

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

Assembly: GCA_018903425.1_ASM1890342v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 9nt PSE: 0.95

[illegible]

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Zap_nig1      -----tatggaagcgcagacaggtttcactttgccccccttgtaattccaagtgcacgtttgcggatgtatgataaaaaacacattgccacaagaatttgacac
Arthropod_75K -----caccctgttactttcttccctttccaaatctctgtataattcccaagtcgtatttccacatcttaadatatataaacaacattcttccaaatattatctc
RNAse_MRP      -----taccacgggcattttcactttctgtctataaattcccaagttgttttgcgcagcttgggcgtatataaatagacagctctgcagagagccatcagcgccgtt
U6            -----ctctctatcatgtttctgttttaccacagacattctataattcccaagttgtgtttgcacagttacagttataaataagctcattgttcaaacacattctc
U6            -----caccacaaaataaagccttttttttaataataatctaccgtataattcccaagtcgttttttccctctctcacatttaaatatccacataatcttaaacatctc
U6            -----aagggacacaaacattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U6            -----gttttaggcattctcattctctgtttattccctgtataattcccaagttgttttttaccacagggcgtatataaataaacgcgaattggccacaagcttt
tRNAse3       -aggcctctgggataaanaacacatttggattttgtctcttggaattcccaagtgccaatttgcacatctctctctctctctctctctctctctctctctctctc
snRNome18S186 -atagatcgttttccctctctatagtcacaaatttgttataaattcccaactgcttcccaactgttccggccagcgcgtatataaacacagttgtataaacgcgcga
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U1            -----catatcaatttttaccacagagatattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U1            -----ttgatcacttttttttgaaattttcagttttgtctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
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U1            -----gagtagtttggccctctcatatctcaactgtctataaagcctataattcccaactgagttctgcacacagatttgtggaatgacgtgtccagagctgcagagaac
U1            -----caataggggttttttttttttttttaccacagagatcattctataattcccaactggtttctacgtgcgcacagatattgaaaccccccttagctgactgcagaaaaac
U2            -----tccccaataaagaaatttttttccacgcgtttttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U2            -----atgcctgttttttaccacagagatattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
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U2            -----aaatcaaaaaaatacattagggcataaaaaattctataaaaaattcttcaaaattggtttctacgtgcgcacagatttgtggaatgacgtgtccagagctgcagagaac
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U2            -----cgaatcatctctcaaaaaatttttaccacacacccctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
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U2            -----gcatgtatgaaacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttacc
U3            -----ctctctctctacatatttttttaccatttaaatctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U3            -----gagcaatgatatattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U3            -----agcagtagtatcatctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U3            -----aaacctcttacttattttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U3            -----cccaagatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatt
U4            -----ctctgtgacttgaagtttcttcttaaatatttttaccataatttcccaaaattttttaaaccatgcaaaatattactacacagaatttttccaaatttctgaattctagc
U4            -----cgatcaatgatctgaaacgttttttaccattttgtctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U4atatic      -tctctacccctttaccatctccaaaattcttaccattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U5            -----taggggttgactctgtgaaattctgaactcatgtttgtttataattccgaatcagtttaccagaaattcaattagggctgactctctctctctctctctc
U5            -----tctctaataggttctctatttttgcacgtcccccctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U5            -----ttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U5            -----acttttggttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatttttaccacaaaatt
U5            -----acagtgcagctggattttaccacagtttttttgcattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U5            -----taacttttggggtttccacatctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U5            -----tctctcttttaaggtttgtatttttgcacaaagcgcgtttataattcccaaccatgctacacgttggaatgactaggtttgaaactctctctctctctctc
U5            -----caacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacac
U11          -----ttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U11          -----atgggaaacattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U11          -----gcgcagcagcttgaaatttttgagatcattctacccctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctc
U11          -----taccagcacagctcttaattctctatgcccaattctataacttcccaactgcgtttaccggccacagtagtaaaatctgattgtctgtctgtggccgtgtg
ORC1         -----

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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.