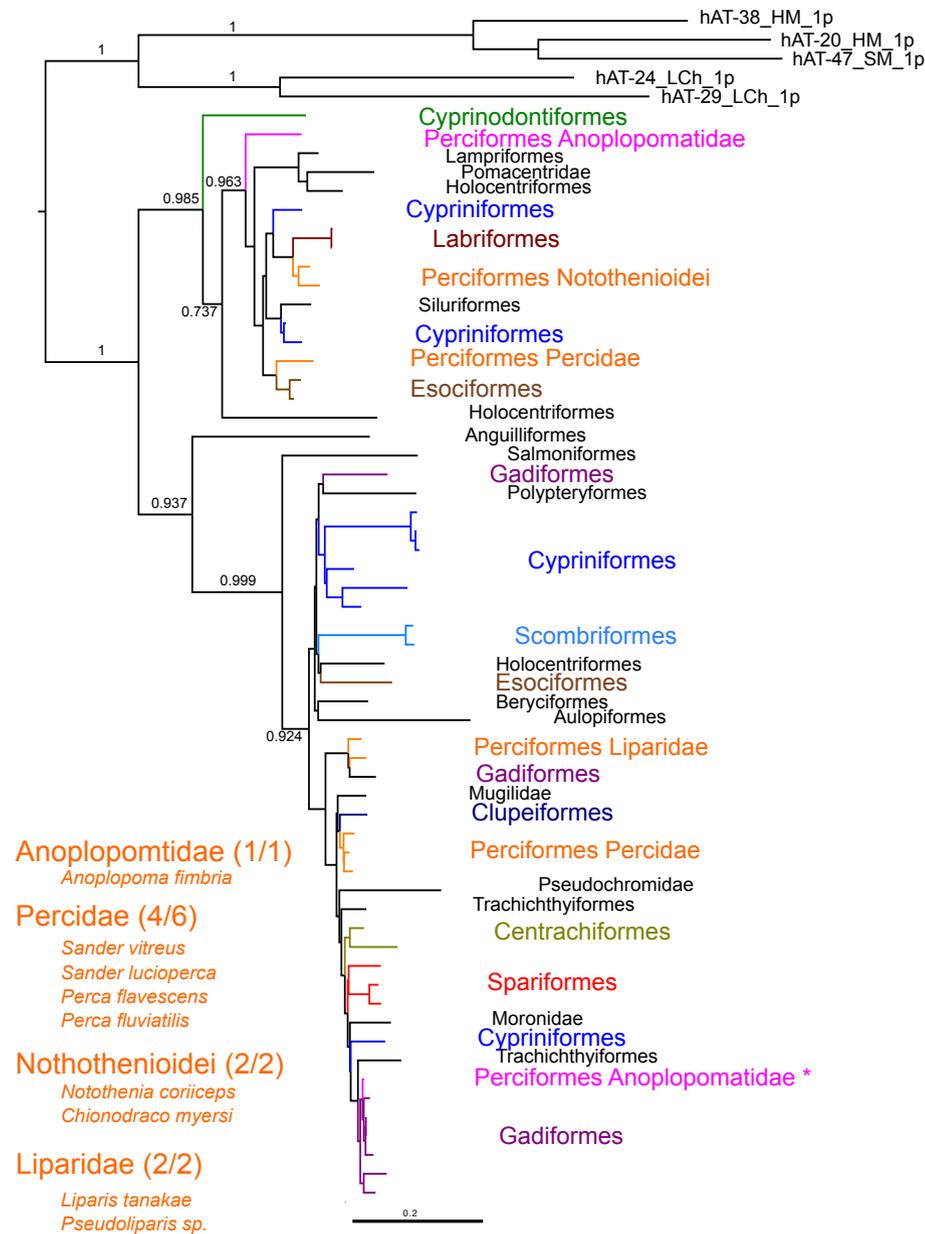


hAT (863 AA)



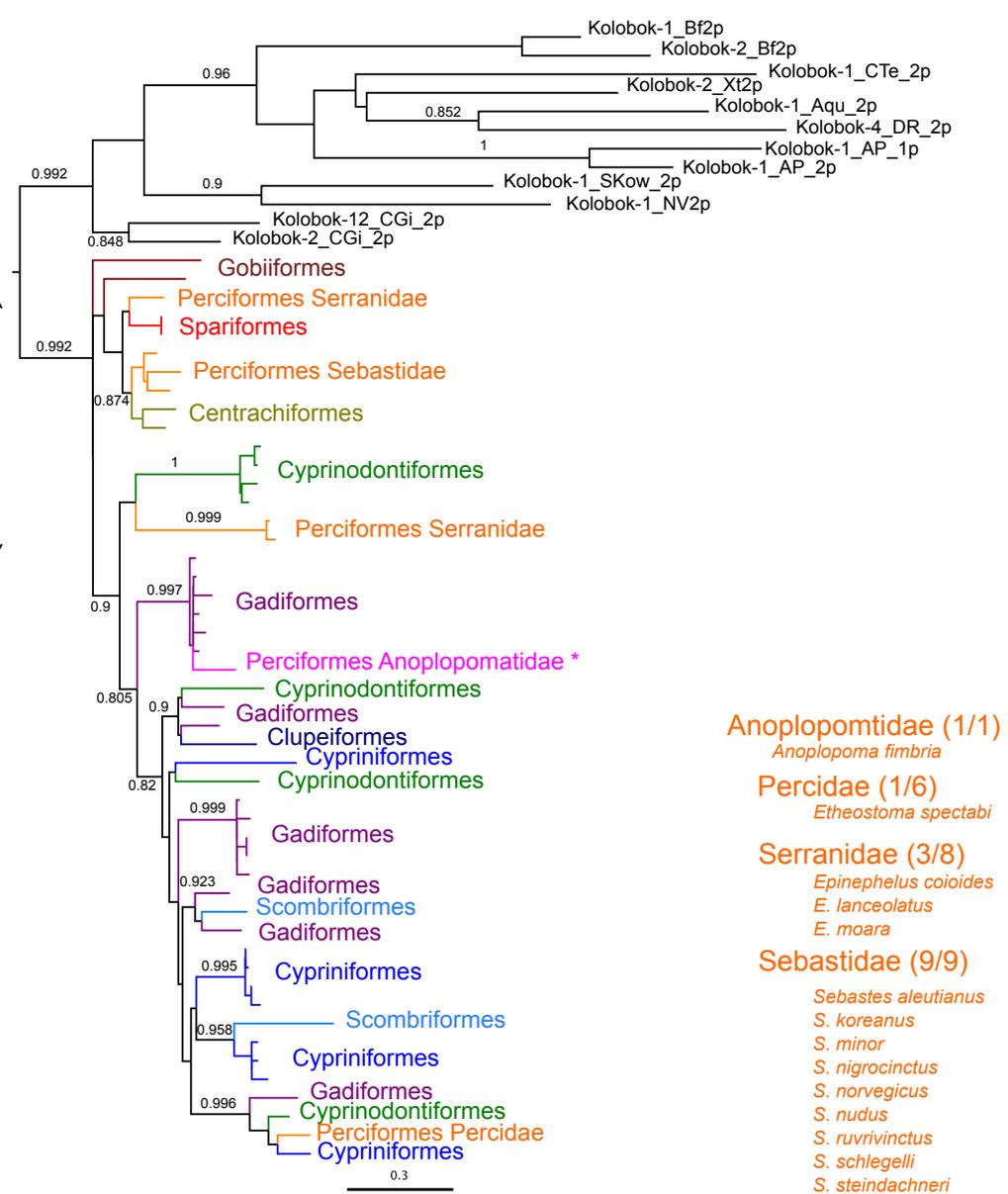
Anoplopomtidae (1/1)
Anoplopoma fimbria

Percidae (4/6)
Sander vitreus
Sander lucioperca
Perca flavescens
Perca fluviatilis

Nothotheniioidei (2/2)
Nothothenia coriiceps
Chionodraco myersi

Liparidae (2/2)
Liparis tanakae
Pseudoliparis sp.

Kolobok (137 AA)



Anoplopomtidae (1/1)
Anoplopoma fimbria

Percidae (1/6)
Etheostoma spectabi

Serranidae (3/8)
Epinephelus coioides
E. lanceolatus
E. moara

Sebastidae (9/9)
Sebastes aleutianus
S. koreanus
S. minor
S. nigrocinctus
S. norvegicus
S. nudus
S. ruvrivinctus
S. schlegelli
S. steindachneri

Supplemental Figure S2. Phylogenetic trees of amino acid sequences of transposases from longer elements related to the Y- (hAT) and X-specific (Kolobok) MITEs. Trees were rooted using Repbase sequences (in black) as an outgroup as they appear more distantly related. Different colors correspond to the different main orders in which related elements have been identified. Numbers above the main branch represent the robustness SH test. Perciformes sequences are in orange, and pink for *Anoplopoma fimbria*. The species names where sequences were found (among Perciformes) are indicated next to the trees, classified by families. Number of species out of number of sequenced species. The asterisk for Anoplopomatidae sequences indicates the sequence found in the new assembly (Other *Anoplopoma fimbria* sequences are from the NCBI assembly).