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 | lncRNA: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 | lncRNA:noe consensus e-value: 3.3e-04

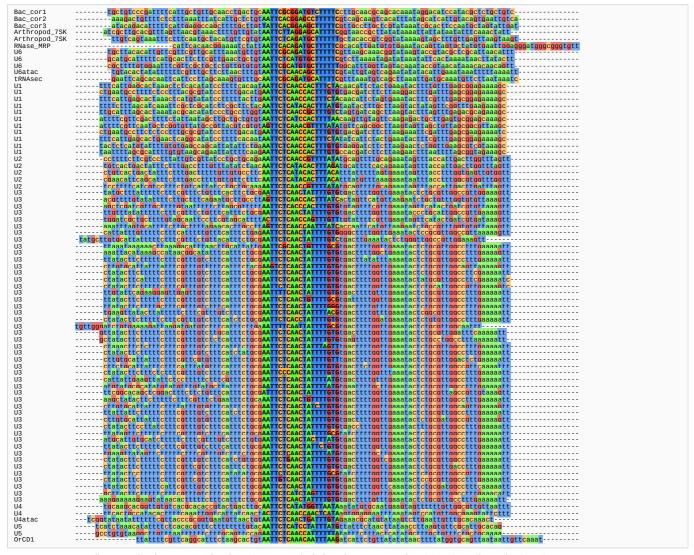5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 7nt   PSE: 0.83

Bac_cor3 | CM050325.1:90329829-90330123 (-) | 295 nt | lncRNA:noe consensus e-value: 2.7e-09

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

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

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