

***Bactrocera tryoni***

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

**Assembly:** GCA\_016617805.2\_CSIRO\_BtryS06\_freeze2\_genomic

**Bac\_try1 | CM028324.1:8522465-8523381 (-) | 917 nt | lncRNA: no consensus e-value: 1.5e-19**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.84

[illegible]

**Bac\_try2 | CM028321.1:10235625-10236064 (-) | 440 nt | lncRNA: noe consensus e-value: 7.3e-03**

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

GCGGTCTGGTGGCCCGGGTGAAGAGGTTGACTGCATGCCCCCGGATGCAACAAAGCAACAAAAAGCAATACTATTTCGCTCTGGTGGATCATCTCTCGGGTACTTTTCGGCGAAAGCTCTGTGACCCTACCATCGTGA  
 GTGTGAAGAGCTCCGCAATATCAACCATCTCTAATTCGGGTGAAAGACCGCTGGTGGGGCTGCACCAAGCATATCAATACCGCAATCGCTCTCTACTACTGACGATATGCAACAGATGCAACAGATATAATAATAATATAATATAA  
 TATCTATATAACCAATCTGCTATGAAATGCAAAATGACCAACAAATATGCAAAACCAATATATTCGCTGACACCTTACGAGGAGAAAGCGTAGTGCCAAATGGGAGCTCGAAAAAAAGGTGTGATCGCTTTTT

**Bac\_try3 | CM028321.1:9994957-9995391 (+) | 435 nt | lncRNA: no consensus e-value: 5.7e-03**

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

6CGGTCCGTA6CCCCATGGTTGAAGGGTTGACTGCATTTCCCTCCCCCAATGACGCAAGCAACAAAAGCAAAAACCAATTCACCTTGGTGGATCATTTCTGCGGTGACTTTTCTAGCGGAAGCTCTGTGACCCTGACCCATCGCA  
GTGTGACACGCGCCGACATCTAGTAAGCTCTCAATTTCCGGTGAAGAACGCTGGTGGTGGTCCCCAGGCATACAAACCAAGATTCGCTCTCTACTTACCTGACCAAGGACGACAGAAAGATTAATAAATGATTTGATTAACAAAATA  
TGTCAAGCAAAAAATCTCATATAGATGCAAAAATTTGAACCAACAAATTAATAACACAAATTTTTCGGCTGACCCCTCTCAGGGGAAGACGCTGCCATGGGAATGCAAGAAAATGTGTGTCBCTTTTTTTT

**Bac\_try4 | CM028323.1:56972100-56972394 (-) | 295 nt | IncRNA:noe consensus e-value: 1.6e-08**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.93

GGCGGGTTCAGATCCTCCCAAGTTGAAAAAGTTGGTCACATCCCTCAATTGTGACAAATGTATACTTTGAAATAAGCAAAACATAAAAAACGCATACGCATACGCATATACAACAAAAACGCAAAAGCAAAAAAATGAATCAACAAACAAAGAA  
TCTATGGTGAAGAACTGAAAAACAACATCAATGATCACTTCTATCCTTAAGAAAGCGATTGAAAAATTAAAGAAAAAATTCCTCAATTTTCGTCGAGGGGTAAATTGATAAGATACTGTGGAGGTCAATGTGATCGCCTTTTTT

	Bac_ try1	Bac_ try2	Bac_ try3	Bac_ try4
Bac_ try1	-	29	30	21
Bac_ try2		-	89	41
Bac_ try3			-	42
Bac_ try4				-

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



the alignment.