Figure S3  Phylogenetic placement of MoTeR1 based on reverse transcriptase and REL-domain alignments. A) based on RT protein sequences; B) based on REL-domain sequences. Evolutionary histories were inferred using the Neighbor-Joining method (Saitou and Nei 1987). Shown are bootstrap consensus trees inferred from 1000 replicates. Evolutionary distances are in the units of the number of amino acid substitutions per site. The sources of sequences included in the analysis are listed in Table S3. For A), branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. There were a total of 485 positions in the final dataset. For B), the percentage of replicate trees in which the associated sequences clustered together in the bootstrap test (1000 replicates) are shown next to each node. There were a total of 66 positions in the final dataset.