Sarcophaga subvicina

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

Assembly: GCA 936449025.2 idSarSubv1.2 genomic

Sar_sub2 | OW388083.2:110558724-110558980 (+) | 257 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 1.00

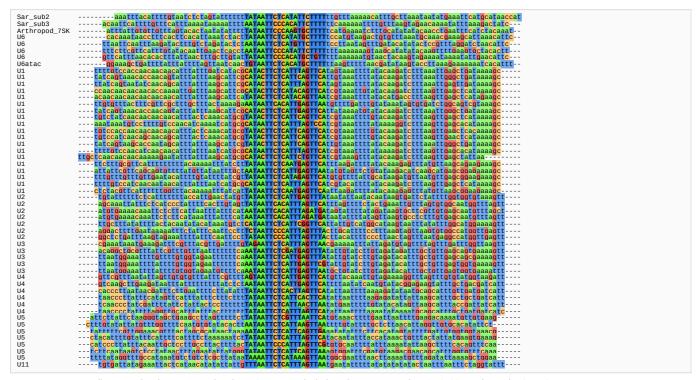
Sar_sub3 | OW388083.2:110306282-110306506 (-) | 225 nt | IncRNA:noe consensus e-value: 1.9e-05

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.99

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| | Sar_sub2 | Sar_sub3 |
|----------|----------|----------|
| Sar_sub2 | - | 47 |
| Sar_sub3 | | - |

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.