# Zaprionus obscuricornis

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

**Assembly:** GCA\_037044475.1\_ASM3704447v1\_genomic

#### Zap\_obs1 | JBAMBR010006508.1:11401-11814 (+) | 414 nt | IncRNA:noe consensus e-value: 6.6e-05

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

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## Zap\_obs2 | JBAMBR010002046.1:51287-51693 (+) | 407 nt | IncRNA:noe consensus e-value: 4.4e-08

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

## Zap\_obs3 | JBAMBR010006507.1:8211-8594 (-) | 384 nt | IncRNA:noe consensus e-value: 2.0e-04

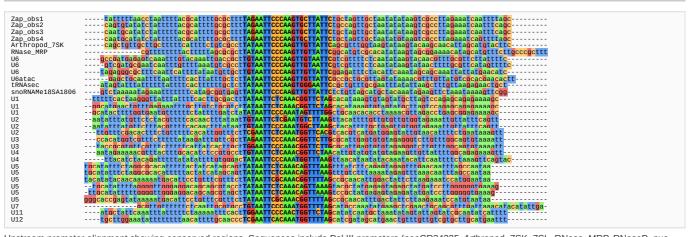
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.89

#### Zap\_obs4 | JBAMBR010000584.1:8049-8430 (+) | 382 nt | IncRNA:noe consensus e-value: 5.1e-05

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

	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 IncRNA sequences.



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.