

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Sarcophagidae > Sarcophaga > Boettcherisca
Assembly: GCA_014635995.1_ASM1463599v1_genomic

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

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

GGCGGGTCTTGAAATCCCTCTGACAAAGGTTGTTACATCCCTTGATTGTGAAATGTTTCAAAATCAAAAAAAGGATTAATAAATCAATGCTTTAAAAACAAAAAGGAAAGTTTGTTAAAAACAAAAACACAACAAAAATACTCAGGAGTT
TGAAGCTTTGGTGCCAGAGTGTGTTAAAAACAAAGCTTAAGAGGAATGAGACCCCATTCAGGGGTGTGACCGCCATTTTTTTTTTTTTTTTTTTTTT

	Sar_per1	Sar_per2
Sar_per1	-	33
Sar_per2		-

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.