Scaeva pyrastri

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Scaeva

Assembly: GCA 905146935.1 idScaPyra1.1 genomic

Sca_pyr1 | LR989929.1:70975622-70975925 (-) | 304 nt | IncRNA:noe consensus e-value: NA

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.82

Sca_pyr2 | LR989929.1:13723765-13724064 (+) | 300 nt | IncRNA:noe consensus e-value: 1.3e-08

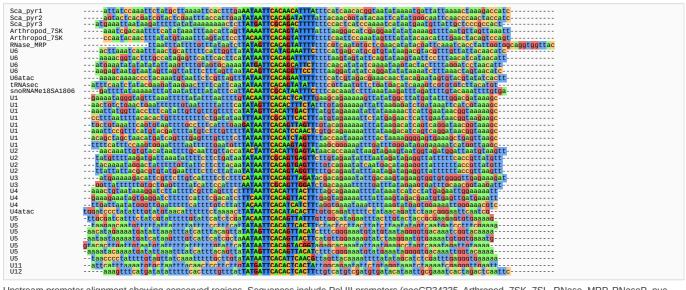
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.97

Sca_pyr3 | LR989929.1:58543835-58544024 (+) | 190 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.90

		Sca_pyr1	Sca_pyr2	Sca_pyr3
	Sca_pyr1	-	51	42
	Sca_pyr2		-	41
	Sca_pyr3			-

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.