

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Ceratitis > Pterandrus
Assembly: GCA_043005495.1 Cquilicii_01_genomic

[illegible]

GGCGGTTGCGTATCTCTCAGTTGAAAAAGGTTGGCTACAAACCTCAATTGTGGCAACGTATAATTTGAATACTATACTATATATGAAACAAACAAAAATGAATCAACAAACAAACCAAGAAACATGGTGAAAACTATAAAACAAAACAACTTCAACGATCAGTTTCTAATTAACTTTAAGAAACGAGTTTGAAAAATTAACTCTCAATTTTCTTCGAGGGGTAAATTGATAAGATACTGAAAGATACACTGTAATCGCCTTTT

GGCGGTTGCGTATCTCTCAGTTGAAAAAGGTTGGCTACAAACCTCAATTGTGGCAACGTATAATTTGAATCTATACTATATATGAAACAAACAAAAATGAATCAACAAACAAACCAAGAAACATGGTGAAAACTATAAAACAAAAAACAACTTCAACGATCAGTTTCTAATTAACTTTAAGAAAGCATTTTGAAAAATTAAAGAAAAAATTTCTCTCAATTTTCTTCGAGGGGTTAATTGATAAGATACTGAAAGATACACTGTAATCGCCTTTT

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

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.