## Gymnocheta viridis

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

Assembly: GCA 956483585.1 idGymViri1.1 genomic

## Gym\_vir2 | OY101442.1:96318852-96319713 (+) | 862 nt | IncRNA:noe consensus e-value: 1.4e-03

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

## Gym\_vir3 | OY101442.1:106670627-106671132 (-) | 506 nt | IncRNA:noe consensus e-value: 3.8e-02

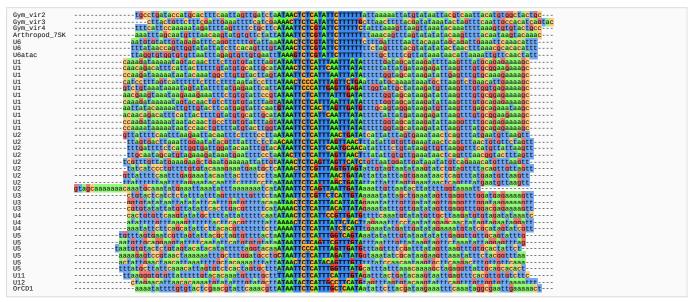
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.84

## Gym\_vir4 | OY101440.1:116334309-116334684 (+) | 376 nt | IncRNA:noe consensus e-value: 1.2e-02

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

	Gym_vir2	Gym_vir3	Gym_vir4
Gym_vir2	-	41	29
Gym_vir3		-	45
Gym_vir4			-

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.