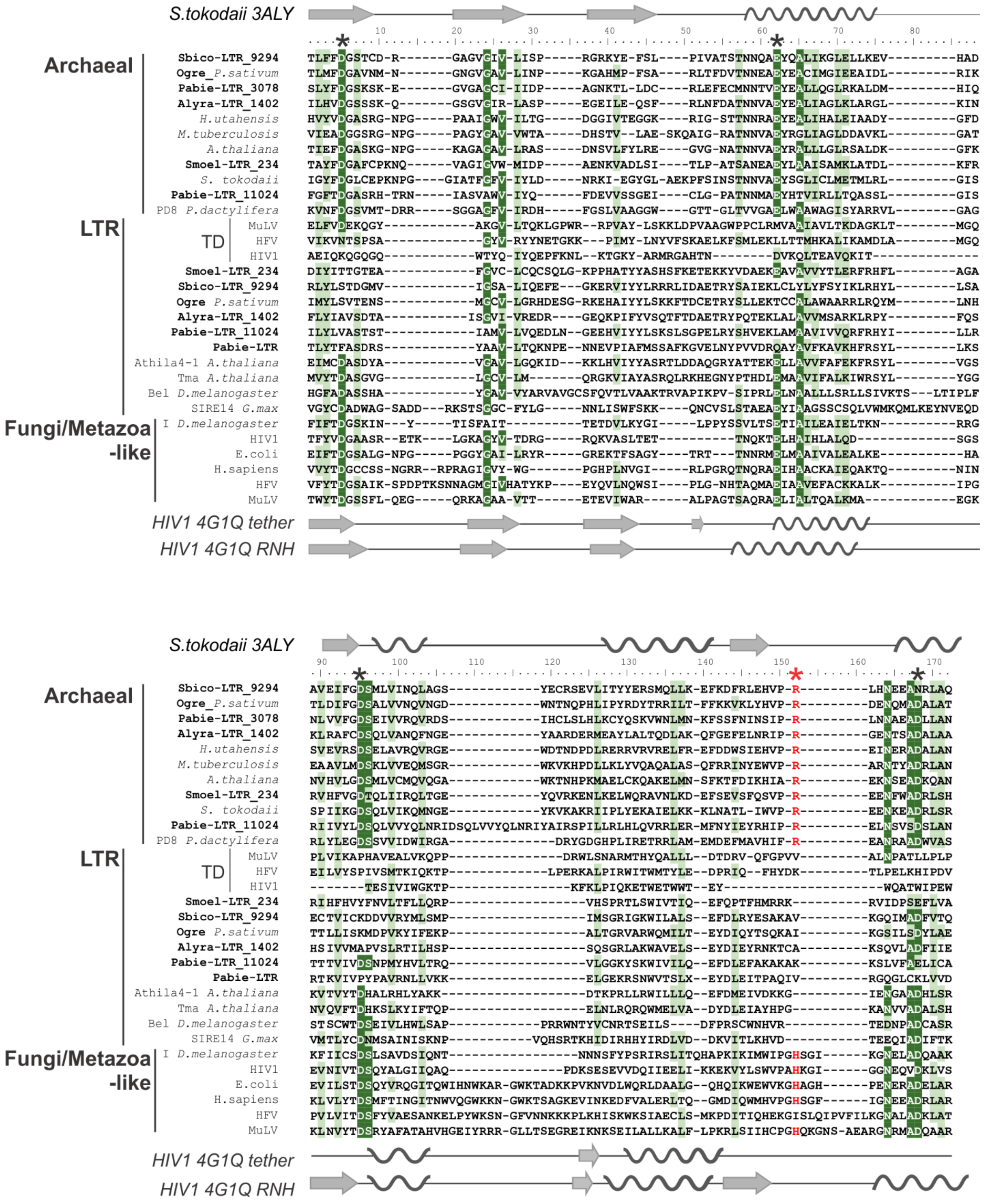

Figure S3. Amino acid sequence alignment of different types of RNHs. The conservative residue varying between aRNH and fungi/metazoa-like RNHs is highlighted in red at position 152 of the alignment. The residues believed to be important for the catalytic mechanism of RNHs are indicated with stars at the top of the alignment. The conserved residues are highlighted in shades of green.

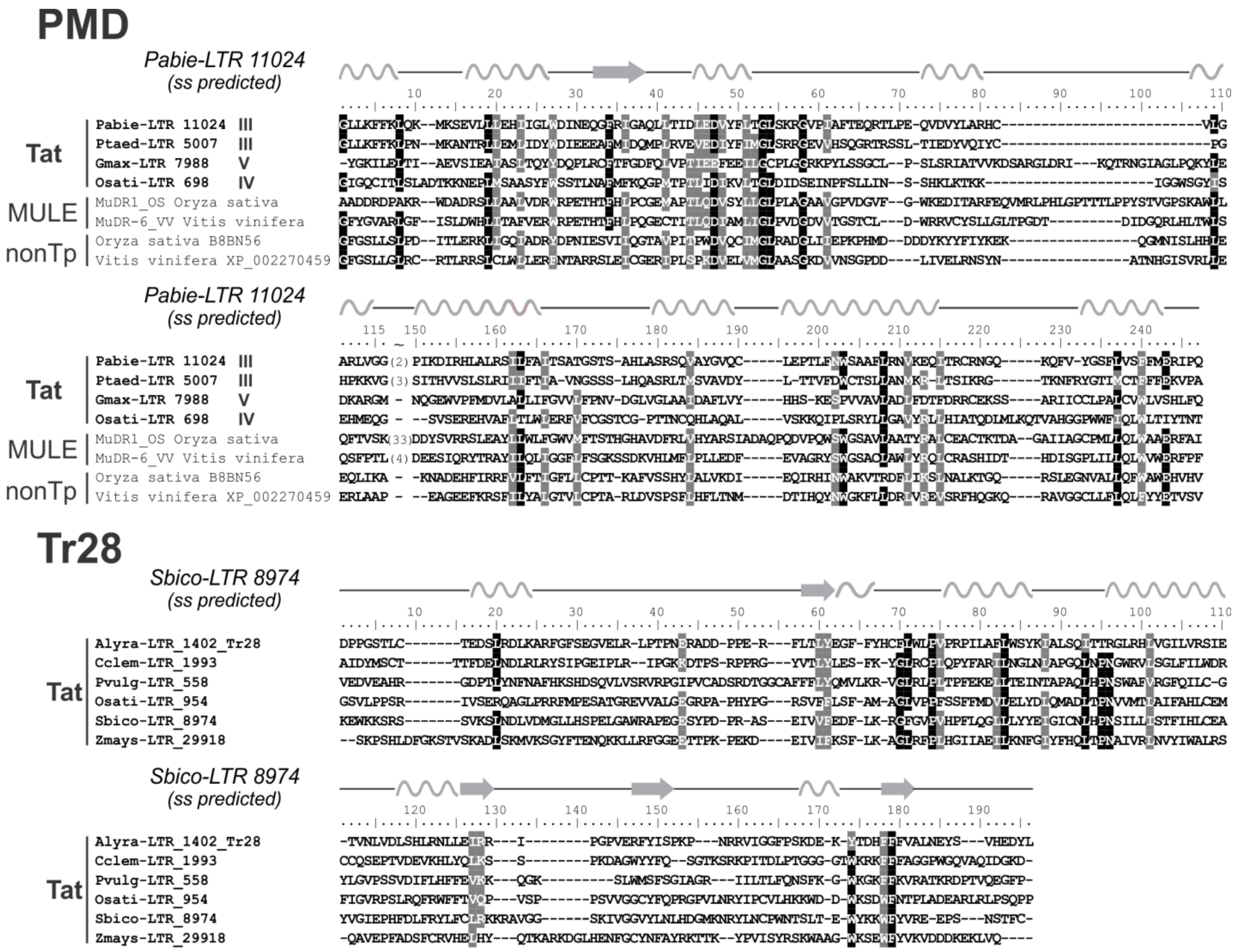

Figure S4. Amino acid sequence alignment of plant mobile domains (PMDs) and transposases 28 (Tr28). Lineages of aRNH-containing Tat LTR retrotransposons are denoted by Latin numerals. Tr28 presents only in elements from lineage VI (see Figure 2B). PMD alignment contains protein sequences from Tat LTR retrotransposons, MULE transposons and from non-transposon (nonTp) genes. The predicted secondary structures for a representative sequence are shown at the top of each of the alignments. The α-helices are depicted as helices, and the β-sheets are shown as arrows.

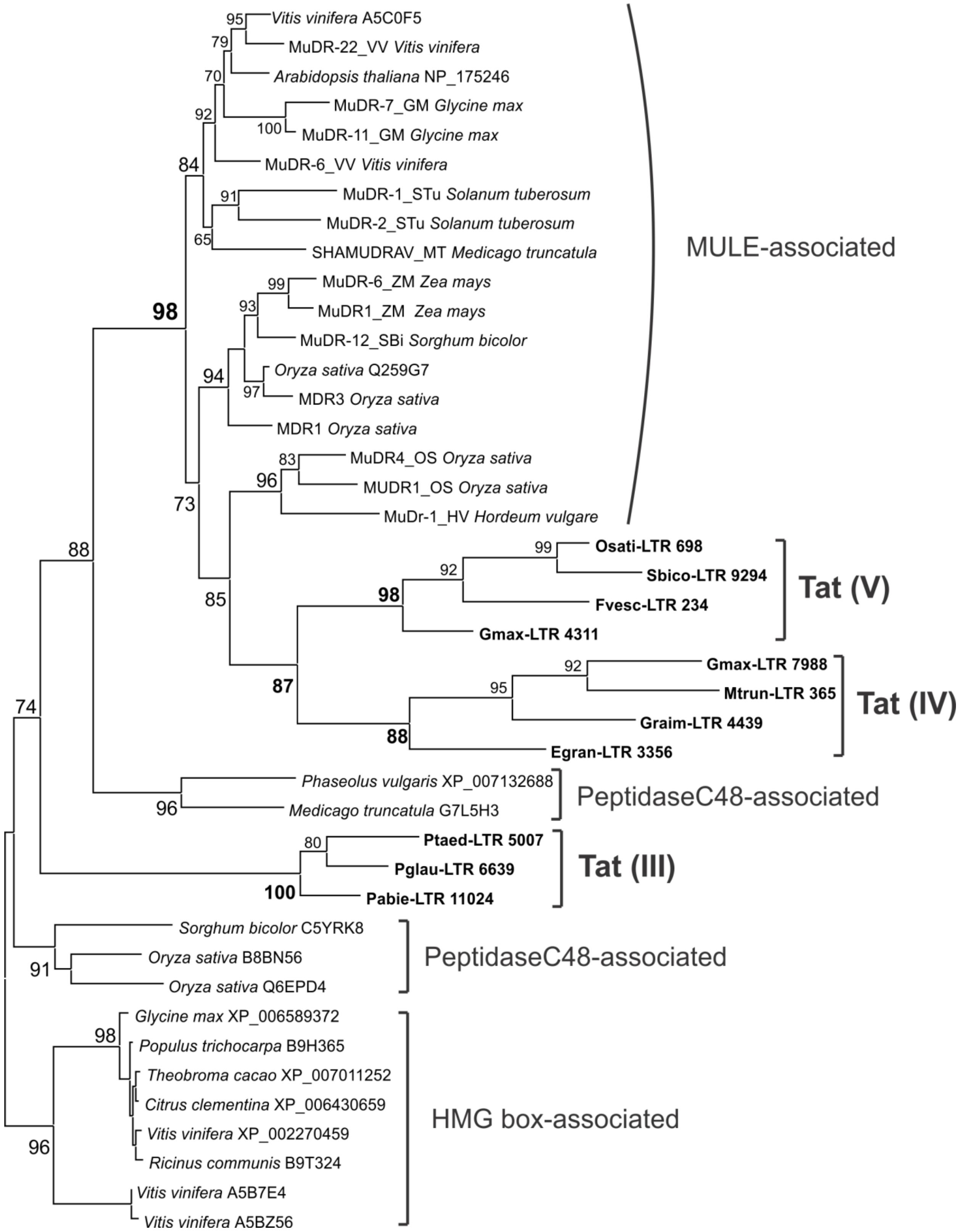

Figure S5. Maximum-likelihood tree based on the amino acid sequences of Plant Mobile Domains (PMDs) from diverse genes. MULE-associated PMDs were extracted from Repbase; non-transposon PMDs, associated with High Mobility Group (HMG) box or with Peptidase48 were extracted from GenBank. Lineages of aRNH-containing Tat LTR retrotransposons are denoted by Latin numerals and the names of the elements are in bold.