Scaptomyza cyrtandrae

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Scaptomyza > Elmomyza

Assembly: GCA 035044605.1 ASM3504460v1 genomic

Sca_cyr3 | JAWNNS010000084.1:2086362-2087407 (+) | 1046 nt | IncRNA:noe consensus e-value: 2e-155

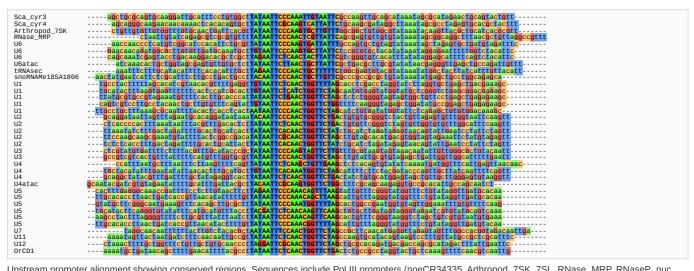
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.86

Sca_cyr4 | JAWNNS010000639.1:5776219-5776602 (+) | 384 nt | IncRNA:noe consensus e-value: 1.4e-08

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

	Sca_cyr3	Sca_cyr4
Sca_cyr3	-	25
Sca_cyr4		-

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.