## Bactrocera correcta

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

Assembly: GCA 027475135.1 ASM2747513v1 genomic

## Bac\_cor1 | CM050326.1:80905289-80906207 (-) | 919 nt | IncRNA:noe consensus e-value: 9.2e-21

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

## Bac\_cor2 | CM050323.1:55344070-55344510 (+) | 441 nt | IncRNA:noe consensus e-value: 3.3e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.83

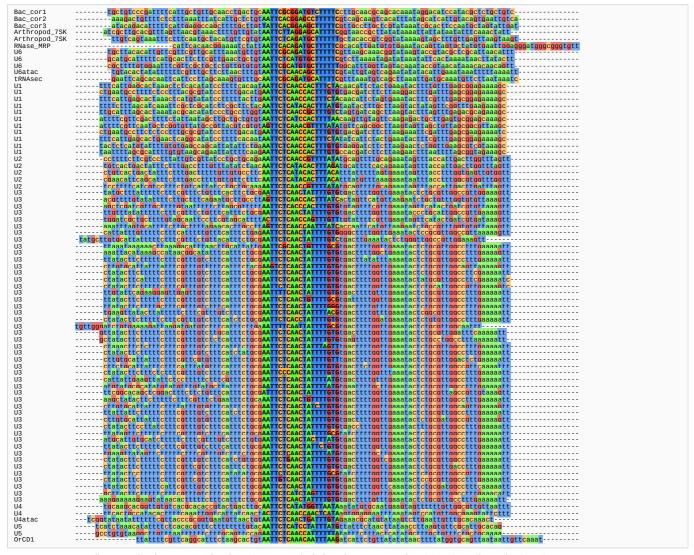
## Bac\_cor3 | CM050325.1:90329829-90330123 (-) | 295 nt | IncRNA:noe consensus e-value: 2.7e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.87

GGCGGTTCABATCCTCCCABTTEAAAAGGTTGGTCACATCCCTCAATTGTGGCAAATGTATACTTTGAATAAGCAAAACATAAAAAACGCATACGCATACGCATATACAACAAAAAAGCAAAAAAATGAATCAACAAAAACAAGA TCTATGGTGAAAACTGTAAAAACAACTTCAATGATCACTTTCTATCCTTAAGAAGCGATTTGAAAAGTTAAGAAAAATTCTCTCAATTTTCGTCGAGGGGTTAATTGATAAGATACTGTGGGGGCATATGTGATCGCCTTTTTTT

		Bac_cor1	Bac_cor2	Bac_cor3
	Bac_cor1	-	30	20
	Bac_cor2		-	41
	Bac_cor3			-

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.