

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Chymomyza > costata group

Assembly: GCA_018150985.1_ASM1815098v1_genomic

Chy_cos1 | JAECWU010000001.1:19340008-19340967 (+) | 960 nt | lncRNA: noe consensus e-value: 7e-181

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.91

[illegible]

Chy_cos2 | JAECWU010000256.1:4816301-4816803 (-) | 503 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.90

[illegible]

Chy_cos3 | JAE CWU010000256.1:4824704-4825084 (+) | 381 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.90

556GCGGTGCGACATCTCATGCGGAGTGAAGGTTGGTCGACGCCGTGACTATTGCGCAAACTACTGAGTTGAATCTCAGGTGCTCGCTCATTAGTGCAGAACATTGTGTGAGCTCCATGTGAGAGCCAAGTAATGCGCGCTGACATTTGTGAGCAAAAAAATATGGAGCTGACACAGAAAGAAATGTAATCGATGCTGCTGACTTAGTTGGTGGAGGACCACACGGAATTGTTGAGAGGGCAGAACCCCTATATGAGATGTGAGTGAATGGGGTAGTTGGG

Chy_cos4 | JAE CWU010000006.1:314557-314899 (-) | 343 nt | lncRNA: no consensus e-value: 1.4e-02

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

GGGCGGTCGAGAGTCTCATGCGTCAGTTGAAGTTGGTCGCAGCCCTGTCTAATTGCGCAAAACAAACATATATGAAAAATTGCAAAATGCAAAAACAAATAAAAATGAATTGAATACACATAAGTATATCGCAAAACAAATGAGTTATAAG
AAAAAAGATATGATCTATATATGATCAACCACTCTTATGACAAACAGCTACAACATGTAATAATGTTTACGCTACAAATTGGAGTGTGTTGGGGAATGGCGCAGTCCCAACACACATATCCGCAACAAAAACAAGGGGCCGTAAACGCCTATACGTG
AGATGTGAGTGTGAGAAAGATCATTGGATGATCCCTTTTTT

	Chy_cos1	Chy_cos2	Chy_cos3	Chy_cos4
Chy_cos1	-	26	23	25
Chy_cos2		-	53	52
Chy_cos3			-	47
Chy_cos4				-

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.