

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Zaprionus > Anaprionus

Assembly: GCA_037044475.1_ASM3704447v1_genomic

Zap_obs1 | JBAMBR010006508.1:11401-11814 (+) | 414 nt | lncRNA: noe consensus e-value: 6.6e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.89

GGGCGGTCGATGGCTCACAGTTATAAAGGGTTGTACACATCCCAGTAAATTGTGTCACTGGGTGGGTCGGGTTTAAATGCATAGTCAATAGTAAAAATTTCAAAATTTAAAGATAAAGTTTGCAATAAATGTAGCTTAAAGAAATATATAGTAGTAGTAAAGTAACTAGTAAAGAAAAATAAAATAGTTCCCATCGCAAAATAGATTATATAGTCAAGTGGAAACACBCTGCACACCAAGCAAGATAAGAAAAAGCABCCAAAAAGAAAAAGGAAAGTCATAGTTCAATCCACCTAAGATATAGTAATATAAAGGGTGGCAGGTTGGGGTATATGTGTGGAAATAAAATCAATGTAGGCAAGCAAGGCTGGGAAGATAAAATCAACGGTTAATCAAAAGTACGCCTAAATTTTTTTTTT

Zap_obs2 | JBAMBR010002046.1:51287-51693 (+) | 407 nt | lncRNA: no consensus e-value: 4.4e-08

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.89

5GGGCGGTCGATGGCTCACAGTTATAAAGGGTTGTACACATCCCGCGATTAATGTGGGTATATATGTGGGTCGGGGGTAGATAATTAATTTTAAATTCATAATCAATCTAGTAAAAATTTATAATTTTAAAGAAATAAAATTTTCAATGG
ATTATTTATGCTTGAACACGATATAATATCTCAAAATCCCAAATATAGATTTTAAAGATAATCCACTCAAAAAACAGAAACGCAAGCCAAAGACCAATTAACBCTCAACTTACTAATATAATATGTTATAACAGGATGCAAGGTTGGG
TATGTTGTTGTTGGTGTAAAAAATACTGTGACGACGCCAGACGGGAGGAAGTACGTCCTTCCGTTCCGGTTAAAAAGATCGATCAAGATCCCAATTTATTTT

Zap_obs3 | JBAMBR010006507.1:8211-8594 (-) | 384 nt | lncRNA: noe consensus e-value: 2.0e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.89

GGGCGGTCGATGCTCACAGTTATAAAGGGTTATACACATCCCGCATTAATTGTTTCACGGACAGGTCATGGGGTATTAAATTAATTTATTAATTTATAAATAATTCATAATCTAAACTTAGTAAATTTACAATTAAGTATTTAACAGTAGCATATAACCAAAAAATAGCACTATTTGTGTAGTAGCAATGAAGAAATCCACAAATATCTCAAATAGATTATTAAGCAGCAGAGAGAGAGAGCCATAGAGAAAGCAGACAAAAGTAATCGTCCGTCGCATTAATTAACACGTCAAATATAAATAAATCTGTGAGCCACAGCCGCGGGGAGATGATGAACCTCGGTTGTATATCATCATGCBCTAAATTTTTTTTTT

Zap_obs4 | JBAMBR010000584.1:8049-8430 (+) | 382 nt | lncRNA: noe consensus e-value: 5.1e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.89

GGGCGGTCGATGGCTCACAGTTATAAAGGGTGTACACATCCCCGATTAATGTTCCTTACGCGCAGGCTGGTGGTATTTAATTAAATTTAATTTAATTTAATTAATTCATAATCTAAACCTAGTAAAAATACAAATTTAGTATTAAACA
GTAGCATATAGCAACAAAATTAAGCCCTTATTTGTGTAGTACGTAAAGCAATCAACCAAAATATCTTCAATATAGATTTAATAAGCAGCAGAGAGAAACCTTAGAGAAAGCAGACAAAGGTATTCGTCCTCCCTCCCATTAATATCAATTAACGTCATAT
AAAAATAAATCAATGTGAGAACCTACACCGCGGGAAGCAGTAAGGCTCCGGTTGTAAATCATCAGATCGCATAAATTTTTTTTTTT

	Zap_obs1	Zap_obs2	Zap_obs3	Zap_obs4
Zap_obs1	-	63	60	56
Zap_obs2		-	60	61
Zap_obs3			-	97
Zap_obs4				-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.