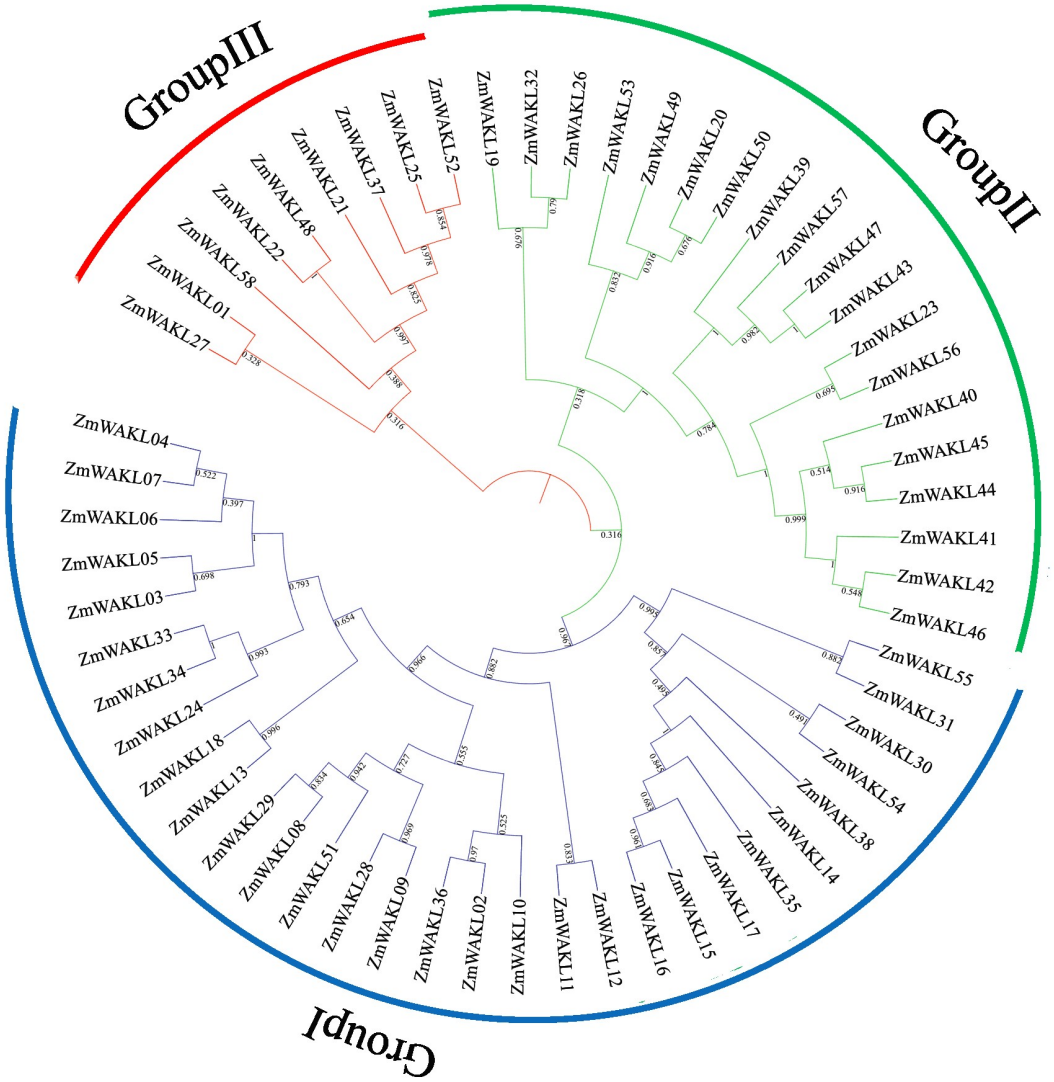

Fig.S1 Phylogenetic tree of ZmWAKL proteins with different color arcs representing distinct clusters of ZmWAKL group. Neighbor-joining (NJ) method with 1,000 bootstrap replicates was utilized to construct the unrooted phylogenetic tree based on the alignment of ZmWAKL domain sequences. The percentages of bootstrap numbers for the nodes are displayed on the branches.