Scaptomyza montana

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

Assembly: GCA 018904305.1 ASM1890430v1 genomic

Sca_mon1 | JAEIGR010000003.1:2514003-2515057 (+) | 1055 nt | IncRNA:noe consensus e-value: 5e-168

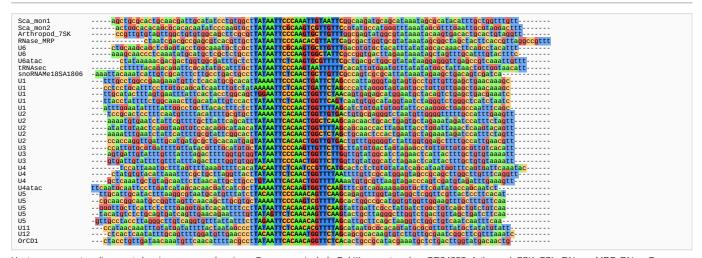
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

Sca_mon2 | JAEIGR010000002.1:20488424-20488785 (+) | 362 nt | IncRNA:noe consensus e-value: 2.0e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.99

	Sca_mon1	Sca_mon2
Sca_mon1	-	24
Sca_mon2		-

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.