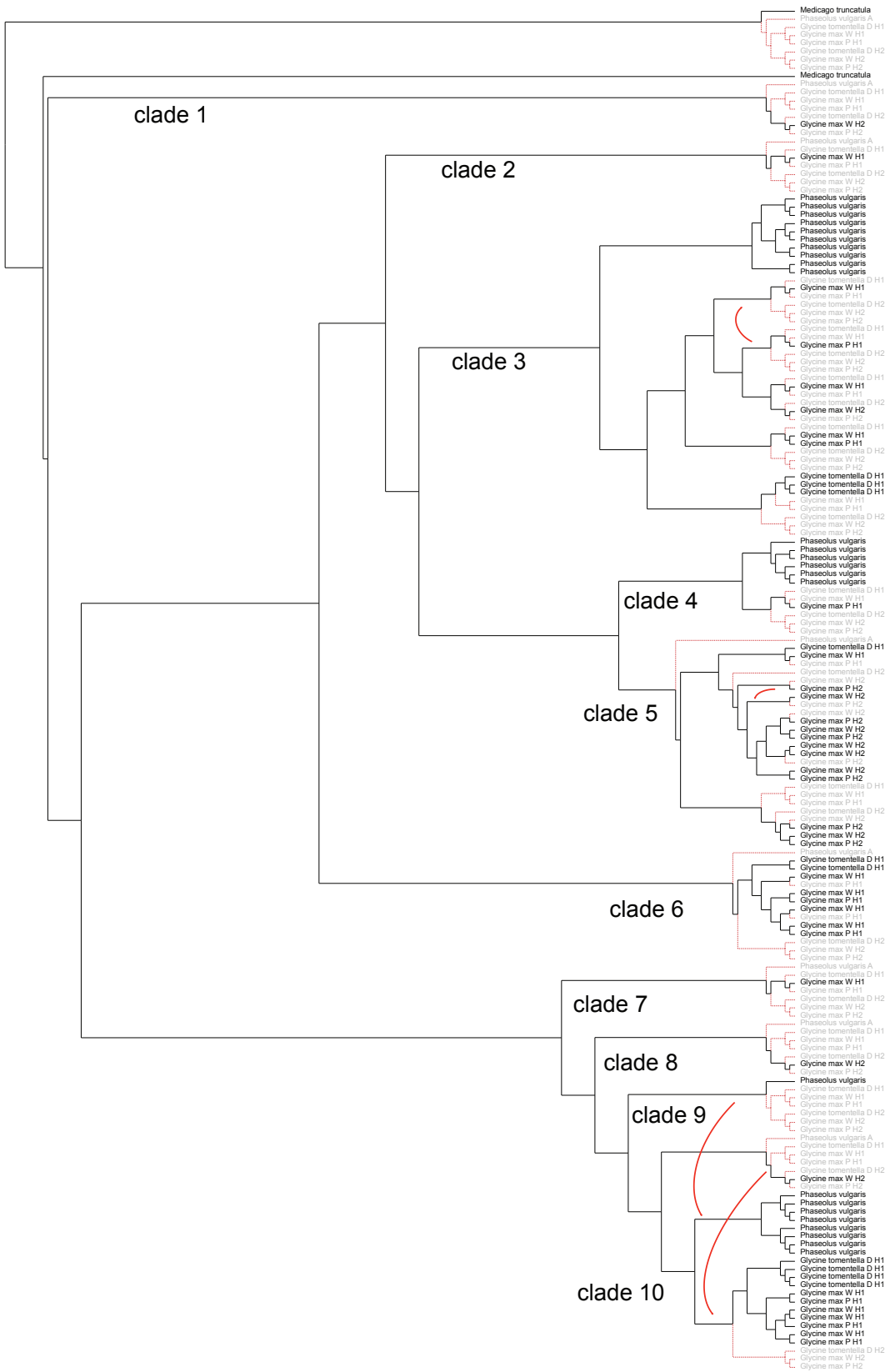Supplementary Figure S1. Using the consensus tree derived from the best analysis under the GTR+G+I model (fig. 3) as input for GeneTree, an estimate of 10 NB-ARC lineages in this genomic location in the most recent common ancestor (MRCA) of *Phaseolus* and *Glycine* was obtained. However, when weakly supported nodes were resolved in favour of fewer duplications and losses (red curves), only nine loci were predicted in the MRCA of these taxa (fig. 4).