## Sarcophaga caerulescens

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Sarcophagidae > Sarcophaga > Robineauella

Assembly: GCA 927399465.1 idSarCaer1.1 genomic

## Sar\_cae2 | OV656867.1:96704713-96704974 (+) | 262 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 11nt PSE: 0.99

## Sar\_cae3 | OV656867.1:96334780-96335021 (-) | 242 nt | IncRNA:noe consensus e-value: 1.4e-03

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 18nt PSE: 0.98

	Sar_cae2	Sar_cae3
Sar_cae2	-	47
Sar_cae3		-

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.