



**Supplementary file 4. Phylogenetic relationships between mir-71 microRNAs in *Schistosoma* and *Schmidtea*.** MicroRNA precursor sequences were aligned with ClustalX 2 [1] and phylogenetic trees built with MEGA 5 [2] using the Maximum-Likelihood (ML) and Neighbor-Joining (NJ) routines are recommended. The tree in the figure shows the topology of the NJ tree and the bootstrap percentages for NJ (above each branch) and ML (below each branch).

#### References

1. Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, et al. (2007) Clustal W and Clustal X version 2.0. *Bioinforma Oxf Engl* 23: 2947–2948.
2. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, et al. (2011) MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Mol Biol Evol* 28: 2731–2739.