

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Bactrocera > Daculus
Assembly: GCA_042242935.1_idBacOlea1_genomic

[illegible][illegible]

CGGGTCCGTTGGTCCCATGGGTGAAGAGGGTTGACTGCGTCCCTTCCCAATTTGACAGCAAGCAACAAAAGCAAAATACCAATTTCTCTCTTCGTGGATCATTTCTGCGTGGCTTTCTGAGCGAAAAGCTTTGTGTAACGCAACCATTCGCTG
TGTGAAGAACTCGCATATAATAGACTCTCTAATTCGAGTGACAAACACATCGGTTGGGACGCTTCCTCTAGGCAATTTAAACCAATACGCTTTCTACTACTAGGAGGTGACAAAGAAATATTAATAGTGTATTAAGAAATAATTTAAACAAAATAAT

GGCGGTTCA⁺GATCCTCCCA⁺GTTGAAAGGGTTGGTCATATCCCTCAATTGTGGCAAA⁺TGATACTTTGAATAAGCAAAACATAAAAACGCA⁺TACGCATACGCATATACAACAAAAACGCAAAACGCAAAAAAATGAATCAACAAACAAAGAA⁺
CTATGGTGA⁺AAACATAAAAACCAC⁺TTCAATGATCACTTTCTATCCTTAAGAA⁺GCGATTTGAAAGGTTAAAGAAAAAATCTCTCAATTTTCGTCGAGGGGTAA⁺TTGATAAGATACTGTGGAGGTCAACGCGATCGCTTTTTT

GGCGGGTTTATGATCCTCCCAAGTTGAAAGGGTTGGTCACATCCCTAAATTGTGGCAAAATATGTATACTTTAAATAAGTTAAACATAAAATACGCATACGTTTACGATTACGAATACGATAAGCACATTGTAAAGTAAAGAAAAAATTCCTCGTCGT
GGGTTTCTCACCTCGGGCATTTTCTTAATGAGCCTTTACAAGTCTTAAAGTAAAGAAAAAATTCCTCGTCGTGGGTTTCTCACCTCGGGCATTTTCTTAATGAGATACGTGGAGGTCGAATGCTATCGCCTTTTTT

	Bac_ole1	Bac_ole2	Bac_ole3	Bac_ole4	Bac_ole5
Bac_ole1	-	30	30	21	20
Bac_ole2		-	95	40	40
Bac_ole3			-	38	40
Bac_ole4				-	63
Bac_ole5					-

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.