Scaptomyza graminum

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

Assembly: GCA 018901835.1 ASM1890183v1 genomic

Sca_gra1 | JAEIFL010000243.1:10591107-10592163 (-) | 1057 nt | IncRNA:noe consensus e-value: 1e-169

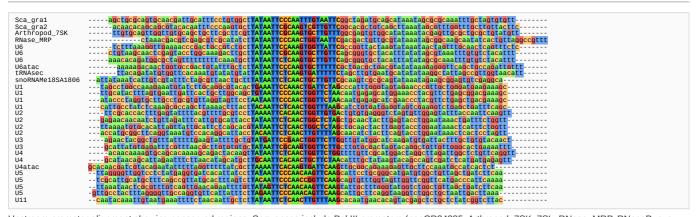
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

Sca_gra2 | JAEIFL010000002.1:14736804-14737196 (+) | 393 nt | IncRNA:noe consensus e-value: 1.6e-12

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

| | Sca_gra1 | Sca_gra2 |
|----------|----------|----------|
| Sca_gra1 | - | 24 |
| Sca_gra2 | | - |

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.