# Bactrocera dorsalis

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

Assembly: GCA\_023373825.1\_ASM2337382v1\_genomic

### Bac\_dor1 | CM041774.1:7431946-7432856 (-) | 911 nt | IncRNA:noe consensus e-value: 4.9e-20

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

## Bac\_dor2 | CM041770.1:106063916-106064357 (-) | 442 nt | IncRNA:noe consensus e-value: 3.6e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.89

## Bac\_dor3 | CM041770.1:105800248-105800679 (+) | 432 nt | IncRNA:noe consensus e-value: NA

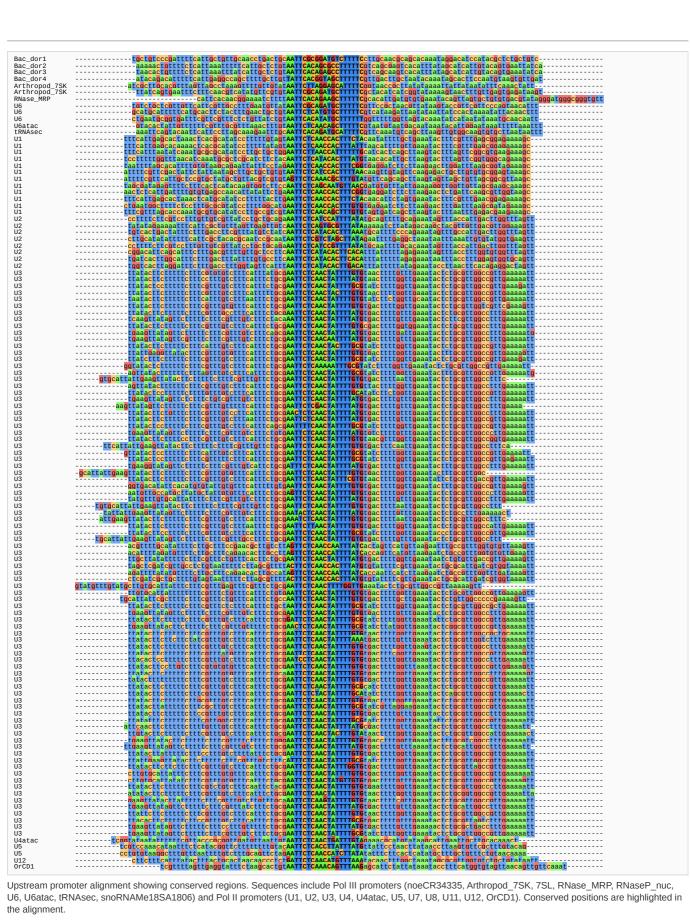
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.90

### Bac\_dor4 | CM041773.1:38736137-38736430 (-) | 294 nt | IncRNA:noe consensus e-value: 1.4e-08

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

	Bac_dor1	Bac_dor2	Bac_dor3	Bac_dor4
Bac_dor1	-	31	31	20
Bac_dor2		-	86	42
Bac_dor3			-	42
Bac_dor4				-

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.