTTAAATATGAGATCATCTGTTTATATCAGAGC
AAAAATGAAGAAAGAAAAACTCTGAAAAAAAGCCAAAAAAACATTAAAAACTGCAAAAACTGCATTGGTGTGTGTGCTCCCGTTCGTGTATATCBCTGGCGCCGCCATAAAGTGAACGGCATCACGGCCCTGGAGGTGCGCTGGAAA
AGGGAGCTCGGGGCTACGAGGGCTCTTTGGAAGGCGGGTTTATATATCAGCATTATAAATCCAGCTTTATCAACAACATATAACATCACAACTACAACTGCGCTACTACTACAGGAACCCATATGAGTGGAGGGGCAAACTCTGAGCA
AGGTABAAACATCTCGAACATAAAATGCTCTCAGCCCTCAGTCTGCATATGCACTCAACCCAGCCCGCCGCGCTCGGTGTGCGGGTACGGCACTGCCCCGCACTCCCTATCTCTAATGTGTGTGAGGAGGCAAGGCTGTGTGAGT
GTGTGCAACACACACATCCCTGGTGTGTGCACATATGGAACCGCATATCGTGTGACCGCTCCCTGTGTGTAGCTAGTTGTATCCAGCCAGGCCCAAGCCCGGTGGGACGCTTGGCGCGCCCTCCATGGCGCTCCACAAAAAATACCC
ATAGAGACGTTTAAAGCAATCTAAATGAGCAAAAAATATAAACCAAAAAAAGCAAAAGCAACAATTTGTGACGABAGAAAAACAATGAATCCAAAAAATAATGAGCAATATGAGCAACATCTATATATGCAAAAAAGCAAAAAAC
AAAAATGCAAAATACBACACACACCTTCGAAAAAGACCTCAGTATAATACAGTAATGCTGGGTGCTGCAAAAGAAATGCTTTGCTGTATCGCCCCTTTTTTT

Zap_meg1 -----ggagaaagctgcagcaggttgcacttggccgccttGTAATTCGCAAGTTGCAAGTTGctgggaattgtggcataaaatccagttgcccaagatgttgcatt-----
Arthropod_7SK -----ccctgttttttcttacttatttccaaatctcctGTAATTCGCAAGTTGCTTATTCcctadattcttgaatataaatacaaatgcttgaatataatctc-----
RNase_MRP -----ctgctatgggcatcttctactgctgtctTAAATTCGCAAGTTGTTTTTggcacgttgcctgtataaataagcgagagctcgcgagacgttcaggccgctt-----
U6 -----agggtaggtacgggcagaaacagccactcgctgtTATAATTCGCAAGTTGTTTTTgcactggtcttcagtataaatagcagacttttatctgtagtcttc-----
U6 -----TaccgaatggttgccttttccaaatgaatttctTATAATTCGCAAGTTGTTTTTccttcttctacttttaataatgacataacccctcgaacttc-----
U6 -----gccccctgattgctgttttaccgtgctctctTATAATTCGCAAGTTGTTTTTgcgacgtgattcgcataaataagctcattgtcaggaattctc-----
U6atac -----ttatttagcattccacttttctgttttccgctTGAATTCGCAAGTTGTTATTCcttcaatcgtcagataaaatgagcagaaagcgcatgtgtttttt-----
tRNAsec -----atccaaagaatcadatttgaatttcttctcctTGAATTCGCAAGTTGCAATTTodcaatctcatttttaaaacgaaccttttatcttadgaacag-----
snoRNA18SA1806 -----atagattgatttgccttcttgcgacaacaattcgtTATAATTCGCAAGTTGTTATTCggtggcaacgctctataaataaacagttgtcaaaaaaccacg-----
U1 -----ttatgctgtgaagaatactgcacgttccactcgctgtTATAATTCGCAAGTTGTTCTAGcagccttctctggtatgctgttccagagcgaaaggaagc-----
U1 -----tatctcaatggttcttcttcttcccaaatctctTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U1 -----tgcaacttctcagttgtttttagttgtgaccTAAGAGTTCTCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U1 -----tagtagttggcctgcattttgagttgtattgcggtTCAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U2 -----caatgccctccatataactatatttaaaattctctTGAATTCGCAAGTTGTTCTAGcctctctcattgaatctcgaattttggtctgaatgtt-----
U2 -----tttctttagaacgatgtttctgcacagcttctctTGAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U3 -----cccttctctcacaatttttccatttgaatctTATAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U3 -----gtttgtgctcatttatttctcgtttgtgctTATAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U3 -----tttgggtcactattttatctcgtttgtgctTATAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U3 -----atccaatataattttcttcttcttcttTATAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U4 -----gtttgtgctcatttatttctcgtttgtgctTATAATTCGCAAGTTGTTCTAGcctctcattgaatctcgaattttggtctgaatgtt-----
U4 -----aaacgtttgctggtcattttctggtgctcactTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U4 -----cctgtgtgcttgaattttcttaaatatttccattTGAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U4atac -----gatcaatgatacaacgcattttttcaatttttgcctTGAATTCGCAAGTTGTTCTAGcctcattgaatctcgaattttggtctgaatgtt-----
U5 -----actttadggttccacatcccaactccacactcattTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U5 -----atgtgctctccaggggtgttcttctactcaagcgtTATAATTCGCAAGTTGTTCTAGcctcattgaatctcgaattttggtctgaatgtt-----
U5 -----actataggggttgccttgccttctgtaggactctTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U5 -----cagcaacatcaaaaaatttttaacatttcttTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U5 -----gacattcgcagtcgacttaaatgtctcttgcacactTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U5 -----tctcagacgttgccttcttcttgcacactcagcactTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U5 -----ctttaggggttgcacatgcgcaactccgactcattTATAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U7 -----tacacagtttttccacatttctccttGTAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U11 -----aatggcaagatctcataatttgcgaagcttgcactAGCAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
U12 -----ggccacagtttgaattttgacacatttcaacctCGAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----
OrCD1 -----tagcagacagcttctatttctcattacgccaacacTAGAATTCGCAAGTTGTTCTAGcagcagatgataaacccttgaatgaatgaataaagc-----

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.