## Zeugodacus cucurbitae

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

Assembly: GCA 028554725.2 idZeuCucr1.2 genomic

## Zeu\_cuc1 | CM053021.1:73501928-73502902 (-) | 975 nt | IncRNA:noe consensus e-value: 1.0e-17

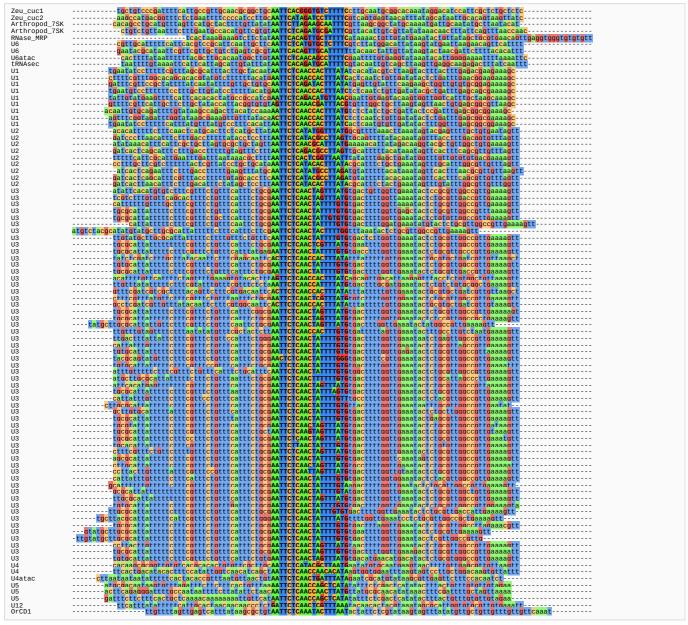
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

## Zeu\_cuc2 | CM053020.1:8836947-8837405 (-) | 459 nt | IncRNA:noe consensus e-value: 6.6e-03

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

	Zeu_cuc1	Zeu_cuc2
Zeu_cuc1	-	31
Zeu_cuc2		-

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.