

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

Assembly: GCA_043005725.1 Crosa_01 genomic

Cer_ros1 | BAAFTF010000025.1:2516026-2517035 (-) | 1010 nt | lncRNA: noe consensus e-value: 1.7e-13

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

[illegible]

Cer_ros2 | BAAFTF010000003.1:13608171-13608448 (+) | 278 nt | lncRNA: noe consensus e-value: 7.5e-08

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.84

GGGCGGGTTCGGTATCTCTCAGTTGAAAAAGGTGGCTACAACCCCTCAATTGTGGCAACGTATAATTTGAATACTATACTATATATATGAAACAAACAAAAATGAATCAACAAAAACAAACAGAAACATGGTGAAAACATATAAACAAAAA
CAACTTCAACGATCACTTTCTAATTAATACTTAAGAAAGCATTTGAAAAAGTTAAGAAAAAATCTCTCAATTTTCTTCGAGGGGTTAATTGATAAGATACTGAAGAGATACACTGTAATCGCCTTTTT

Cer_ros3 | BAAFTF010000003.1:13602794-13603070 (+) | 277 nt | lncRNA: noe consensus e-value: 2.2e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.84

GGCGGGTTGCGGTATCTCTCAGTTGAAAGGGTTGGCTACAACCCCTCAATTGTGGCAACGTATAATTTGAATACTATACTATATATATGAAACAAACAAAAATGAATCAACAAACAAACAAAGAAACATGGTGAAACCTATAAAACAAAAAAC
AAGTTCAACGATCACTTTCATTAATAATACTTAAGAAAGCGATTGAAAAAGTTAAGAAAAAATTCCTCAATTTCTCTGAGGGGTTAATTGATAAGATACTGAAGAGATACACTGTAAATCGCCTTTTT

Cer_ros4 | BAAFTF010000003.1:13614343-13614619 (+) | 277 nt | lncRNA: noe consensus e-value: 2.2e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.84

GGCGGGTTCGGATCTCTCAGTTGAAAAGGTTGGCTACAACCCCTCAATTGTGGCAACGTATAATTTGAATACTATACTATATATATGAACAACAAAAATGAATCAACAAAAACAACAAGAAACATGGTGAAAACTATAAAACAAAAAAC
AACTTCAACGATCACTTTCATTAATAACITTAAGAAAGCATTTGAAAAGTAAAGAAAAAATTCCTCAATTTTCCTCGAGGGGTAAATTTGATAAGATACGAAAGAGATACACTGTAATCGCCCTTTTT

	Cer_ros1	Cer_ros2	Cer_ros3	Cer_ros4
Cer_ros1	-	20	19	19
Cer_ros2		-	100	100
Cer_ros3			-	100
Cer_ros4				-

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.