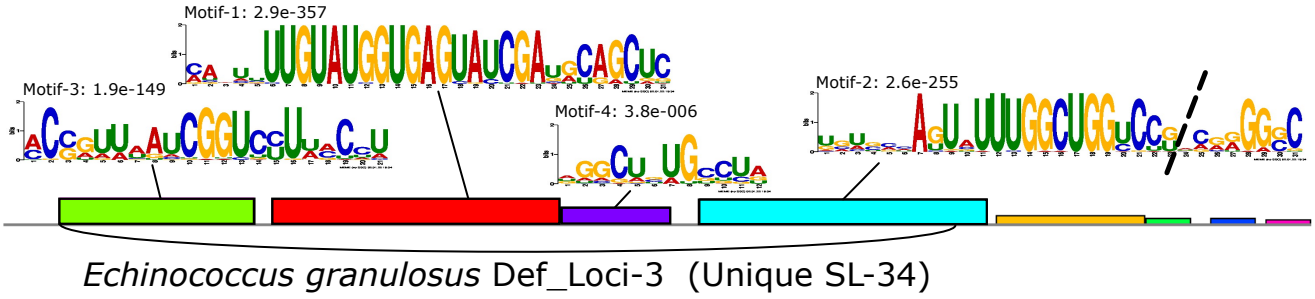
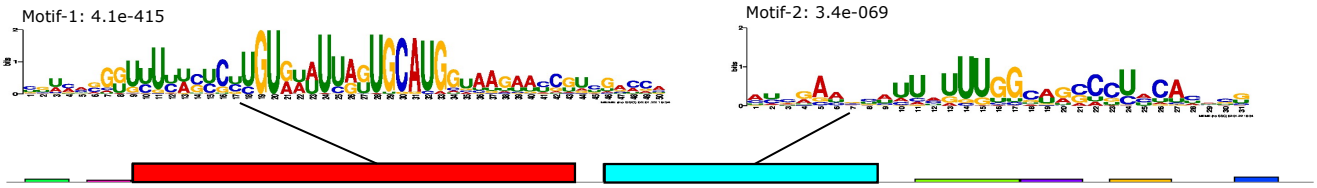
A) SL-RNA Trimming Cestoda

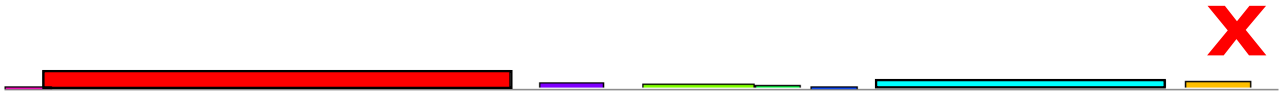


Echinococcus granulosus Def_Loci-3 (Unique SL-34)

B) SL-RNA Trimming Trematoda Round 1

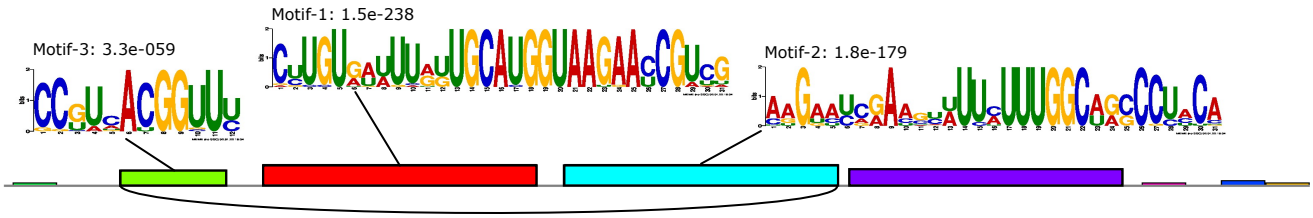


Schistosoma mansoni Def_Loci-15 (Unique SL-57)



Paragonimus westermani Def_Loci-44 (NA)

C) SL-RNA Trimming Trematoda Round 2



Schistosoma mansoni Def_Loci-15 (Unique SL-57)

Clonorchis sinensis Def_Loci-85/86 (Unique SL-1)

Supplementary Figure 1: Overview of the trimming process based on MEME motifs. A) In Cestodes the process was straightforward as 4 highly conserved motifs were identified. The trimming was decided to be conducted at the start of Motif-3 and inside Motif-2. This was done because the second less conserved half was less recognizable outside Taeniidae. Trematoda on the other hand required one round of filtration B) as only two motifs were predicted with unclear boundaries. After the exclusion of sequences with poor matches for Motif-2, like Paragonimus westermani Def_Loci-44, the analysis was repeated in a second round C). Here 3 Motifs were identified consistently in both the selected sequences and the reference SL-RNAs for Trematoda. The boundaries of Motifs -2 and -3 were again selected as the boundary of SL-RNAs. The loci Def_Loci-85 and -86 of Clonorchis sinensis were included in the final analysis despite lacking Motif-2 because it's SL TAG "Trematoda_E" was found in the species C. sinensis, Fasciola gigantica, Fasciola hepatica and Fasciolopsis buski. Despite this SL TAG low numbers, its phylogenetic distribution suggests there are SL-RNAs with "Trematoda_E" exists within this lineage, even if they possess limited functionality, and no better representative could be found.