

Taxonomic lineage: Brachycera > Muscomorpha > Sphaeroceroidea > Heleomyzidae > Suillia

Assembly: GCA_949127995.1_idSuiVari3.1_genomic

Sui var1 | OX421845.1:22379843-22380667 (-) | 825 nt | lncRNA: noe consensus e-value: 1.1e-29

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.87

[illegible]

Sui var2 | OX421842.1:60449687-60449996 (-) | 310 nt | IncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.94

GGCGGTGGAAGTCTTCGAATAGAAGTGTTGCTGCATCCCCGCCAATCAATTGCTGGAATTTTTAAAAAAATCACACAGAGATCGTAACAGATCAGTCAGGAGAGATAAAAAAAAAATGTCGCTAAAAAAAAGCTTTTAATTCGTCGAGGG
TTTGGGTTTGGAAAGGCGATTAACATATCGATTCTCCCATTCCTTCGATTCAATAATGAAAAAATGGTACCTATCCGCTGGACCATGGATACGGTCGCTCTACATGAGAAATTTTCGCTATGAGACCATTTTGAACACGGTGTGATCGCCC

	Sui_var1	Sui_var2
Sui_var1	-	24
Sui_var2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.