## Ceratitis rosa

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

Assembly: GCA 043005725.1 Crosa 01 genomic

### Cer\_ros1 | BAAFTF010000025.1:2516026-2517035 (-) | 1010 nt | IncRNA:noe consensus e-value: 1.7e-13

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

#### Cer\_ros2 | BAAFTF010000003.1:13608171-13608448 (+) | 278 nt | IncRNA:noe consensus e-value: 7.5e-08

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

# Cer\_ros3 | BAAFTF010000003.1:13602794-13603070 (+) | 277 nt | IncRNA:noe consensus e-value: 2.2e-07

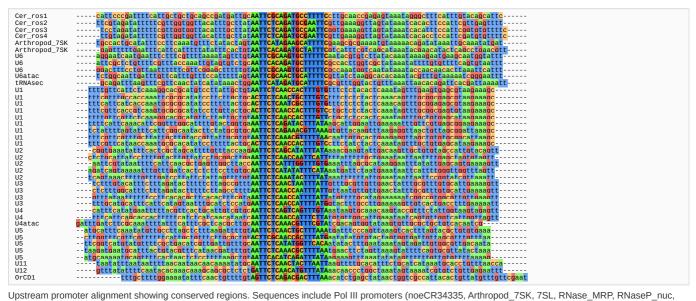
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.84

#### Cer\_ros4 | BAAFTF010000003.1:13614343-13614619 (+) | 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: 0.84

	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 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.