Scaptomyza polygonia

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

Assembly: GCA 035044585.1 ASM3504458v1 genomic

Sca_pol1 | JAWNNU010001672.1:2063245-2064265 (-) | 1021 nt | IncRNA:noe consensus e-value: 2e-165

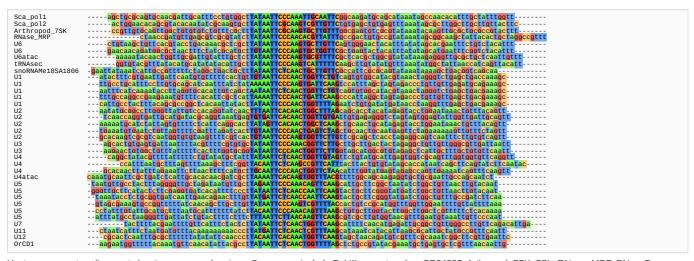
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.82

Sca_pol2 | JAWNNU010001642.1:260348-260748 (-) | 401 nt | IncRNA:noe consensus e-value: 6.9e-06

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

	Sca_pol1	Sca_pol2
Sca_pol1	-	25
Sca_pol2		-

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.