

Cistogaster globosa

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

Assembly: GCA_937654795.1 idCisGlob1.1 genomic

Cis_glo1 | OW569403.1:59869590-59869984 (+) | 395 nt | lncRNA: no consensus e-value: 2.3e+00

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

GCGGGTTCATTAACCTCTGCATTGAAAGGGGTGTTCACATTCCTTAACTAATGTGAAATTTCTTAAATAAAAAAAAATTTCTCTTAAAGCGGTCTCAATGACGCTCATACATTCAGAAATATAAATAAATCTTACAAATCTCTCTCCAT
 CAAAAAAGCAATCTCTCAAACTCAAGCTTTAAAAATGTTTATCTGTCAAAATTAATGAAATGACAAAAACGCTTCTCAATTTCAATTTACATAAAAAATAAATGTCAAAACTTTCTTAACACTTTCTCT
 CAAATGACGCAAAAAAGTTTAAATAAAAAAATTTGACGCAAAATCAAAATTAAGAAATGTCAGAGGTACAAAAAGGTTATGCGCATTTTTT

Cis_glo2 | OW569406.1:106344733-106344997 (+) | 265 nt | lncRNA: noe consensus e-value: 1.6e-12

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

GGCGGGTCCCCTTACTCTCAGTTGAAACGGTGGCCACATTCGGTAATTGTGCGATTTTCATATAGTTATCTATATAATATGTTAAGAATTAATTTCTCCACAAAAAACAAACAAAAAACAAATTCAAAAACACAAAAAATATTCAAGGAT
CACTCTCTTCTTAGATTGCGATTAAAGAACACGTTAGCATTATAATGTTAATAAAACAAACAAAAAAAAAAAAACCTTTAGAAGTGAAGGTAACATTGTGATCGGCTTCTTTTTT

	Cis_glo1	Cis_glo2
Cis_glo1	-	48
Cis_glo2		-

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, snoRNAm18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.