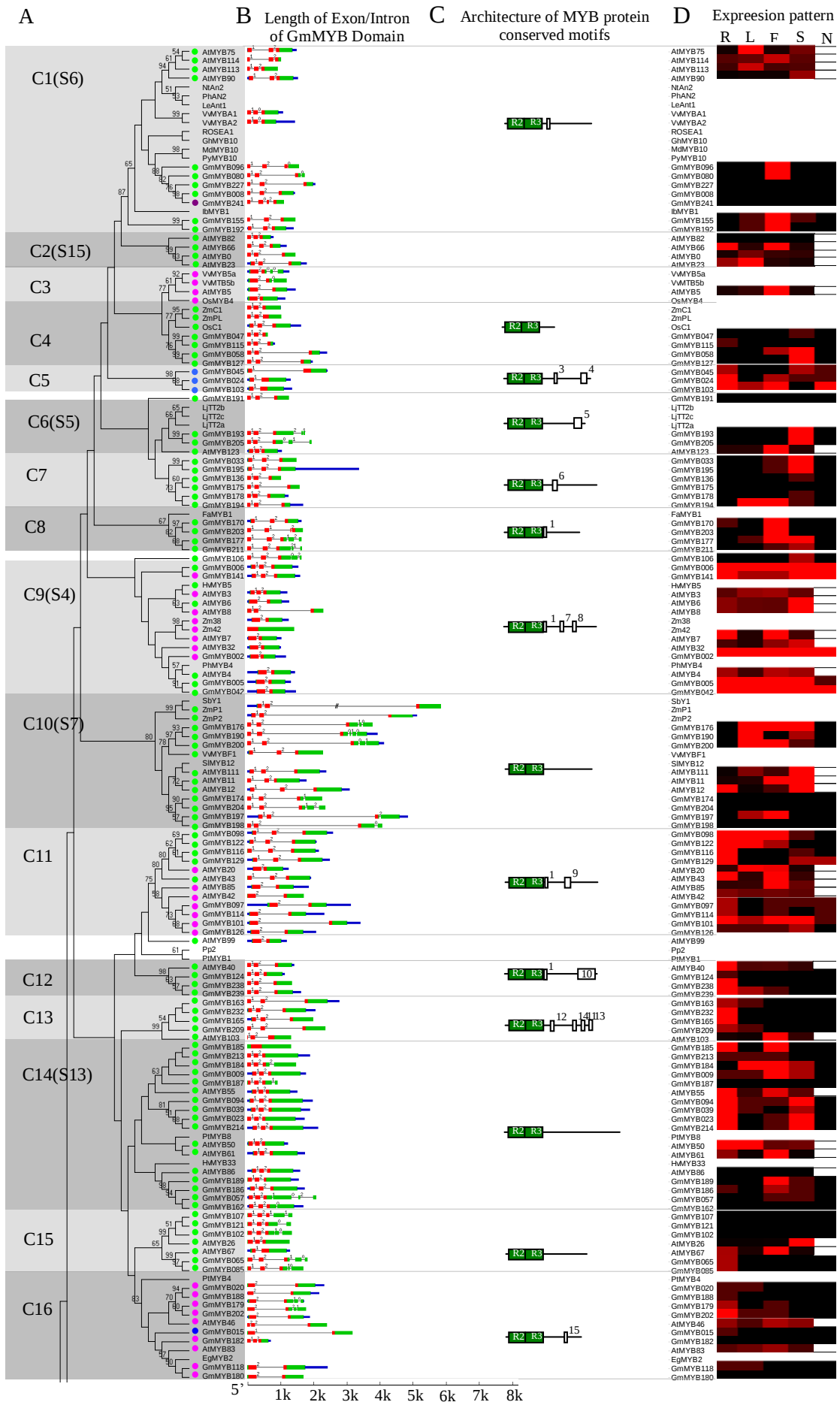
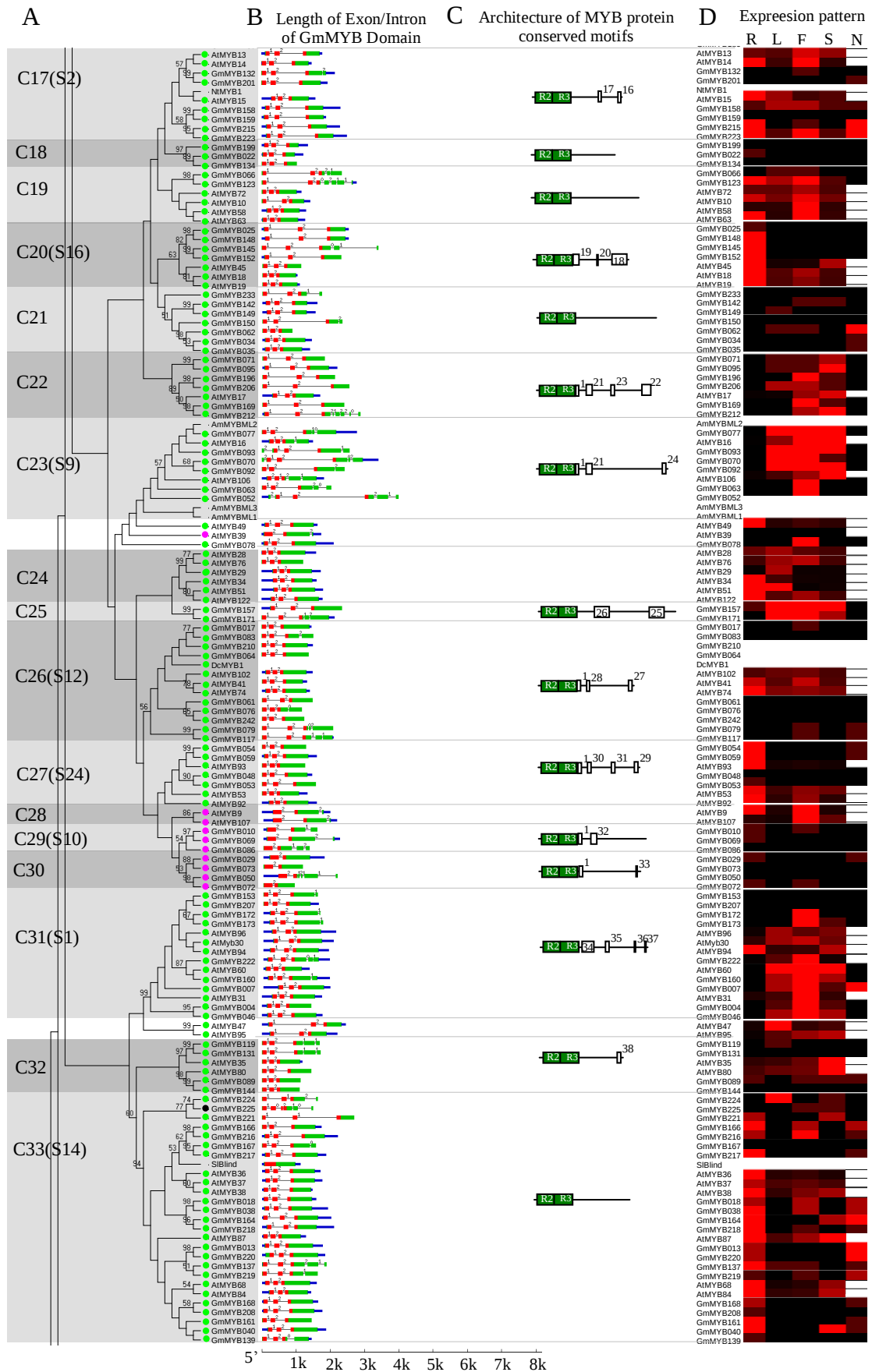
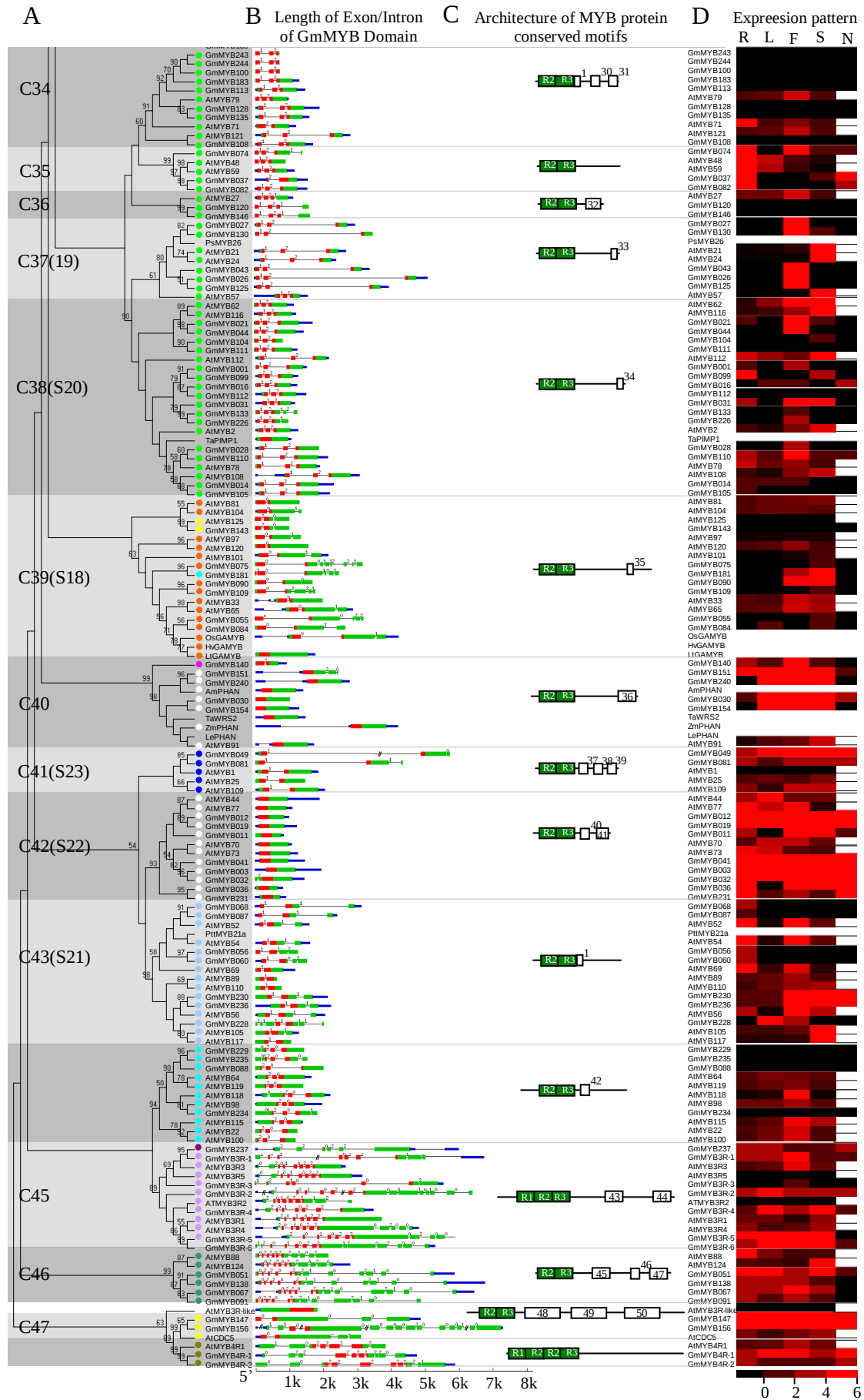








Additional file 3. The complete version of Figure 2: Phylogenetic relationships and subgroup designations in MYB proteins from soybean (Gm), *Arabidopsis* (At) and other plants. (a) Neighbor-joining tree representing relationships among 252 MYB proteins from soybean and 132 MYB proteins from *Arabidopsis*, including five 3R-MYB proteins from *Arabidopsis* and six 3R-MYB proteins from soybean. The proteins are clustered into 47 subgroups, which are designated with a subgroup number (e.g., C1) and marked with different alternating tones of a gray background to facilitate subfamily identification with high predictive value. The numbers beside the branches represent bootstrap support values (>50%) from 1000 replications. Sixteen proteins did not fit well into clusters. Colored circles indicate the corresponding intron distribution patterns, as shown in Figure 3. (b) Structure of MYB genes in soybean and *Arabidopsis*. Exon(s) are indicated by green boxes, MYB domain(s) by red boxes, untranslated region(s) by blue boxes, and spaces between the colored boxes correspond to introns. The sizes of exons and introns can be estimated using the horizontal scale bar. (c) Architecture of conserved protein motifs in 47 subfamilies. The motifs on the right were detected using MEME and are graphically represented as white boxes drawn to scale for a representative plant MYB protein of each subfamily. (d) Expression patterns of MYB genes in soybean and *Arabidopsis* in different organs. R, root; L, leaf; F, flower; S, seed; N, legume-specific nodulation. In this expression pattern analysis, the highest values among the expression values of the four organs published in the AtGenExpress and SoySeq databases were selected.