Panzeria rudis

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Tachinidae > Panzeria

Assembly: GCA 956483635.1 idPanRudi1.1 genomic

Pan_rud3 | OY101448.1:172800555-172801072 (-) | 518 nt | IncRNA:noe consensus e-value: 3.9e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

Pan_rud4 | OY101447.1:166306526-166306889 (-) | 364 nt | IncRNA:noe consensus e-value: 1.8e-01

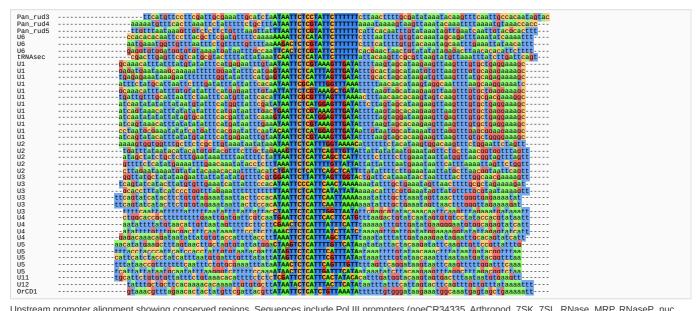
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 1.00

Pan_rud5 | OY101451.1:8381793-8382021 (+) | 229 nt | IncRNA:noe consensus e-value: 2.6e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

		Pan_rud3	Pan_rud4	Pan_rud5
	Pan_rud3	-	42	27
	Pan_rud4		-	43
	Pan_rud5			-

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.