## Ceratitis capitata

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

Assembly: GCA 000347755.4 Ccap 2.1 genomic

## Cer\_cap1 | AOHK02000180.1:485475-486474 (-) | 1000 nt | IncRNA:noe consensus e-value: 1.9e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95

## Cer\_cap2 | KZ344513.1:333769-334049 (+) | 281 nt | IncRNA:noe consensus e-value: 2.7e-07

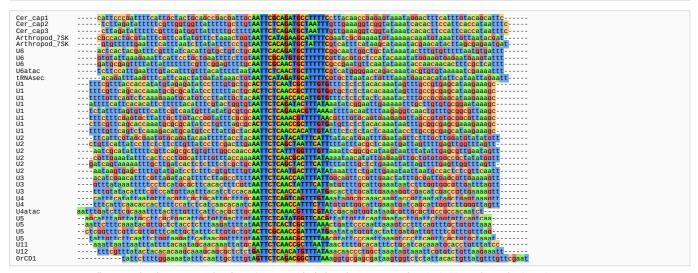
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

## Cer\_cap3 | KZ344513.1:340502-340782 (+) | 281 nt | IncRNA:noe consensus e-value: 5.7e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

		Cer_cap1	Cer_cap2	Cer_cap3
	Cer_cap1	-	20	21
	Cer_cap2		-	100
	Cer_cap3			-

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.