

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

[illegible]

Gym_rot2 | OU744336.1:65190086-65190492 (-) | 407 nt | lncRNA: noe consensus e-value: NA

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

5'GGGGGTTTCATCAACCTGTCATTAAAGGGTGGTCACATTCCCTAACTAATTGTGAAATTTGTTAAATAAATAAAAAATAAAATTTCTCTTTAAAGCCGCTGCAACACGACTTAATTCAGAACTGCAAAAATAACTTTACAAATATATCTCTATCTCAAAAAAGCAATTTCTCAAGCTCAAGCTTTAAAAATGGTTATCATCAAAATAAATAAGAAAAACAACACACACAAATAAAACACACAAAAAGGCTCTTCAATTCCAATTCACAAAAAATAATAAATGTCAAACTTTCTAAATCTATCTCTCCCAAGTGAAGCAGAAAAATTAATAAATGAATTTAGCTGATTTAAATAATTTCAAAATGTCAGAGGTACAAAAAGGGTCAATGTCBCCAATTTCTCAAA

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

GGCGGGTCCGTGTCCTTTGTTACTAGGTTGTTCACAGCCCTTAATTGTGGAGCCAAACAACTTTAAATCGAAACAAAACTTTAAAACTACTAAACTTTGTAAGGAATTATAATTGCATAAATTAACTTGTAAATAAAAGTACCGCAAG
GTCTTAGGATTTAATAACAGGAGTGCCTGAAAAAGCATCGCATTATTTTTT

Gym_rot6 | OU744336.1:72375571-72375715 (-) | 145 nt | lncRNA: noe consensus e-value: 5.1e-02

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

GC GG TCT GT CT CT CC GT AAC AAG GT GT CAC AG CT TAA TT GC GG AG CT AAA TTT ATA AAT CCA AAA CAAA ACT CAAA GAA CT ACT ACA AG CT AG ATA TAAAA TTACA GGGG ATA AG CT GAAAA GT GAT CGC TTTTTT

	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 lncRNA sequences.

[illegible]

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.