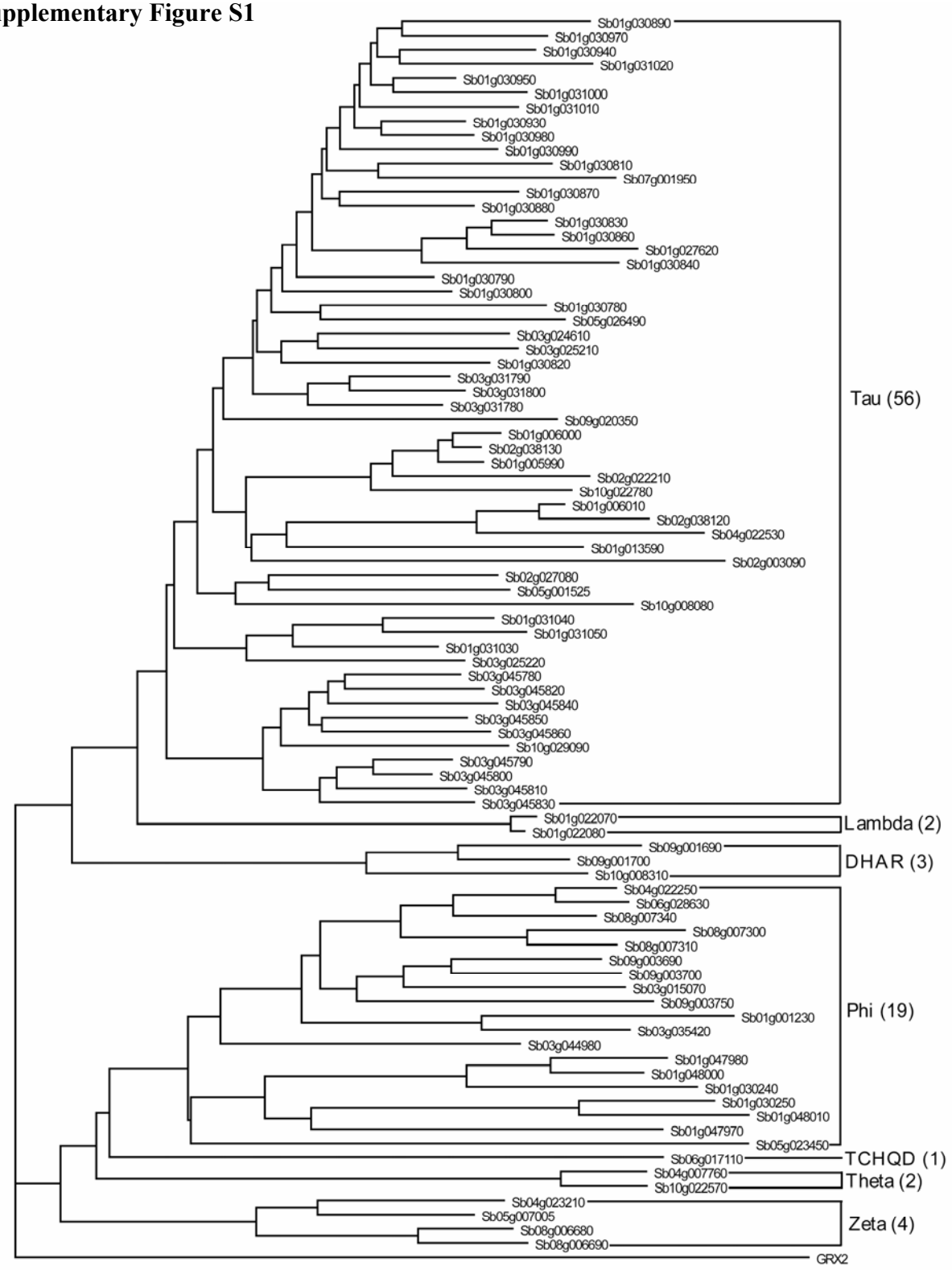
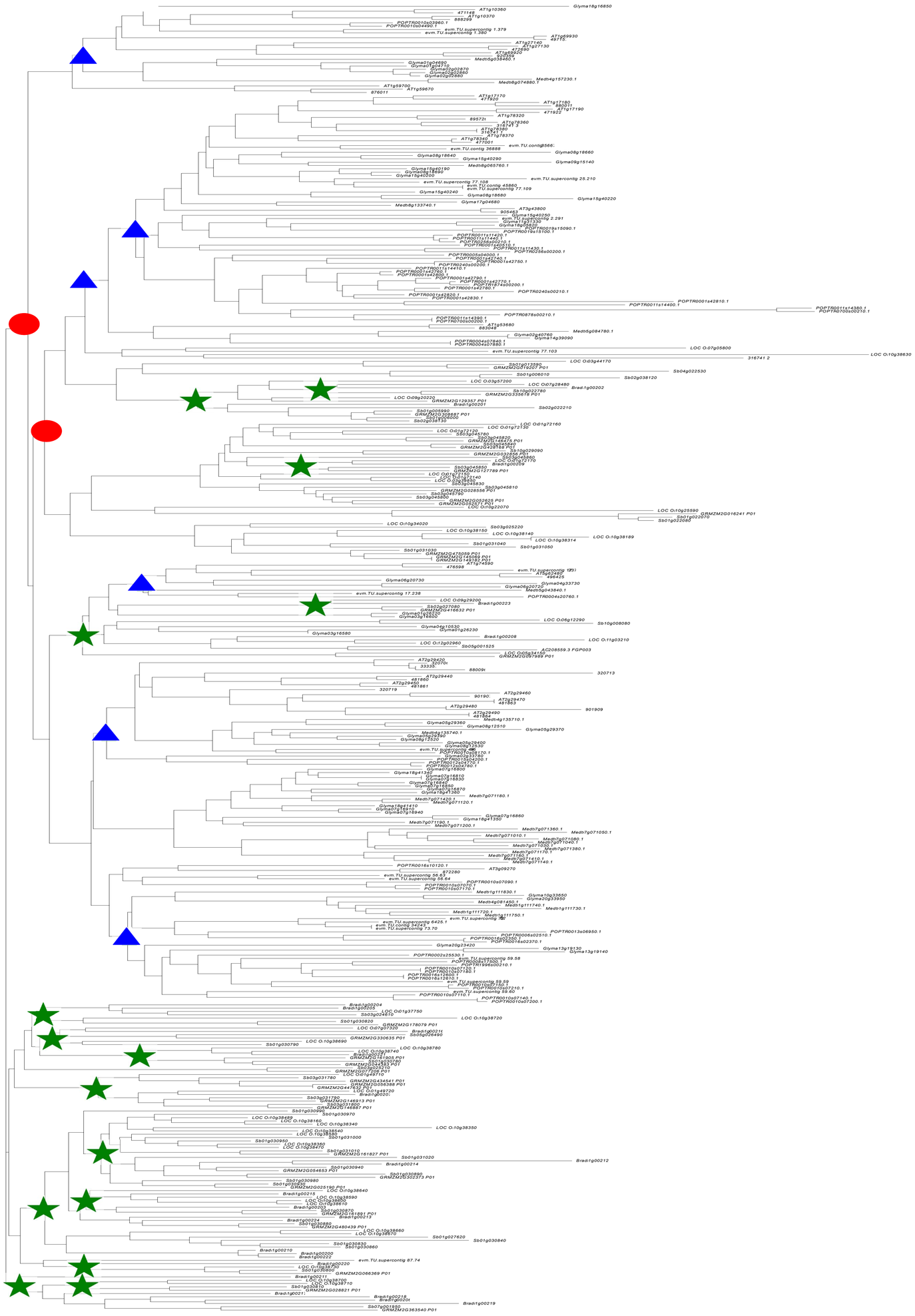
Supplementary Figure S1



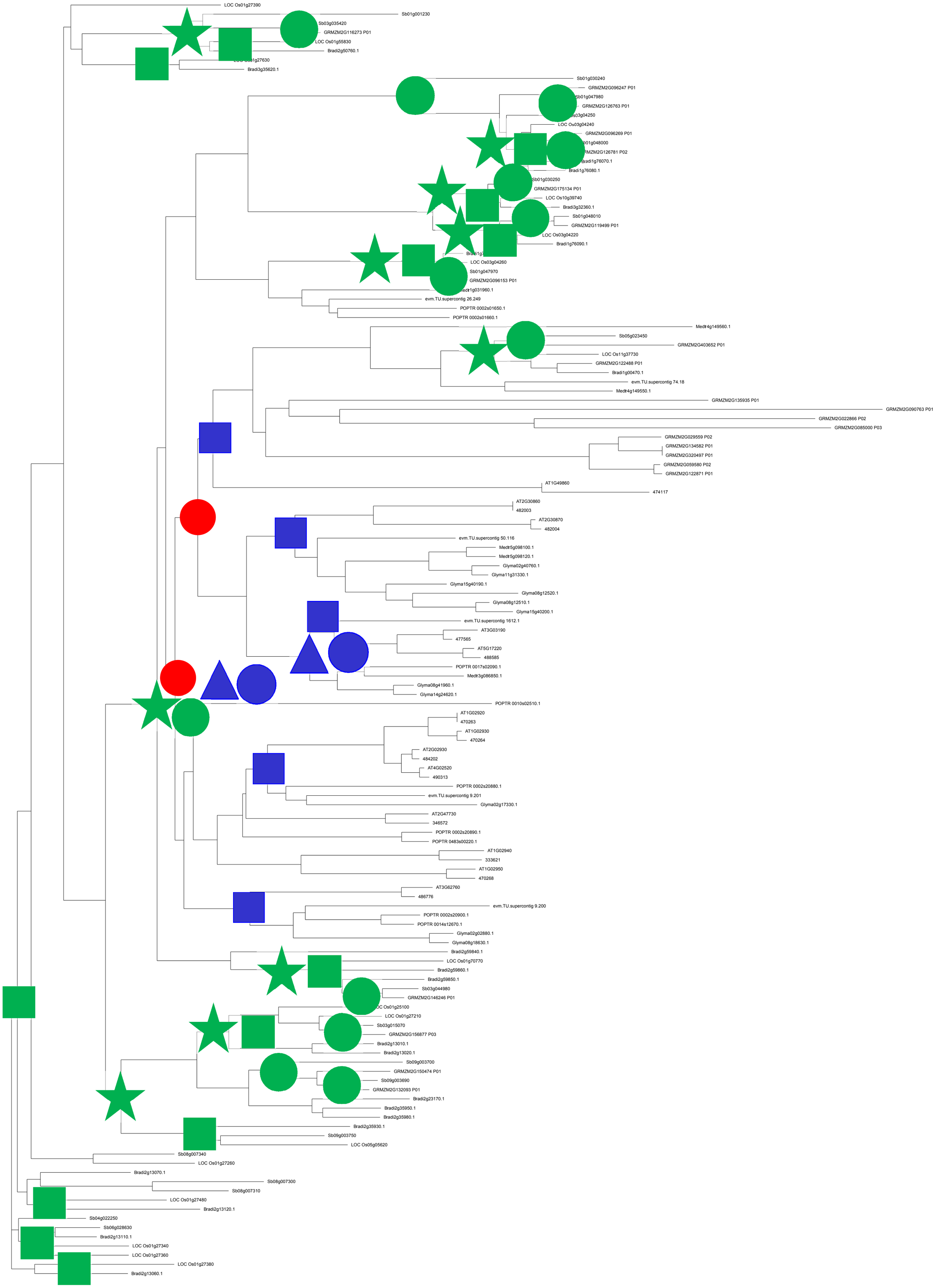
Supplementary Figure S1. Phylogenetic Relationships among the sorghum GSTs and their classification. GST_N domain amino acid sequences were employed to construct phylogenetic trees using the bootstrap method with a heuristic search of the PAUP 4.0b8 program as described in the methods section. One of genes encoding glutaredoxin in sorghum, GRX2, was used to root the tree.

Supplementary Figure S2



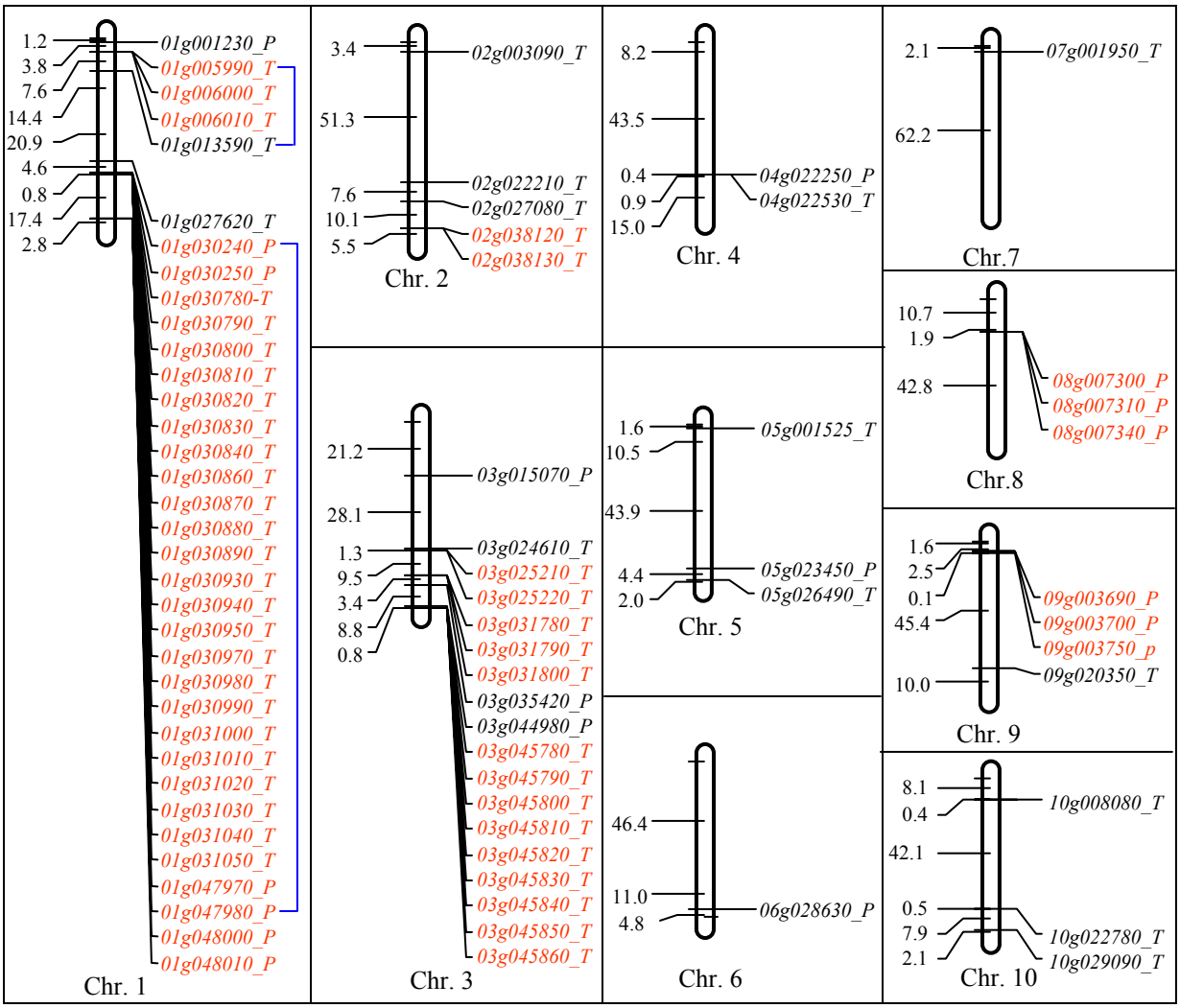
Supplementary Figure S2. An enlarged phylogenetic tree and its analysis from Fig. 1A

Supplementary Figure S3



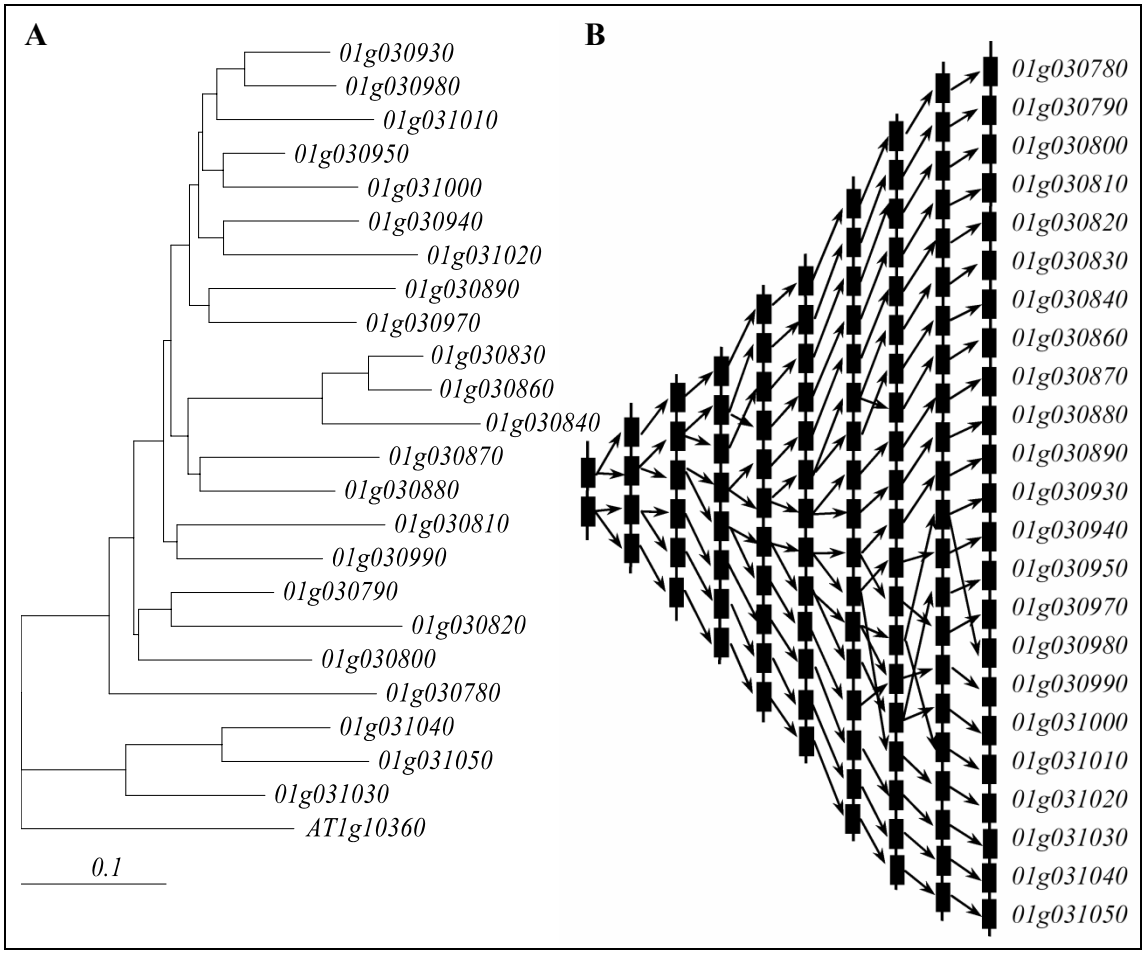
Supplementary Figure S3. An enlarged phylogenetic tree and its analysis from Fig. 1C

Supplementary Figure S4



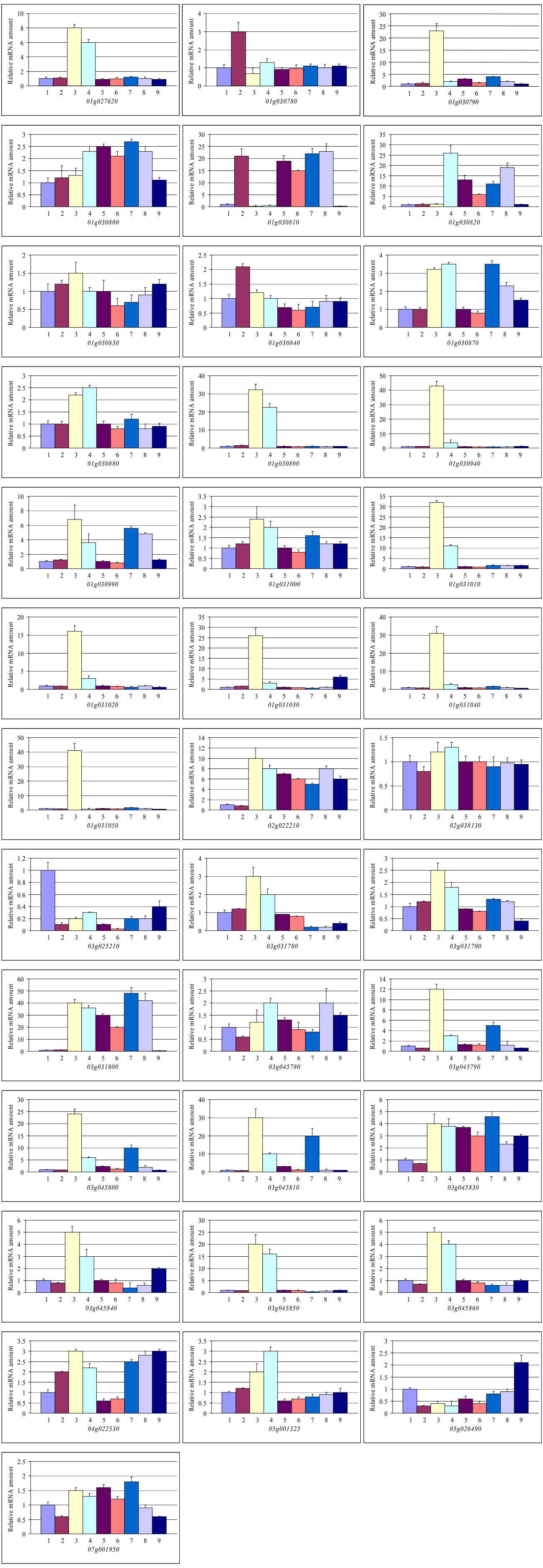
Supplementary Figure S4. Chromosomal distribution of the Tau and Phi classes of GST members and detection of duplicated genes in the sorghum genome. Tandemly duplicated genes are indicated with red fonts and the blue line represents the segmentally duplicated pairs. The prefix "Sb" of gene locus names in this figure and in the all other figures have been omitted for convenience.

Supplementary Figure S5



Supplementary Figure S5. Detail analysis in the expansion of the largest tandem cluster in the sorghum Tau sub-family. (A) Phylogenetic relationships of 23 members from the tandem cluster. (B) Hypothetical origins of tandemly duplicated genes.

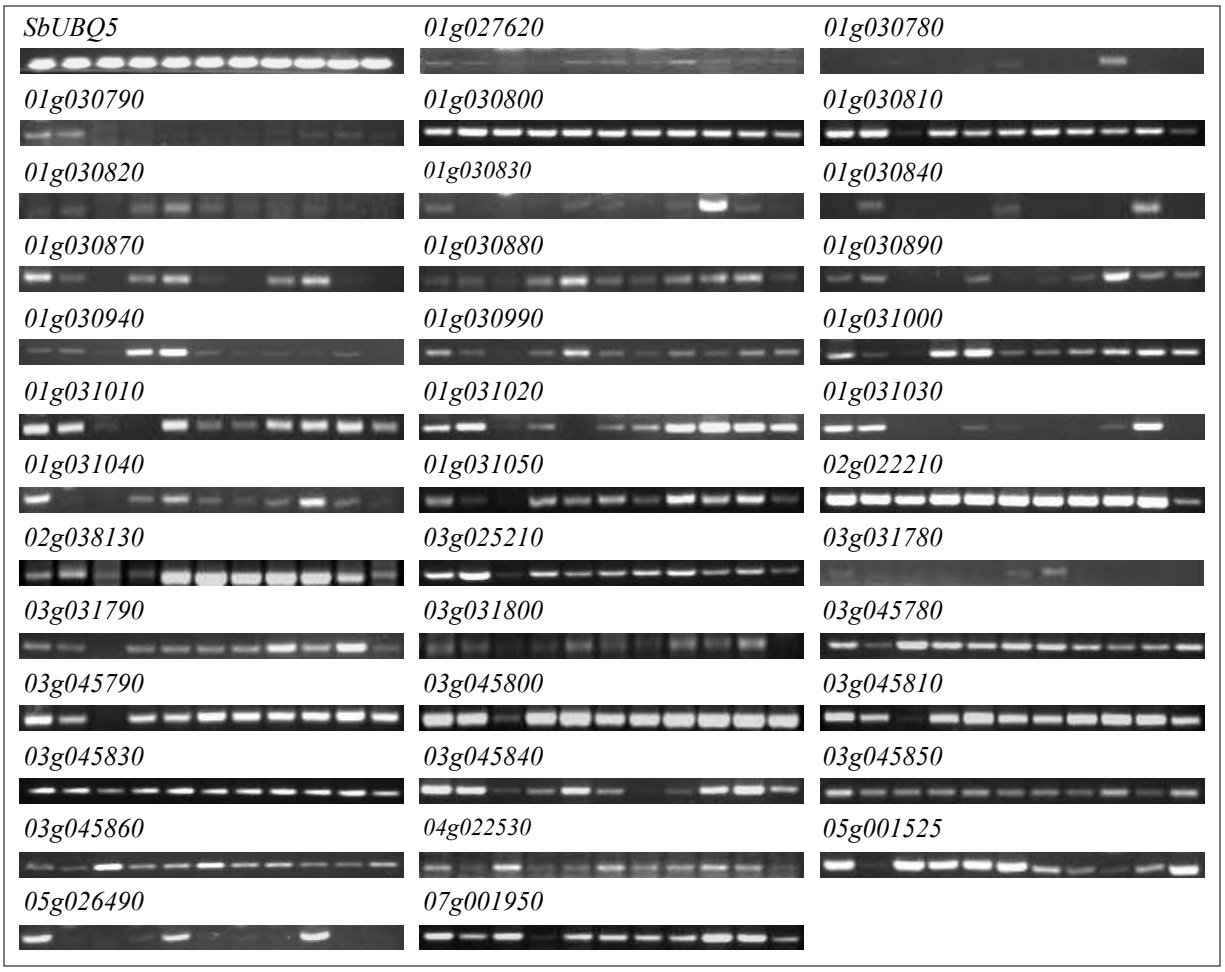
Supplementary Figure S6



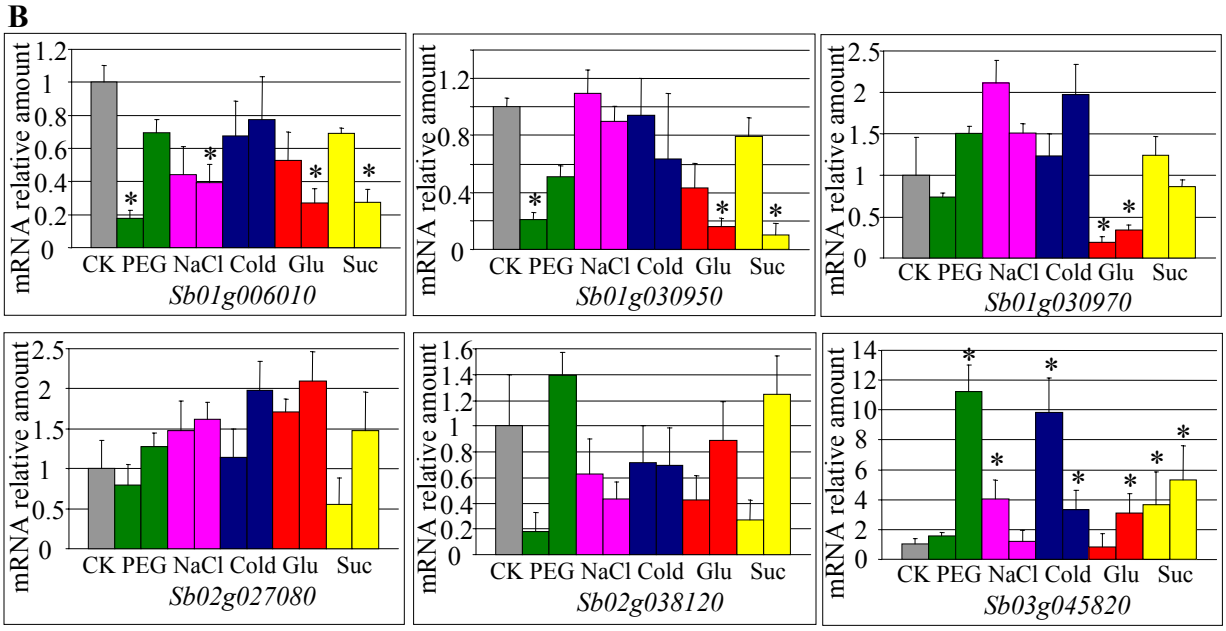
Supplementary Figure S6. Transcript profiles of the sorghum Tau class of GST superfamily members in 9 different sorghum tissues shown by qRT-PCR analyses. Nine columns from left to right for each gene represent relative mRNA signals from young leaves, mature leaves, young roots, mature roots, young panicles, mature panicles, young seeds, mature seeds and stems, respectively. The gene *SbUBQ5* was used as an internal control to normalize the data for qRT-PCR analysis.

Supplementary Figure S7

A

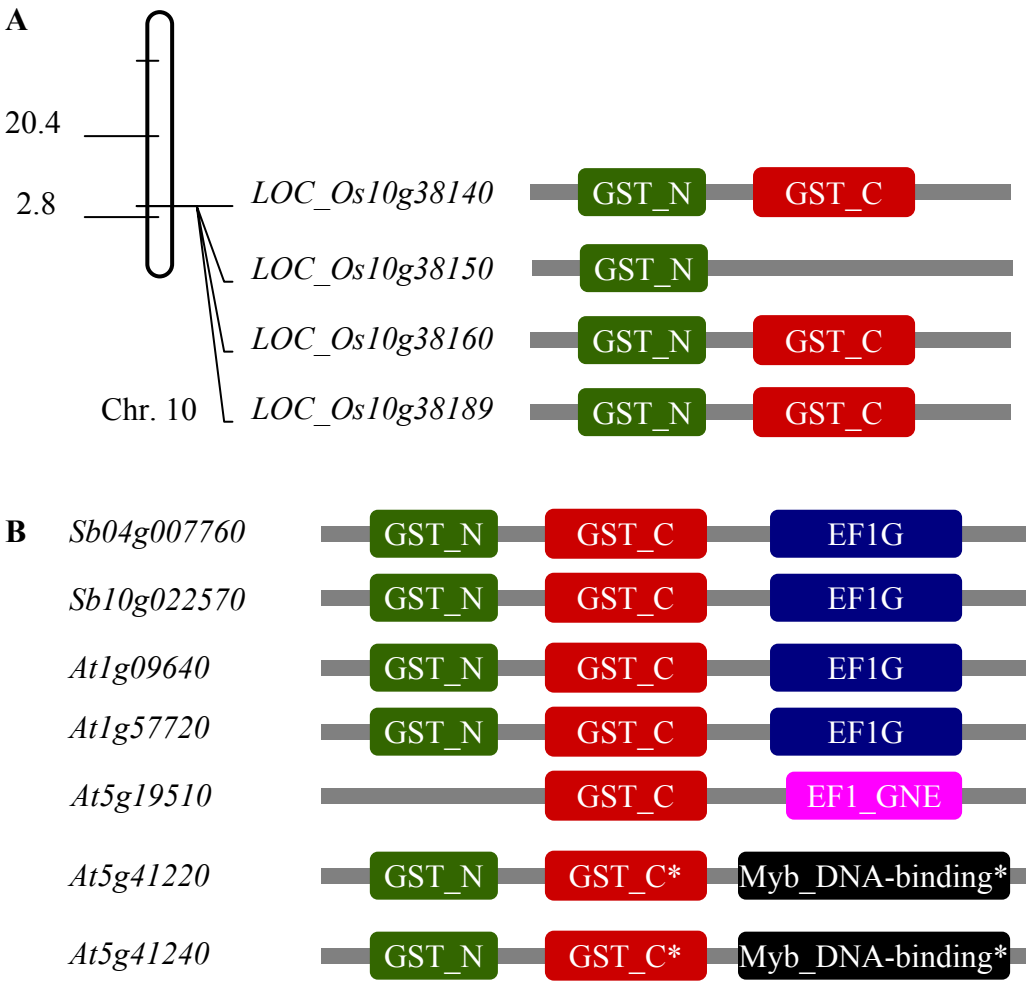


B



Supplementary Figure S7. Expression patterns of the sorghum Tau class of GST superfamily members under various abiotic stresses and sugar treatments shown by RT-PCR and qRT-PCR analyses. Both RT-PCR (A) and qRT-PCR (B) were employed to analyze the expression profiling under various treatments. Eleven bands in (A) or columns in (B) from left to right for each gene indicate amplified products from the following tissues: 1, control (un-treated tissue); 2 and 3, stressed by 30% PEG for 0.5 and 2 h, respectively; 4 and 5, stressed by 250 mM NaCl for 2 and 8 h, respectively; 6 and 7, stressed by cold at 4oC for 2 and 8 h, respectively; 8 and 9, treated by 5% glucose for 2 and 6 h, respectively; 10 and 11, treated by 5% sucrose for 2 and 6 h, respectively. Asterisks indicate significant differences among different treatments with at least $P < 0.05$ by *t*-test. The gene *SbUBQ5* was used as an internal control to normalize the data for qRT-PCR analysis.

Supplementary Figure S8



Supplementary Figure S8. Domain loss and combination in GSTs. (A) an example of possible domain loss after tandem duplication. The figure shows a tandem cluster consisting of 4 rice GSTs and their domain organizations. (B) Domain combinations found in sorghum and Arabidopsis GSTs. The figure shows the extra domains except for GST_N or GST_C. EF1G, Elongation factor 1 gamma domain; EF1_GNE, EF-1 guanine nucleotide exchange domain; Myb_DNA-binding, Myb transcription factor domain. The star "*" indicates the domains detected with e-value > 0.01.