Scathophaga stercoraria

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Scathophagidae > Scathophaga

Assembly: GCA 040938175.1 ASM4093817v1 genomic

Sca_ste1 | CM082079.1:57302406-57302882 (+) | 477 nt | IncRNA:noe consensus e-value: 3.1e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

Sca_ste2 | CM082077.1:97985855-97986152 (+) | 298 nt | IncRNA:noe consensus e-value: 4.0e-04

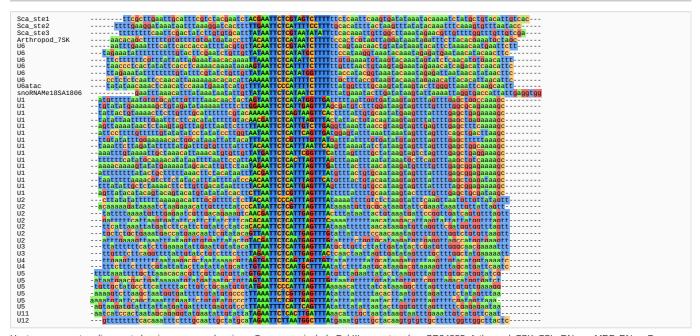
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.90

Sca_ste3 | CM082078.1:74764220-74764511 (-) | 292 nt | IncRNA:noe consensus e-value: 9.0e-07

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.88

	Sca_ste1	Sca_ste2	Sca_ste3
Sca_ste1	-	45	45
Sca_ste2		-	57
Sca_ste3			-

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.