# Tachina grossa

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

Assembly: GCA 949987645.1 idTacGros1.1 genomic

## Tac\_gro1 | OX465276.1:57664909-57665463 (-) | 555 nt | IncRNA:noe consensus e-value: 9.5e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.94

## Tac\_gro2 | OX465276.1:30956773-30957303 (+) | 531 nt | IncRNA:noe consensus e-value: 2.1e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.93

## Tac\_gro3 | OX465274.1:155956826-155957242 (-) | 417 nt | IncRNA:noe consensus e-value: NA

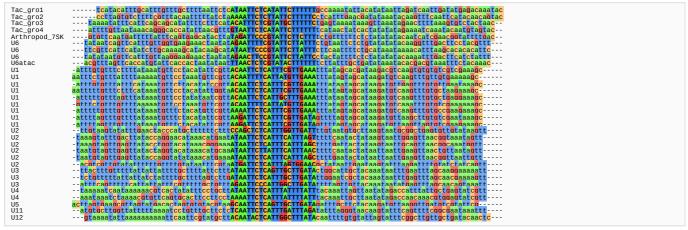
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

## Tac\_gro4 | OX465277.1:72930441-72930755 (+) | 315 nt | IncRNA:noe consensus e-value: 2.0e-02

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.90

	Tac_gro1	Tac_gro2	Tac_gro3	Tac_gro4
Tac_gro1	-	47	43	39
Tac_gro2		-	46	41
Tac_gro3			-	46
Tac_gro4				-

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.