Chymomyza fuscimana

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

Assembly: GCA_949987675.1_idChyFusc2.1_genomic

Chy_fus1 | OX465089.1:30537618-30538586 (+) | 969 nt | IncRNA:noe consensus e-value: 6e-189

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.92

Chy_fus2 | OX465090.1:18001058-18001828 (+) | 771 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.94

Chy_fus3 | OX465090.1:18007602-18008082 (+) | 481 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

Chy_fus4 | OX465088.1:54316782-54317148 (-) | 367 nt | IncRNA:noe consensus e-value: NA

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

| | Chy_fus1 | Chy_fus2 | Chy_fus3 | Chy_fus4 |
|----------|----------|----------|----------|----------|
| Chy_fus1 | - | 38 | 33 | 27 |
| Chy_fus2 | | - | 53 | 38 |
| Chy_fus3 | | | - | 51 |
| Chy_fus4 | | | | - |

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.