# Chymomyza caudatula

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

Assembly: GCA\_035041775.1\_ASM3504177v1\_genomic

### Chy\_cau1 | JAWNKW010000133.1:160457-161405 (-) | 949 nt | IncRNA:noe consensus e-value: 8e-193

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.94

### Chy\_cau2 | JAWNKW010000195.1:908132-908577 (+) | 446 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.97

## Chy\_cau3 | JAWNKW010000195.1:917459-917873 (+) | 415 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.94

#### Chy\_cau4 | JAWNKW010000200.1:852327-852649 (+) | 323 nt | IncRNA:noe consensus e-value: 6.2e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.88

### Chy\_cau5 | JAWNKW010000217.1:3788383-3788670 (-) | 288 nt | IncRNA:noe consensus e-value: 1.2e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

### Chy\_cau6 | JAWNKW010000147.1:8473416-8473682 (+) | 267 nt | IncRNA:noe consensus e-value: NA

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

	Chy_cau1	Chy_cau2	Chy_cau3	Chy_cau4	Chy_cau5	Chy_cau6
Chy_cau1	-	32	27	23	19	18
Chy_cau2		-	48	52	46	42
Chy_cau3			-	43	47	43
Chy_cau4				-	50	55
Chy_cau5					-	48
Chy_cau6						-

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.