

## *Tetanops myopaeformis*

**Taxonomic lineage:** Brachycera > Muscomorpha > Tephritoidea > Ulidiidae > Tetanops

**Assembly:** GCA\_050613955.1\_idTetMyoa1.1\_genomic

**Tet\_myo1 | CM115762.1:63518839-63519621 (-) | 783 nt | lncRNA: noe consensus e-value: 9.4e-25**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

[illegible]

**Tet\_myo2 | CM115765.1:35256221-35256693 (+) | 473 nt | lncRNA: noe consensus e-value: NA**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.81

[illegible]

	Tet_myo1	Tet_myo2
Tet_myo1	-	36
Tet_myo2		-

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.