## Scaptomyza pallida

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

Assembly: GCA 018152965.1 ASM1815296v1 genomic

## Sca\_pal1 | JAECXP010000238.1:5543804-5544886 (-) | 1083 nt | IncRNA:noe consensus e-value: 2e-163

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

## Sca\_pal2 | JAECXP010000128.1:3386937-3387418 (-) | 482 nt | IncRNA:noe consensus e-value: 2.3e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.90

	Sca_pal1	Sca_pal2
Sca_pal1	-	26
Sca_pal2		-

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.