Chymomyza amoena

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

Assembly: GCA 037043745.1 ASM3704374v1 genomic

Chy_amo1 | JBAMAX010000009.1:418884-419846 (+) | 963 nt | IncRNA:noe consensus e-value: 3e-184

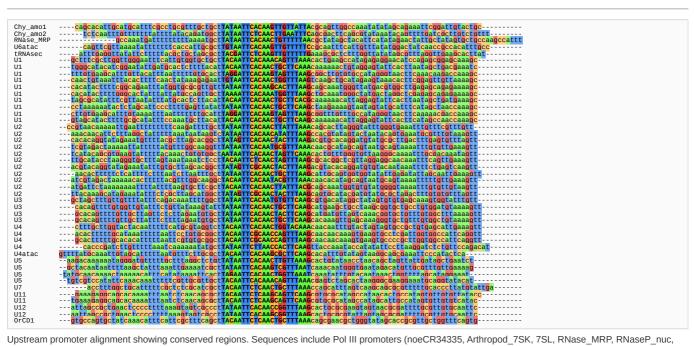
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95

Chy_amo2 | JBAMAX010003218.1:1243-1776 (+) | 534 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.89

	Chy_amo1	Chy_amo2
Chy_amo1	-	33
Chy_amo2		-

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.