## Bactrocera minax

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

Assembly: GCA 021498325.1 ASM2149832v1 genomic

## Bac\_min1 | JAKEEE010000059.1:1186259-1187187 (+) | 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\_min2 | JAKEEE010000003.1:8911201-8911716 (+) | 516 nt | IncRNA:noe consensus e-value: NA

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

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## Bac\_min3 | JAKEEE010000049.1:1211941-1212222 (-) | 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_min1	Bac_min2	Bac_min3
Bac_min1	-	29	21
Bac_min2		-	34
Bac_min3			-

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.