# Bactrocera neohumeralis

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

Assembly: GCA\_024586455.2\_APGP\_CSIRO\_Bneo\_wtdbg2-racon-allhic-juicebox.fasta\_v2\_genomic

### Bac\_neo1 | CM044978.1:8317169-8318093 (-) | 925 nt | IncRNA:noe consensus e-value: 8.3e-20

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

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## Bac\_neo2 | CM044975.1:10331670-10332109 (-) | 440 nt | IncRNA:noe consensus e-value: 1.2e+00

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

## Bac\_neo3 | CM044975.1:10077181-10077616 (+) | 436 nt | IncRNA:noe consensus e-value: 3.2e-03

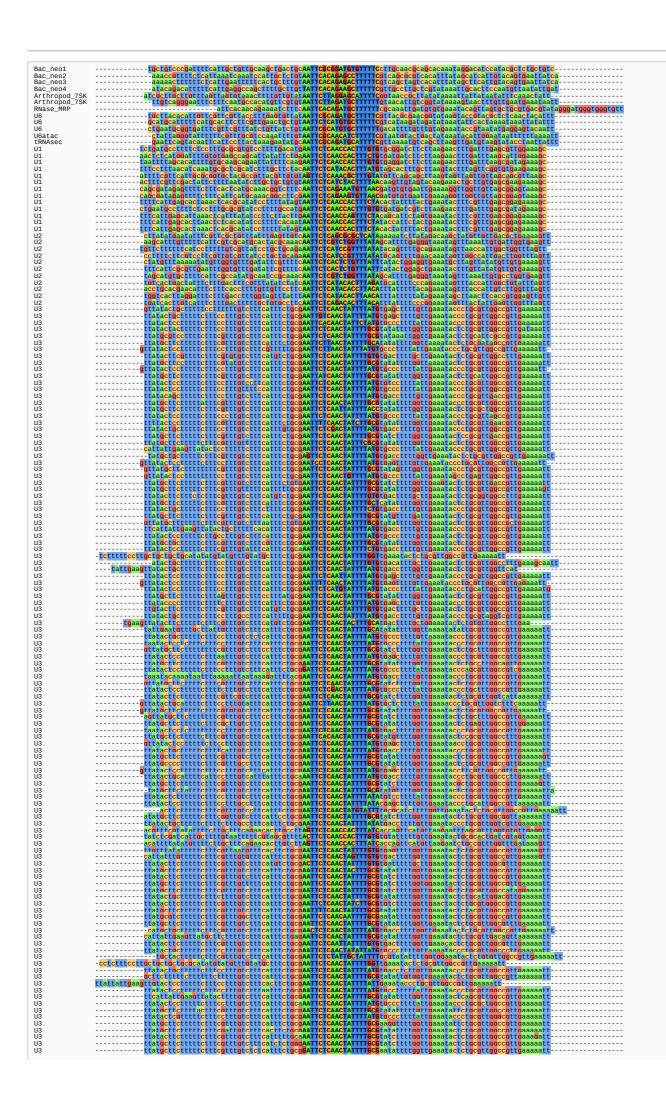
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.90

### Bac\_neo4 | CM044977.1:56095089-56095385 (-) | 297 nt | IncRNA:noe consensus e-value: 2.0e-08

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

|          | Bac_neo1 | Bac_neo2 | Bac_neo3 | Bac_neo4 |
|----------|----------|----------|----------|----------|
| Bac_neo1 | -        | 30       | 30       | 21       |
| Bac_neo2 |          | -        | 89       | 41       |
| Bac_neo3 |          |          | -        | 40       |
| Bac_neo4 |          |          |          | -        |

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.