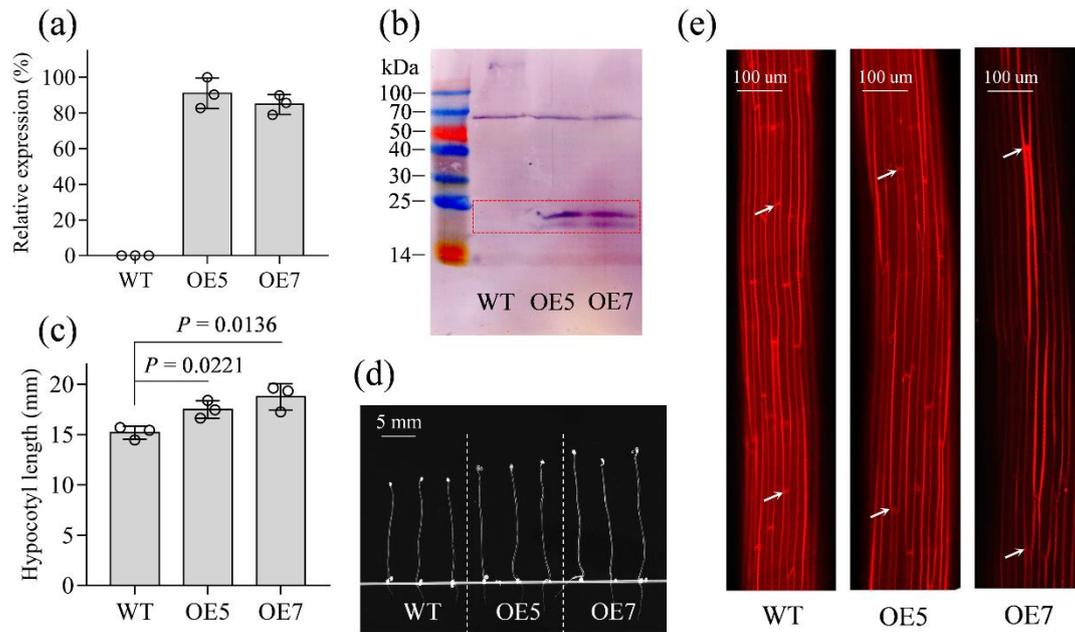
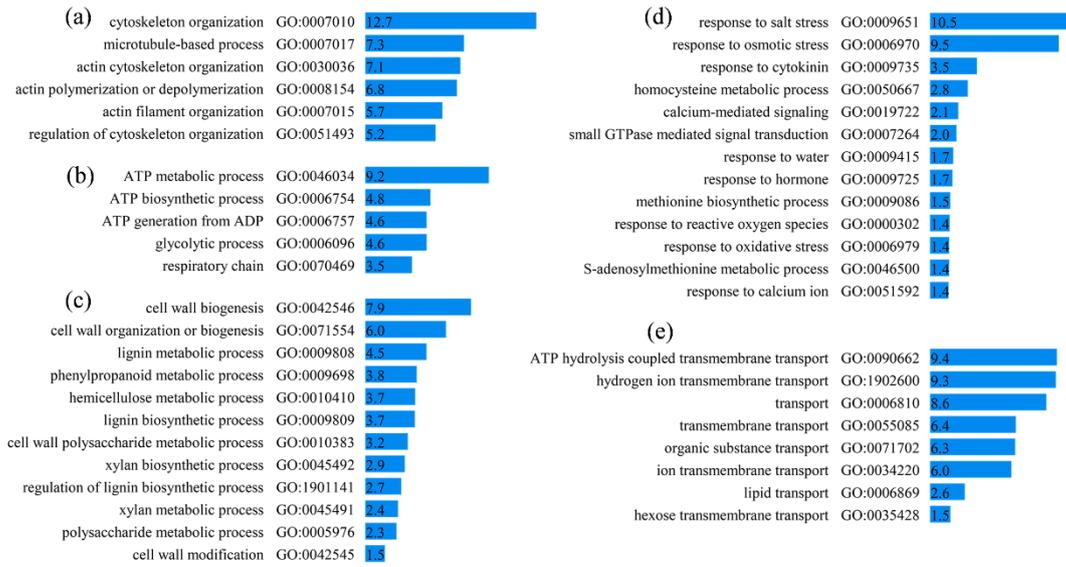


Supplementary Figure S1 Expression patterns and GO enrichment analysis of DEGs.

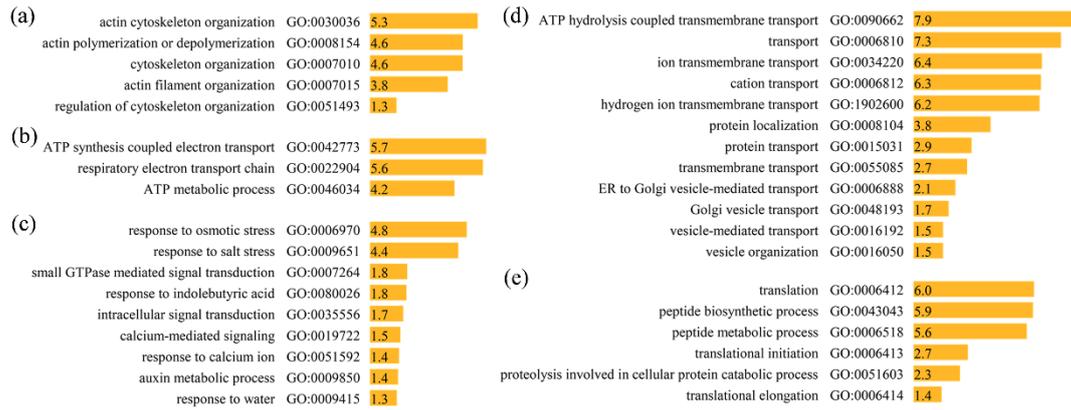
(a) Expression patterns of DEGs during cotton fiber development in *G. barbadense* acc. Pima90-53 and Hai7124. DEGs were up-regulated or down-regulated significantly at 5, 10, 15, 20, 25 and 30 DPA as compared with 0 DPA. DEGs were divided into six categories based on expression trends. **(b)** GO enrichment analysis of DEGs in the different categories. The common genes of Pima90-53 and Hai7124 in each category were used for GO enrichment analysis. GO terms with $Q\text{-value} < 0.05$ were considered significantly enriched.



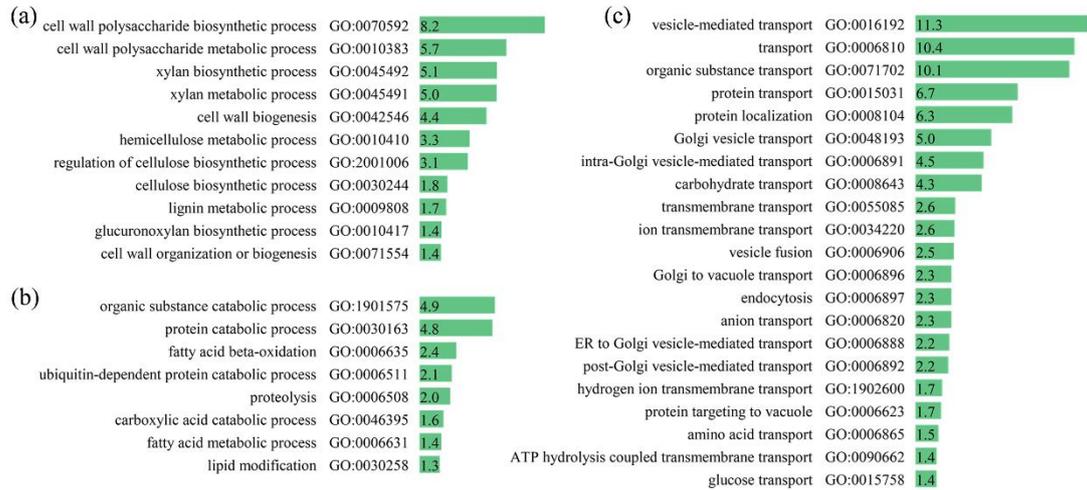
Supplementary Figure S2 Functional analysis of *GbTWS1* in *Arabidopsis*. **(a)** Expression of *GbTWS1* in *GbTWS1*-overexpressed *Arabidopsis* plants, detected by qRT-PCR. **(b)** Western blot of GbTWS1 in *GbTWS1*-overexpressed *Arabidopsis* plants. **(c-d)** *Arabidopsis* plants with overexpression of *GbTWS1*, compared with wild type, showed significantly longer dark-grown hypocotyls. **(e)** Microscopic inspection of hypocotyl epidermal cells. The arrows mark the ends of representative epidermal cells.



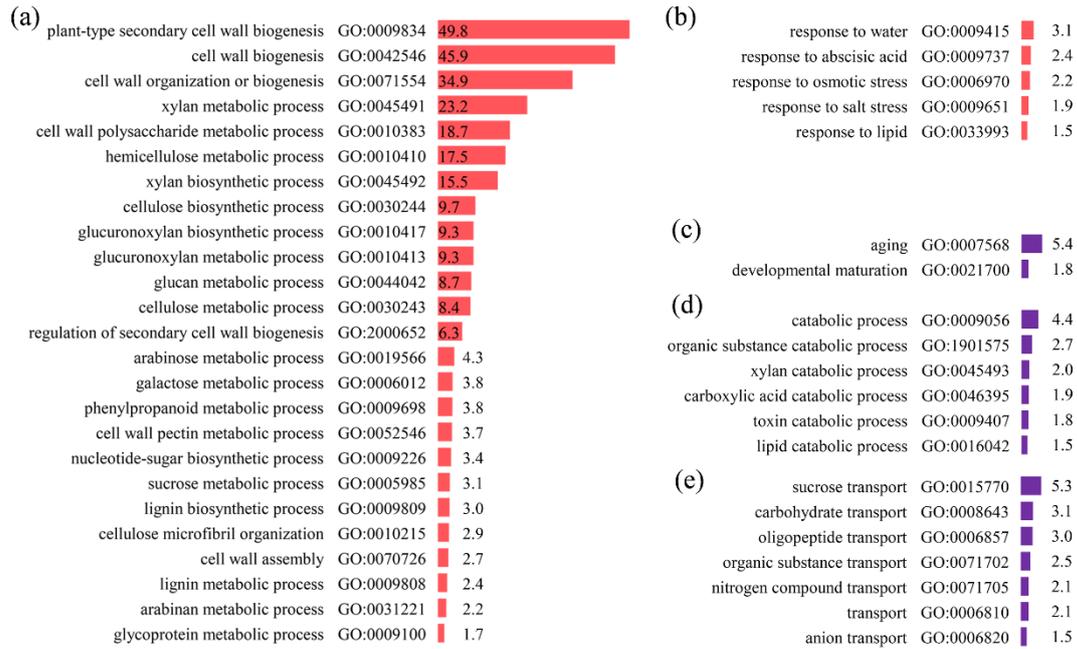
Supplementary Figure S3 GO enrichment analysis of the group I preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into five categories: cytoskeleton organization **(a)**, ATP metabolism **(b)**, cell wall development **(c)**, gene expression regulation **(d)**, and transport **(e)**. GO terms with Q -value < 0.05 were considered significantly enriched. The bars show Q -value with a $-\log_{10}$ transformation.



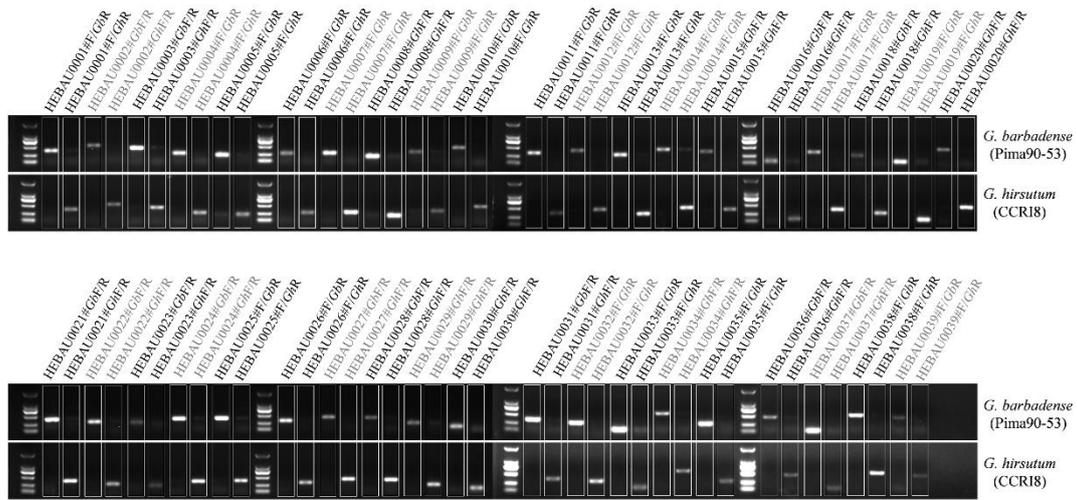
Supplementary Figure S4 GO enrichment analysis of the group II preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into five categories: cytoskeleton organization **(a)**, ATP metabolism **(b)**, gene expression regulation **(c)**, transport **(d)**, and protein metabolism **(e)**.



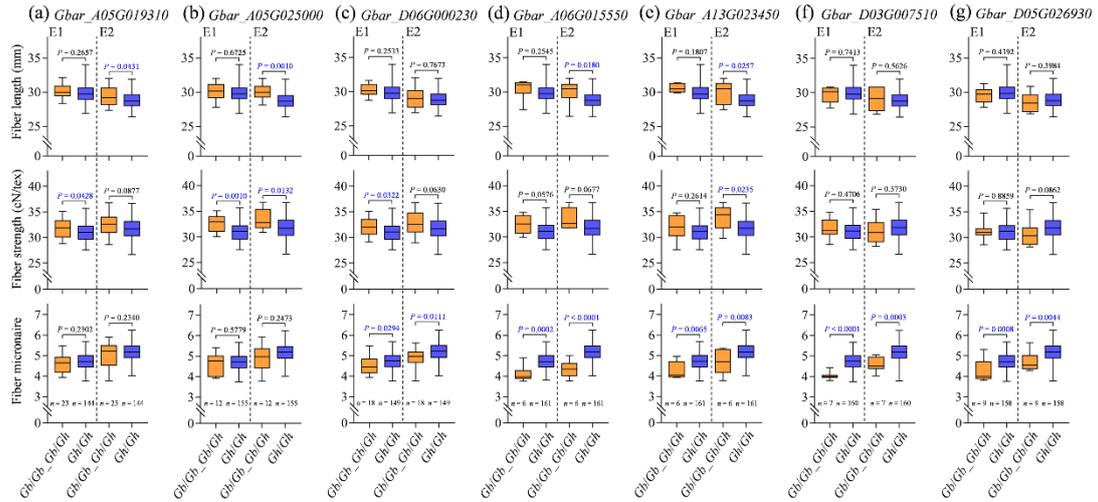
Supplementary Figure S5 GO enrichment analysis of the group III preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into three categories: cell wall development **(a)**, protein and lipid metabolism **(b)**, and transport **(c)**.



Supplementary Figure S6 GO enrichment analysis of the group IV (a-b) and V (c-e) preferentially expressed genes during SCW biosynthesis. Diagram exhibits the significantly enriched GO terms related to cell wall development (a), gene expression regulation (b), maturation (c), catabolism (d) and transport (e).



Supplementary Figure S7 Detection of SNP molecular markers in *G. barbadense* and *G. hirsutum*.



Supplementary Figure S8 The influence on cotton fiber quality with the introgression of *Gbar_A05G019310* (a), *Gbar_A05G025000* (b), *Gbar_D06G000230* (c), *Gbar_A06G015550* (d), *Gbar_A13G023450* (e), *Gbar_D03G007510* (f) and *Gbar_D05G026930* (g).