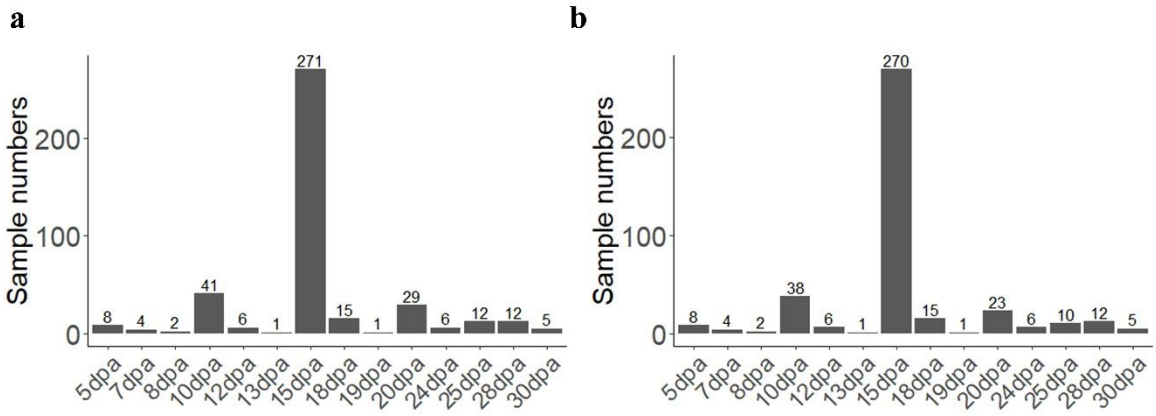
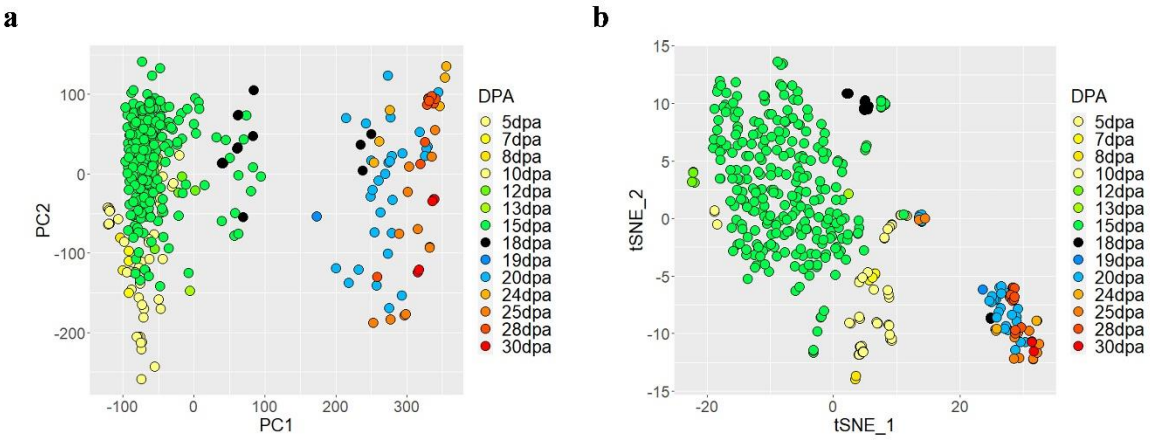
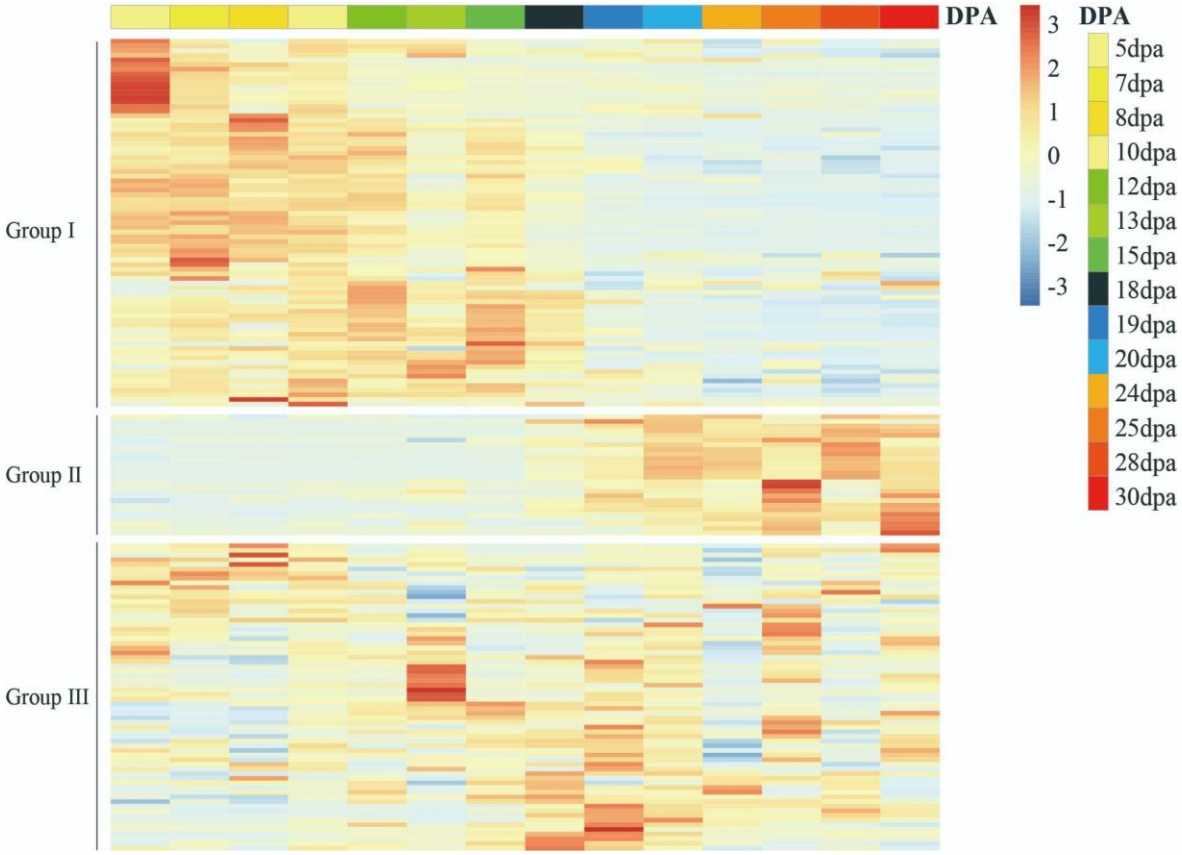
Supplementary Figures



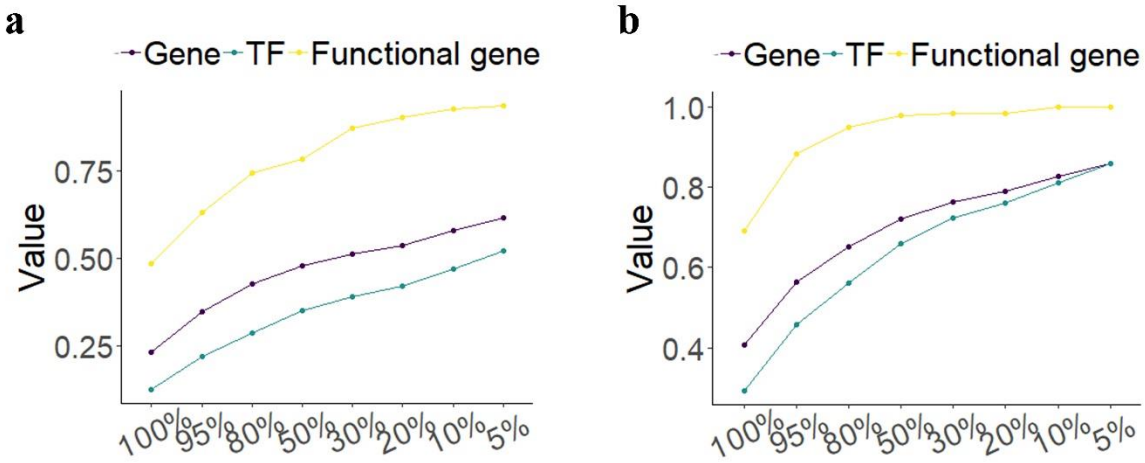
Supplementary Fig. 1. Number of RNA-seq samples representing each time point before (**a**) and after (**b**) quality control.



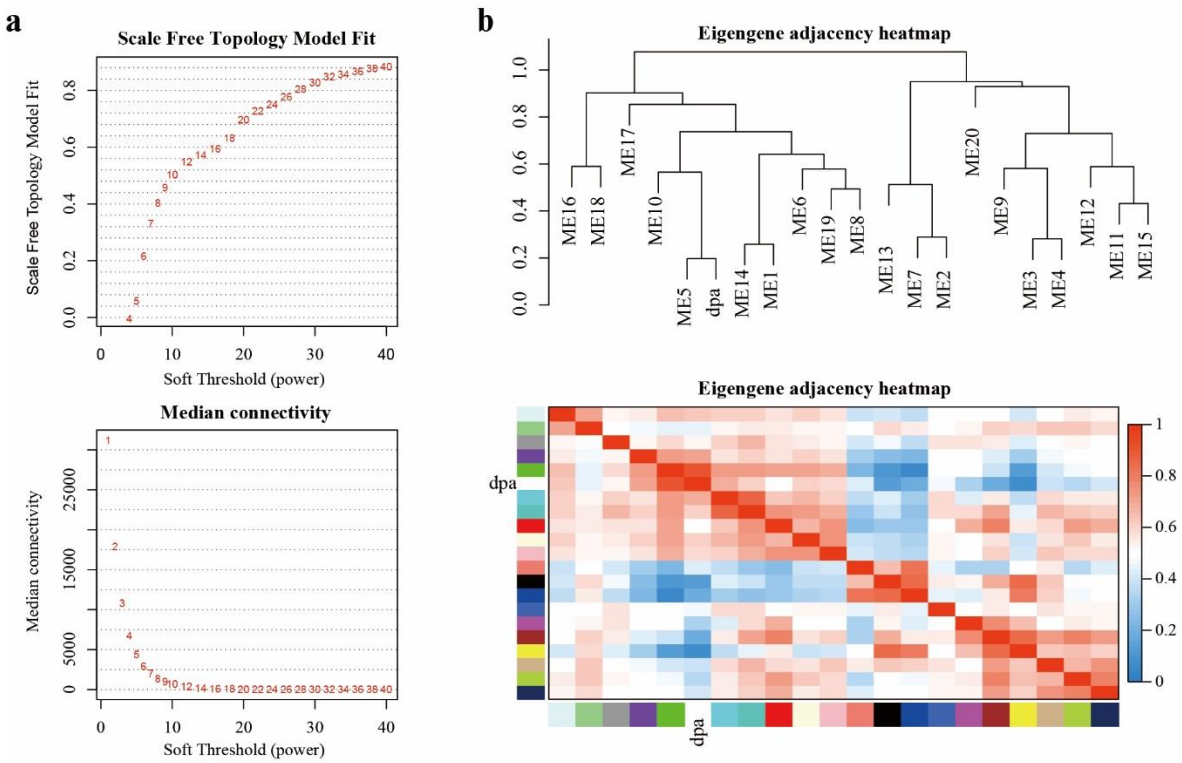
Supplementary Fig. 2. Dimensionality reduction and visualization of gene expression profiles for the 413 public RNA-seq samples passing quality control before removing 12 outlier samples. **a** Principal component analysis. PC1 and PC2 captured 15.5% and 12.3% of the variance, respectively. **b** T-distributed stochastic neighbor embedding.



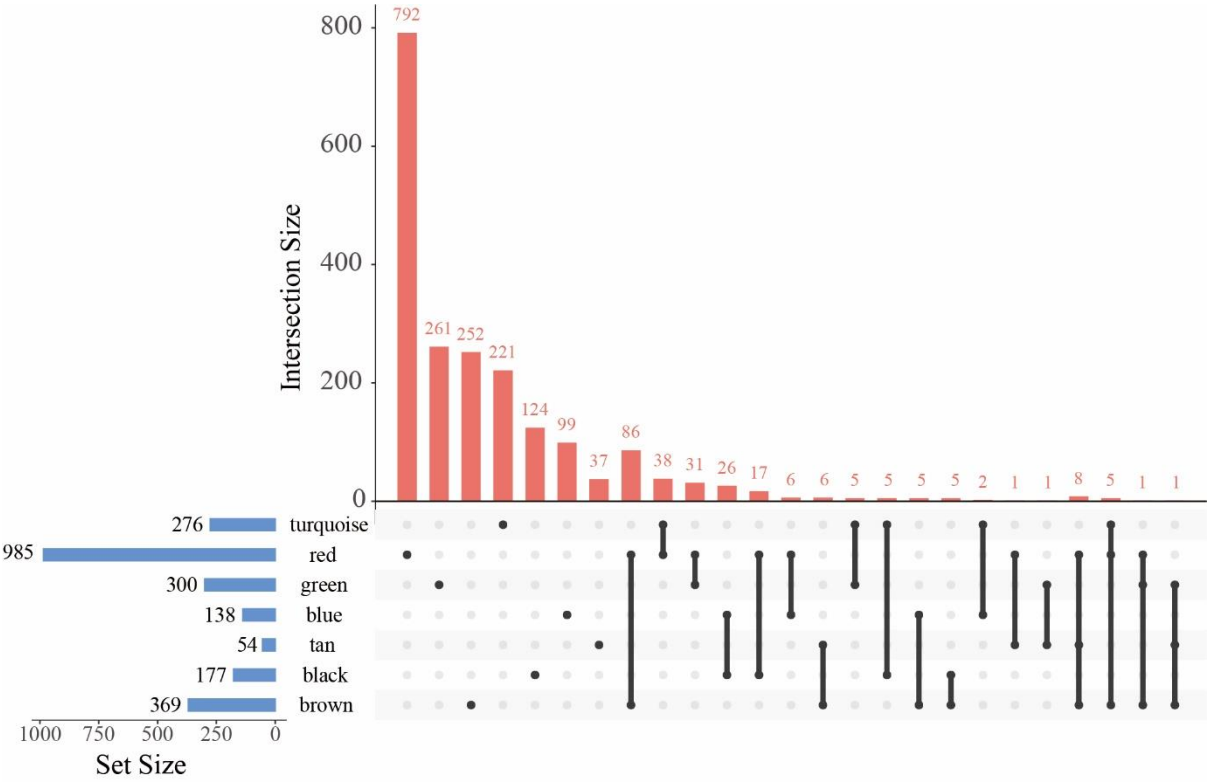
Supplementary Fig. 3. Expression analysis of 192 fiber-related functional genes clustered into three groups: group I, early expressed during fiber elongation; group II, later expression during secondary cell wall synthesis; and group III, expressed peaked at various time points. Heatmap displays the averaged TPM values per DPA.



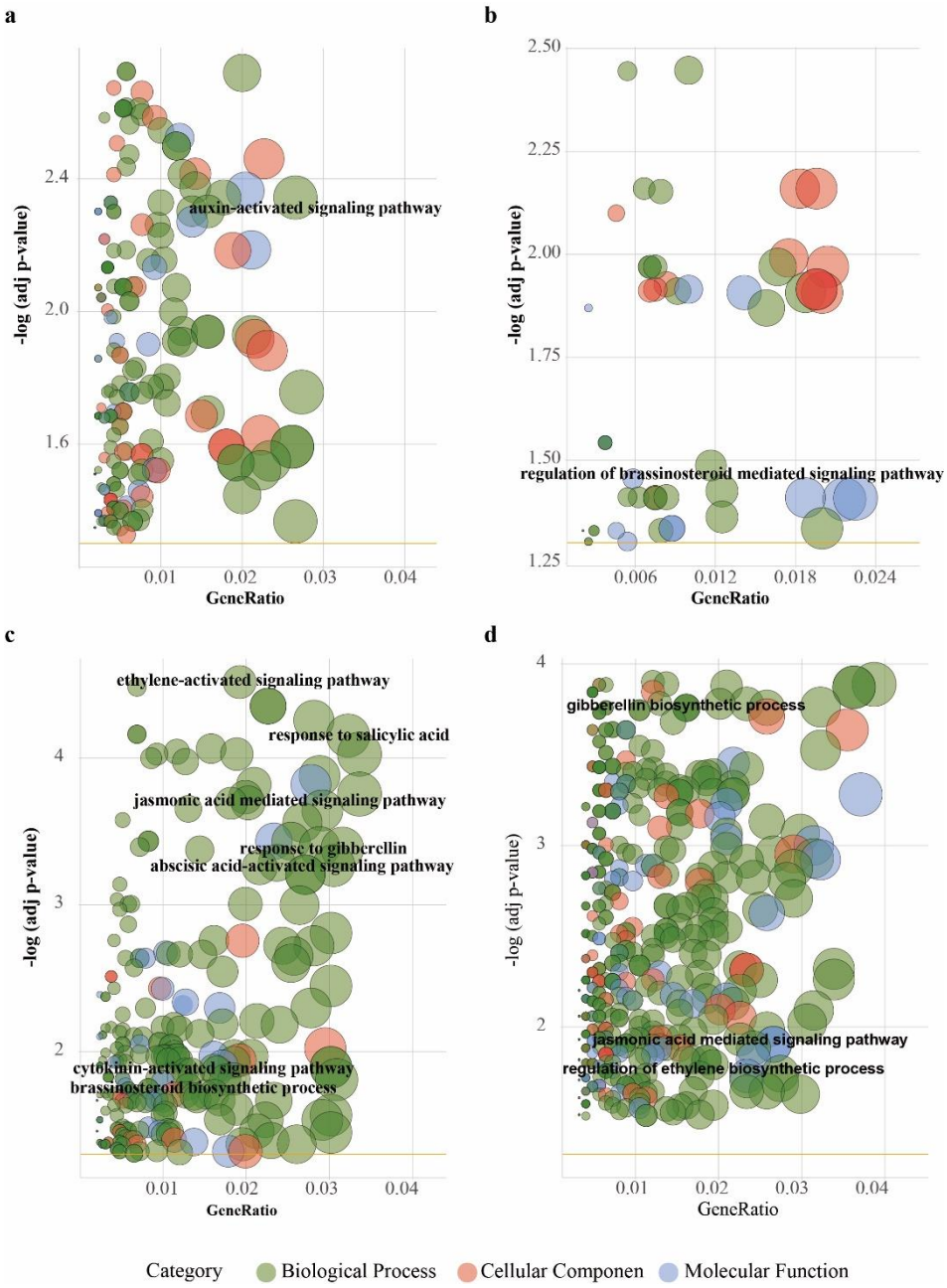
Supplementary Fig. 4. Criterion testing for filtering fiber-expressed genes. Applying the TPM cutoffs across varying percentages of the 401 RNA-seq samples (x-axis) determined the proportions of expressed genes (y-axis). Proportions examined include all genes (purple), transcription factors (TFs; blue), and genes with known functions related to fiber development. **a** TPM cutoff >1. For example, with TPM >1 in at least 5% of the samples, 64.5% of the total 74,901 genes were considered expressed, including 93.7% of 192 fiber-related genes and 58.3% of 5,036 TFs. **b** TPM cutoff of >0. Choosing TPM>0 in 30% of samples as the final criterion, 76.3% of the total genes were considered expressed, including 98.28% of fiber-related genes and 72.22% of TFs.



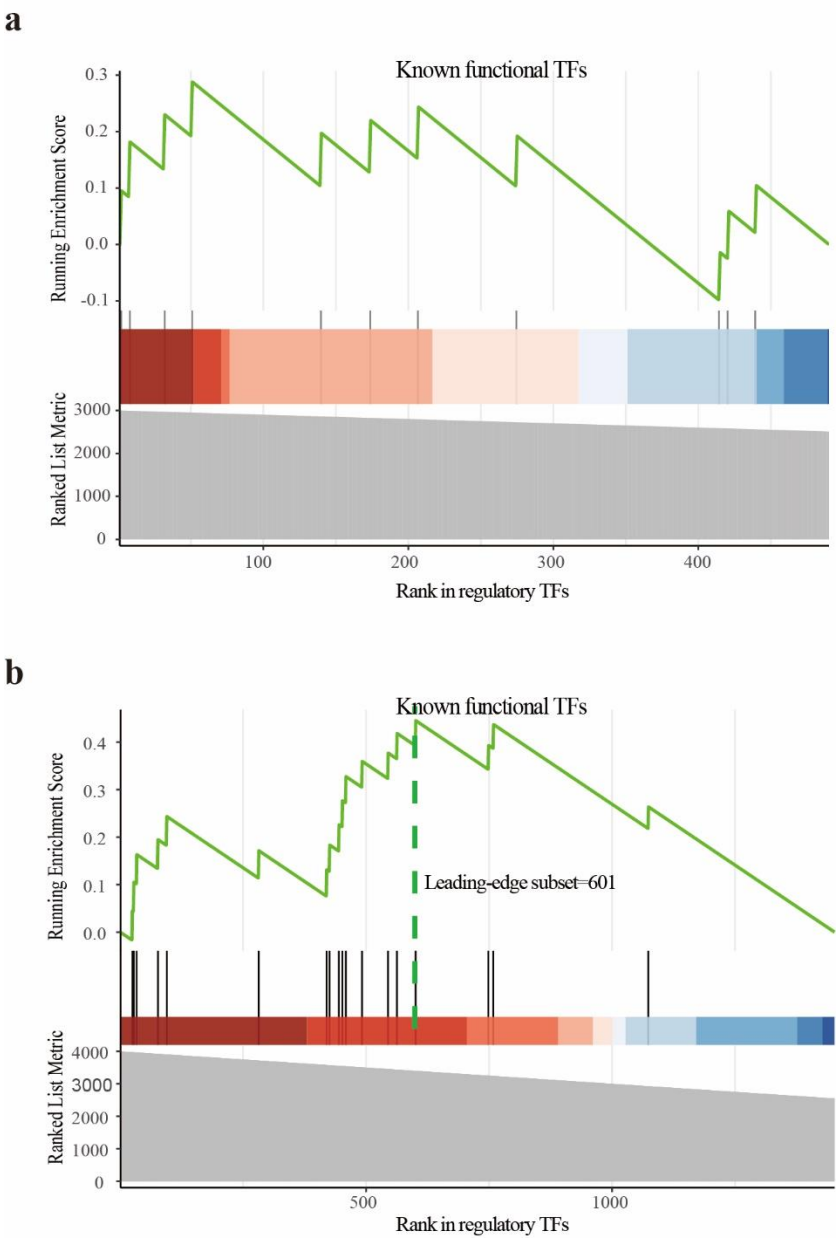
Supplementary Fig. 5. Weighted gene co-expression network analysis of 57,151 fiber-expressed genes. **a** Selection of soft-thresholding powers (x-axis) based on scale-free fit index and median connectivity (y-axis). **b** Eigengene dendrogram (up) and correlation heatmap (down) show the inter-modular co-expression relationships, as measured by adjacencies. Red and blue show high and low adjacencies, respectively.



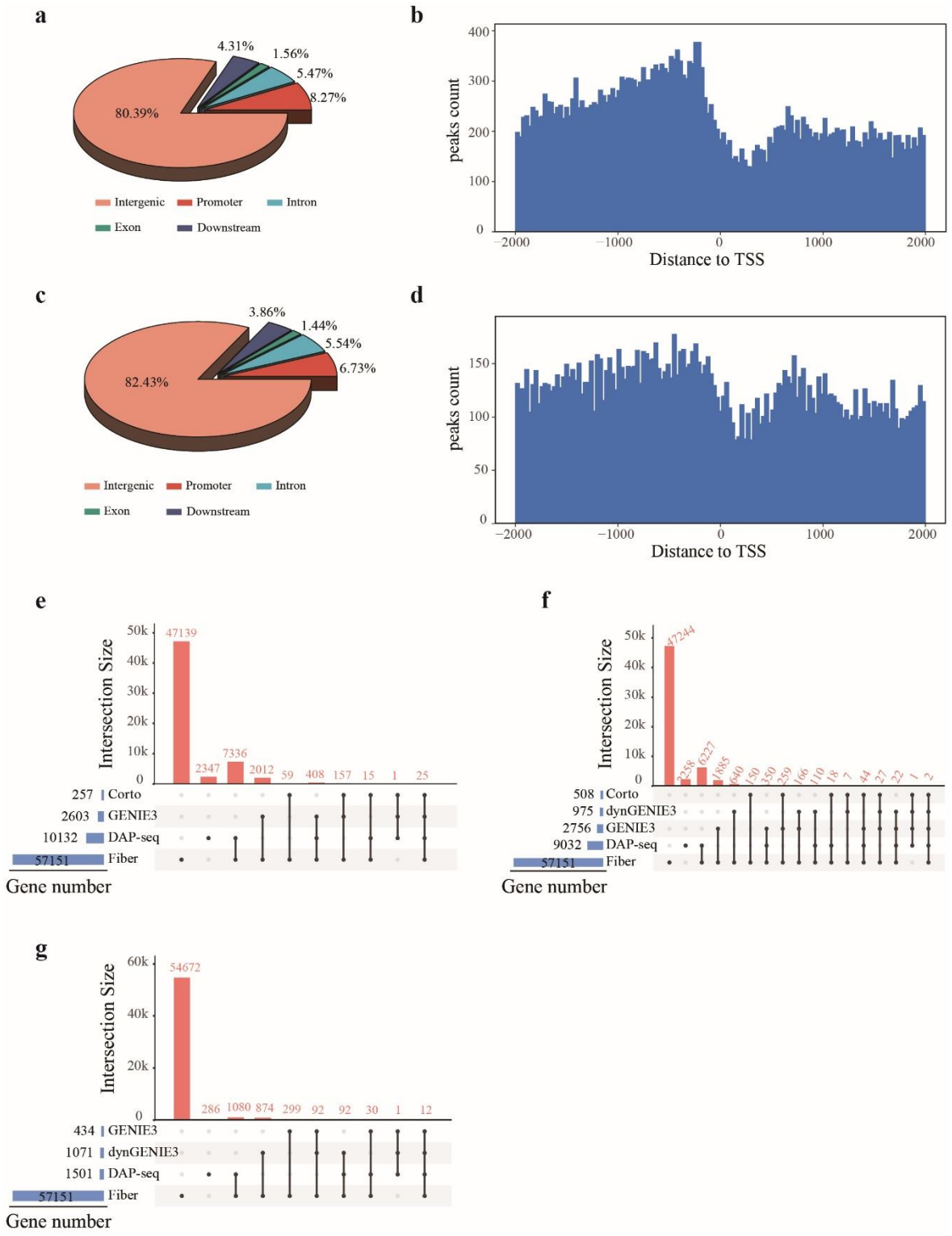
Supplementary Fig. 6. Enriched GO terms of the seven largest modules as illustrated by an UpSet plot.



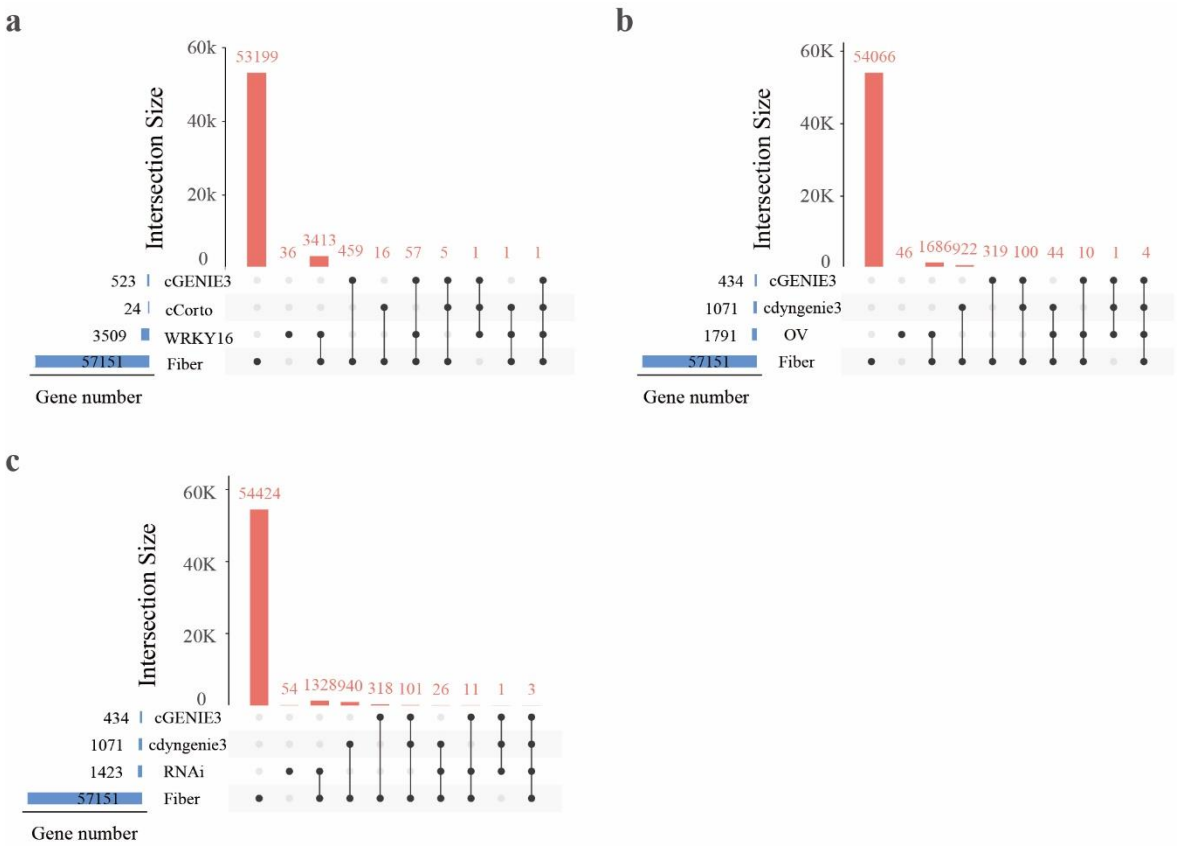
Supplementary Fig. 7. Plant hormone-related GO pathways enriched in the brown (**a**), tan (**b**), turquoise (**c**), and red (**d**) modules.



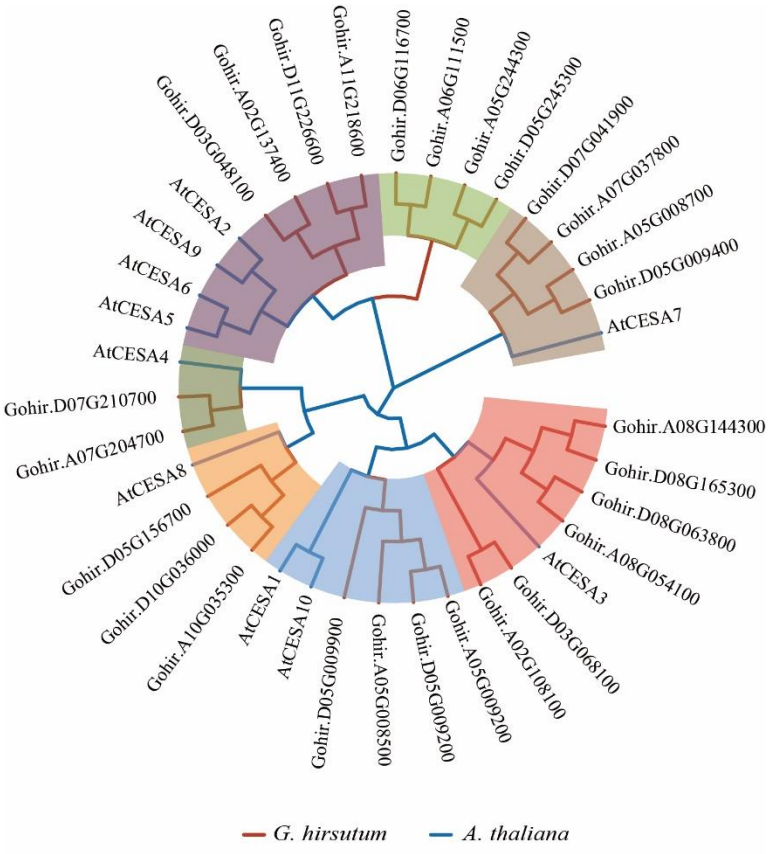
Supplementary Fig. 8. GSEA shows enrichment of known functional TFs in TFs identified by cdynGENIE3(**a**), and cCorto(**b**).



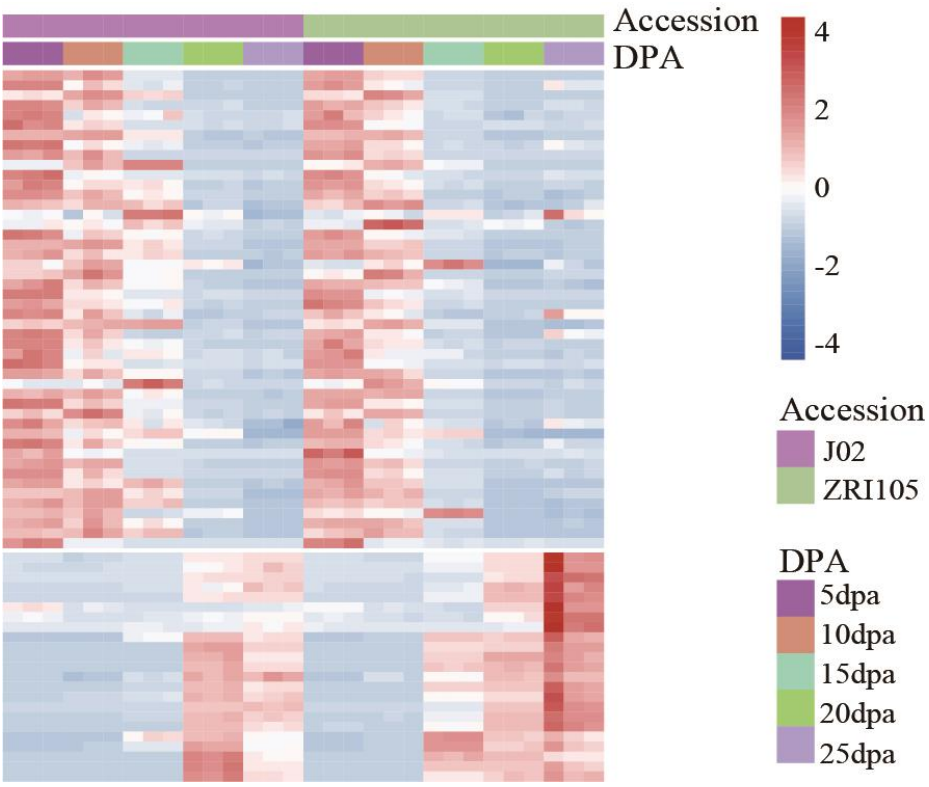
Supplementary Fig. 9. Evaluation of GRN inferences by DAP-seq. (**a-b**), Statistics of distribution regions of binding sites for GhMYS1_A10 (**a**), GhMYS1_D10 (**b**). (**c-d**), Distance from the center of the binding site to TSS for all GhMYS1_A10 (**c**) and GhMYS1_D10 (**d**) target genes. (**e-g**), The intersection of target genes identified in the GhMYS1_A10 (**e**) and GhMYS1_D10 (**f**), and, GhBES1.4 (**g**) DAP-seq with target genes identified using different GRNs methods.



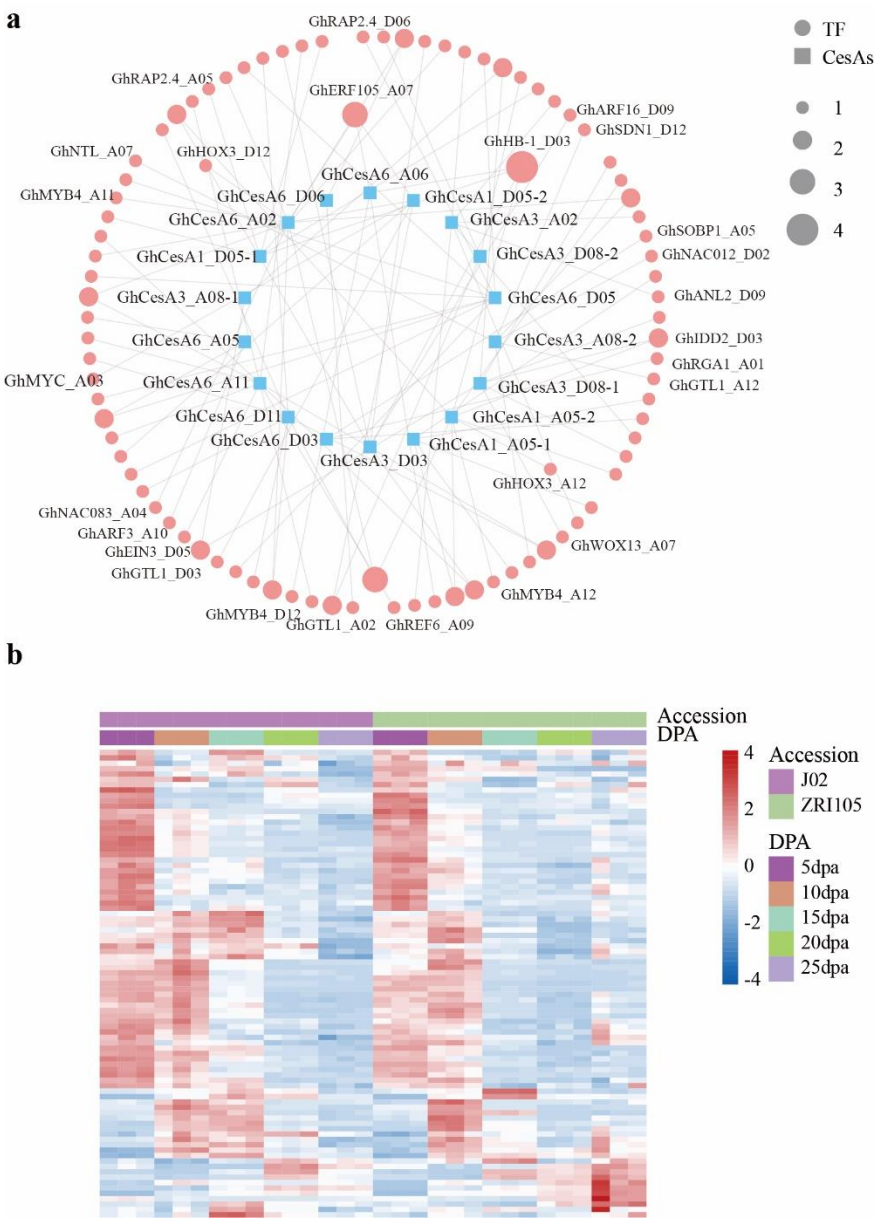
Supplementary Fig. 10. Evaluation of GRN inferences by RNA-seq. The intersection of differentially expressed genes (DEGs) identified in the *GhWRKY16* RNAi line (**a**), *GhBES1.4* overexpression line (**b**), and, *GhBES1.4* RNAi (**c**) line with target genes identified using different GRNs methods.



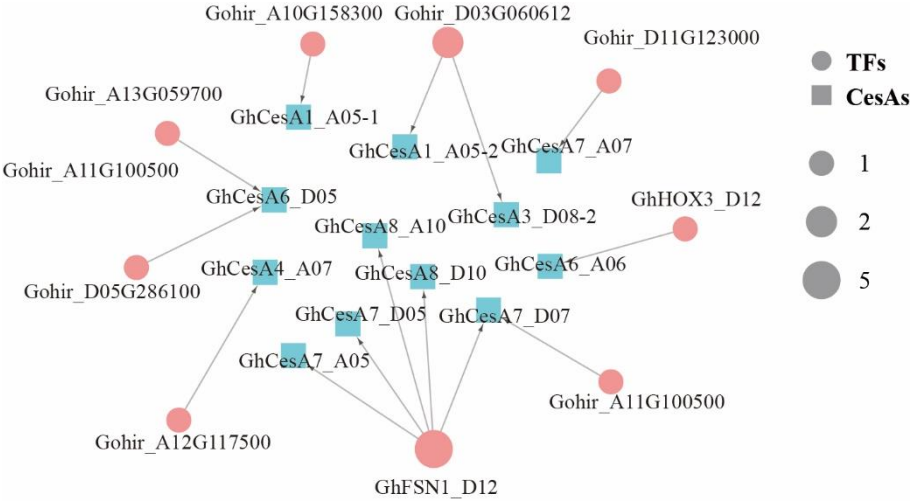
Supplementary Fig. 11. Genome-wide characterization of CesA coding genes in *G. hirsutum*. The phylogenetic trees of 27 GhCesAs and ten AtCesA proteins were constructed by the Neighbor-Joining (NJ) method in MEGA 7.0 with a bootstrap value of 1,000.



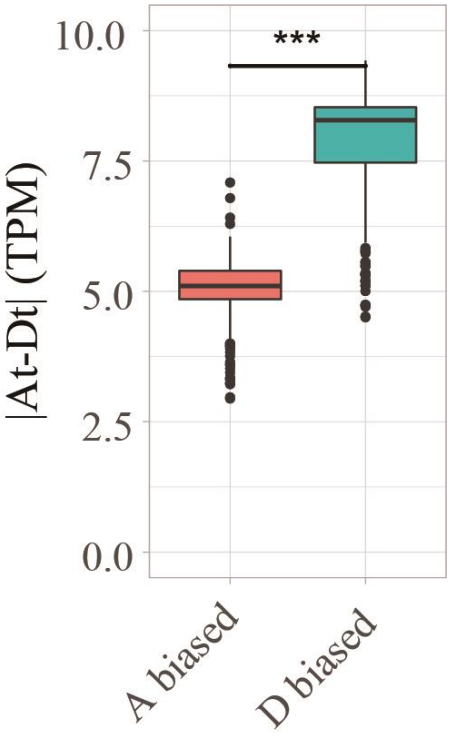
Supplementary Fig. 12. Expression pattern analysis of TFs regulating cellulose synthase identified by cGENIE3 in long fiber and short fiber cotton varieties.



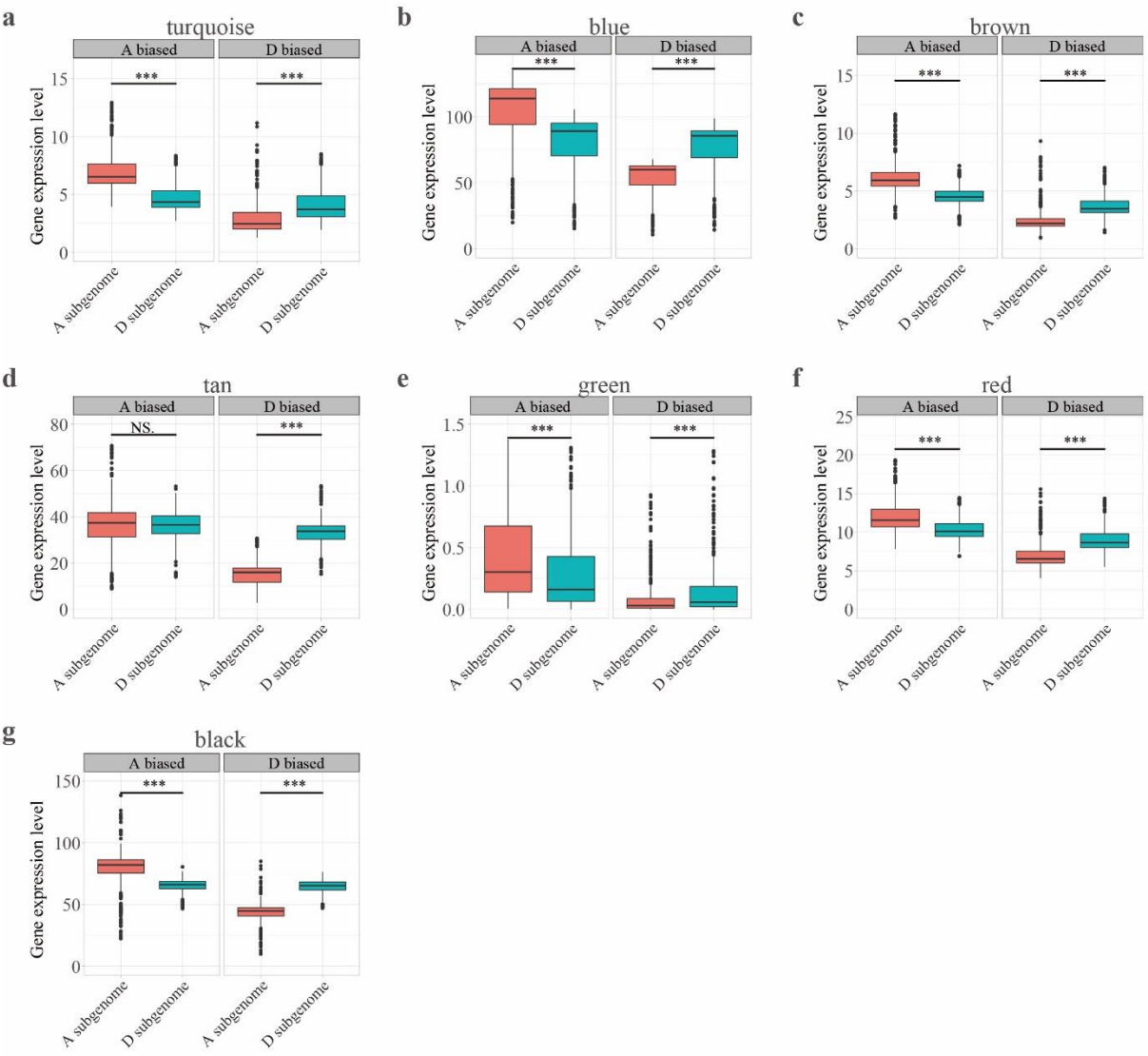
Supplementary Fig. 13. cdynGENIE3 predicted GRN for cotton cellulose synthesis. (A) Regulatory interactions between TFs and regulated cellulose were identified by dynGENIE3. Circles and squares represent transcription factors and cellulose synthases, respectively. The size of the shape represents the number of target genes for the transcription factor. (B) Expression pattern analysis of TFs regulating cellulose synthase by dynGENIE3 in long fiber (J02) and short fiber (ZRI015) cotton varieties.



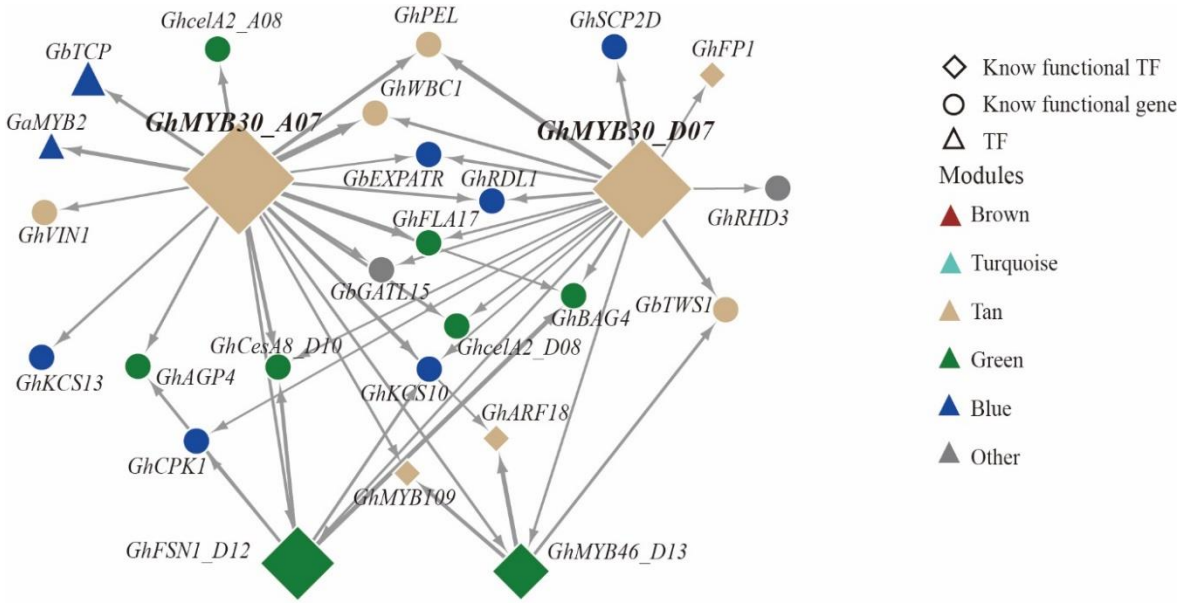
Supplementary Fig. 14. cCorto predicted GRN for cotton cellulose synthesis. Circles and squares represent transcription factors and cellulose synthases, respectively. The size of the shape represents the number of target genes for the transcription factor.



Supplementary Fig. 15. Absolute expression differences compared between A-biased and D-biased scOGs.



Supplementary Fig. 16. Gene expression levels compared for scOGs pairs exhibiting homoeolog expression bias (HEB) in co-expression modules.



Supplementary Fig. 17. GRN of known functional genes regulated by *GhMYB30_A07* and *GhMYB30_D07*.