Eudasyphora cyanicolor

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Muscidae > Eudasyphora

Assembly: GCA 963930755.1 idEudCyai1.1 genomic

Eud_cya1 | OZ005734.1:246091354-246091969 (-) | 616 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 1.00

CGGTTCGAAAGCCTCTTCGTGAAAGGGTTGCTCGCATCCCCTTCAAATTGCGTTAATCGACCA GTTGTTCTCCACATTCTCATTCTCATTCTCCTCTTCTCCATCTCAAACAAACACATCACAAA

Eud_cya2 | OZ005735.1:134089649-134090131 (-) | 483 nt | IncRNA:noe consensus e-value: 1.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

	Eud_cya1	Eud_cya2
Eud_cya1	-	43
Eud_cya2		-

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.