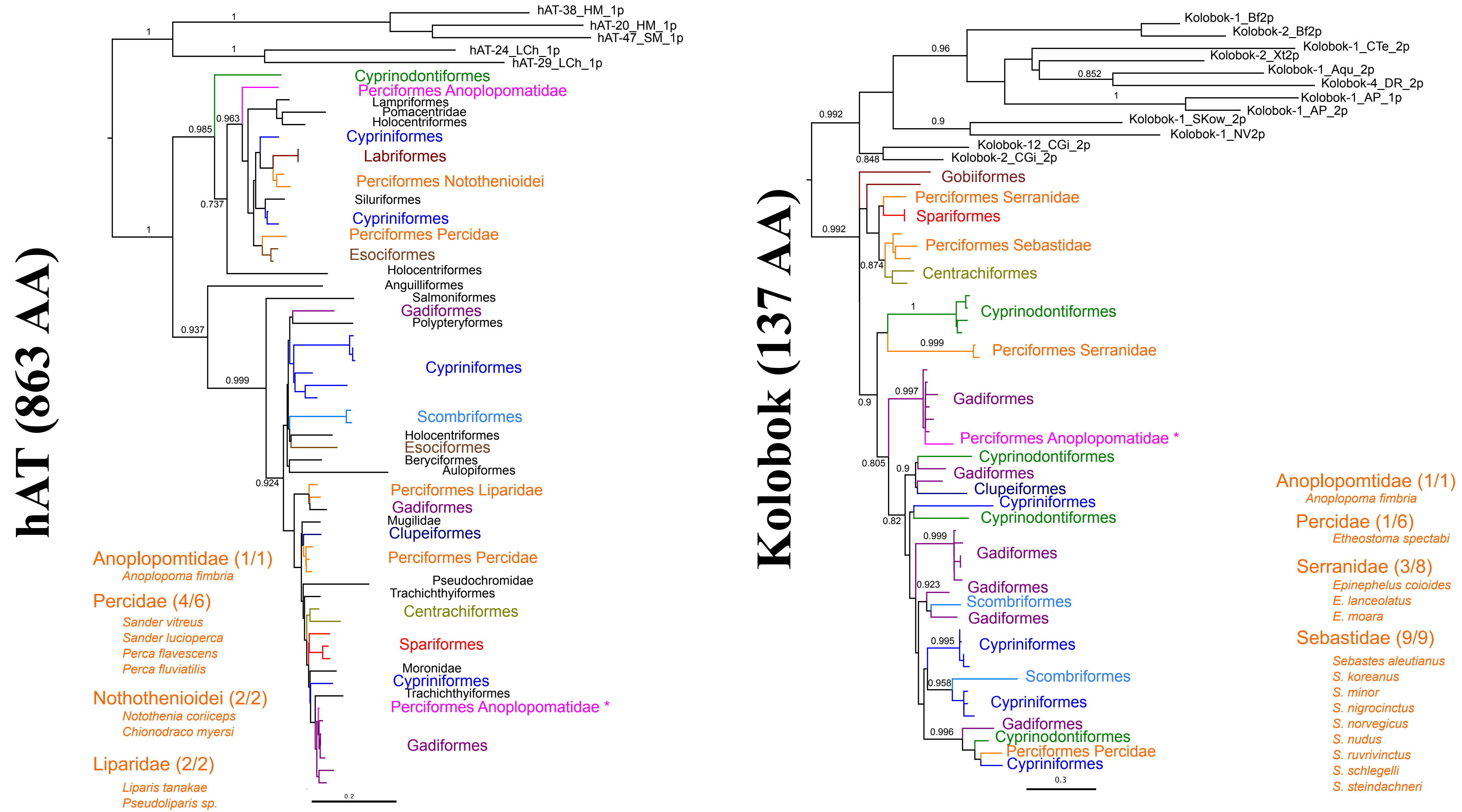

Supplemental Figure S2. Phylogenetic trees of amino acid sequences of transposases from longer elements related to the Y- (hAT) and X-specific (Kolobok) MITEs. Trees were rooted using Repbase sequences (in black) as an outgroup as they appear more distantly related. Different colors correspond to the 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).