Bactrocera latifrons

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

Assembly: GCA 001853355.1 ASM185335v1 genomic

Bac_lat2 | MIMC01000264.1:23693-24142 (-) | 450 nt | IncRNA:noe consensus e-value: 2.7e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.83

Bac_lat3 | MIMC01000001.1:4576654-4576944 (-) | 291 nt | IncRNA:noe consensus e-value: 4.9e-09

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

GGCGGTTCAGATCCTCCCAGTTGAAAAAGGTTGGTCACATCCCTTAATTGTGGCAAATGTATACTTTGAATAAGCAAACATAAAAAACGCATATACAACAAAAAACGCAAAAGCAAAAAAATGAATCCAGCAAAATCTAT GGTGAAAACTGTAAAAACAACTTCAATGATCACTTTCTATCTCAGAAGAAGCGATTTGAAAAGTTAAGAAAAAATTCTCTCAATTTTCGTGAGGGGTTTATTGATAAGATACTGTGGAGGTCATTGTGATCGCCTTTTTT

	Bac_lat2	Bac_lat3
Bac_lat2	-	41
Bac_lat3		-

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.