Supplementary Material to "Comparative genome analysis of the SPL gene family reveals novel evolutionary features in maize"

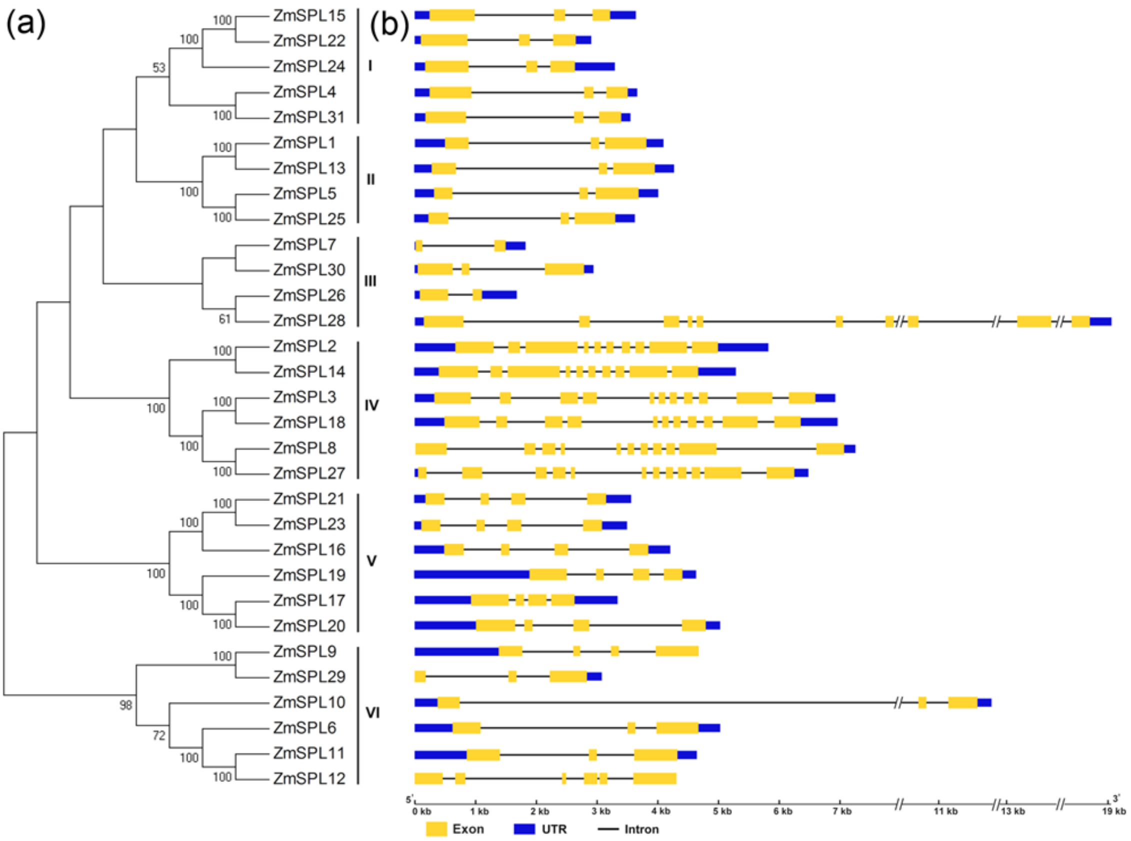

Figure S1 - Phylogenetic relationships and gene structure of the *ZmSPL*s. (a) The unrooted tree was generated using MEGA4.0 program with the NJ method. Bootstrap values above 50% from 1,000 replicates are shown at each node. (b) Yellow rectangles and thin lines represent exons and introns, respectively. Blue lines represent the untranslated regions (UTRs).