Sarcophaga rosellei

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

Assembly: GCA 930367235.1 idSarRose1.1 genomic

Sar_ros1 | OV884017.1:60420551-60421089 (-) | 539 nt | IncRNA:noe consensus e-value: 2.0e+00

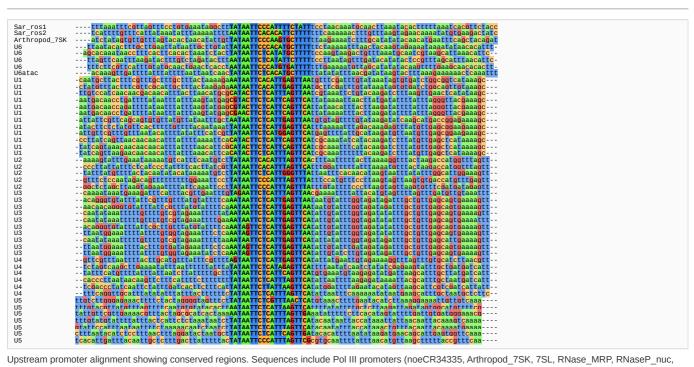
5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 12nt PSE: 0.89

Sar_ros2 | OV884020.1:89459762-89460003 (-) | 242 nt | IncRNA:noe consensus e-value: 5.9e-04

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 16nt PSE: 0.94

	Sar_ros1	Sar_ros2
Sar_ros1	-	34
Sar_ros2		-

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.