Bactrocera tsuneonis

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

Assembly: GCA 046562955.1 ASM4656295v1 genomic

Bac_tsu1 | CM102042.1:58895486-58896414 (-) | 929 nt | IncRNA:noe consensus e-value: 1.8e-16

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

Bac_tsu2 | CM102038.1:54946820-54947340 (+) | 521 nt | IncRNA:noe consensus e-value: 6.5e+00

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

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Bac_tsu3 | CM102039.1:22371851-22372132 (+) | 282 nt | IncRNA:noe consensus e-value: 2.1e-06

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.88

	Bac_tsu1	Bac_tsu2	Bac_tsu3
Bac_tsu1	-	36	21
Bac_tsu2		-	35
Bac_tsu3			-

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.