Tephritis formosa

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Tephritis

Assembly: GCA 965654245.1 idTepForm3.1 genomic

Tep_for2 | OZ294581.1:264629979-264630939 (-) | 961 nt | IncRNA:noe consensus e-value: 4.7e-12

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 1.00

Tep_for3 | OZ294580.1:275448021-275448280 (+) | 260 nt | IncRNA:noe consensus e-value: NA

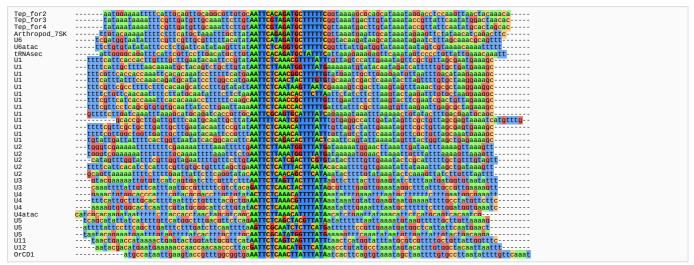
5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.95

Tep_for4 | OZ294580.1:275458473-275458720 (+) | 248 nt | IncRNA:noe consensus e-value: 2.4e-08

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

	Tep_for2	Tep_for3	Tep_for4
Tep_for2	-	15	14
Tep_for3		-	92
Tep_for4			-

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.