

Bactrocera dorsalis

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

Assembly: GCA_023373825.1_ASM2337382v1_genomic

Bac_dor1 | CM041774.1:7431946-7432856 (-) | 911 nt | lncRNA: noe consensus e-value: 4.9e-20

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

GGGGGGTCTGGTGTTCGCGAGTACACACGGTTGGGACACACCCGTTTCAAAATTTGTCACCTTACTACACACACAAATTAATTAACAAAAACACTGATTAATCTACTAAAAACAATGAATATCTGAACATGGGCATTAATAAGAAA
TGAATTAACCATTTACATACACACGACATATAGCAAACTTTCTGCACACTAATAGGGAAATGATTACAGATTTAGCAACACAAAGCAAAAGCAAAATTTGAATCTGACTTTAGGAAATCTCCATTTGTGGGACACGATAT
ATAAAGCAACCTTACAGATCTATAAAAAATCAATGAATTTTTCGCAAAAGCAAAACCCATTCAGATTTAACACGATTTGAAAAACAAATACGAATCAAGAACGAAATGCGCAATATGGAAATTAACCTTCAAAATACCCGAAACGCT
ATATGATTAATCTTAAAAATCGAAATGTCATCTGTGTGCTGGCTTTGTGTATGATGACGAAAGCCGAGATCCGATCTCGCTGCTGTCGGCCAGATTTGTGAGCTGCTGCGACACACACCGGCAACACGCCGACACACGATGCTGAC
CTGTCGATGTTGGTGTATGCGCCAGATTTGTGTCGATTTACBAGAGCAAAAAACBAGGAGACGACGATCTCCCGGTTGACBAGGAGACGTCGCAAGGGGCGAACACBACGCGCGATATGGATCTGCAAAATTAATAACCAATATGATGTTTG
AGAAATATCTAGACAAACGAACGCAAAAAAATACCACTATAAATGGACAGATTGAAAAAATCTACTTAACAAAAACACACACAAAGAAATGTCACGAAAAACGAACCAATATATAATACTTGGCAAACTGCCGGAACCAATCTGGTAT
GCCGCTTTTITTT

Bac_dor2 | CM041770.1:106063916-106064357 (-) | 442 nt | lncRNA: noe consensus e-value: 3.6e-03

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

CGCGTCCGTAACCCCGTGGTGAAGGGTGTACTGCATTTCCCTCCCCAATTGCAGCAAGCAATAAAAGCAAAACCAATTCACCTTCGTGGATCATTCCGCGGGTACTTTTCTAGCGAAGAGCTTCTGTACCCTACCAATCGCAGTGTCAAAAGCCGCAATGTAATGATGATCTAATGTGGCTGAAAGAACCAACCTCGTGGCAGTACCCCTAGGCATATATGCAAGACCCATTTCGTTCTACCACTGATGACGACAGCAAGCAATAAAATATGGAATAAGAAATTAATTAATTAATATGATATAATCAAAAACAAAAATCTCTCATATGATATGCAAAAATGATGACCAACCAATTAATAAAACACCAATTAATTTGGCTGACCCCTCTTATGGGAAAGGCGGCGCATGAGGAGTACGAAAAATGTGTGTGATCGCTTTT

Bac_dor3 | CM041770.1:105800248-105800679 (+) | 432 nt | lncRNA:noe consensus e-value: NA

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

CGCGTCTGTTGGTCCCATGGTTGAAAGGGTTGACTGCATTTCCTCCCCCAATTGCAGCAAGCAACAAAAGCAATACAAATTCGCCTTCGAGGATCATTCGCGGTGACTTTTCGAGCGAAAGCTTCGTGATCGCTACCATCGCAG
TGTAAAAAGCCCGCAATGTAATGAATCTCTCAATTCGCGTGAAAAAGCAATCGGTGGCGATCTCCGAGGCGCATAGACCCCAATTCACGGTCTTCACTATGAGCAGAGCAGCAAGAAAATAAAATAGAAATAAAAAGTAATTAATAA
AATTACTATATAAAAAAATCTGCTATGAATGAGCAAAACAAATTAATACATCATTCGCGTCGCCCTCATAGGAAAGAGGCGTGGCCCAATGGGATCGGAAAAAATTTGTGATCGCTTTTT

Bac_dor4 | CM041773.1:38736137-38736430 (-) | 294 nt | lncRNA: noe consensus e-value: 1.4e-08

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.84

GGCGGGTTGAGATCCTCCCAAGTTGAAAAAGGTTGGTCACATCCCTCAATTGTGGCAAAATGTATACTTTGAATAAGCAAACTAAAAACGCATACGCATACGCATATACAACAAAAACGCAAAAGCAAAAAAATGAAATCAACAAAAACAAGAAATCTATGGTGAAGAACTGTAAAAACAACATTCATGATCACTTTCTATCTTTAAGAAAGCGATTTGAAAAAGTTAAGAAAAAATTCCTCAATTTTCCTGAGGGGTAAATTGATAAGGATCATGTGGAGGTCAATGTGATCGCCTTTTTT

	Bac_dor1	Bac_dor2	Bac_dor3	Bac_dor4
Bac_dor1	-	31	31	20
Bac_dor2		-	86	42
Bac_dor3			-	42
Bac_dor4				-

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

