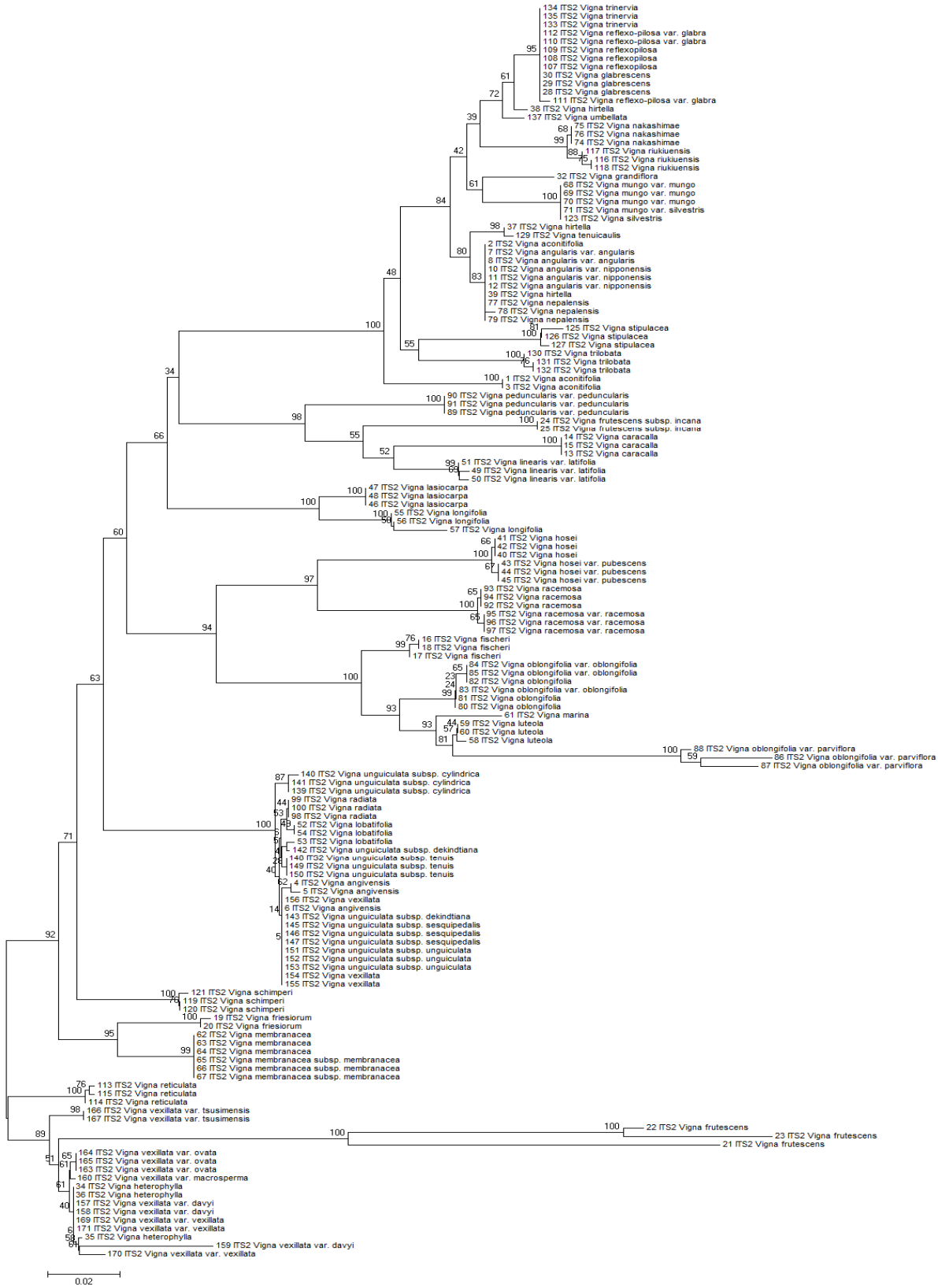

Figure S1. Phylogenetic analysis of 52 *Vigna* species based on the nucleotide sequences of the ITS2 region. The NJ tree was developed using the Kimura 2-parameter method with nucleotide sequences of the ITS2 region. Numbers next to the branches are the bootstrap test values.