

Fig. 1: expression profile of genes encoding the proteins involved in the miRNA pathway found in *Schistosoma haematobium* Egypt.

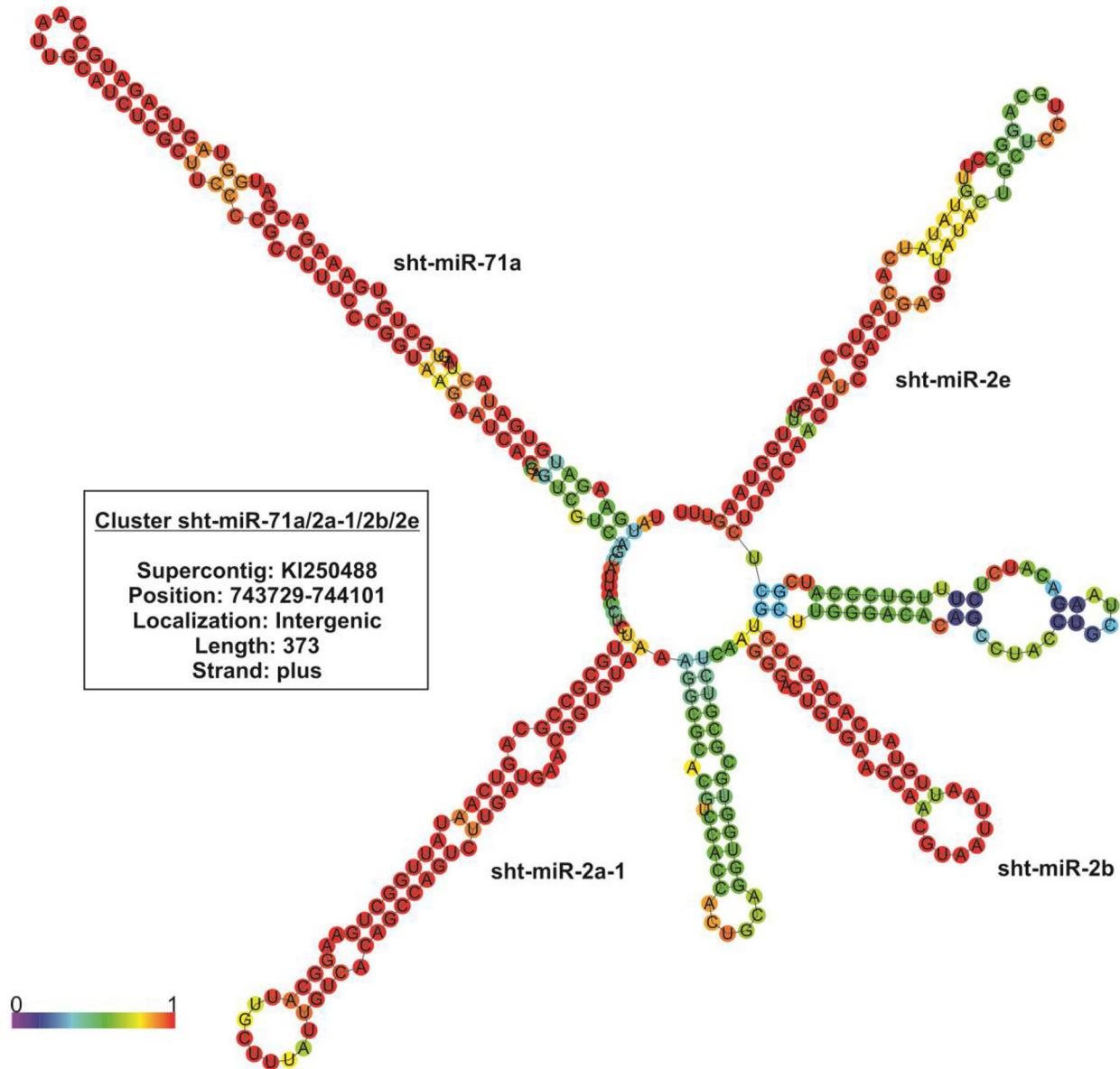
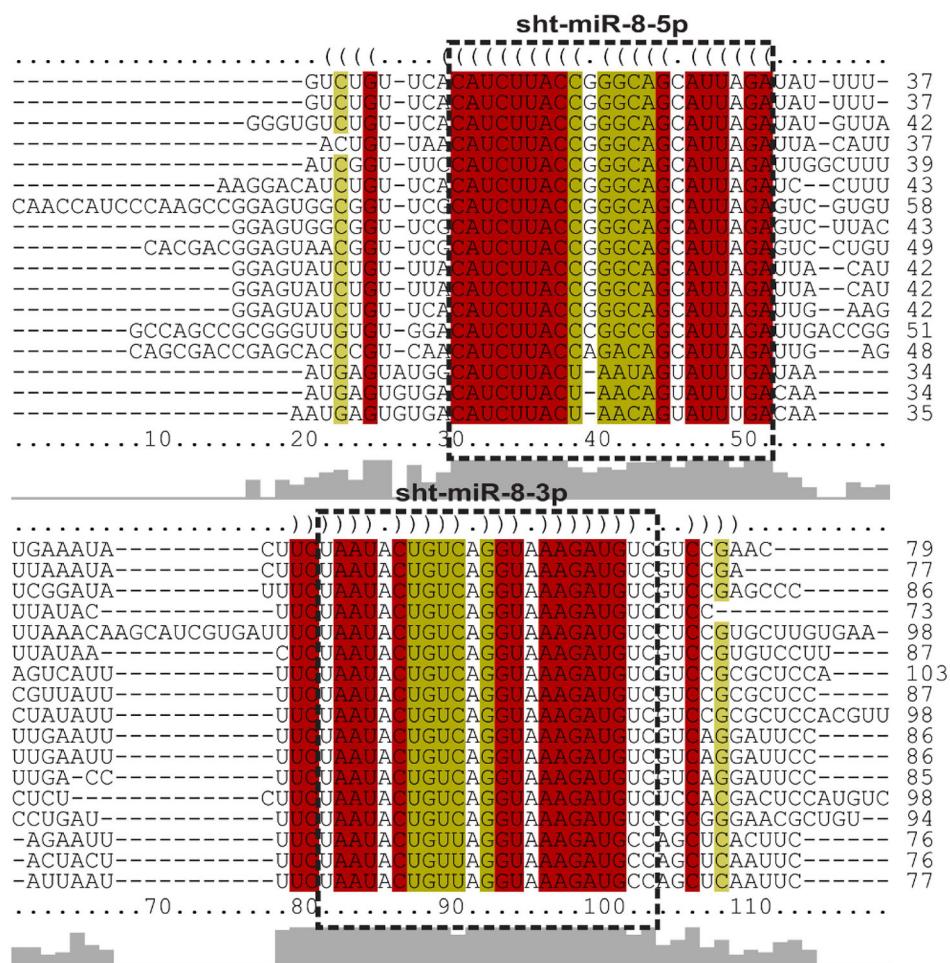


Fig. 2: RNA secondary structure of the cluster sht-miR-71a/sht-miR-2a-1/sht-miR-2b/sht-miR-2e; sht: *Schistosoma haematobium*.

**sht-miR-8**

aae-mir-8/1-79  
cqu-mir-8/1-77  
aga-mir-8/1-86  
tca-mir-8/1-73  
dpu-mir-8/1-98  
dme-mir-8/1-87  
mse-mir-8/1-103  
hme-mir-8/1-87  
bmo-mir-8/1-102  
nvi-mir-8/1-86  
nlo-mir-8/1-86  
ame-mir-8/1-85  
cte-mir-8/1-98  
isc-mir-8/1-94  
sjp-mir-8/1-76  
smp-mir-8/1-76  
sht-miR-8/1-77



aae-mir-8/1-79	79
cqu-mir-8/1-77	77
aga-mir-8/1-86	86
tca-mir-8/1-73	73
dpu-mir-8/1-98	98
dme-mir-8/1-87	87
mse-mir-8/1-103	103
hme-mir-8/1-87	87
bmo-mir-8/1-102	CGUC 102
nvi-mir-8/1-86	86
nlo-mir-8/1-86	86
ame-mir-8/1-85	85
cte-mir-8/1-98	98
isc-mir-8/1-94	94
sjp-mir-8/1-76	76
smp-mir-8/1-76	76
sht-miR-8/1-77	77

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Fig. 3: alignment of sht-miR-8 pre-miRNA and their orthologs; sht: *Schistosoma haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*; isc: *Ixodes scapularis*; cte: *Capitella teleta*; ame: *Apis mellifera*; nlo: *Nasonia longicornis*; nvi: *Nasonia vitripennis*; bmo: *Bombyx mori*; hme: *Heliconius melpomene*; mse: *Manduca sexta*; dme: *Drosophila melanogaster*; dpu: *Daphnia pulex*; tca: *Tribolium castaneum*; aga: *Anopheles gambiae*; cqu: *Culex quinquefasciatus*; and aae: *Aedes aegypti*.

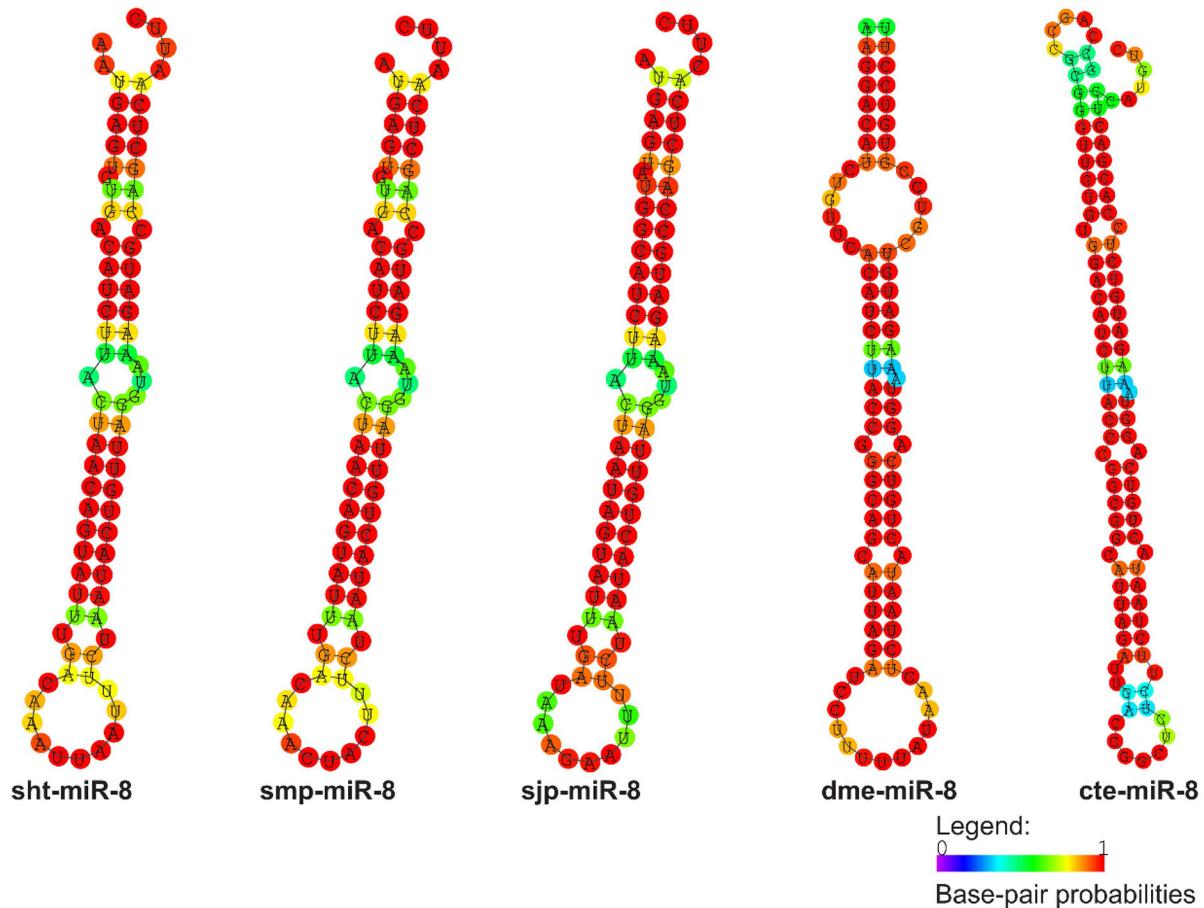


Fig. 4: secondary structures of the sht-miR-8 pre-miRNA and their orthologs; sht: *Schistosoma haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*; dme: *Drosophila melanogaster*; and cte: *Capitella teleta*.

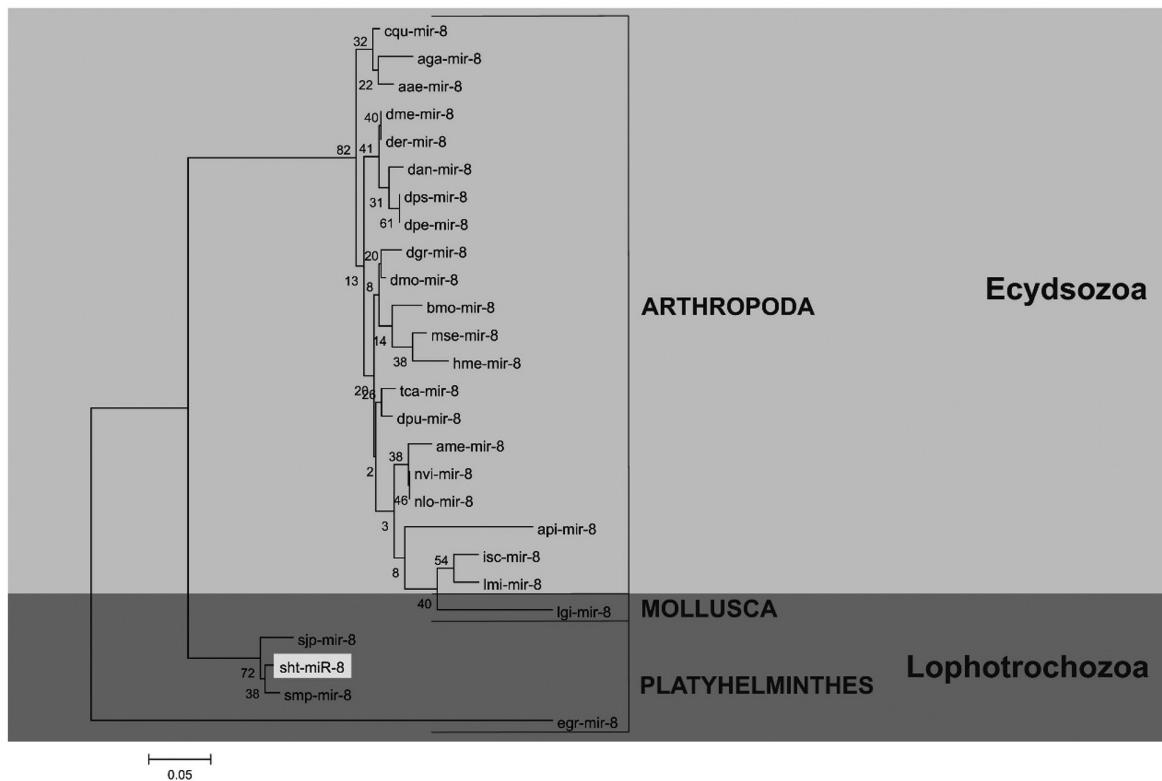


Fig. 5: phylogenetic tree generated by phylogenetic analysis to sht-miR-8 precursor miRNAs found in *Schistosoma haematobium* Egypt and their orthologs; sht: *S. haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*; egr: *Echinococcus granulosus*; lgi: *Lottia gigantean*; nvi: *Nasonia vitripennis*; ame: *Apis mellifera*; dpu: *Daphnia pulex*; tca: *Tribolium castaneum*; hme: *Heliconius Melpomene*; mse: *Manduca sexta*; bmo: *Bombyx mori*; dmo: *Drosophila mojavensis*; dgr: *Drosophila grimshtwi*; dpe: *Drosophila persimilis*; dps: *Drosophila pseudoobscura*; dan: *Drosophila ananassae*; der: *Drosophila erecta*; dme: *D. melanogaster*; aae: *Aedes aegypti*; aga: *Anopheles gambiae*; and cqu: *Culex quinquefasciatus*.

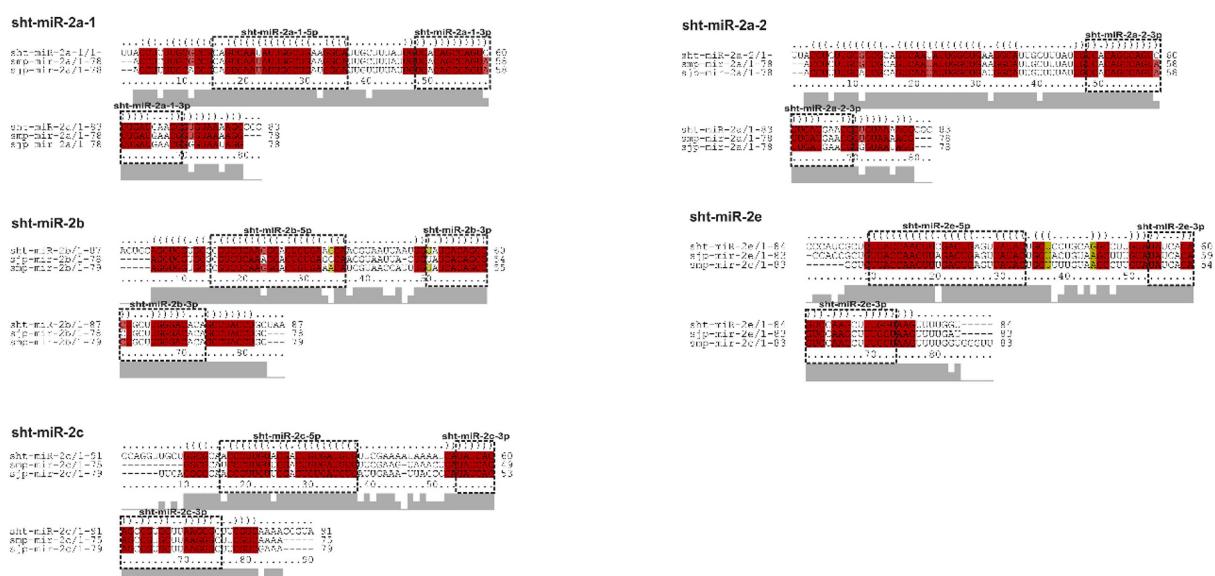


Fig. 6: alignment of the sht-miR-2 family pre-miRNAs and their orthologs; sht: *Schistosoma haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*.

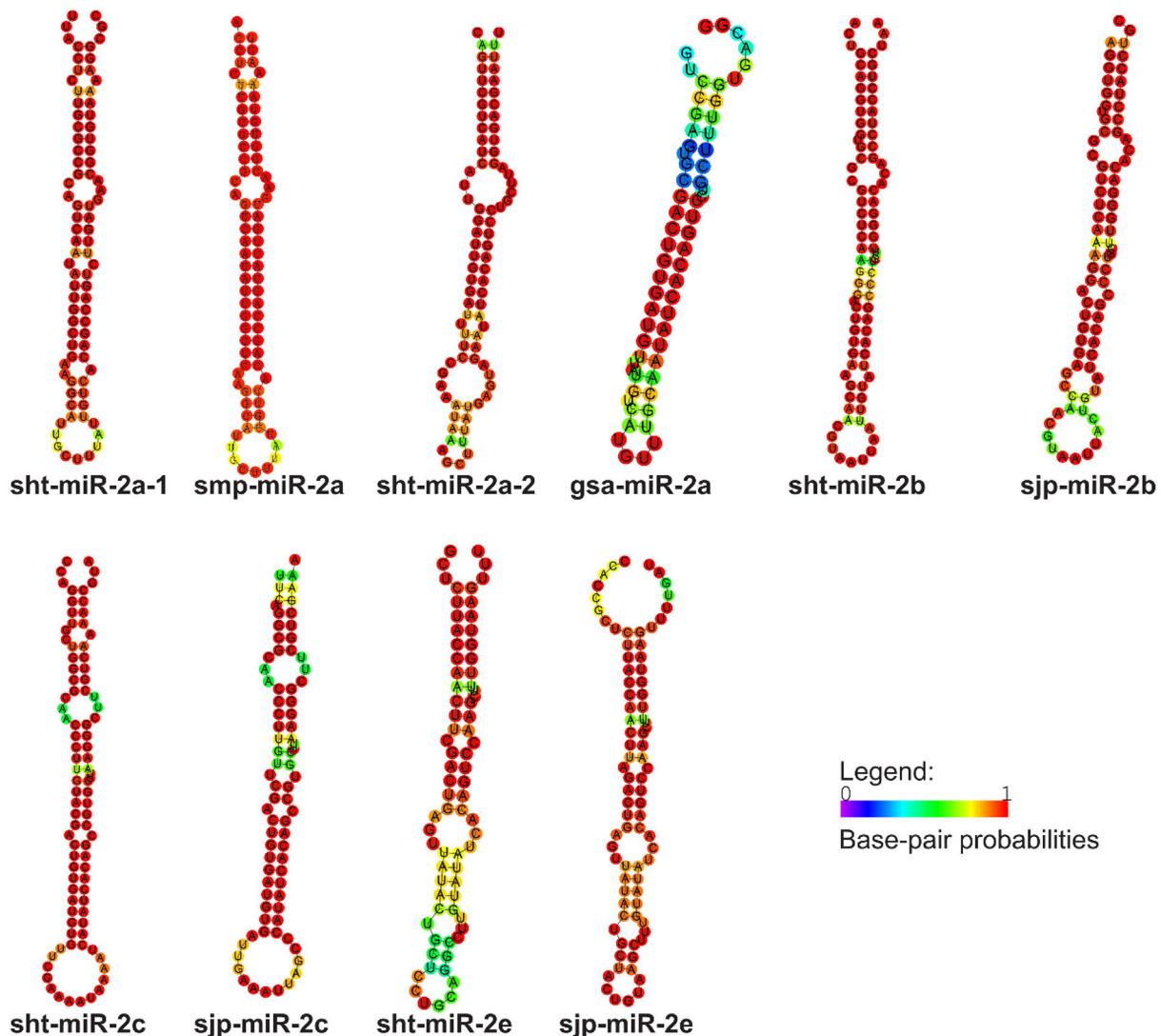


Fig. 7: secondary structures of the sht-miR-2 family pre-miRNAs and their orthologs; smp: *Schistosoma mansoni*; sht: *S. haematobium*; gsa: *Gyrodactylus salaris*.

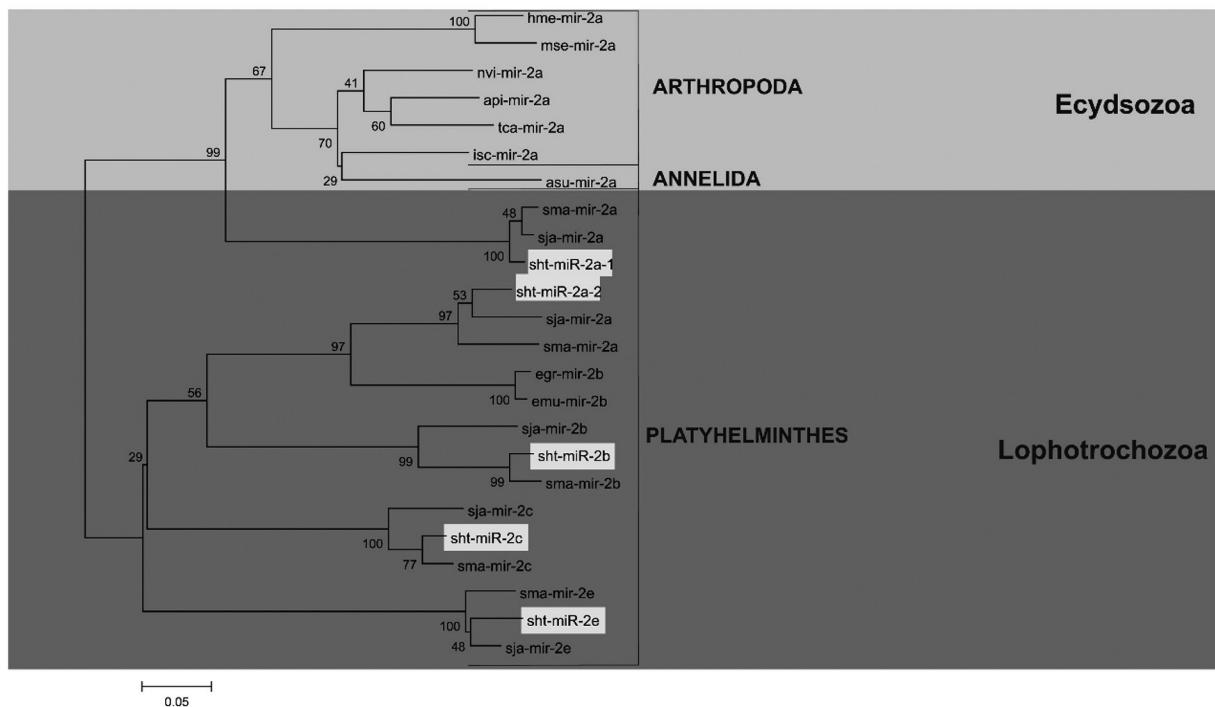


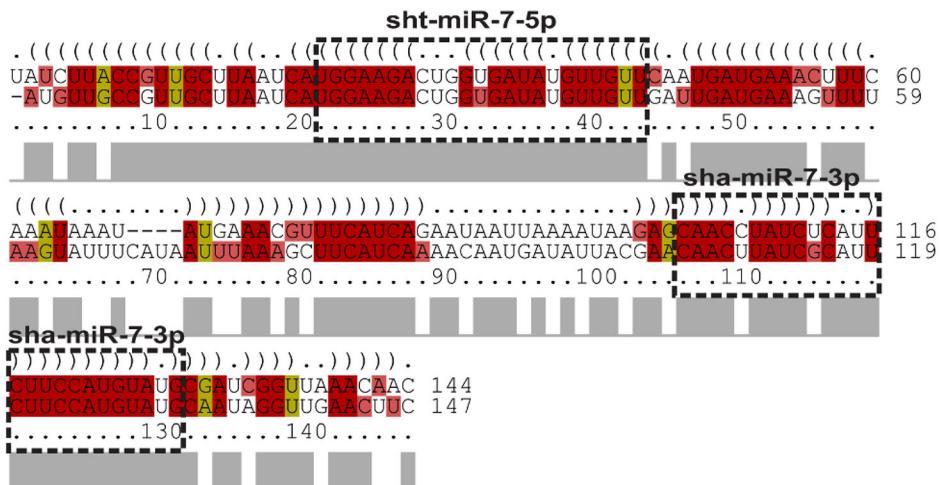
Fig. 8: tree generated from the phylogenetic analysis to sht-miR-2 family precursor miRNAs and their orthologs; sht: *Schistosoma haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*; emu: *Echinococcus multilocularis*; egr: *Echinococcus granulosus*; asu: *Ascaris suum*; isc: *Ixodes scapularis*; tca: *Tribolium castaneum*; api: *Acyrthosiphon pisum*; nvi: *Nasonia vitripennis*; mse: *Manduca sexta*; and hme: *Heliconius melpomene*. Fig. 8: tree generated from the phylogenetic analysis to sht-miR-2 family precursor miRNAs and their orthologs; sht: *Schistosoma haematobium*; smp: *S. mansoni*; sjp: *S. japonicum*; emu: *Echinococcus multilocularis*; egr: *Echinococcus granulosus*; asu: *Ascaris suum*; isc: *Ixodes scapularis*; tca: *Tribolium castaneum*; api: *Acyrthosiphon pisum*; nvi: *Nasonia vitripennis*; mse: *Manduca sexta*; and hme: *Heliconius melpomene*.

**sht-miR-7**

sht-miR-7/1-144  
sjp-mir-7/1-147

sht-miR-7/1-144  
sjp-mir-7/1-147

sht-miR-7/1-144  
sjp-mir-7/1-147

**sht-miR-7b**

mmu-mir-7b/1-111  
rno-mir-7b/1-110  
cgr-mir-7b/1-80  
sht-miR-7b/1-125

mmu-mir-7b/1-111  
rno-mir-7b/1-110  
cgr-mir-7b/1-80  
sht-miR-7b/1-125

mmu-mir-7b/1-111  
rno-mir-7b/1-110  
cgr-mir-7b/1-80  
sht-miR-7b/1-125

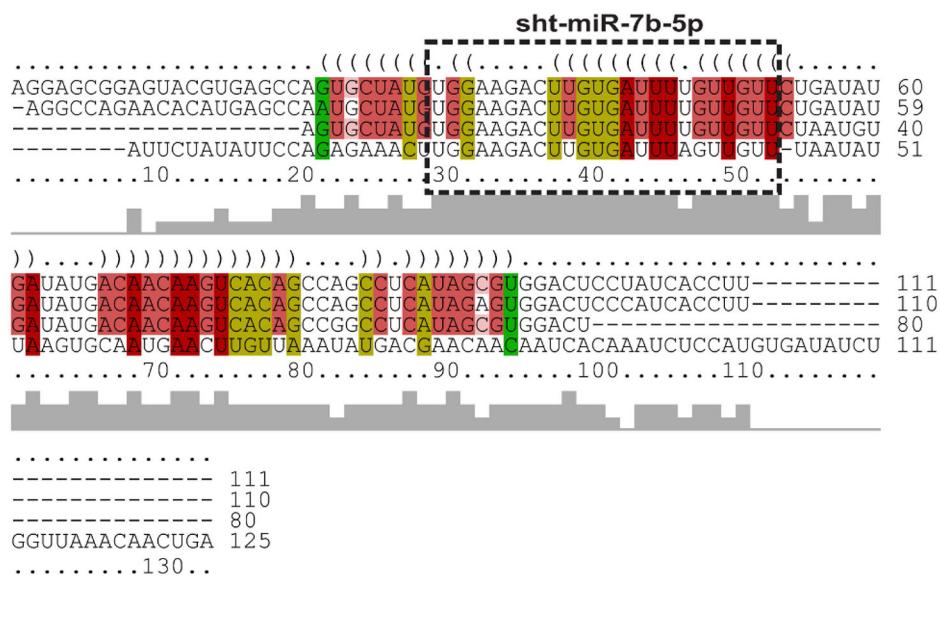


Fig. 9: alignment of the sht-miR-7 and sht-miR-7b sequences and their orthologs; sht: *Schistosoma haematobium*; sjp: *S. japonicum*; mmu: *Mus musculus*; rno: *Rattus norvegicus*; cgr: *Cricetulus griseus*.

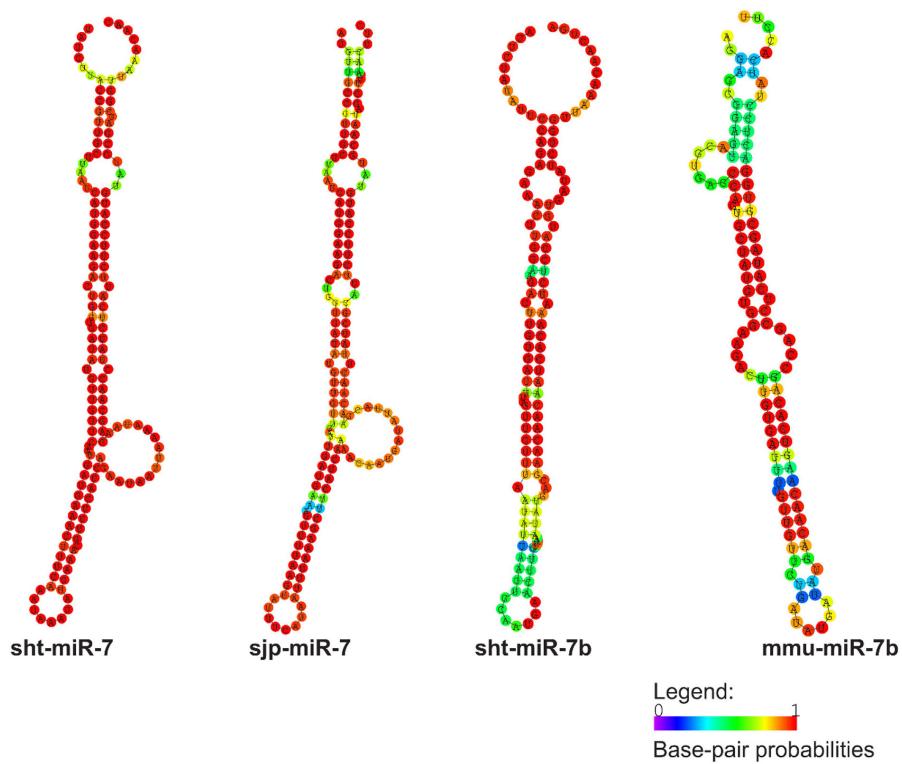


Fig. 10: secondary structures of the sht-mir-7 and sht-mir-7b pre-miRNAs and their orthologs; sht: *Schistosoma haematobium*; sjp: *S. japonicum*; mmu: *Mus musculus*.

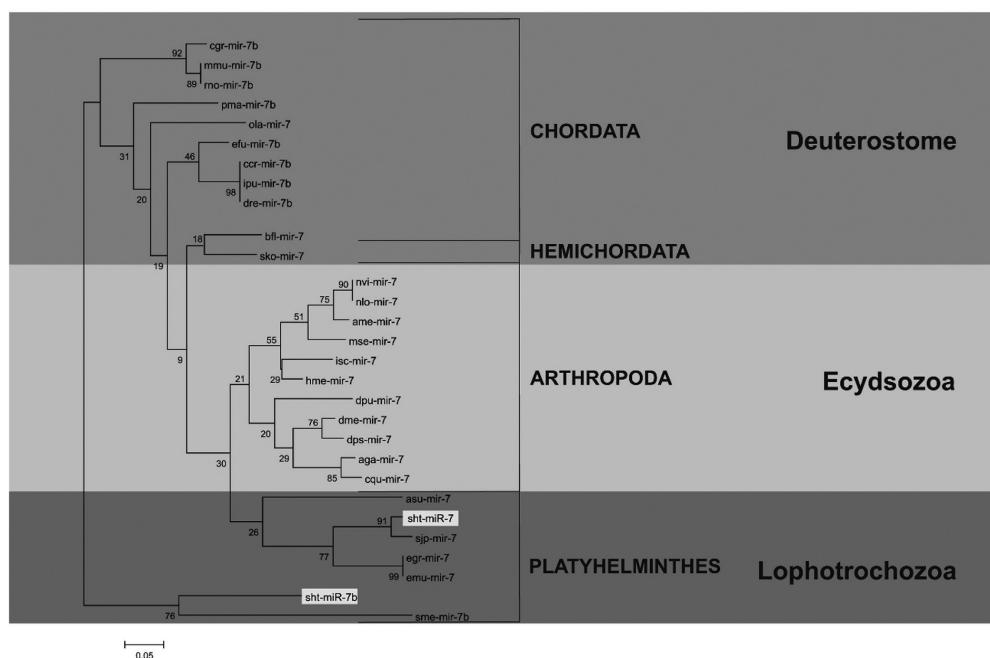


Fig. 11: phylogenetic tree of sht-miR-7 family precursor miRNAs and their orthologs; sht: *Schistosoma haematobium*; sjp: *S. japonicum*; sme: *S. mediterranea*; egr: *Echinococcus granulosus*; emu: *E. multilocularis*;asu: *Ascaris suum*; cqu: *Culex quinquefasciatus*; aga: *Anopheles gambiae*; dps: *Drosophila pseudoobscura*; dme: *D. melanogaster*; dpu: *Daphnia pulex*; hme: *Heliconius Melpomene*; isc: *Ixodes scapularis*; mse: *Manduca sexta*; ame: *Apis mellifera*; nlo: *Niphona longicornis*; nvi: *Nasonia vitripennis*; sko: *Saccoglossus kowalevskii*; bfl: *Branchiostoma floridae*; dre: *Danio rerio*; ipu: *Ictalurus punctatus*; ccr: *Cyprinus carpio*; efu: *Eptesicus fuscus*; ola: *Oryzias latipes*; pma: *Petromyzon marinus*; rno: *Rattus norvegicus*; mmu: *Mus musculus*; and cgr: *Cricetulus griseus*.