Bactrocera zonata

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

Assembly: GCA 043005645.1 Bz 01 genomic

Bac_zon3 | BAAFTE010000002.1:8378168-8379081 (-) | 914 nt | IncRNA:noe consensus e-value: 8.8e-20

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.84

Bac_zon4 | BAAFTE010000005.1:8883755-8884195 (-) | 441 nt | IncRNA:noe consensus e-value: 7.0e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.89

Bac_zon5 | BAAFTE010000005.1:8567653-8568090 (+) | 438 nt | IncRNA:noe consensus e-value: 4.5e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.83

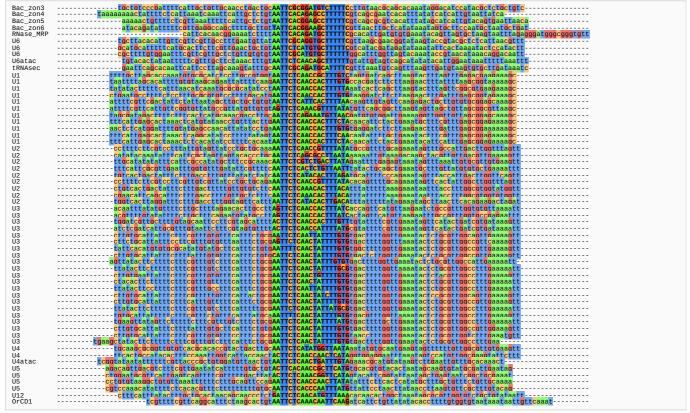
Bac_zon6 | BAAFTE010000003.1:40320849-40321144 (+) | 296 nt | IncRNA:noe consensus e-value: 4.2e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.87

GGCGGTTCAGATCCTCCCAGTTGAAAAGGTTGGTCACATTCCCTCAATTGTGGCAAATGTATACTTTGAATAAGCAAACATAAAAAACGCATACGCATATACAACAAAAAAGCAAAAAGCAAAAAAGTAAATGAATCAACAAAAAAGTAAATGAATCAACAAAAAAGTAAAAAAATTCTCTCAATTTTTCGTCGAGGGTTAATTGATAAGATACTGTGGAGGTCATTGTGATCGCCTTTTTT

	Bac_zon3	Bac_zon4	Bac_zon5	Bac_zon6
Bac_zon3	-	26	30	21
Bac_zon4		-	89	41
Bac_zon5			-	42
Bac_zon6				-

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