Scaptomyza tumidula

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

Assembly: GCA 035044465.1 ASM3504446v1 genomic

Sca_tum1 | JAWNNW010000536.1:1568272-1569321 (+) | 1050 nt | IncRNA:noe consensus e-value: 4e-152

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

Sca_tum2 | JAWNNW010000843.1:703653-704023 (-) | 371 nt | IncRNA:noe consensus e-value: 1.9e-09

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

	Sca_tum1	Sca_tum2
Sca_tum1	-	24
Sca_tum2		-

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.