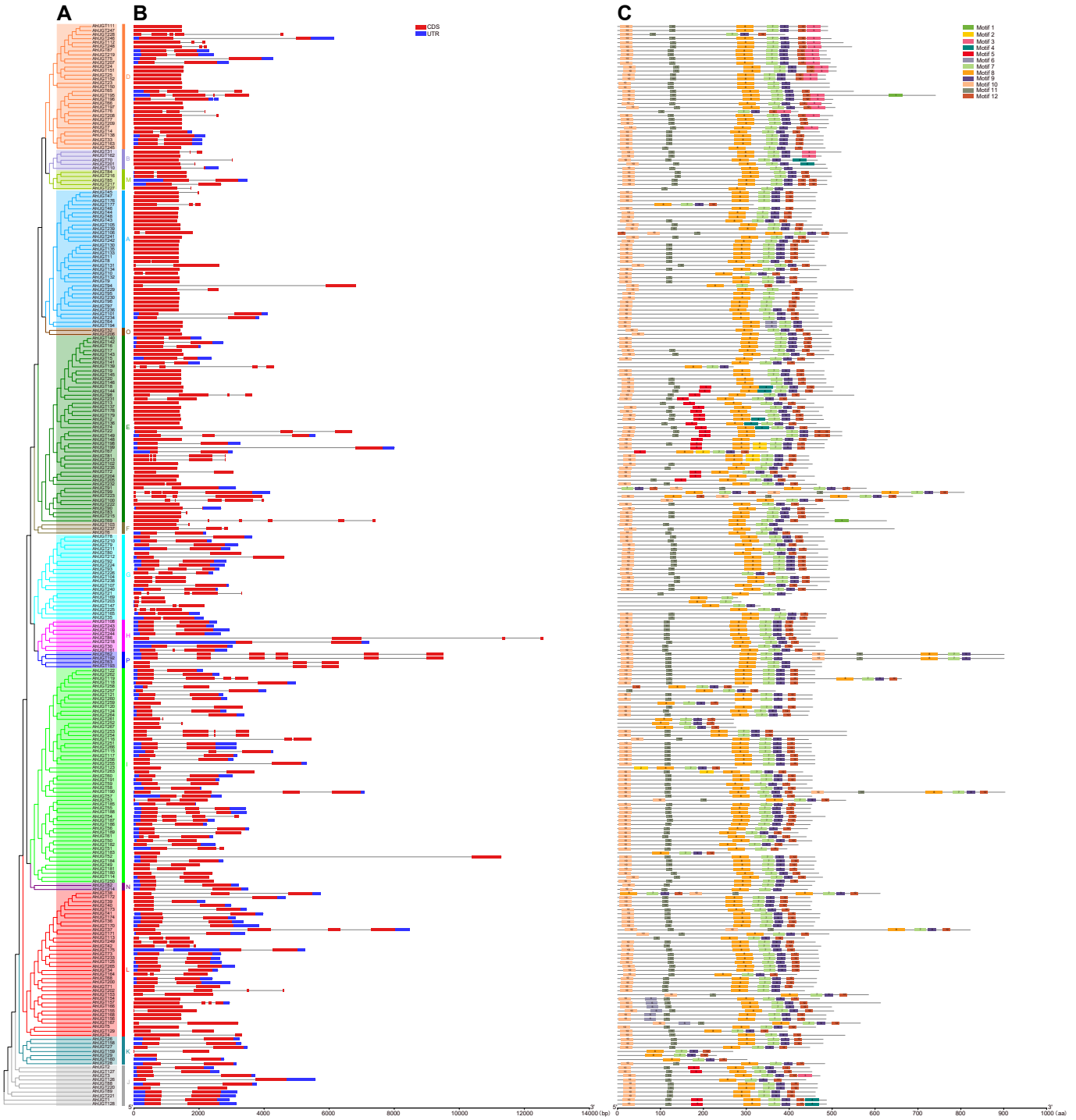

Fig. S1 Gene structure and conserved protein motifs of AhUGT family members. A The phylogenetic tree of AhUGTs. **B** Exon-intron structure of *AhUGT* genes. Red boxes represent coding sequences, blue boxes are untranslated regions, and black lines indicate introns. **C** Conserved protein motifs in AhUGTs.

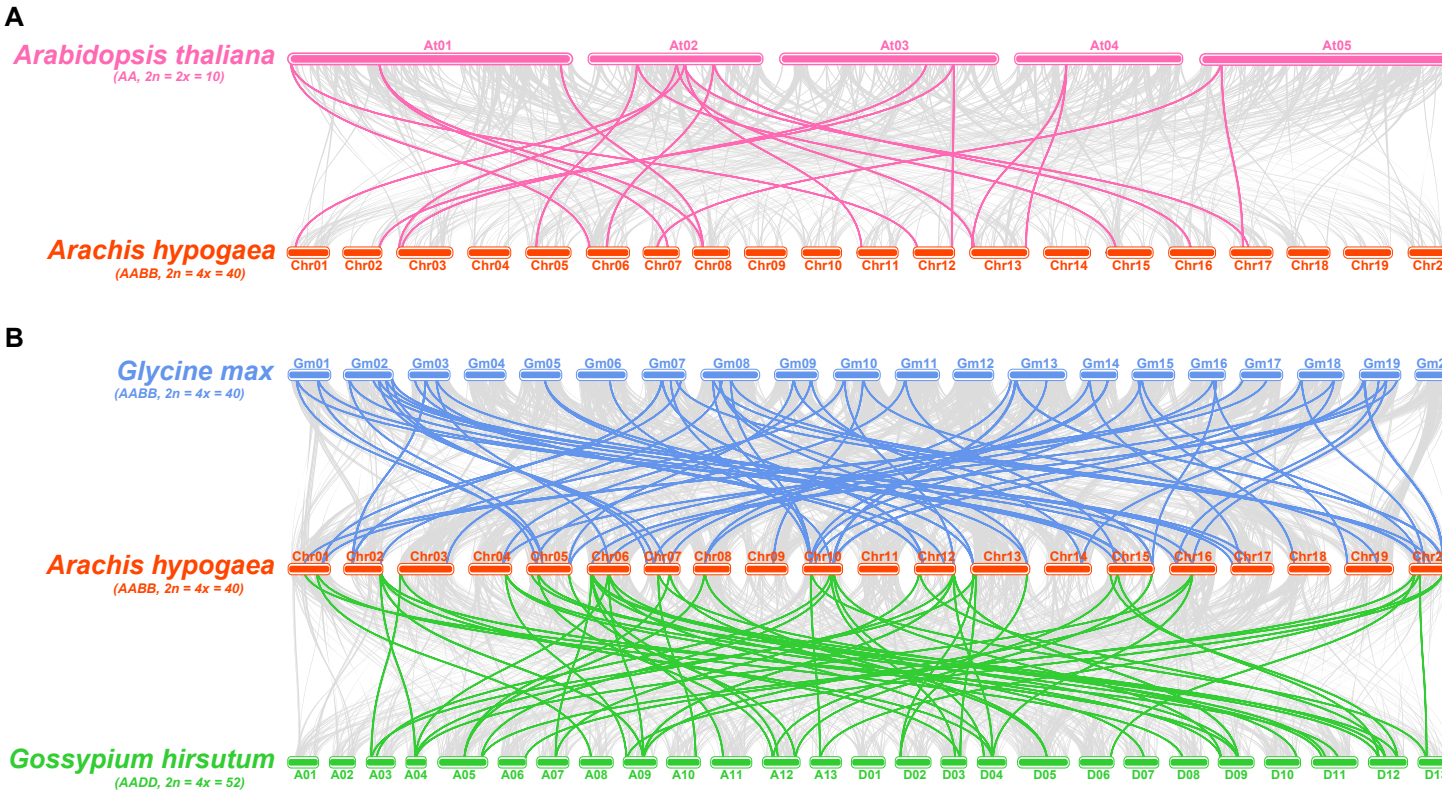

Fig. S2 Syntenic relationship analysis of UGTs between *A. hypogaea* and other plant species. MCScanX program was used to analyze the orthologous genes between *A. hypogaea* and Arabidopsis, *G. max* and *G. hirsutum*. Gray lines represent all orthologous gene pairs, and color lines highlight UGT orthologous gene pairs.

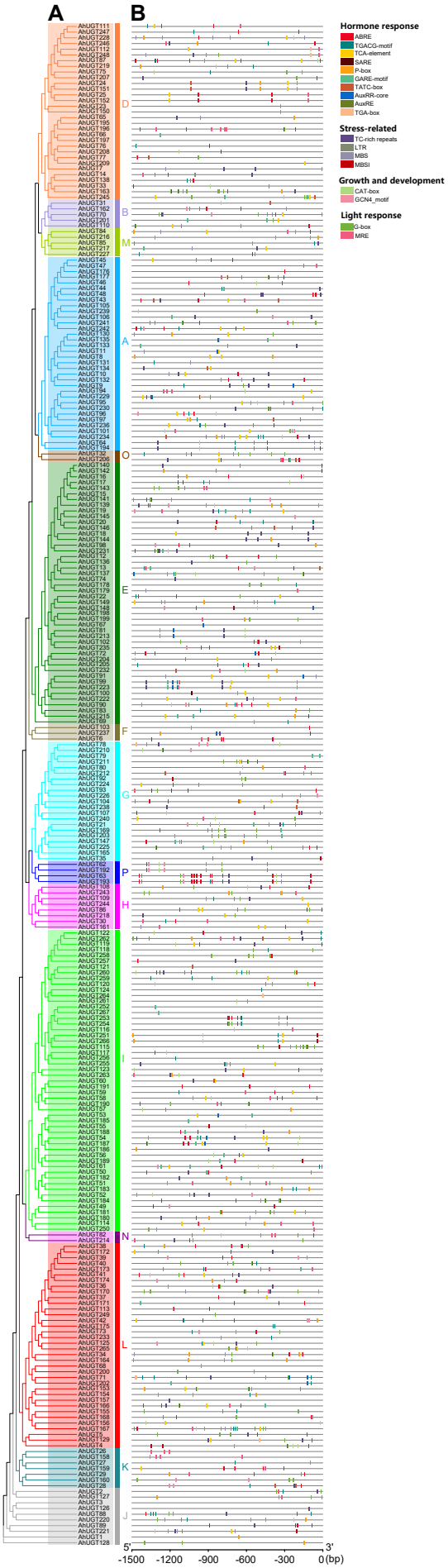

Fig. S3 Predicted *cis*-acting elements in the promoter regions of *AhUGT* genes. A The phylogenetic tree. **B** Prediction of *cis*-acting elements in the 1500 bp upstream region of *AhUGT* gene transcription start site.

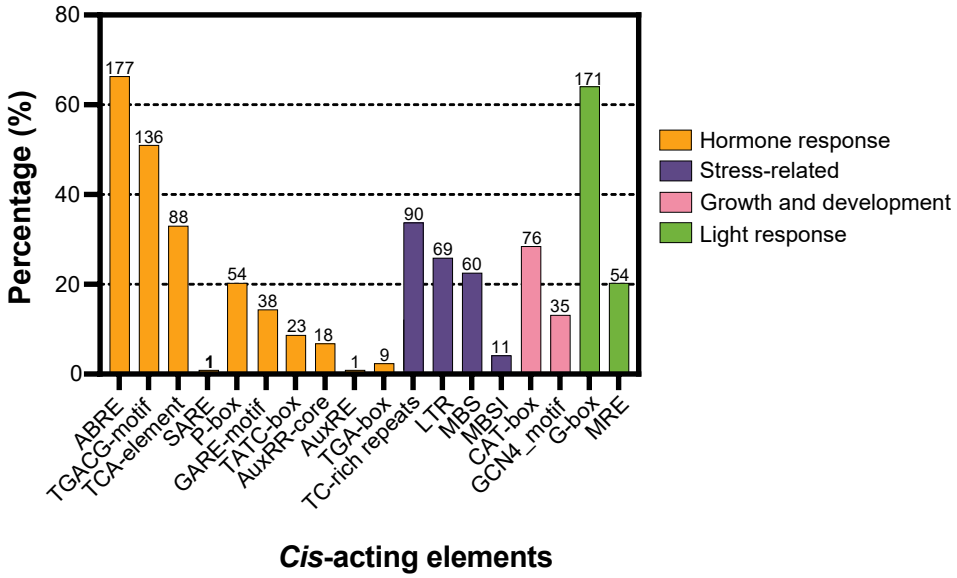

Fig. S4 Classification and annotation of *cis*-acting elements in the promoter regions of *AhUGTs*. The values on the top of bar indicate the number of *cis*-acting elements.

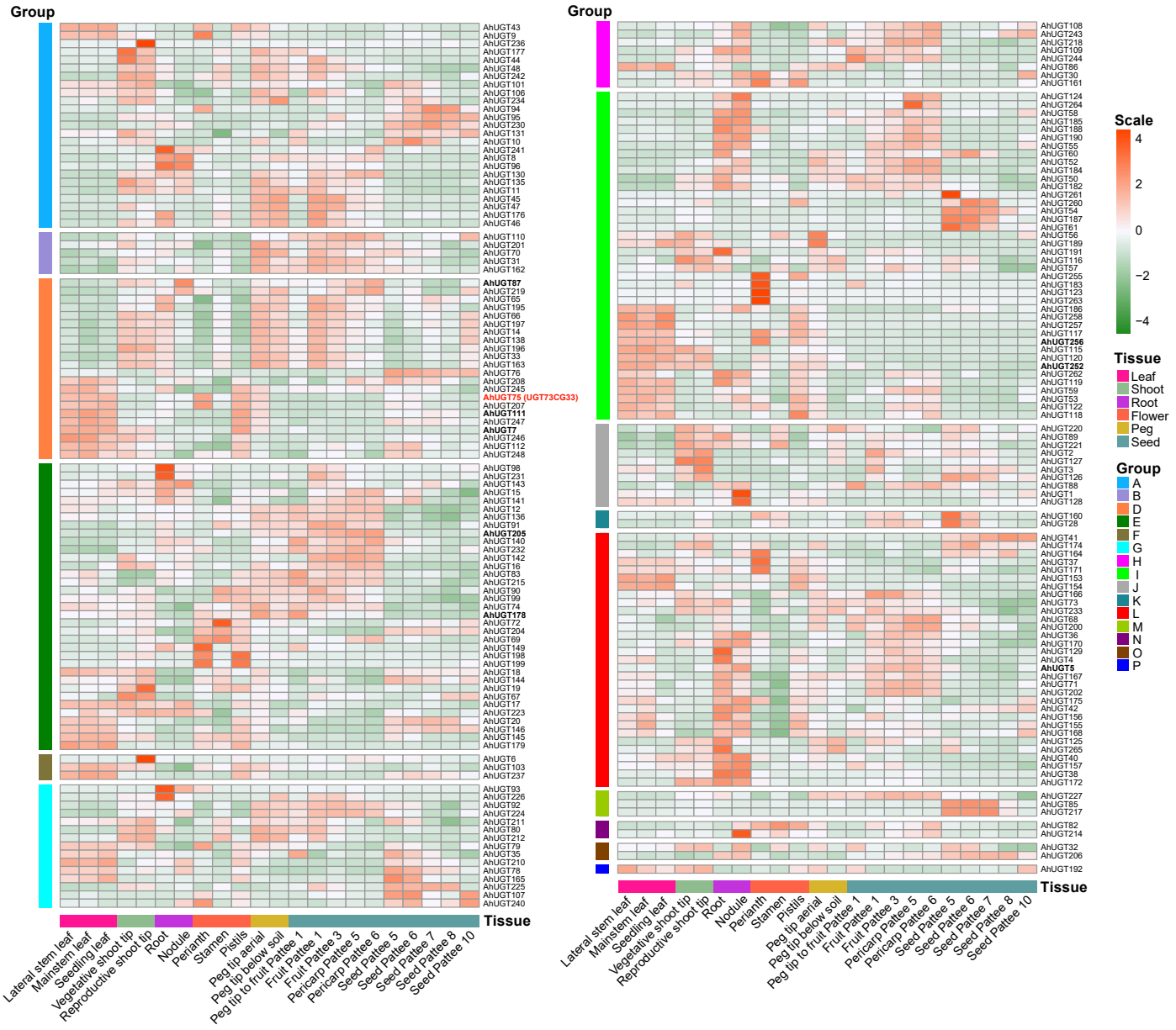

Fig. S5 Transcriptional expression profiles of *AhUGTs* in various peanut tissues and different developmental stages. The *AhUGTs* were classified into 15 different groups with different color based on phylogenetic tree. FPKM values were obtained from the RNA-seq data, and the expression levels of *AhUGTs* were normalized by log2 (FPKM+1), with red to green indicating high to low gene expression level in the heatmap.

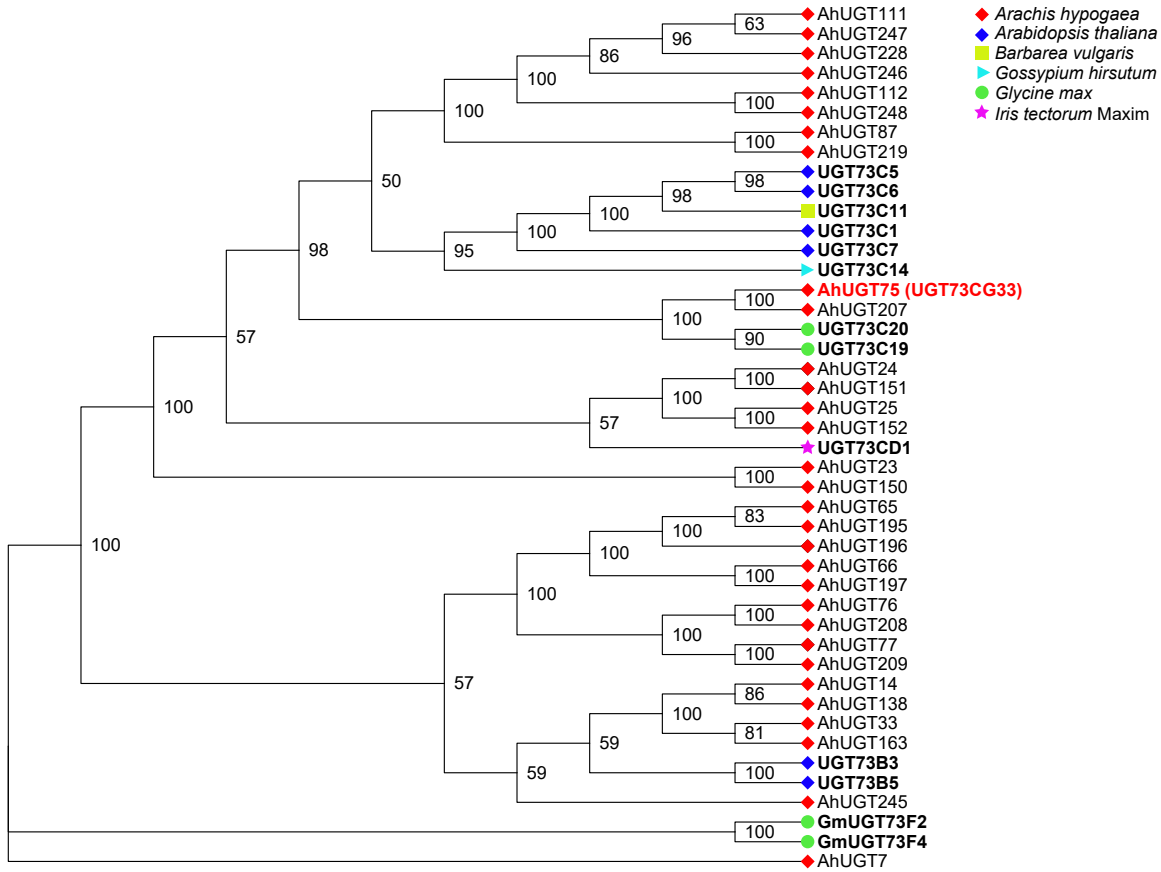

Fig. S6 Phylogenetic analysis of AhUGTs from group D. The phylogenetic tree was constructed using the maximum likelihood method by aligning the amino acid sequences of 31 AhUGTs from group D with those of functionally characterized UGT73 subfamily members from other plant species.

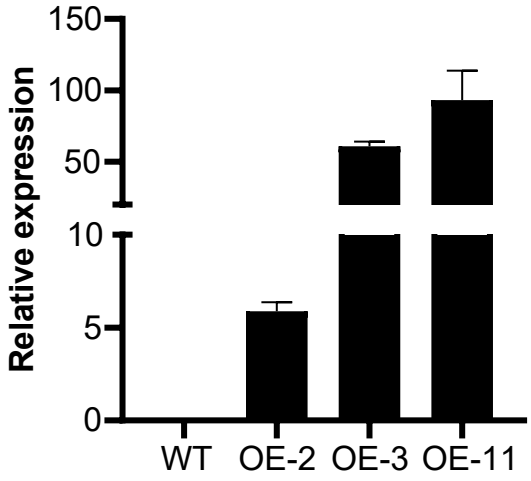

Fig. S7 qRT-PCR analysis of relative transcript level of *AhUGT75* in three overexpressing lines and wild type Arabidopsis plants. Tubulin was used as an internal reference gene. Data were derived from three biological replicates and are presented as means ± SEM.