Sarcophaga bullata

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

Assembly: GCA 005959815.1 ROC SBull 1.0 genomic

Sar_bul1 | QOCX01000147.1:90044-90583 (+) | 540 nt | IncRNA:noe consensus e-value: 1.6e+00

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.93

Sar_bul2 | QOCX01009253.1:1507-1729 (-) | 223 nt | IncRNA:noe consensus e-value: 1.1e-04

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.98

Sar_bul3 | QOCX01013547.1:3251-3474 (+) | 224 nt | IncRNA:noe consensus e-value: 1.5e-05

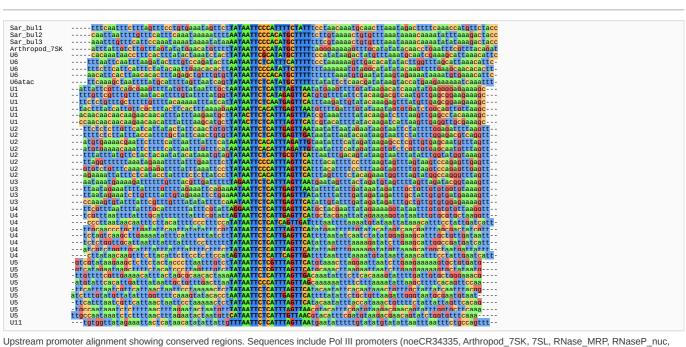
5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.98

GGCGGTCTTGAATTCCCTGTGACAAGGTTGTTCACATCCCTTAATTGTGAAAATTTCCAAATTCAAAAAAAGAATTAAAAGTTAAAAATTAATGCTTAAAAATATGAAAGGAAAGTTTGTTAAAAACAAAAACACAACATATTCAGGAGTTTTGAAGCCTTAAGGGTGACCGCCAACTTTTTTT

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	Sar_bul1	Sar_bul2	Sar_bul3
Sar_bul1	-	31	32
Sar_bul2		-	97
Sar_bul3			-

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.