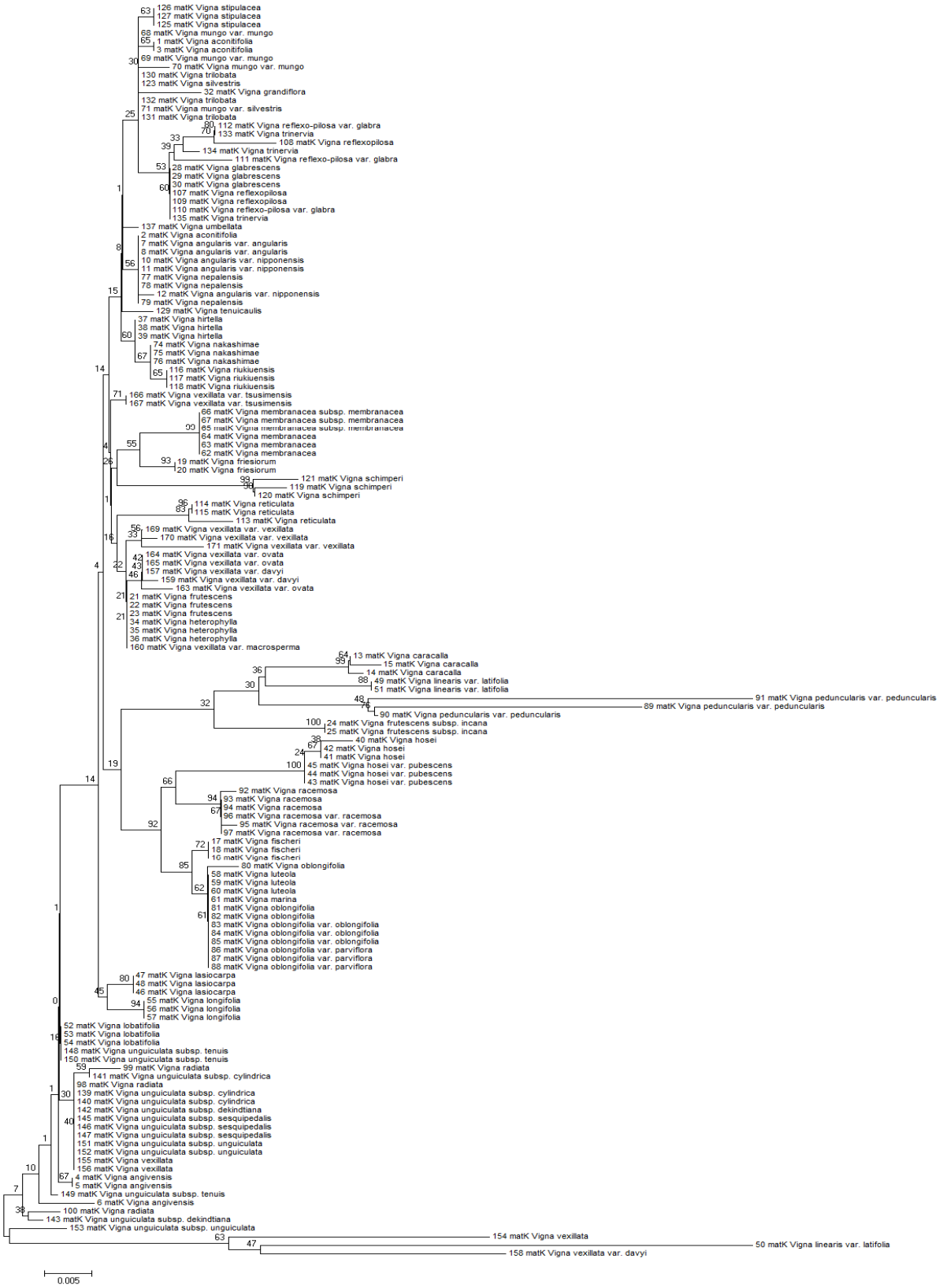

Figure S2. Phylogenetic analysis of 52 *Vigna* species based on the nucleotide sequences of the *matK* region. The NJ tree was developed using the Kimura 2-parameter method with nucleotide sequences of the *matK* region. Numbers next to the branches are the bootstrap test values.