Scaptomyza reducta

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

Assembly: GCA 035044485.1 ASM3504448v1 genomic

Sca_red1 | JAWNNV010000206.1:67700-68736 (+) | 1037 nt | IncRNA:noe consensus e-value: 1e-152

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

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Sca_red2 | JAWNNV010000533.1:459467-459834 (+) | 368 nt | IncRNA:noe consensus e-value: 4.8e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.91

	Sca_red1	Sca_red2
Sca_red1	-	23
Sca_red2		-

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.