

# Zaprionus indianus

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

**Assembly:** GCA\_043643915.1\_UR\_Zind\_1.0\_genomic

**Zap\_ind1 | JAU1ZU010000004.1:17300835-17302236 (-) | 1402 nt | IncRNA: noe consensus e-value: 1e-176**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.96

GGGGCGGTCSTGCATTCCGCACTAACCGCTTGGACACATCCGCTCTACCTCCTCTGAAATGTGTCCGTGCGAGGGGCGAGCTTTAAAAAATAAGAGAGAGGAACAACAACTACACAAGGAGGAGGATTAGCAAAATTTCTGTCATATTCTGGAAGCAAAACAAATTTGCAACBCAAAGCGAGCGAAAGGCAAGCTAAGCAGACAAAGCAAAAGCTTTTGCAAAGCGAGGCCAACACAGCAAGATGGATGCAACTAGTCTGCTCCBCTTGGCCGAAATGCTGCATTCAAAACATBAAGAAAGACACAAAGACAAACATATATAAACAACTATAAAACAAAGAAACAAACAAACAAAGACTTAAAGCAAGAAATACGAAACBCAATGATAAAAACGAAAGACAAACAAATATCAGACCAATCGAATATCATGCAAAACAAAAACCTATAAAACACATAAAAACAAATGAAATGAAGAGGAAACAAACACAACTAAATGTGACCTAGTAGTTAAATGAAGATCATCATCGTGTATATCAGGACAAATBAAGAAACCTGCAAAAGGCCAAAAAACAATTAAGAACTGCAAAACATGCAATGGTGTGTGTGTCGCGCTTCBTGTATACGCTGGCCGCBCCACTAAAAATGACGGCATCACGGCCCTGGAGGCCGCTGGAAAGAGGAGCTCGGGCTAGAGGGCTCTTCGGGGGCGGGGTTGTATATCAGCATTATGAATCCAGCCATCTATAATACATAACATCAAACTACAACGGCTACTACTACAGGAACCCATATGACCCAGAGGGGGTGGACTCCTTCTGAGCAGATAGAACATCTACAACATATAATGCTCTTAGCCCCCTCACTGCATATGACGCTCAACCCAGCCGCGCGCTCGGTGTGCGGGCGGGGCTTCCTGCTCCTTAGTGTTCAGGACGAGGAGGCTTCCTGAGCATGTGCACACCCCAACATCCTGGTGGCATGTGGAAACCGCATATCCTGTGTCCGGTCACTGTGCTAGCTAGTGTATCCAGCCAGGCCAGCCGCTGGGACGCTTGGCCGGCCCTCCATGGCGCTCCACAAAAAATAACCATAGAGACGTTTAAAGCAAAATCTAAATGAGCAAAAGTATATAACCAAAAAACAAAGCGCAACATTTGACGAGAGAAACAAATGAATCCAAAAAATATGAGCAATATGAGCAACATACTATATGGCAAAAAACAAAAACGAAAAATGCAAAATACGACACACACAGCTTCGAAAAAGACCTAGTATATATCATATATGCTGGGTGCAAAAGAAATGCCCTTCCTGTATCGCCCTTTTCTT

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Zap_ind1      -----aatggaagactgcagcaggttcacatttccaggttgaattctcaagtgcagttcgtggagttgtgcataaaaaacagttgccacacgatgttgca-----
Arthropod_7SK  -----ccctgttttttcttactcttttaaatatctctgtaattcccaactgccttatttcaatctatctgaatataaatcaaacctatgttaatatctc-----
RNase_MRP     -----actacggacgttttcacgtctgctgtcttaaaatcccaagtatgttttggcctgttgagcgcataaatagcaacagctcgccgaacggtcaggccgtt-----
U6            -----gcaactcagctacctaaggggtgggtacagtcgaattataattcccaactgtttatttggctgacgcctgtataaaaaccaactttgctgatctagtctct-----
U6            -----tgaacaaadatatgcctatttttaataaatttcttacaattcccaactgccccttttcaactctcttacttotaatagcacaatttcttadaacttct-----
U6            -----cgggttcacctgtgagttgagttgagttgagttcttataattctcaagtgttcttgcgaatgattcagatttaaatgctatttgcgtgcacctc-----
U6atac        -----ttataaagcattccacatttgcgcttctgcttgaattcccaagtgtgtatttttcaaaatcccgataaaaataagcgaacggaacttagcattt-----
tRNAsec       -----cttgaataaagccadatttgaatttattctcattggaattcccaagtggcaatttgaatataatcttataaaacaaactatttaataaagaaatgaac-----
snoRNA18SA1806  -----agtagatttttgccttatagtagcaacaggttcttaaaatcccaactgtttatttgcctggcactgcgcataaaatagctttatttaaaccaatgcagg-----
U1            -----tgcataatctggggcatttttcaacagagttcccttataattctcaaaaggttctggcagcagtgatgcgaacccctagccagagcggaagaaagc-----
U1            -----ttdatgttcccttgcacaactaacttgaadgaatcttcaaaatcccaactgcttgcacccagatcttgaatgcttctccagaaacaaadgaagc-----
U1            -----ctcgcctgtagggaaacttttcaggttgccttgccttataattcccaactggttctgacccagatcttgaatgcttctccagaaacaaadgaagc-----
U2            -----tttgatagttacgcttcaattttacacatcagcgtgttttaattctcaactgggttctagcagtaagcagtatggatgctcgaagtgtgggttacagtt-----
U2            -----aacdatattacccctacacattttacacatcagcgtgttttaattctcaactgggttctagcagtaagcagtatggatgctcgaagtgtgggttacagtt-----
U2            -----acagttatgcttcaggaaacgttttcaccagtggtctcaattctcaactgggttctagcagtaagcagtatggatgctcgaagtgtgggttacagtt-----
U3            -----cagcagtaactaaattcttttgcatttgccttataattctcaactgggttctggttgcgtggtgagaggtgtgttttggcgttggaagatt-----
U3            -----ctcttcttcttccatcttttgcacatttcaacttcttataattctcaactgggttctggttgcgtggtgagaggtgtgttttggcgttggaagatt-----
U3            -----cggcagcgtctatgttcttcttgccttgccttataattctcaactgggttctggttgcgtggtgagaggtgtgttttggcgttggaagatt-----
U4            -----tagattagcttgccttcttgcacatttgcagtgcgaattcccaatttttataagctcatalacaaggtaaacctacaattataaattctggtt-----
U4            -----aaaacttcttctacatttttcatatgtatctcattataattcccaactggttctagcagccacaaactgaadgaatccttcttcttcttctacatt-----
U4            -----acagcaacccttggaagttcttaaatctttcccaataattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U4atac        gatcaatgatcataaagcgtttttcccatcttttgccttgcgaattctcaactggtttaaagcgttttatacttgcctgagtgccgcatgaatccaacgactc-----
U5            -----cccttgaadtttccacattcccaatttcccaactcatttataattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U5            -----actttagggttgcgcagctcttactctgtatgatatcttataattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U5            -----aaaactgaaaatattatttctcagcagcttgcatttataattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U5            -----aagaaactcattaaaatattttataacttttccacttataattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U5            -----ttccctctttaaaggtgattcttcaagtgctgccacttacaattccgaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U5            -----tctttccaaacttacttcttattttcaaccccttctacttataattctcaattgagttcaagcgcagcgcctgttaaggttggttcttcccttgcaaaa-----
U7            -----acacatttttacacatttcttgaatttcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U11           atgggaagattcattatttgcgaagcttgcacgaattcccaactggtttaaagcgaatgaagcattttatgccaagttttcttaagttcagtag-----
U12           ggcagcatttgaatttgcacatttgcaccccttcaacttcaacttgcacccactcagctgcgcgattcgcctgacagaaatt-----
OrCD1        tagcagcagctcttacttcttcatagcgaacacatagaattcccaattggttctagctgcgacgttaggaagattaatagagtgctgttagcaagtg-----
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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, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.