# Gymnosoma rotundatum

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

Assembly: GCA 916610165.2 idGymRotn1.2 genomic

### Gym\_rot1 | OU744338.1:34981956-34982489 (+) | 534 nt | IncRNA:noe consensus e-value: 1.3e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.90

### Gym\_rot2 | OU744336.1:65190086-65190492 (-) | 407 nt | IncRNA:noe consensus e-value: NA

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

## Gym\_rot5 | OU744336.1:72336296-72336495 (-) | 200 nt | IncRNA:noe consensus e-value: 1.3e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

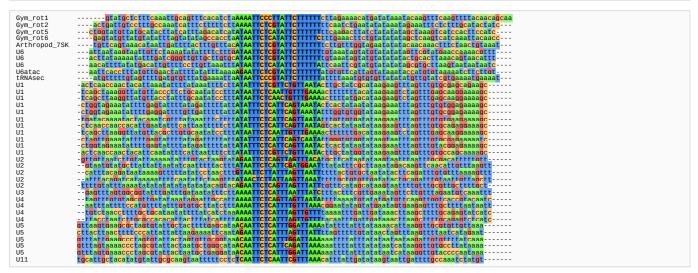
#### Gym\_rot6 | OU744336.1:72375571-72375715 (-) | 145 nt | IncRNA:noe consensus e-value: 5.1e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95

GCBGTCTTGTCTCCTGTAACAAGGTTGTTCACAGTCCTTAATTGCGGAGCTAAATTTATAAATCCAAAACTAAAACTCAAAGAACTACTACAAGCTAGATATAAAAATTACAGGGGATAAGCTGAAAGTGATCGCTTTTTTT

	Gym_rot1	Gym_rot2	Gym_rot5	Gym_rot6
Gym_rot1	-	44	28	19
Gym_rot2		-	37	24
Gym_rot5			-	60
Gym_rot6				-

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.