## Zeugodacus tau

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Zeugodacus > Zeugodacus subgenus Zeugodacus

Assembly: GCA 031772095.1 ASM3177209v1 genomic

## Zeu\_tau1 | CM062653.1:67282634-67283613 (+) | 980 nt | IncRNA:noe consensus e-value: 1.1e-15

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

## Zeu\_tau2 | CM062651.1:70517070-70517528 (+) | 459 nt | IncRNA:noe consensus e-value: 1.2e-04

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

	Zeu_tau1	Zeu_tau2
Zeu_tau1	-	29
Zeu_tau2		-

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.