Bactrocera oleae

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Bactrocera > Daculus

Assembly: GCA 042242935.1 idBacOlea1 genomic

Bac_ole1 | CM090311.1:72206903-72207801 (-) | 899 nt | IncRNA:noe consensus e-value: 1.1e-19

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

Bac_ole2 | CM090308.1:8713660-8714092 (+) | 433 nt | IncRNA:noe consensus e-value: 1.2e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.90

Bac_ole3 | CM090308.1:8708214-8708647 (+) | 434 nt | IncRNA:noe consensus e-value: 1.8e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.90

Bac_ole4 | CM090310.1:39023863-39024156 (-) | 294 nt | IncRNA:noe consensus e-value: 7.6e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

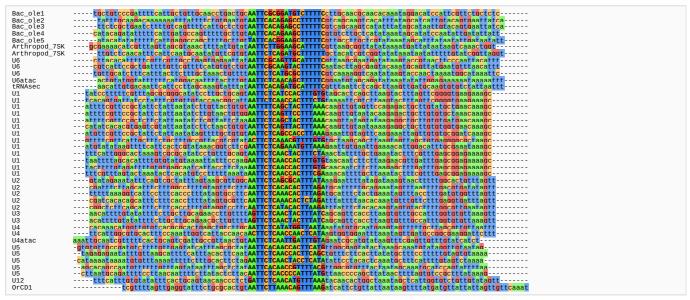
Bac_ole5 | CM090310.1:43757245-43757529 (-) | 285 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.92

GGCGGTTTAGATCCTCCCAGTTGAAAAGGTTGGTCACATCCCTAAATTGTGGCAAATATGTATACTTTAAATAAGTTAACATAAAATACGCATACGTTTACGATTACGATAAGCACTTGTAAAGTAAAGAAAAATTCTCGTCGT GGGTTTCTCACCTCGGGCATTTTCTTAATGAGCCTTTACAAGTGCTTAAGTAAAGAAAAATTCTCGTCGTCGTGTGTTACCACCTCGGGCATTTTCTTAATGAGATACTGTGGAGGTCAATGCTATCGCCTTTTTT

	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 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.