Cacoxenus indagator

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

Assembly: GCA 035041755.1 ASM3504175v1 genomic

Cac_ind1 | JAWNKX010000176.1:4879214-4879997 (+) | 784 nt | IncRNA:noe consensus e-value: 8.6e-33

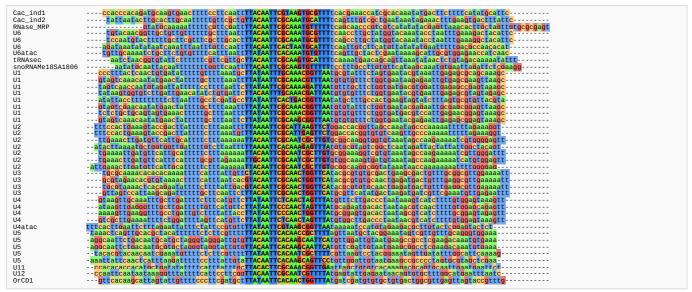
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Cac_ind2 | JAWNKX010000233.1:7616379-7616897 (-) | 519 nt | IncRNA:noe consensus e-value: 3.9e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 9nt PSE: 1.00

	Cac_ind1	Cac_ind2
Cac_ind1	-	42
Cac_ind2		-

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.