Ceratitis quilicii

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

Assembly: GCA 043005495.1 Cquilicii 01 genomic

Cer_qui1 | BAAFTC010000004.1:40886583-40887593 (+) | 1011 nt | IncRNA:noe consensus e-value: 5.6e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Cer_qui2 | BAAFTC010000003.1:13741143-13741419 (-) | 277 nt | IncRNA:noe consensus e-value: 1.5e-07

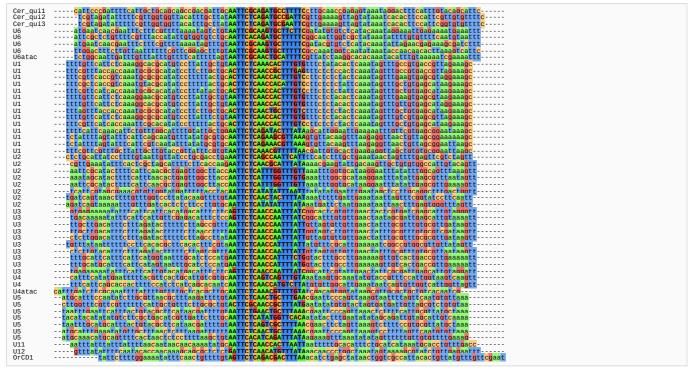
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.79

Cer_qui3 | BAAFTC010000003.1:13755356-13755632 (-) | 277 nt | IncRNA:noe consensus e-value: 2.2e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.79

	Cer_qui1	Cer_qui2	Cer_qui3
Cer_qui1	-	19	19
Cer_qui2		-	100
Cer_qui3			-

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.