

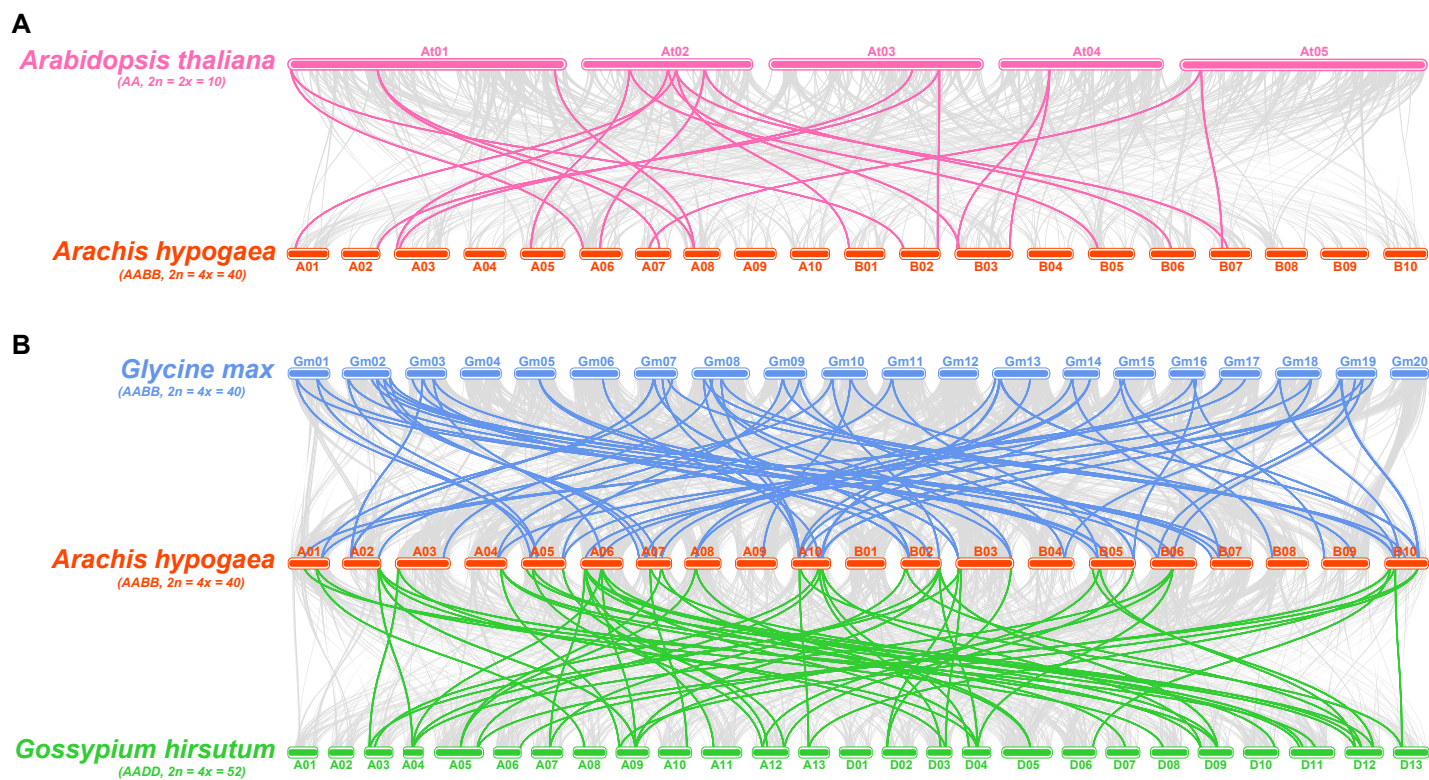


Fig. S2 Syntenic relationship analysis of UGTs between *A. hypogaea* and other plant species. MCSScanX program was used to analyze the orthologous genes between *A. hypogaea* and *A. thaliana*, *G. max* and *G. hirsutum*. Gray lines represent all orthologous gene pairs, and color lines highlight UGT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

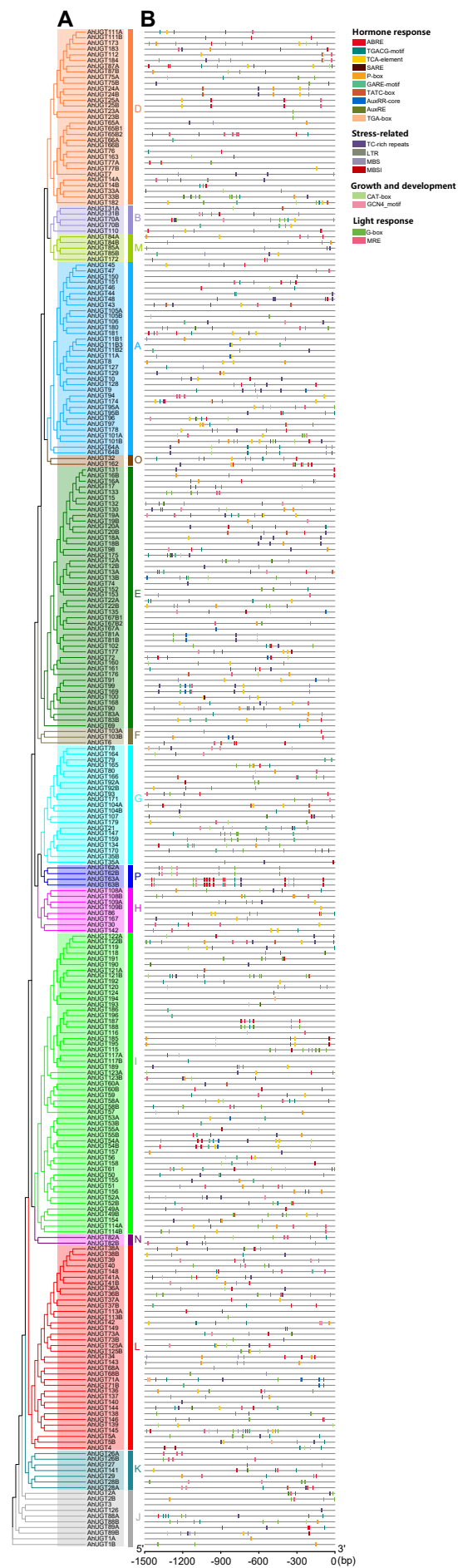


Fig. S3 Predicted *cis*-acting elements in the promoter regions of *AhUGT* genes. A The phylogenetic tree. **B** Prediction of *cis*-acting elements in the 1500 bp upstream region of *AhUGT* gene transcription start site

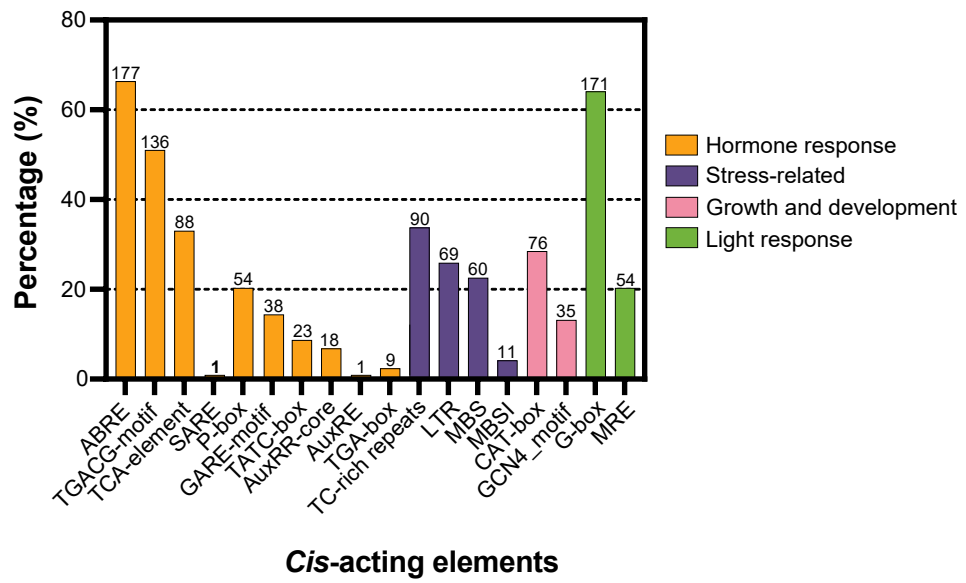


Fig. S4 Classification and annotation of *cis*-acting elements in the promoter regions of *AhUGTs*. The values on the top of bar indicate the number of *cis*-acting elements

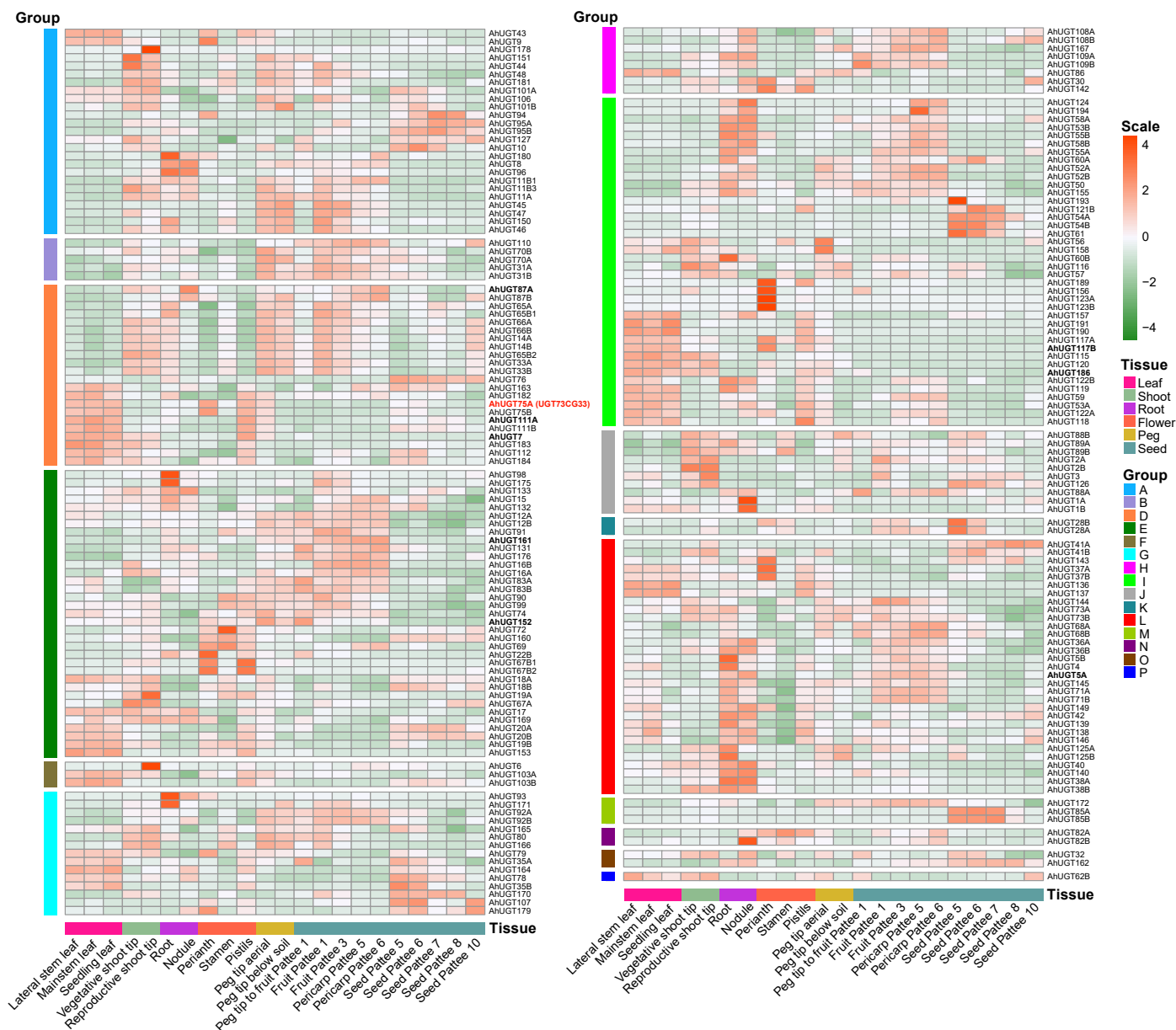


Fig. S5 Transcriptional expression profiles of *AhUGTs* in various peanut tissues and different developmental stages. The *AhUGTs* were classified into 15 different groups with different color based on phylogenetic tree. FPKM values were obtained from the RNA-seq data, and the expression levels of *AhUGTs* were normalized by $\log_2(\text{FPKM}+1)$, with red to green indicating high to low gene expression level in the heatmap

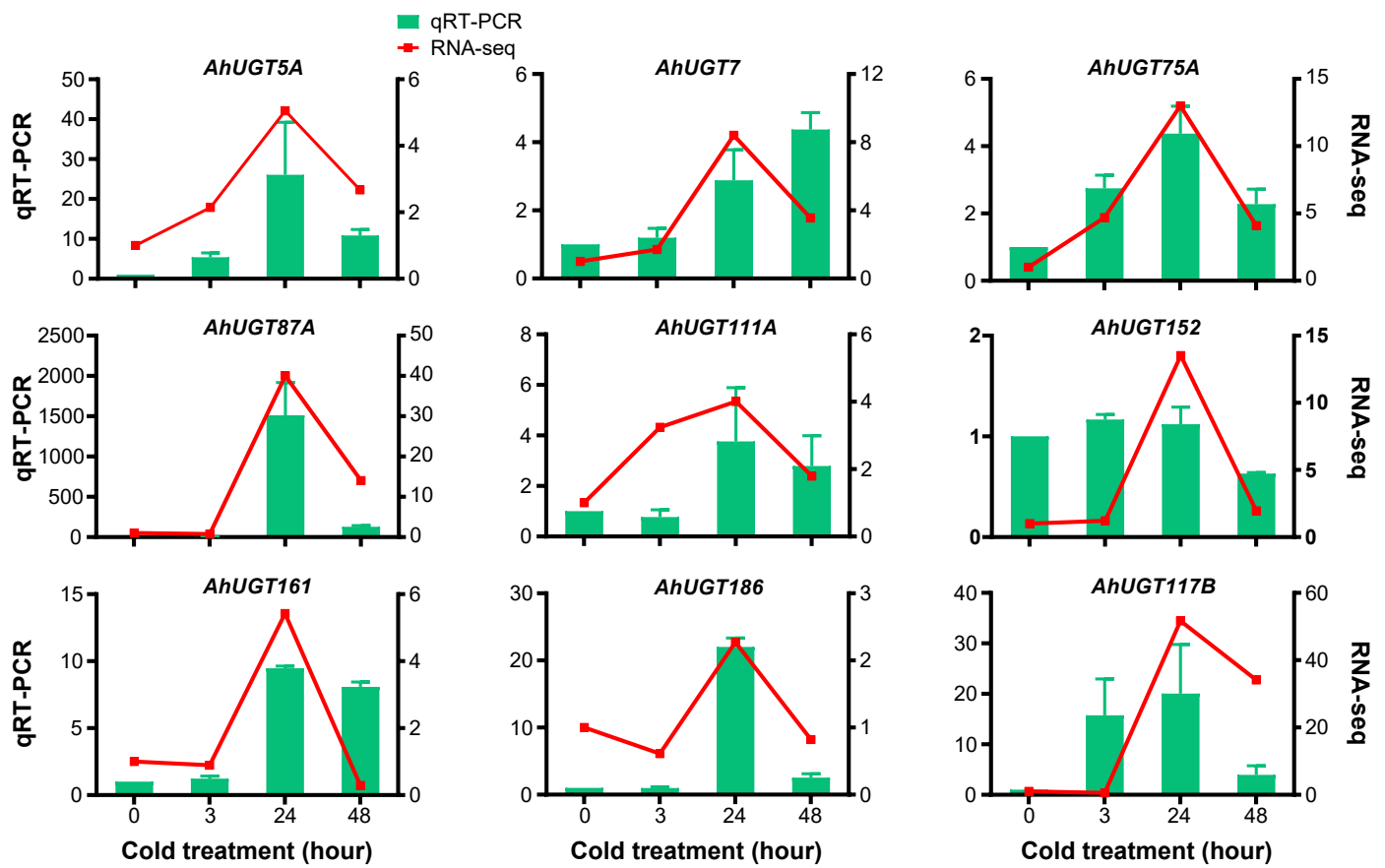


Fig. S6 Analysis of transcriptional patterns of nine selected *AhUGTs* in response to cold stress. The expression levels of *AhUGTs* were analyzed by qRT-PCR (shown by green bars) and transcriptome data (indicated by red lines). No treatment control (0 h) was normalized as “1”. Error bars indicate the standard error of three biological replicates. The expression profiles of most *AhUGTs* (except *AhUGT152*) correlated well between qRT-PCR results and transcriptome data

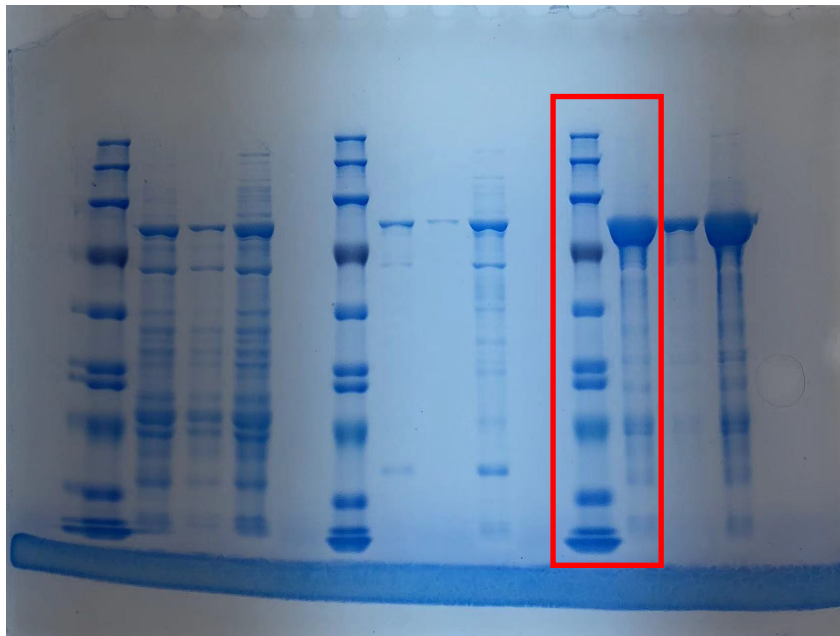


Fig. S8 SDS-PAGE analysis of purified recombinant AhUGT75A. This is the original uncropped image of protein gel electrophoresis. The red rectangle region in this image corresponds to Figure 6A

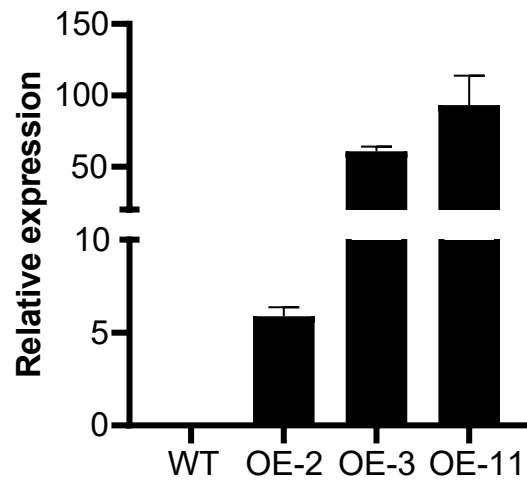


Fig. S9 qRT-PCR analysis of relative transcript level of *AhUGT75A* in three overexpressing lines and wild type *Arabidopsis* plants. Tubulin was used as an internal reference gene. Data were derived from three biological replicates and are presented as means $\pm$ SEM