Metopia argyrocephala

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Sarcophagidae > Metopia

Assembly: GCA_963576795.1_idMetArgy1.1_genomic

Met_arg1 | OY756210.1:49545379-49545972 (-) | 594 nt | IncRNA:noe consensus e-value: 4.5e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.84

Met_arg2 | OY756210.1:21865608-21865835 (+) | 228 nt | IncRNA:noe consensus e-value: 1.1e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

| | Met_arg1 | Met_arg2 |
|----------|----------|----------|
| Met_arg1 | - | 28 |
| Met_arg2 | | - |

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.