Sarcophaga peregrina

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

Assembly: GCA 014635995.1 ASM1463599v1 genomic

Sar_per1 | CM025789.1:71515331-71515889 (-) | 559 nt | IncRNA:noe consensus e-value: 1.1e+00

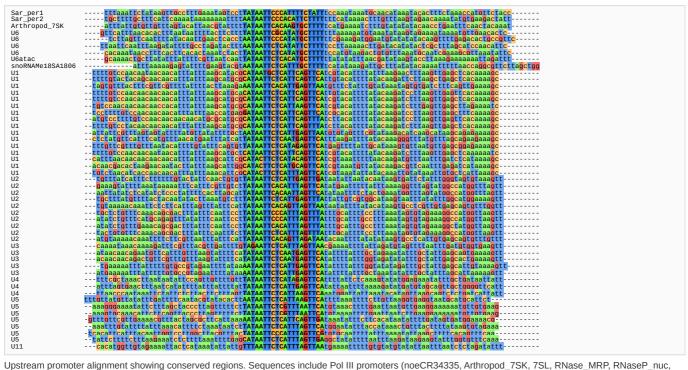
5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.92

Sar_per2 | CM025792.1:95096047-95096294 (-) | 248 nt | IncRNA:noe consensus e-value: 1.2e-03

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 22nt PSE: 0.97

	Sar_per1	Sar_per2
Sar_per1	-	33
Sar_per2		-

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.