## Scaptomyza hsui

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

Assembly: GCA 018152825.1 ASM1815282v1 genomic

#### Sca\_hsu1 | JAECXO010000165.1:2232359-2233474 (-) | 1116 nt | IncRNA:noe consensus e-value: 5e-167

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.87

#### Sca\_hsu2 | JAECXO010000001.1:3224149-3224632 (-) | 484 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

### Sca\_hsu3 | JAECXO010000001.1:15285777-15286104 (+) | 328 nt | IncRNA:noe consensus e-value: 8.1e-15

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

### Sca\_hsu4 | JAECXO010000269.1:10354667-10354883 (-) | 217 nt | IncRNA:noe consensus e-value: 1.2e-08

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.93

# Sca\_hsu5 | JAECXO010000269.1:10351671-10351886 (-) | 216 nt | IncRNA:noe consensus e-value: 5.9e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.93

BACBTBABABATAMACAACCACBTBCBTAATTCBBBTCBAATTAACATAATBATCBCCTTTTT

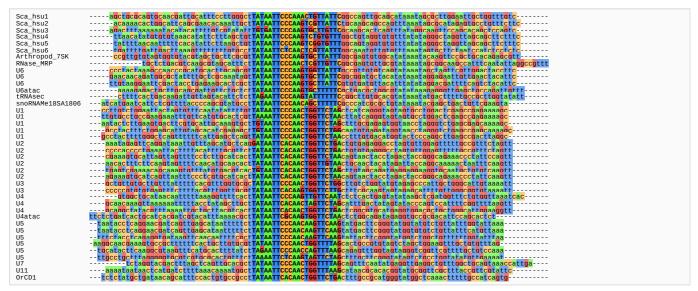
#### Sca\_hsu6 | JAECXO010000269.1:12864086-12864214 (-) | 129 nt | IncRNA:noe consensus e-value: 1.4e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

GGCSGTCEASCGTCTCACAATGTTAAASGTTSATCACATCCCCSACTAATTGTSACTAAACAACTCCAGTAAATTGTSAGCACGCTCCGASAAGGGAATCATATTCASCTCSGTTTSATCACCTATTTCASCTC

	Sca_hsu1	Sca_hsu2	Sca_hsu3	Sca_hsu4	Sca_hsu5	Sca_hsu6
Sca_hsu1	-	27	21	14	15	7
Sca_hsu2		-	43	33	34	19
Sca_hsu3			-	48	47	30
Sca_hsu4				-	91	48
Sca_hsu5					-	50
Sca_hsu6						-

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.